GENETIC DIVERSITY AND ADMIXTURE STUDY OF ETHIOPIAN THIN-TAILED AND FAT-TAILED SHEEP POPULATIONS USING MORPHOLOGICAL TRAITS AND LOW-DENSITY SNP MARKERS

A DISSERTATION SUBMITTED TO THE SCHOOL OF GRADUATE STUDIES COLLEGE OF NATURAL AND COMPUTATIONAL SCIENCES ADDIS ABABA UNIVERSITY, IN FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY IN BIOLOGY (APPLIED GENETICS)

BY

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DECLARATION

I, the undersigned, declare that the thesis submitted to the Department of Microbial, Cellular, and Molecular Biology, Addis Ababa University for the Degree of Doctor of Philosophy (Ph.D.) in Biology (Applied Genetics) is my own work and has not been submitted at another university. The materials obtained from other sources are duly acknowledged in the thesis.

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ABSTRACT

GENETIC DIVERSITY AND ADMIXTURE STUDY OF ETHIOPIAN THIN-TAILED AND FAT-TAILED SHEEP POPULATIONS USING MORPHOLOGICAL TRAITS AND LOW-DENSITY SNP MARKERS

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The study was conducted to characterize the fat-tailed and thin-tailed sheep breeds based on morphological traits and low-density SNP markers. Six hundred and five animals were used from both fat-tailed and thin-tailed sheep breeds for phenotypic observation and body linear measurements and two hundred and seventeen animals were used for molecular studies. Both qualitative and quantitative data were collected and analyzed using SAS 9.4. The measure of the genetic diversity within the breed and genetic relationships and distance between breeds were analyzed using ARLEQUIN 3.5.2 software. Genetic structure among breeds was analyzed using a model-based clustering algorithm implemented in the software ADMIXTURE v. 1.2.3 and the pattern of breed admixture was further analyzed through principal component analysis (PCA) using the GenABEL R package. Diverse coat color pattern and coat color type were observed in both fat-tailed and thin-tailed sheep breeds. Least square means and standard error of body weight and linear body measurements of fat-tailed and thin-tailed female sheep showed a significant ($p<0.05$) variability between breeds and age groups. Discriminant analysis of variance revealed tail length, rump length, ear length, and body weight were the most discriminating variables among the studied sheep breeds. The canonical discriminant analysis revealed that the greatest Mahalanobis distance was observed between Begayit and Afar sheep populations and least Mahalanobis distance was observed between Begayit and Rutana sheep populations living more closely. A dendrogram based on quantitative traits and the molecular analysis of PCA and admixture results at k=2 were identified two main clusters that separate fat-tailed (Afar, Tumele and SSFT) and thin-tailed (Gumz, Rutana and Begayit) sheep populations. The observed heterozygosity was estimated at 0.36 ± 0.15 for Begayit and Gumz, 0.37 ±

0.15 for Rutana, Afar, Tumele, and SSFT. The expected heterozygosity values were 0.37 ± 0.14 for Begayit, Gumz, Afar and SSFT and 0.38 ± 0.14 for Rutana and Tumele. All sheep populations demonstrated positive FIS values ranged from 0.004 (Afar) to 0.032 (Begayit). The analysis of molecular variance results revealed that the greatest variation existed within the individual across all populations (93.37%). F_{ST} values for all pairs of populations were significantly different from zero ($P<0.001$). The highest F_{ST} values were observed between Begayit and Afar ($F_{ST} = 0.062$) breeds, similar to mahalanobis distance while the lowest one was observed between Afar and Tumele populations ($F_{ST} = 0.015$). The Afar and small short fat-tailed sheep breeds in the fat-tailed sheep had the minimal case of admixture while thin-tailed sheep population and Tumele sheep had a high level of admixture. The F_{IS} result showed low to moderate inbreeding coefficient. Both the PCA and genetic admixture analysis indicated that the thin-tailed and Tumele sheep population had high level of admixture. The present morphometric information, inbreeding coefficient (FIS), genetic differentiation (FST), population pattern and level of admixture found in this study will have paramount importance for future decision on the management, conservation, and improvement of the studied sheep genetic resources.

Keywords: - Genetic diversity, morphological characterization, fat-tailed and thin-tailed sheep

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ABBREVIATIONS

ADG	Average Daily Gain
AFLP	Amplified Fragment Length Polymorphisms
AnGR	Animal Genetic Resource
BW	Body Weight
DNA	Deoxy Nucleic Acid
EDTA	Ethylene Diamine Tetra Acetic Acid
FAO	Food and Agriculture Organization
ISSR	Inter-Simple Sequence Repeat
m.a.s.l.	Meter above sea level
PC	Principal components
PCA	Principal Components Analysis
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphisms
SNP	Single Nucleotide Polymorphism
SSR	Simple Sequence Repeats
STS	Sequence-Tagged Sites
VNTR	Variable Number of Tandem Repeats
HWE	Hardy-Weinberg equilibrium
WWT	Weaning weight

CHAPTER-1

1. Introduction

1.1.Background and Justification

Sheep (*Ovis aries*) became important farm animals across the globe through adaptation to a various range of environments and varied production systems. Its domesticated started about 10,000 years ago in south western Asia (Melaku Tefera, 2013). African sheep were domesticated outside Africa. Indigenous African sheep genetic resources are classified into two main groups, fat-tailed and thin-tailed sheep. The fat-tailed sheep are the foremost cosmopolitan, being found in a wider part of North Africa and in Eastern and Southern Africa (Muigai and Hanotte, 2013). The thin-tailed sheep are present mainly in Morocco, Sudan, West Africa, and in west Ethiopia along border of Sudan. They share a standard ancestry with European and Asian sheep (Muigai and Hanotte, 2013). The Eastern African sheep are further sub-classified as either fat-tailed or fat-rumped (Wilson, 2011).

Ethiopia's sheep population is estimated to be about 31.1 million and out of this 99.8 % of the population are indigenous breeds (CSA, 2017). Ethiopia has diverse sheep populations of 14 traditionally classified sheep breed types and nine distinct breeds (Solomon Gizaw *et al.*, 2008b). The existence of this diversity is due largely to the geographical location being near the historical entry point of many livestock populations from Asia, its diverse topographic and climatic conditions; the huge livestock populations size and a wide range in production systems (Workneh Ayalew *et al.*, 2004; Solomon Gizaw *et al.*, 2007). Ethiopian sheep are described as fat-tailed, fat-rumped and thin-

tailed based on tail type. The fat-tailed sheep type is widespread in the country (Solomon Gizaw *et al.*, 2008b). Indigenous sheep breeds have rich gene pool that shaped by exposure to different climatic conditions and is reflected in their ability utilize the limited and poor-quality feed resources and their tolerance to a range of diseases found in these regions (Ibeagha-Awemu *et al.*, 2019) .

Sheep production plays a very important role in Ethiopian farming systems. Resource-poor farmers can afford to keep sheep on small plots and improve their economic and nutritional status. Sheep contribute considerably to the livelihoods of rural households as a source of income, food (meat and milk), and industrial raw materials (skins and wool). Besides these, sheep contribute socioeconomic and cultural functions, risk-mitigating during crop failures, increase property security, and serve as a form of investment (Markos Tibbo, 2006). Despite the large population of sheep and the importance of sheep both to the livelihood of resource-poor farmers and to the national economy, the current level of on-farm productivity in the smallholder production systems is low, with an off-take rate of about 33% (FAO, 2009) and an average lamb carcass weight of 10 kg which is less than African average 14kg and world average 15.8kg (Skapetas and Kalaitzidou, 2013). Therefore, genetic improvement of economically important traits is vital.

The basis for genetic improvement of livestock is identification of traditionally recognized breeds and characterization of their environment, and their adaptive and production capabilities. The initial step for long-term genetic improvement of indigenous livestock is, therefore, identification of the breed types, estimation of their population

size, and documentation of their common uses and description of the management system in which they are maintained (Kosgey and Okeyo, 2007). Genetic diversity among breeds enables the existence of livestock in different environmental conditions and provides a range of products and functions necessary for the human population. Characterization of animal genetic resources (AnGR) encompass all activities associated with the identification, qualitative and quantitative description of breed productions and natural habitat and production systems to which they are or not adapted (FAO, 2012). Livestock Genetic diversity can be determined based on morphological, biochemical, and molecular markers (Yang *et al.,* 2013). Characterization of livestock breeds/populations based on morphological trait variations is the first step towards the available Animal Genetic Resources (AnGR) (Lanari *et al.,* 2003). Morphological characterization involves the description and documentation of a physical traits of a breed (Scherf and Pilling, 2015). Morphological characterization has been an accessible and easy-to-use tool in conservation and breeding programs. Description of the physical characteristics of livestock breeds is very important for developing a breeding strategy in a particular production system. Sheep biodiversity have been studied using morphological traits and DNA based markers (Tesfaye Getachew 2015; Zewdu Edea *et al.,* 2017; Michailidou *et al.*, 2018; Helen Nigussie *et al.*, 2019).

The phenotypic variation in a population arises due to evolutionary forces such as mutation, drift, selection, and migration that contribute to change in allelic frequency in space and time (Groeneveld, 2010). Their magnitude in phenotypic variability among deems could differ under different environmental conditions and farming practices of

sheep. The morphometric variation between populations can provide a basis for understanding flock structure and maybe more applicable for studying, environmentally and human-induced variation (Agaviezor *et al.,* 2012). According to Solomon Gizaw *et al.* (2007), morphological description is an essential component of breed characterization that can physically identify, describe, and recognize a breed, and also to classify livestock breeds into broad categories. Dossa *et al.* (2007) reported that morphological measurements such as heart girth, height at withers and body length can be used for the rapid selection of large size individuals in the field to enable the establishment of elite flocks. So far, the characterization of Ethiopian sheep population based on morphological markers were reported extensively at district level (Tassew Mohammed *et al.,* 2014; Wossenie Mebratie *et al.,* 2014; Helen Nigussie *et al.,* 2016; Mengstie Taye. *et al.,* 2016). But the characterization of sheep population based on molecular markers were limited. Some genetic diversity studies were reported using molecular markers such as microsatellite (Solomon Gizaw *et al.,* 2007; Helen Nigussie *et al.,* 2019) and genome-wide based genetic diversity and admixture studies (Tesfaye Getachew 2015; Zewdu Edea *et al.,* 2017). SNP is one of the molecular markers rapidly becoming the markers of choice for many applications in genome analysis due to their abundance, stability, low error rate, ease of automation and standardization between laboratories. SNPs, represent sites in the genome where DNA sequence differs by a single base when two or more genomes are compared. They occur about once every 300-500bp in sheep, within the coding and non-coding regions. For a variation to be considered an SNP, it must occur in at least 1% of the population (Mburu and Hanotte, 2005). SNPs are used in genome-wide

association studies, genetic prediction of breeding values, for the estimation of genetic diversity and population genetic parameters (Engelsma *et al.*, 2012; Kijas *et al.*, 2012). These genetic resources could be threatened by several factors such as indiscriminate crossbreeding with cosmopolitan breeds and uncontrolled intermixing (Hanotte *et al.*, 2010). Genetic variability existing within and among-breeds is important for sustaining breeding planning of genetic improvement programs to enhance the productivity of local breeds based on their real potential to one of or both traits of interest such as meat, wool, and milk productions and to identify divergent breeds that may harbor distinct genotypes (FAO, 2012; Biscarini *et al.*, 2015). Knowledge of the genetic relationship among neighboring sheep populations is crucial for conservation efforts (Mukhongo *et al.*, 2014) while genetic diversity serves as a way for populations to adapt to changing environments.

There are some populations not characterized at molecular level in the previous studies (Solomon Gizaw *et al.*, 2013a). For example, Begayit, Rutana in northwestern and Tumele sheep population in the Northeastern part of the country.

The Rutana sheep population had long-thin tailed and found in the Northwestern of the country on the border with Sudan are believed to be indigenous to Sudan (Workneh Ayalew *et al.*, 2004). It is increasingly dominating in the Gumz sheep breeding zone (Solomon Gizaw, 2009). The genetic relationship within breeds and among the neighboring populations is not yet known. The Begayit sheep is found in the Northwestern part of the country in Tigray Region and one of the populations that did not

reported in the previous molecular characterization.

The ‘Tumele’ sheep populations in the Rift valley (from Shewa Robit to “Moheni” along the main road, Addis Ababa to Mekele) is one of the fat-tailed sheep that did not included in the previous molecular characterization. However, there is no genetic information on the genetic diversity, genetic structure, level of admixture and classification, *i.e.* whether it is a distinct or a similar population with neighboring Afar sheep breed and SSFT sheep breed or admixed population.

Thus, the characterization of sheep populations then determining admixture is essential for rational designing of conservation and improvement strategies. This study focuses on sheep populations of Tumele in the Northeastern part of Ethiopia and Rutana and Begayit sheep population in the Northwestern part of Ethiopia, where limited information is available about the extent of genetic diversity that exist among and within populations and level of admixtures among populations. The populations represent all the thin-tailed populations and the fat-tailed populations of Ethiopia.

Therefore, this study analyzed the genetic diversity and extent of admixture level of thin-tailed and fat-tailed/rumped sheep populations by using both morphological traits and low-density ovine 15K SNP as molecular markers. Low-density 15K SNP chips are considered as a way to reduce the cost of high-density SNP panels in livestock breeding and would enable cost-effective implementation of genomic studies. The information generated from the study would be used for designing appropriate breeding program,

conservation and management strategies for the studied sheep populations genetic resources.

1.2. Research Questions

1. What are genetic variation between and within thin-tailed and fat-tailed sheep groups?
2. What are genetic admixture between populations sharing same breeding tracts and contiguous populations?
3. Is it influencing the phenotypic and genetic variability of purebred indigenous sheep and threatening the genetic diversity of Ethiopian sheep?
4. What are the relationship between Tumele sheep population in the Northeastern rift valley region and the highland fat-tailed and the lowland fat-rumped Afar sheep?

1.3. Objectives of the study

1.3.1. General objective

The main objective of this study was to characterized the morphological and genetic diversity of thin-tailed and fat-tailed sheep populations of Ethiopia.

1.3.2. Specific objectives

- To describe the physical characteristics of thin-tailed and fat-tailed sheep populations of Ethiopia using morphological traits

- To determine the extent of genetic diversity and population structure within and between fat-tailed and thin-tailed sheep population using low-density genetic markers
- To determine the extent of genetic admixture of fat-tailed and thin-tailed populations using low-density SNP markers

1.4. Thesis outline

This dissertation has eight sections where chapter one comprises a general introduction, the statement of the problem, and general and specific objectives. The second chapter is literature review that gives details of origin and domestication of sheep, sheep breed type of Ethiopia, production system, growth and reproductive performance, the importance of phenotypic and genetic characterization, methods of characterization and related works were reviewed. Chapter three addressed the description of the study area, the materials used in this study and the methods that have been used to collect data, the statistical tools and analytical methods. Chapter four covered the result of the description of the production system, agroecology, geography and the breeds using both qualitative and quantitative data. Chapter five addressed on regression and multivariate analysis of morphological traits and classification of breeds using morphological traits by discriminant analysis. Chapter six discussed on the genetic diversity and genetic admixture between breeds and within a breed. Chapter seven encompassed a general discussion of the results by comparing with the previous similar studies. Chapter eight comprised the summary, conclusion and recommendation for future study and then list of reference and appendixes are presented.

CHAPTER-2

2. LITERATURE REVIEW

2.1. Origin and domestication of sheep

The process of domestication of sheep started about 10,000 years ago in southwestern Asia (Melaku Tefera, 2013). Sheep (*Ovis aries*) became important livestock across the globe through adaptation to a various range of environments and varied production systems. They belong to the family Caprine in suborder Ruminantia of the order Artiodactyla and genus *Ovis* (Dong *et al.*, 2018). Domestic breeds of sheep are most likely descended from the wild mouflon (*Ovis aries/Ovis orientalis)* from Asia (McManus *et al.*, 2010). Wild species are found in some areas of the world: the Mouflon in Mediterranean countries; the Asian Mouflon in western Asia and the Argali in eastern Asia (Atavliyeva and Tarlykov, 2018). No wild sheep were domesticated in Africa but sheep appeared in the tomb and cave painting in Egypt by about 7000 years ago (Muigai and Hanotte, 2013).

Sheep, probably, entered Sub-Saharan Africa with cattle in the period 6000-5000 years ago possibly slightly later than goat (Gifford-Gonzalez and Hanotte, 2011). The thin-tailed hairy sheep was the first introduced to Africa. They were likely introduced by the same Hamitic pastoralists migrating from western Asia who introduced the longhorn cattle. Fat-tailed coarse-woolly sheep in Africa were probably introduced to Africa about 3000 years after the thin tail breeds and probably through the Isthmus of Suez at the northern end of the Red Sea and via the Babel, El Mandeb strides at its southern end. The origin of fat-rumped breeds remains unknown but they occur in two disjunction and

ecologically different regions (Wilson, 2011; Muigai and Hanotte, 2013). African sheep are described as thin-tailed, fat-tailed or fat-rumped with thin-tailed further segregated into hairy or woolly types (Wilson, 2011; Muigai and Hanotte, 2013). The Eastern African sheep are classified as either fat-tailed or fat-rumped(Muigai and Hanotte, 2013).

2.2 Importance of sheep production in Ethiopia

Ethiopia is believed to have the largest livestock population in Africa (CSA 2018). The livestock subsector makes an enormous contribution to the national economy and the livelihoods of many Ethiopians. The subsector contributes about 16.5% of the national Gross Domestic Product (GDP) and 35.6% of the agricultural GDP (Samson and Frehiwot, 2014). As described by the same authors, it contributes 15% of export earnings and 30% of agricultural employment. Livestock plays vital roles in generating income to farmers, creating job opportunities, ensuring food security, providing services, contributing to an asset, social, cultural and environmental values, and sustain livelihoods.

Sheep production plays a very important role in Ethiopian farming systems. At the smallholder level, sheep are the major source of food security serving diverse function including cash income, savings, fertilizer, socio-cultural functions, and fiber (Pollott and Wilson, 2009). Sheep are important for the pastoralist/agro-pastoralist and for farmers in the subalpine highlands where crop production is unreliable. Sheep are also important foreign currency earners accounting for 34% of the live animal exports (Solomon Gizaw *et al.*, 2013a). Resource-poor farmers can also afford to keep sheep on smaller land areas

and improve their economic and nutritional status (Solomon Gizaw *et al.*, 2007; Solomon Abegaz *et al.*, 2011; Bettencourt *et al.*, 2015). Studies in Ethiopia show substantial within and between breed variations, and hence genetic improvement is feasible among indigenous sheep breeds (Solomon Gizaw *et al.*, 2007; Helen Nigussie *et al.*, 2016). Despite the massive numbers and importance of adapted indigenous small ruminants within the tropics, information on sustainable breeding strategies for them is scarce and sometimes unavailable.

2.3 The sheep production system in Ethiopia

Sheep production in developing regions of the world is generally a traditional system characterized by small flock-size, communally shared grazing, uncontrolled mating, and the absence of pedigree and performance recording (Kosgey *et al.*, 2004; Zewdu Edea *et al.*, 2012). In Ethiopia, most sheep are kept in a traditional, low input and subsistence-oriented production system (Yenesew Abebe *et al.*, 2013; Yohanse Dagnew *et al.*, 2018). Sheep in Ethiopia are kept in a wide range of production systems reflecting the diversity of the environment (Solomon Gizaw *et al.*, 2007; Abegaze Beyene *et al.*, 2018). There are several ways to classify production systems depending on the purpose of classification. Based on the prevalence of agricultural activity, Getahun (2008) classified traditional small ruminant production systems into four subsystems: (a) small ruminant in annual crop-based system in northern, Northwestern, and central highlands; (b) small ruminant in perennial crop-based, mostly found in southern and southwestern highlands; (c) small ruminants in cattle based systems, these systems usually exist in agro-pastoral and semi-arid areas; (d) small ruminant dominated systems found in pastoral and arid

areas of eastern and northeastern Ethiopia, where sheep and goats are the dominant livestock species. The basis of classification of sub production systems is the type and dominance of agricultural activities.

Solomon Gizaw *et al.* (2008b) also classified sheep production system into five: (a) sub-alpine sheep–barely system which is characterized by high altitude (above 3000 meters above sea level), steep terrain, recurrent droughts, cold temperature, and windy climate, which limit crop production. In such an area, sheep played a higher role in maintaining the income and the livelihood of smallholder farmers (Solomon Gizaw *et al.*, 2008b). Samson and Frehiwot (2015) reported the highest sheep density in the cool highlands of Ethiopia. Similarly, Markos Tibbo (2006) reported about 75% of the sheep population inhabited the highland part of the country while the remaining 25% is distributed in the lowlands. The same authors explained that sheep breeds of this system are apparent to be the hardiest sheep types evolved under stressful environments. (b) The highland cereal–livestock system which covers areas in altitudes between 2000 and 3000 meters above sea level in which sheep are kept in small flocks along with other livestock species like cattle, goats, and equines. The area is suitable for grain production due to it has adequate rainfall and moderate temperature. Integrating crops and livestock is high in most areas except lower in the perennial crop-livestock system (coffee growing areas) in southern Ethiopia (Solomon Abegaz *et al.*, 2008). (c) Agro-pastoral and a pastoral system are usually practiced in arid and semi-arid lowland areas of below 1500 meters above sea level in which livestock rearing is the mainstay of people. Sheep production in this system is mainly for cash income, meat and milk (Markos Tibbo, 2006). (D) Highland

perennial crop system which covers areas in altitude between 1500-2000m above sea level which is found in south and southwestern mid-highlands. Farmers in the area mainly engaged in perennial crop production like coffee, inset and khat and sheep rearing is a minor activity and (E) the lowland crop-livestock system which covers wet lowland up to 1000 meters above sea level in this area livestock production is the major activities and farmers also produce cereals, sesame, and cotton.

2.3.1 Sheep breeds of Ethiopia

Ethiopia has a large genetic diversity of farm animals. The existence of this diversity is due largely to the geographical location being near the historical entry point of many livestock populations from Asia, its diverse topographic and climatic conditions; the huge livestock population size and a wide range in production systems (Workneh Ayalew *et al.*, 2004). The sheep population in Ethiopia is estimated to be about 31.30 million and out of this 99. 81 % of the population are indigenous breeds (Central Statistical Agency, 2018). Ethiopian sheep are described as fat-tailed, fat-rumped and thin-tailed based on tail type. The fat-tailed sheep type is widespread in the country (Solomon Gizaw *et al.*, 2008b).

Sheep types in Ethiopia are highly associated with specific ethnic communities and geographical distribution. According to Solomon Gizaw *et al.* (2007), Ethiopia has 14 traditionally classified sheep breed types. The fourteen sheep types were categorized into four groups: sub-alpine short-fat-tailed, highland long-fat-tailed, lowland fat-rumped, and lowland thin-tailed based on their ecological distribution, geographic proximity, tail types, and tail form/shape.

Sub-alpine short-fat-tailed sheep inhabit a contiguous central-northern highland area of altitude ranges from 2000 to 3500 meters above sea level. In this group, seven sheep types were included which are characterized by their short fat tail well above the hocks, small size, coarse wool and low ewe reproduction (Solomon Gizaw *et al.*, 2007). This group is further classified into three breeds: Semin, Washera and Small Short-fat Tailed sheep (Sekota, Farta, Menz, Wollo and Tikur).

Highland long-fat-tailed sheep breed is distributed over the southern and south-western mid-highlands of 1,500 to 2,500 meters above sea level. The sheep breeds in this group are characterized by fat and a long tail reaching the hocks, broad at the base and upper third with a long tapering end, large-sized, short-haired, predominantly brown and prolific (litter size = 1.29±0.06 - 1.55±0.12). The group includes Horro, Arsi-Bale, Bonga and Adilo sheep. These groups are classified into three distinct breeds: Horro, Arsi (Arsi Bale and Adilo) and Bonga (Solomon Gizaw *et al.*, 2008b).

Lowland fat-rumped sheep include Afar and Black-Head-Somali (BHS) which are distinguished by the short and fat-tail, with the rump being also fatty. This group includes two distinct breeds, Afar and Black Head Somali (BHS)(Solomon Gizaw *et al.*, 2008b).

Lowland thin-tailed sheep are represented by a single population Gumz sheep and are found adjacent to the thin-tailed sheep region of the Sudanese desert. They are moderately prolific (litter size = 1.28±0.06). There are three additional traditional sheep

breeds identified based on phenotypic features in northern Ethiopia (Zelealem Tesfay and Anal, 2014) which are not molecularly characterization in the previous study by Solomon Gizaw *et al.* (2007), Begayit sheep population in Northwestern Ethiopia is one of the population their genetic diversity and genetic structure based on molecular marker not known.

2.4. Importance of Genetic diversity

The wide range of breeds and species that have evolved in various environments represent unique sets of genetic diversity. Genetic diversity has been defined because sort of alleles and genotypes present throughout a population, and this is often reflected in morphological, physiological and behavioral differences between individuals and populations (Frankham *et al.*, 2002). Farm animal biodiversity includes all animal species, breeds, strains, and their wild relatives of economic, scientific and cultural interest to humankind in terms of food and agricultural production for the present and future generations. There are over 1,400 modern domestic sheep breeds worldwide (Taberlet *et al.*, 2008; Goldammer *et al.*, 2009). However, the Food and Agricultural Organization of the United Nations (FAO) estimates that at least one breed of traditional livestock becomes extinct every week (FAO, 2011). According to FAO (2011) report, nearly 800 farm animal genetic resources have been lost and about 30% of all those remaining are associated with some risk.

The utilization of farm animal genetic resources to achieve and maintain sustainable production systems capable of responding to human needs is necessary for national and

global food security. Sustainable utilization of livestock genetic diversity requires the characterization of the available resources and development of sustainable genetic improvement strategies that consider the needs and perceptions of target groups and that minimize loss of genetic diversity (Solomon Gizaw, 2011). Thus, studying the genetic diversity of existing sheep populations has paramount importance to develop conservation strategies for the breeds.

Information on both within and among-breed diversity is important for management at the breed level and to identify divergent breeds that may harbor distinct genotypes hence worthy of conservation efforts even though their within-breed diversity is comparatively high (Abdelkader *et al.*, 2020). An understanding of the evolutionary history of domestic breeds and data on genetic variation within and among breeds is vital to these initiatives to provide critically important data for the decision-making process (Rege and Gibson, 2003). In developing countries, cross-breeding between local breeds and with exotic breeds represents one of the main threats to the livestock diversity, leading to genetic dilution and loss of unique allelic combination underlying essential local adaptive traits (Harkat *et al.*, 2017). Loss of diversity in domestic species including sheep has important economic, ecological, scientific, and social implications (Tisdell, 2003). Loss of genetic diversity will likely decrease the ability of animals to respond to environmental change and will cause a loss of genetic resources potentially useful for breeding improvement (Oldenbroek and van der Waaij, 2014). Losing livestock diversity limits our efforts towards poverty alleviation, improved food security and promoting sustainable agriculture.

To develop conservation strategies for the breeds, their genetic diversity and genetic distinctness must be first characterized. Comprehensive knowledge of the existing genetic variability is the first step for the conservation and exploitation of domestic animal biodiversity (Li *et al.,* 2002; Ciani *et al.,* 2013). Thus, study of genetic diversity and population structure of sheep populations which are not studied in previous works like Tumele, Begayit and Rutana sheep with their neighboring breeds may improve the understanding of the existing genetic resources of our sheep breeds.

2.5. Population structure and admixture

Knowledge of genetic diversity and population structure is beneficial for designing effective strategies to enhance the assembly, management, and conservation of livestock genetic resources. Inference of population structure is essential in both population genetics and association studies and is often performed using principal component analysis (PCA) or clustering-based approaches (Meisner and Albrechtsen, 2018). Population structure is often estimated using the Bayesian method STRUCTURE (Pritchard *et al.,* 2000); however, in recent years full maximum-likelihood approaches like ADMIXTURE (Alexander *et al.,* 2009) have become popular especially for large data sets. This is due to efficient expectation-maximization (EM) algorithms that allow for simultaneous optimization of millions of parameters.

Admixture occurs when isolated populations interbreed and their offspring represent a mixture of alleles from different ancestral populations (Skotte *et al.,* 2013; Mersha,

2015). Admixture analysis is important for many scientific fields. Estimating population structure and individual ancestry is important both for population genetics and for association studies. Methods and models for locating population structure and admixture require exact knowledge of the individual genotypes. Applying admixture mapping should build on knowledge regarding the genetic makeup of the admixed population, and of the specific ancestral populations that contributed to the admixture. Genetic admixture can be studied at the population, individual or specific regions along the chromosome (locus level) (Mersha, 2015; Tesfaye Getachew 2015).

Estimating the admixture proportions of a distinct population is a valuable tool in both population genetics and genetic epidemiology. In population genetics, admixture analysis is used to classify individuals with unknown ancestry into discrete populations. Knowing the individual admixture proportions is additionally useful in genetic association studies. Applying admixture mapping to the identification of genes influencing complex traits (including disease) in populations tracing their ancestry to genetically differentiated populations (McKeigue, 2005; Zhu *et al.*, 2008). Admixture mapping is potentially more powerful and economical than high-density whole-genome association studies and should also allow the identification of trait-related genetic variants fixed in one of the parental populations. Population genetics linked with the study of evolution principle and provide information how and why the frequencies of alleles and genotypes change over time within and between populations (Ewens, 2012; Jamieson, 2015). Population structure is the existence of differing levels of genetic relatedness among some subgroups within a sample. Two of the most commonly used approaches to describe population structure in a

sample are principal component analysis (Abraham and Inouye, 2014; Yano *et al.*, 2019) and admixture proportion inference (Harkat *et al.*, 2017; Wu, 2020). Admixture analysis is equally important in population genetics where is it used to infer information on the history of a sample or population. Principal component analysis of five Ethiopian sheep population using high-density SNP showed that PC1 and PC2 accounted for 26.7% and 25.2% of the total variation and clustered according to their tail type (Zewdu *et al.*, 2015).

2.6 . Characterization of Sheep Breed of Ethiopia

Characterization of the animal genetic resource (AnGR) encompasses all activities related to the identification, quantitative and qualitative description of populations and therefore the natural habitat and production systems to which they are or are not adapted (Fao, 2007; Asamoah-Boaheng, 2016). Characterization means the distillation of all knowledge, which contributes to the reliable prediction of the genetic performance of an animal genetic resource in a defined environment and provides a basis for distinguishing between AnGR and for assessing diversity (Asamoah-Boaheng, 2016).

Research on identification, classification, and description of sheep resources of Ethiopia began in the 1970s with the classification of the sheep populations into broad categories of the tail and fiber types (Solomon Gizaw *et al.*, 2013a). Ethiopian sheep were initially categorized into fat-tailed (Arsi-Bale sheep), thin-tailed (Horro sheep) and coarse-woolen sheep (Menz and Tikur sheep), the classification that distinguished rather few populations (Solomon Gizaw *et al.*, 2013b). Solomon Gizaw *et al.*, (2013b) described the

characterization and classification of Ethiopian sheep based on body size into these breeds: small (Menz, Wollo, and Tikur sheep), medium (Sekota and Simien sheep), large (Black Head Somali (BHS), Adilo, Farta, and Arsi-Bale sheep) and very large (Gumz, Afar, Washera, Horro and Bonga) sheep types. The very large breeds are more prolific than the smaller breeds, with litter sizes varying from 1.0 to 1.09 within the small breeds and 1.28 to 1.55 within the very large breeds (Solomon Gizaw *et al.*, 2013b).

2.7. Methods of characterization

2.7.1. Phenotypic characterization

It includes productive and reproductive performance and physical characterization of populations. We discussed here focused on litter size and morphological characterization that used for this study to characterized the thin-tailed and fat-tailed sheep population of Ethiopia

Litter size is essentially determined by the ovulation rate but is additionally modified by fertilization rate and embryonic and fetal losses (Da Silva *et al.*, 2016). Breed, level of nutrition, season and age, can determine ovulation rate. The age of the dam can affect several lambs per lambing. Litter size is influenced by genotype, parity, season, and ewe weight at mating and therefore the management system may be a major source of variation in litter size(Sánchez-Dávila *et al.*, 2015).

2.7.2. Morphological characterization

Genetic diversity can be determined based on morphological, biochemical, and molecular markers (Yang *et al.*, 2013). Morphological markers are based on visible traits. The

description of breeds regarding coat color, horns, physical body measurements, and productive traits is based upon observation of the phenotype which can be obtained by direct visual observation and measurement are called morphological markers. Morphological characterization of the animal genetic resource generally refers to identifying distinct breed populations and describing their external and production characteristics within a production environment (FAO, 2012).

The first phase of characterization involves the identification of populations based on morphological descriptors important to identify and document diversity within and between distinct breeds. Phenotypic characters have the advantages of being easily seen and measured and usually much lower costs are incurred during phenotypic characterization compared to genetic characterization. Phenotypic characters have been used extensively for the characterization and identification of breeds (Tassew Mohammed *et al.*, 2014; Addisu Hailu and Addis Getu, 2015; Helen Nigussie *et al.*, 2016).

Most phenotypic characters are polygenetically inherited and many are influenced by environmental effects and, sometimes, strong genotype by environment interaction (Duijvesteijn *et al.*, 2018). Phenotypic characters are affected by natural selection (Linnen and Hoekstra, 2009). Therefore, due to the influence of different environmental conditions and different selection pressure on different characters indigenous breeds of animals resistant to any diseases and better adapted to the changing environmental

conditions (Ozerov *et al.*, 2020). Morphological characterization of Ethiopian sheep population was done by several MSc students

2.7.2.1. Qualitative traits

This includes traits like presence or absence of horns, coat color pattern, color type, horn orientation, tail type, presence or absence of ruff and wattle, ear type, ear orientation and hair type (wool versus hair) and head profile. Some of these (e.g. Presence or absence of horn) have simple Mendelian inheritance and have been studied extensively at least in temperate livestock. Physical characteristics are possibly the most commonly used criteria for breed or strain definitions. Attempts have been made to use these traits in classifying previously uncharacterized population.

The characterization of indigenous sheep breeds and breed diversity are essential for the conservation of their genetic sources and determination of the flock's potential for breeding and to meet future needs. A good description comparison or characterization based on morphological properties can provide, to some extent, a reasonable insight about the differences among populations (Yakubu, 2011).

Despite the many sheep populations in the country, characterization of Animal Genetic Resource (AnGR) in Ethiopia has largely been limited to description of production systems and phenotypes classification of traditional breeds using multivariate morphological traits (Tassew Mohammed *et al.*, 2014; Zelealem Tesfay and Anal, 2014; Mengstie Taye. *et al.*, 2016). Characterization of livestock breeds supported their

morphological traits variations is that the initiative towards evaluating the available animal genetic resources (Lanari *et al.*, 2003). According to {Aberra Melesse, 2013 #27} coat color pattern of indigenous sheep of Southern Regional State of Ethiopia dominated by plain and followed by patchy, with long fat-tailed, short and smooth hair type and absence of wattle and ruff. Helen Nigussie *et al.* (2016) studied on indginous sheep breeds in eastern Ethiopia based on phentypic variation and protin polymorphism and found significant variation in most qualitative characters among eastern Ethiopia sheep breeds. Based on their finding multiple correspondence analysis BHS breed was clustered together with black head and white body coat color type, fat rump and having tail shape both cylindrical and straight. Afar breed was closely associated with light brown coat color type and cylindrical and twisted tail shape while Harergie High Land sheep population was closely associated with dark brown, black and combination of both colors with white coat color type, having tail shape cylindrical and turned up at the end. Similarly, a study by Bosenu Abera *et al.* (2014) on indgenous sheep population of Selale Area, Centeral Ethiopia based on phenotypic vairation found that majority of the studied sheep had plain coat color pattern followed by patchy, having medium and smooth coat cover and long fat-tailed with semi-pendulous ear formation. Qualitative traits may represent some adaptive mechanisms related to adaptation and survival in different ecological zones (Mdladla *et al.*, 2017). Dark coat colors have been linked to environmental adaptation in Gana as described by Hagan (2012). Black-colored animals are believed to have superior adaptation to seasonal cold weather as the dark pigment helps them to absorb heat and warm up faster than other coat colors (Fsahatsion Hailemariam *et al.*, 2018).

2.7.2.2. Quantitative traits

The quantitative traits such as height at withers, chest girth, body length, pelvic width, rump length, rump height, ear length, tail length, horn length, and head length are used to evaluate the characteristics of varied breeds of animals and will provide information on the suitability of animals for selection (Yakubu *et al.*, 2010) and for further characterization studies using modern molecular methods.

Linear body traits have been suggested as objective measures of body conformation in sheep. Body conformation highly influences the market value of meat sheep in traditional markets (Solomon Gizaw *et al.*, 2008b). Body measurements are quantitative growth indicators that reflect the conformational changes during the lifespan of animals (Asamoah-Boaheng and Sam, 2016; Sam, 2017). Linear body measurements are divided into skeletal and tissue measurements. The height at withers is part of the skeletal measurements, whereas the chest girth is part of the tissue measurements. Information on body weight and physical linear measurements of specific sheep population at constant age have paramount importance in the selection of genetically superior animals for production and reproduction purposes . Several scholars (Bosenu Abera *et al.*, 2014; Tassew Mohammed *et al.*, 2014; Zelealem Tesfay and Anal, 2014) used these traits for breed characterization. Morphometric characterization of indigenous sheep using multifactorial discriminant analysis could be identified discriminant traits (Yunusa *et al.*, 2013; Tariq *et al.*, 2014; Asamoah-Boaheng, 2016; Arandas *et al.*, 2017). The value of linear body measurements varies due to the gene difference and the environmental, production system and management difference of the sheep populations.

2.7.3. Genetic characterization of Ethiopian sheep

2.7.3.1. Molecular genetic characterization

Developing tools for the analysis of DNA in the last few decades has increased our capacity to characterize variation within and between breeds (Toro *et al.*, 2009). An increasing number of molecular markers and developing sophisticated statistical techniques for their analysis can now complement the physical characterization with phenotypic attributes. The study of genetic diversity at the molecular level has been proposed as a valuable complement to evaluating phenotypes and production systems (Ajmone-Marsan *et al.*, 2014).

There are three general types of DNA markers based on their basic marker technique. 1. non-PCR-based techniques or hybridization-based techniques such as Restriction Fragment Length Polymorphisms (RFLP) and Variable Number of Tandem Repeats (VNTR); 2. PCR-based DNA markers such as Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR), Sequence-Tagged Sites (STS), Amplified Fragment Length Polymorphisms (AFLP), Inter-Simple Sequence Repeat (I-SSR) and 3. Sequence-based molecular markers like Single Nucleotide Polymorphism (SNP) (Benjelloun *et al.*, 2015). Of these, microsatellite and SNPs are widely used and preferred for population studies in livestock.

SNP is a type of molecular markers that recently has gained greater popularity. Single nucleotide polymorphism SNPs, represent sites in the genome where DNA sequence differs by a single base when two or more genomes are compared. They occur about once

every 300-500bp in sheep, within the coding and non-coding regions. For a variation to be considered an SNP, it must occur in at least 1% of the population (Mburu and Hanotte, 2005; Kijas *et al.*, 2012).

SNPs are rapidly becoming the markers of choice for many applications in genome analysis due to their abundance, stability, low error rate, ease of automation and standardization between laboratories (Kijas *et al.*, 2012). In recent years, the SNP array has been developed, based on the discovery of numerous SNPs through genome sequencing. The availability of many thousands of single nucleotide polymorphism (SNP) markers distributed across the genome has led to a new approach for genetic studies and applications. SNPs are used in genome-wide association studies, genetic prediction of breeding values, for the estimation of genetic diversity and population genetic parameters (Engelsma *et al.*, 2012; Kijas *et al.*, 2012).

Marker panels could be considered as either high- or low-density depending on the genome size, the extent of linkage disequilibrium (LD) and the traits of interest (Ballesta *et al.*, 2020). Larger genomes and rapid breakdown of linkage disequilibrium (LD) would imply that a higher density of SNP loci. High-density SNPs are used as highly favored makers to analyze genetic diversity and population structure, to construct high-density genetic maps and provide genotypes for genome-wide association analysis (Xia *et al.*, 2019). The high-density (HD) SNP chips provide best coverage of genome but still very expensive for routine use of genetic improvement of livestock (Aliloo *et al.*, 2018). Low-density SNP panels has been design based on the use of evenly spaced markers and

maximization of minor allele frequency (MAF) with some enrichments at chromosomal ends (Bolormaa S, 2015). Low-density SNP chips are considered as a way to reduce the cost of high-density SNP panels in livestock breeding and would enable cost-effective implementation of genomic studies (Shashkova *et al.*, 2019).

A study on molecular characterization of Ethiopian sheep breed is very limited. So far only few studies have been reported, indicating genetic diversity of sheep populations at the national level based on microsatellite markers by Solomon Gizaw *et al.* (2007). Helen Nigussie *et al.* (2019) also assess genetic variation and matrilineal genetic origin and relationship of fat-rumped sheep found in eastern Ethiopia using microsatellite markers and sequenced for the mitochondrial DNA displacement loop (mtDNA d-loop) region. The authors found the overall H_O and H_E were 0.57 and 0.75, respectively and a high proportion (97%) of the total genetic variation was explained by differences between individuals within populations. The mtDNA D-loop sequences analysis shown the matrilineal genetic origin of eastern Ethiopia sheep is from two haplotype groups (types A and B) among the five haplotypes globally observed. Genetic diversity and admixture analysis of Ethiopian fat-tailed (Menz and Wollo) and Awassi sheep using SNP markers by Tesfaye Getachew (2015) and Genetic diversity and population structure of some Ethiopian sheep population based on high-density SNP markers by Edea *et al.* (2017). In their study, only five breeds (Arsi-Bale, Horro, Menz, Adilo, and Blackhead Somali) included. They found that the mean genetic diversity ranged from 0.29 in Arsi-Bale to 0.32 in Menz sheep, while estimates of genetic differentiation among populations ranged from 0.02 to 0.07, indicating that low to moderate FST value. There are sheep

populations that did not included in the previous study and yet have not described. For example Begayit and Nuer sheep populations that need further characterization as reviewed by (Solomon Gizaw *et al.*, 2013a).

2.7.3.2. Quantitative genetic characterization

Estimates of genetic parameters are necessary to determine the selection method to be used, to estimate the maximum genetic gain that can be achieved and to obtain correct estimates of breeding values (Lôbo *et al.*, 2009). However, there have been few estimates of the genetic parameters for growth, reproductive and maternal traits in sheep (Safari *et al.*, 2005). Studying the genetic variability of important traits and co-variability between these traits is considered an important primary step in the planning and implementation of any successful selection or breeding program that aims to improve the genetic gain of production animals (Jawasreh *et al.*, 2018).

Direct heritability estimates for birth weight of Afar sheep (0.13 to 0.38) and BHS (0.20 to 0.58) using univariate analysis; for Horro sheep (0.18 - 0.32) and Menz sheep (0.46) by fitting a multi-trait individual animal model. The weaning weight direct heritability estimates for sheep in Ethiopia, Afar sheep (0.11 - 0.37) and BHS (0.00 - 0.29), Horro sheep (0.10 - 0.26) and Menz sheep (0.48). Ewe productivity could be improved by increasing the number and weight of lambs weaned per ewe within a specific year (Cloete *et al.*, 2002). The reproductive traits included age at first lambing (AFL), number of lambs born (NLB/EL) and weaned (NLW/EL) per ewe in each lambing, total weight of lambs born (TWLB/EL) and weaned (TWLW/EL) per ewe in each lambing, total number

of lambs born (TNLB) and weaned (TNLW) per ewe, total weight of lambs born (TWLB) and weaned (TWLW) per ewe.

CHAPTER-3

3. Material and methods

3.1. The study areas and sheep populations studied

The study was conducted in two major areas of Ethiopia. The first area of study includes the Amhara region of North Gonder (Metema and AbraJira woredas) and Western Administrative zones (Kafta Humera Woreda) of the Tigray regional state. These areas were selected because they are the main production area of the thin-tailed sheep populations, especially (Gumz, Rutana and Begayit). The Rutana and Begayit sheep populations are not addressed in the previous molecular characterization.

The thin-tailed sheep breeds (Gumz, Rutana, and Begayit) were reared in the Northwestern areas in which small-scale, commercial farming and mixed crop-livestock production system is common. The area is characterized by hot to warm, moist and sub-moist tropical climate, a vast area of plains lowlands suitable for commercial farming and subsistence agriculture including crop and livestock production systems. Cattle, sheep and goats are the major livestock in the area.

The Gumz sheep breed mainly found in the Benishangul regional state and moist lowland area of north Gondar. The majority of the farmers in Metema Woreda were kept Gumz and Rutana sheep breeds and their crosses. Rutana is a Sudanese sheep breed found in Metema and Abra Jira area. Farmers preferred this sheep breed due to its twining ability and fast growth.

Begayit sheep breed types found distributed entirely in Western and North Western Tigray including districts such as Kafta Humera, Setit Humera, Tsegede, and Tahtay–Adyabo. The present study conducted in Kafta Humera in which commercial farming sheep production practice common by private farms with the production of sesame and cotton.

The other main study area includes North Shewa, South Wollo, and North Wollo administrative zones of Amhara regional state and zone one of the Afar regional state. These areas were also selected to characterized Tumele sheep with the neighboring breed of Afar and SSFT (Menz, Wollo and Tikur) in the Ethiopian Rift valley (from Shewa Robit to Moheni along the main road Addis Ababa to Mekele), which have mixed phenotypic features.

The fat-tailed sheep populations found in the sub-alpine cool highland, hot to humid semi-arid and arid climate in northeastern Ethiopia. The mid-altitude and lowland area of these zone up to the border of the Afar region is the main breeding tract for 'Tumele' sheep populations. The altitude ranges from 1200 to 2200 meters above sea level and mixed crop-livestock production system is predominant. Northeastern highland area of North Shewa, South Wollo, and North Wollo zones are breeding areas of small short fat-tailed sheep breeds. The altitude ranges from 1700-3500 meters above sea level in which sheep production is a major practice and the mainstay for people. The area is characterized by recurrent drought and cool weather (frost) which is a limiting factor for crop production.

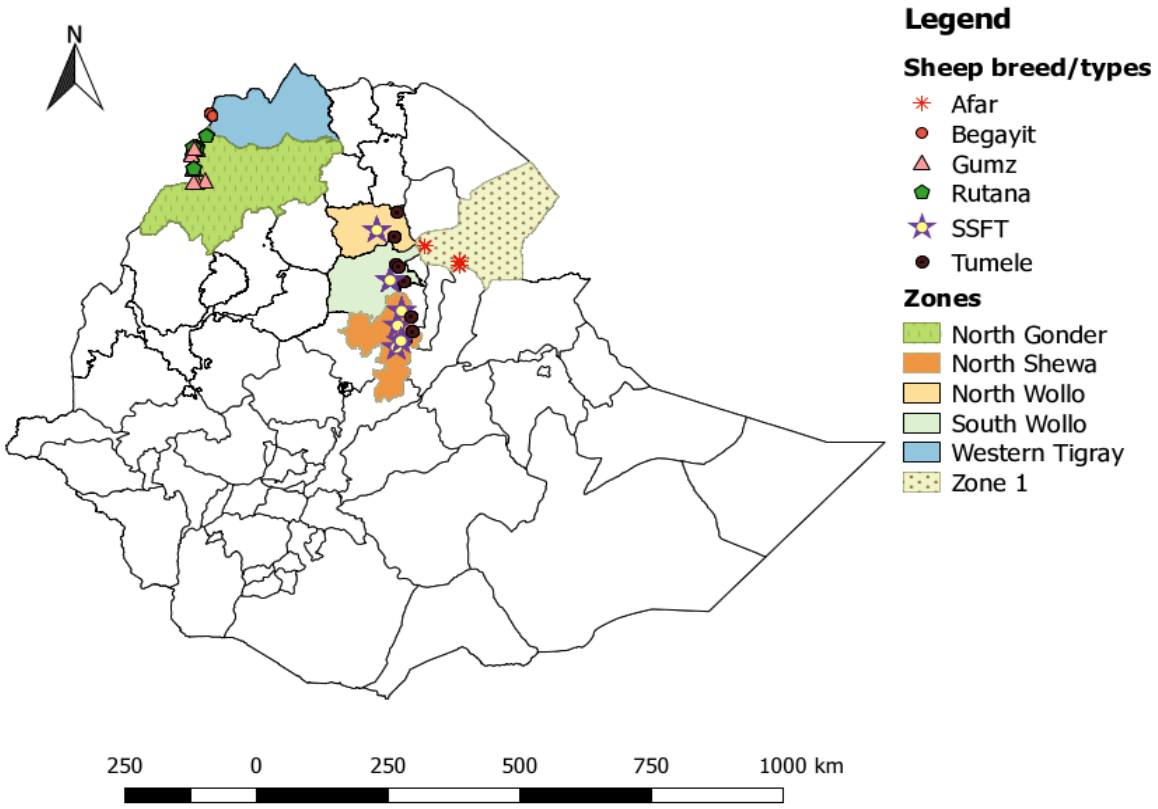

Figure 1. Map of Ethiopia showing the study areas

Afar region is the main breeding tract of Afar sheep populations which was characterized by arid to a semi-arid climate with low and erratic rainfall with annual average rainfall less than 555 mm. Most of the pastoralists in the area based their livelihood on livestock rearing with limited irrigation agriculture along the river basins. They rear multiple species including cattle, goats, sheep, camel, and donkeys. An extensive livestock production system has been the predominant livelihood system, which subsists pastoral households (Afar National Regional State Chifra Woreda, 2011).

Table 1. Description of agroecology, geography, and production system of fat-tailed sheep populations

Breed/type	Agroecology zones	Geography	Production system	Altitude
Afar	Hot to warm semi-arid and arid lowland and characterized by arid to a semi-arid climate with low (less than 500 mm) and erratic rainfall.	Afar regional state; bordering Tigray, Amhara and Oromia zone of eastern Shewa	Semi- pastoral and Pastoral	Below sea level to 1200 m.a.s.l
Small Short fat-tailed	Sub-alpine highlands. it is characterized by cool to very cold sub-moist/ dry alpine mountains and plateaus, low vegetation, 1102 mm rain, maximum 22.1 ^{o}c, minimum 7.6 ^{o}c.	North Shewa, south Wollo and North Wollo zone of the Amhara region of the central highland area.	Mixed crop-livestock and at the higher altitude (above 3000 m.a.s.l.) sheep-barely production system is predominant	1700-3500 m.a.s.l.
Tumele	Humid lowland to hot lowland	Low land of North Showa, South Wollo and North Wollo along the main road from Addis Ababa to Mekele at the bottom of the northeastern steep landscape	Mixed crop-livestock	1200-2200 m.a.s.l.

Table 2. Description of agroecology, geography, and production system of thin-tailed sheep populations

Breed/type	Agro-ecology zones	Geography	Production system	Altitude
Begayit	Hot to warm semi-arid lowland plains. Characterized by hot temperature, erratic rainfall, a vast area of plains lowlands suitable for comercial farming and subsistence agriculture including crop and livestock production systems.	Western and northwestern Tigray: including districts such as Tahtay–Adyabo, Tsegede, and Kafta Humera.	Mixed crop-livestock	568 -1861 m.a.s.l.
Rutana	Hot to warm semi-arid lowland plains. Characterized by hot temperature, erratic rainfall, a vast area of plains lowlands suitable for comercial farming and subsistence agriculture including crop and livestock production systems.	Sudanese Desert sheep found in Metema and AbraJira area of Amhara Region	Mixed crop-livestock	560–1849 m.a.s.l.
Gumz	Hot humid lowland characterized by hot to warm, moist and sub-moist tropical climate, a vast area of plains lowlands suitable for large-scale and subsistence agriculture including crop and livestock production systems.	Benishangul regional state and moist lowland area of north Gondar (Metema and Qura district)	Mixed crop-livestock	550-1680 m.a.s.l.

3.2. Data collection

The zone, woreda and kebele which have fat-tailed and thin-tailed sheep population were selected using purposive sampling technique. The individual animals at village was selected randomly from small holder farmers and private farms. Phenotypic observation and measurement were done on 660 mature female sheep (ewe) based on the phenotypic characterization descriptive format recommended by FAO (2012). Blood samples were collected from only two hundred forty-three female ewes.

Table 3. Studied sheep populations Region, Zone and number of Female animals sampled

Tail type	Populations	Region	Zone	No of animal[1]	No of animal[2]
Fat-tailed	SSFT	Amhara	North Shewa, Wollo and south Wollo	112	40
	Tumele		North Shewa, Wollo and South Wollo	128	43
Thin-tailed	Gumz	Amhara	North Gondar	109	41
	Rutana		North Gondar	115	42
	Begayit	Tigray	Western Tigray	96	39
Fat-rumped	Afar	Afar	Zone 1	117	38
			Total number of animals	677	243

[1] morphological data collection; [2] blood sample collection

3.2.1. Morphological traits studied

Both qualitative and quantitative traits were collected based on the phenotypic characterization guideline recommended by FAO (2012).

Qualitative traits

Coat color pattern (CCP), hair type (HT), coat color type (CCT), head profile (HP), ear formation (EF), horn, wattle and ruff presence or absence were observed and recorded.

Quantitative traits

Body length (BL), chest girth (CG), chest depth (CD), rump height (RH), rump length (RL), wither height (WH), tail length (TL), pelvic width (PW), Ear Length (EL), horn length (HL) and body weight (BWT) were measured. The live body weights of the sheep were measured using the Salter scale (50 kg capacity with 200 g precision) and other linear body measurements were taken after restraining and holding the animals in a natural position using measuring tape. Litter size and parity of female animals were collected using farmers recalling method during the morphological traits data collection. Information regarding flock size and composition, productive and reproductive performance, and production system characterization were collected through all the way through field observation, literature review, and personal communication.

3.2.2. Blood Sample Collection

Blood samples of two hundred forty-three animals were collected from unrelated full-mouth mature ewes (Table 3). The age of the animals was estimated based on dentition. The samples were collected from different households with a maximum number of two to three distinct animals per household based on the flock size to avoid sampling closely related animals.

Blood samples were collected according to the recommendations of (FAO, 2011). Blood samples were taken from individual animals by trained personnel (veterinarian) with one supporter to restrain the animals. Blood from the jugular vein was collected using 4ml of Vacutainer tubes with EDTA (Ethylene Diamine Tetra Acetic Acid) as an anticoagulant. The blood samples were transported from field to laboratory in an icebox and stored at −20 °C until genomic DNA was extracted.

DNA extraction and quantification

The DNA extractions were performed at Holeta National Agricultural Biotechnology Research Center based on modified salting-out methods (Nasiri *et al.*, 2005).

Testing purity, concentration, and integrity of isolated DNA.

The quantity and quality of genomic DNA for all samples were quantified using the Nanodrop spectrometer (Nanodrop ND-8000). A260 and A260/A280 ratios were used to determine DNA concentration and purity, respectively. Gel electrophoresis was carried out to evaluate the probability of DNA degradation, by loading of extracted DNA in parallel with DNA isolated by the standard salting-out procedure on 1% agarose gel.

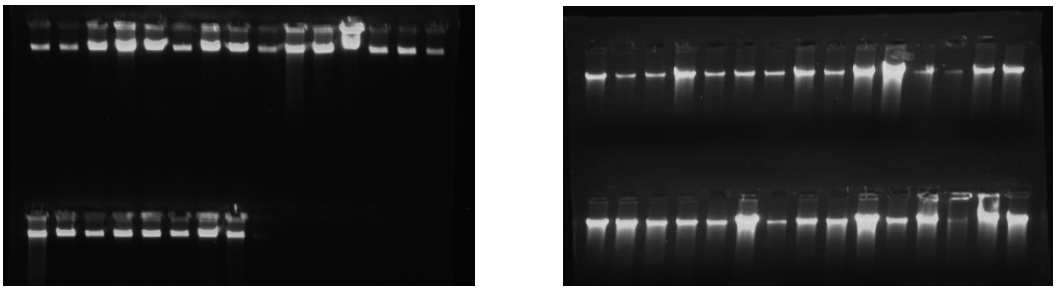

Figure 2. DNA band produced by loading sample DNA on 1% Agarose gel electrophoresis

Genotyping and SNP quality control

DNA genotyping was done at AgResearch, New Zealand, using the low-density ovine Illumina 15K SNP Bead Chip developed by the International Sheep Genome Consortium (ISGC; https://www.sheephapmap.prg/). The SNP data were subjected to quality control using PLINK software (Purcell *et al.*, 2007). SNPs with a call rate of <95% and SNPs with a minor allele frequency of below 0.001 were excluded from the analysis.

3.3. Data analysis

3.3.1. Morphological data analysis

Description of frequency and percentage of qualitative traits among populations were analyzed using the FREQ procedure of SAS 9.4. The relationship of qualitative traits and populations was analyzed using the SAS procedure of correspondence analysis. Least square means and their corresponding standard errors were obtained for each quantitative trait by population level using the PROC GLM procedure of SAS 9.4 {Institute, 2015} with the model that includes population and dentation as a fixed effect. Adult sheep were classified into three age groups based on the number of pairs of permanent incisors (PPI) following the finding of Wilson and Durkin (1984) for African sheep breed: 2 PPI = 22.5 to 27.0 months, 3 PPI = 28.0 to 38 months and 4 PPI= above 39.0 months. The litter size was calculated using the GLM procedure of SAS 9.4. with the model that includes breed, tail type and parity as a fixed effect.

Differences among sheep populations for quantitative variables were analyzed using the following linear model:

$$Y_{ik} = \mu + B_i + D_k + \varepsilon_{ik}$$

Where Y_{ik} = observation (body weight, body length, ear length, wither height, chest girth, and pelvic width) on the n^{th} individual sheep of the i^{th} populations and the k^{th} Dentation.

μ = the overall means common to all animals in the study

B_i= fixed the effect of i^{th} population effect (i^{th}= Afar, Tumele, SSFT, Begayit, Gumz and Rutana)

D_k = fixed effects of the k^{th} dentation (k^{th}= 2PPI, 3PPI and 4PPI)

ε_{ik} is the random error term assumed to be normally distributed with a variance equal to δ^2 and a mean =0

The mean separation was done using the Tukey students test.

Litter size was analyzed using the following model

$$Y_{ijk} = \mu + B_i + T_j + P_k + \varepsilon_{ijk}$$

Where

Y_{ijk} = observation (litter size) on the n^{th} individual sheep of the i^{th} breed and the j^{th} tail type and k^{th} parity.

μ = the overall means common to all animals in the study

B_i= fixed the effect of i^{th} population effect (i^{th}= Afar, Tumele, SSFT, Begayit, Gumz and Rutana)

T_j = fixed effects of the j^{th} tail type (j^{th}=fat and thin)

P_k = fixed effects of the k^{th} Parity (k^{th}= parity 1, parity 2, parity 3, parity 4, parity 5 and parity >=6)

ε_{ijk} is the random error term assumed to be normally distributed with a variance equal to δ^2 and a mean =0

3.3.2. Correlation and regression analysis

Correlations (Pearson's correlation coefficients) between body weight and different body measurements were computed only for female sheep.

The correlation coefficient, r, is calculated using:

$$r = \frac{cov(x,y)}{\sqrt{var(x)var(y)}}$$

Where, $var(x) = \frac{\sum_{i=1}^{n}(x-\bar{x})^2}{n-1}$ is the variance of x from the sample n,

$var(y) = \frac{\sum_{i=1}^{n}(y-\bar{y})^2}{n-1}$ is the variance of y, and

$var(x,y) = \frac{\sum_{i=1}^{n}(x-\bar{x})(y-\bar{y})}{n-1}$ is the covariance of x and y.

Stepwise REG procedures of SAS 9.4 were employed to predict live weight from body measurements. The choice of the best-fitted regression model was selected using the coefficient of determination (R^2), mallow's CP and Mean standard error (MSE). The multiple regression models were followed to estimate body weight from body measurements for each breed in separate analyses. The default significant level was 0.15 taken. Prediction of body weight from linear body measurements using the stepwise multiple regression procedure was carried out adopting the multiple linear regression model:

$$Y = \alpha + \beta_i x_i + \beta_2 x_2 + \ldots\ldots + \beta_k x_k + \varepsilon$$

Where: Y = dependent variable (body weight), α = intercept, β's = regression coefficients, X's = independent variables (BL, CD, EL, CG, PW, WH, RH, RL and TL), and ε= error term, normally distributed with mean = zero and variance=one.

3.3.3. Multivariate analysis

The discriminant analysis which describes the variation among groups and identifies variables with greater discriminatory power between groups was examined by using Stepwise discriminant procedure (PROC STEPDISC) of SAS 9.4. The relative importance of the morphometric variables in discriminating between the populations was assessed using the level of significance, partial R^2, and an F-statistic. The CANDISC procedure was used to enable differentiation between the populations, to estimate Mahalanobis distances and derive canonical functions. The DISCRIM procedure SAS 9.4 was used to compute canonical functions to assign each individual sheep to its sampling breed and to calculate the percent of the correct assignment.

The form of the equation or function is:

$$D = v_1 X_1 + v_2 X_2 + v_3 X_3 + \cdots + v_i X_i + \partial$$

Where D = discriminate function

v = the discriminant coefficient or weight for that variable

X= the measurement of predictor variable

∂ = a constant

i = the number of predictor variables

Cluster analysis was done using SAS 9.4 of seven quantitative traits (body length, chest girth, tail length, rump height, rump length, pelvic width and chest depth) based on ward methods. Ward method is most appropriate for quantitative traits and it involves an agglomerative clustering algorithm based on Euclidean distance.

3.3.4. Genetic diversity analysis

Observed heterozygosity (H_o) and expected heterozygosity (H_e) and Wright's inbreeding coefficient (FIS) were calculated for each breed to measure the genetic diversity within

the populations. The proportion of minor allelic frequency (MAF) for each population were calculated using PLINK (Purcell *et al.*, 2007). Pairwise FST values and analyses of molecular variance (AMOVA) were also calculated to test genetic relationships and distance between populations, using ARLEQUIN 3.5.2.2 software (EXCOFFIER *et al.*, 2005). PGDSpider version 2.0.8.2 (Lischer and Excoffier, 2012) was used to convert PLINK.MAP and PED files to Arlequin format and Arlequin, 1023 permutations were used for the AMOVA based on Weir and Cockerham (1984). Animal relatedness was estimated as the proportion of gene identity-by-descent between sample pairs within the population as an average relatedness (PI_HAT) value using PLINK (Purcell *et al.*, 2007).

3.3.5. Genetic structure and admixture analysis

Genetic structure and admixture among populations were analyzed using a model-based clustering algorithm implemented in the software ADMIXTURE v. 1.2.3 (Alexander *et al.*, 2009). Prior population information was ignored, and K-values of 2-10 were tested. The most probable number of population in the data set (K) was estimated using the default cross-validation procedure by which prediction errors were obtained for each K values (Alexander and Lange, 2011). The cross-validation (CV) procedure was used to choose the optimal number of inferred clusters by identifying the K-value with the lowest cross-validation error estimate. The K value that minimizes this estimated prediction error was assuming the most appropriate. The individual coefficient of ancestry proportion produced by ADMIXTURE software was graphically visualized using R software (R Development Core Team, 2013).

The pattern of breed admixture was further analyzed through principal component analysis (PCA) using the GenABEL R package (Aulchenko *et al.*, 2007). GenABEL R package was used for the PC analysis in the R environment (R Development Core Team, 2013). The PCA was conducted to determine the breed relationships based directly on allele frequencies using a multivariate method, which condenses the information from many alleles and loci into a few synthetic variables.

CHAPTER -4

4. Results

4.2. Description of qualitative traits of the sampled sheep populations

The frequency and percentage of coat color pattern of fat-tailed and thin-tailed female sheep was presented in Table 4. The most frequent coat color patterns observed in Tumele sheep population was plain (72%) and followed by patchy (28%). The most frequent coat color patterns observed in the female Afar sheep breed was plain (53%), patchy (45%) and spotted (1.71%). Similarly, in SSFT, the most frequently observed coat color pattern was plain (78%) followed by patchy (22%).

Table 4. Frequency and percent of coat color pattern of female fat-tailed and thin-tailed sheep

Sex	breed group	breed/type	Coat color pattern		
			Plain (%)	Patchy (%)	Spotted (%)
Female	Northeastern Fat-tailed	Afar	62(52.99)	53(45.30)	2(1.71)
		Tumele	78(71.56)	31(28.44)	-
		SSFT	87(77.68)	25(22.32)	-
	Northwestern thin tailed	Gumz	62(56.88)	41(37.61)	6(5.50)
		Rutana	63(54.31)	53(45.69)	-
		Begayit	34(33.33)	62(60.78)	6(5.88)

The most frequent coat color patterns observed in the thin-tailed Begayit sheep breed were patchy (61%), plain (33%) and spotted (6%). The most frequent coat color patterns

observed in Rutana sheep was plain (54%) followed by patchy (46%) respectively. the most frequent coat color patterns observed in Gumz sheep were patchy (57%), plain (38%) and spotted (6%).

In the fat-tailed sheep populations, most dominant coat color observed in the female of the Tumele sheep population were plain brown color (40%), plain white color (23%) and patchy coat color white with brown (14%), respectively. The most dominant coat color observed in neighboring Afar sheep breed was plain brown (32%), followed by patchy white with black (23%), then plain white (15%), and patchy white with brown (15%), respectively. In a patchy coat color pattern, the first color indicates that the dominant coat color. The dominant coat colors observed in the SSFT sheep were plain white (26%), plain red (19%), plain brown (15%) and plain black (13%), (Table 5).

In the thin-tailed sheep populations the most dominant coat colors observed in Begayit sheep population were plain white (28%), patchy white with black (18%), and patchy black with white (17%) (Table 5). The dominant coat colors observed in Rutana sheep were plain brown (24%), plain red (20%) and patchy red with black (13%), respectively (Table 5). The dominant coat colors observed in Gumz sheep were red (20%) and brown (12%) in plain coat color pattern, white with brown (15%) and red with white (12%) in patchy coat color pattern (Table 5).

Table 5. The frequency and percentage of coat color type of the fat-tailed and thin-tailed female sheep populations.

CCP	CCT	Afar	Tumele	SSFT	Gumz	Rutana	Begayit
plain	Black	6(5.1)	1(0.9)	15(13.4)	2(1.8)	2(1.7)	1(1.0)
	Brown	37(31.6)	51(39.8)	17(15.2)	13(11.9)	28(24.1)	1(1.0)
	Gray	-	1(0.9)	5(4.5)	1(0.9)	3(2.6)	-
	Red	2(1.7)	4(3.7)	21(18.8)	22(20.2)	26(22.4)	4(3.9)
	White	17(14.5)	25(22.9)	29(25.9)	3(2.8)	4(3.5)	28(27.5)
patchy	black red	-	-	1(0.9)	-	1(0.9)	-
	black white	8(6.8)	1(0.9)	7(6.3)	8(8.3)	3(2.6)	17(16.7)
	brown black	-	-	-	1(0.9)	2(1.7)	2(1.0)
	brown white	-	7(6.4)	3(2.7)	9 (8.3)	10(8.6)	3(2.9)
	gray white	-	-	1(0.9)	1(0.9)	-	1(1.0)
	Red black	1(0.9)	-	-	1(0.9)	-	-
	red white	-	3(2.8)	4(3.6)	13(11.9)	15(12.9)	4(3.9)
	white black	27(23.1)	3(2.8)	3(2.7)	5(4.6)	3(2.6)	18(17.7)
	white brown	17(14.5)	15(13.8)	3(2.7)	16(14.7)	6(5.2)	-
	white gray	-	-	-	3(2.8)	1(0.9)	-
	white red		1(0.9)	4(3.6)	5(4.6)	9(7.8)	9(8.8)
spotted	G+R+W	-	-	-	-	2(1.7)	-
	R+W+B	1(0.9)	-	-	1(0.9)	-	1(1.0)
	W+R+B	1(0.9)	-	-	-	-	3(2.9)
Total		117	112	113	104	115	102

CCP=coat color pattern, CCT=coat color type, figures in parenthesis are %, G+R+W=Gray red white mixed color, R+W+B=Red white black mixed color, and W+R+B=white red black mixed color

The frequency and percent of hair type, head profile, presence or absence of wattle and ruff and ear formation of fat-tailed and thin-tailed female sheep are presented in Table 6. Tumele sheep breed type had short and smooth (53%) and rough and coarse (46%) of

hair type. The only hair type observed in Afar breed was short and smooth (100%) and 98% of rough and coarse hair type was observed in SSFT breed.

The most frequent hair type in the northwestern thin-tailed sheep was short and smooth (92%, 84%, and 86%) for Begayit, Gumz and Rutana sheep breed, respectively and the rest of the percentage is rough and coarse. The higher percent of coarse hair type was observed in the small short fat-tailed sheep found in the cool central highland of Ethiopia. But sheep populations that are found in semi-arid, arid and sub-humid lowland area had mainly short and smooth hair type.

The most dominant head profiles in all the studied fat-tailed sheep populations are straight. The straight head profile observed in Afar, Tumele and SSFT sheep populations were 100%, 91%, and 100%, respectively. Whereas the head profile observed in Begayit, Gumz and Rutana sheep were 87%, 33%, and 85% convex, respectively. But the majority (66%) of Gumz sheep had a semi-convex head profile.

The ear formation that are commonly observed in all fat-tailed sheep populations was lateral whereas pendulous and semi-pendulous ear formation was common for northwestern thin-tailed sheep populations. Ear formation was pendulous (92%, 44%, and 88%) for Begayit, Gumz and Rutana, respectively. The horn was not seen in all sampled female animals in all populations.

Table 6. The frequency and percent (in the parenthesis) of hair type, head profile, presence or absence of wattle and ruff, and ear formation of fat-tailed and thin-tailed female sheep

Traits		Afar	Tumele	SSFT	Gumz	Begayit	Rutana
Hair type	Short and smooth	117(100)	68(53.1)	2(1.8)	109(91.7)	86(84.3)	100(86.2)
	Coarse	-	60(46.9)	110(98.2)	9(8.3)	16(15.7)	16(13.8)
Head profile	Convex	-	-	-	33(33.3)	87(87.3)	99(85.3)
	Semi-convex	-	11(8.6)	-	72(66.1)	15(14.7)	17(14.7)
	Straight	117(100)	117(91.4)	112(100)	4(3.7)	-	-
Wattle	Present	22(18.8)	7(5.5)	15(13.4)	15(13.8)	12(11.8)	16(13.8)
	Absent	95(81.2)	121(94.5)	97(86.6)	94(86.2)	90(88.2)	100(86.2)
Ruff	Present	1(0.9)	2(1.6)	-	10(9.2)	29(28.4)	19(16.4)
	Absent	116(99.2)	126(98.4)	112(100)	99(90.8)	73(71.6)	97(83.6)
Ear	Pendulous	-	-	-	48(44.0)	95(93.1)	99(75.3)
Formation	Semi-Pendulous	4(3.4)	18(14.1)	-	49(45.0)	5(4.9)	12(10.3)
	Lateral	113(96.6)	110(85.9)	112(100)	12(11.0)	2(1.96)	5(4.3)

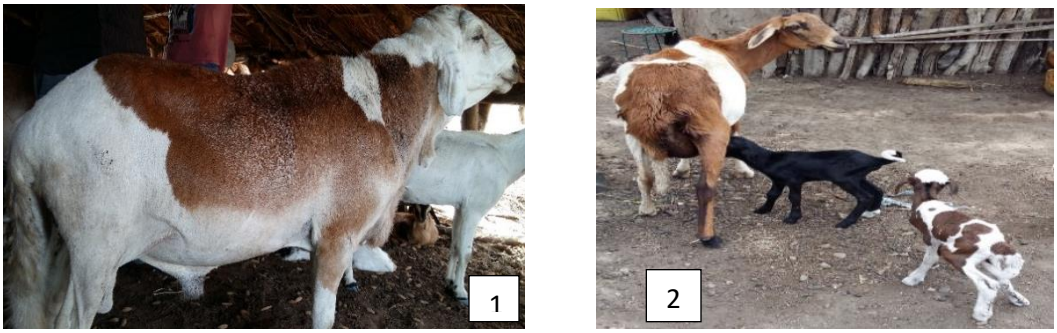

Figure 3. Picture of Gumz ram (1) and Gumz ewe with twin lambs (2)

Figure 4. Picture of Rutana rams (1) and Begayit Ram (2)

Figure 5. Picture of Female Tumele sheep

4.3. Multiple Correspondence analysis of qualitative traits

Begayit and Rutana sheep populations were associated with a convex head profile and pendulous ear formation. Likewise, Gumz sheep breed also associated with semi-pendulous ear formation and semi-convex head profile (Figure 6).

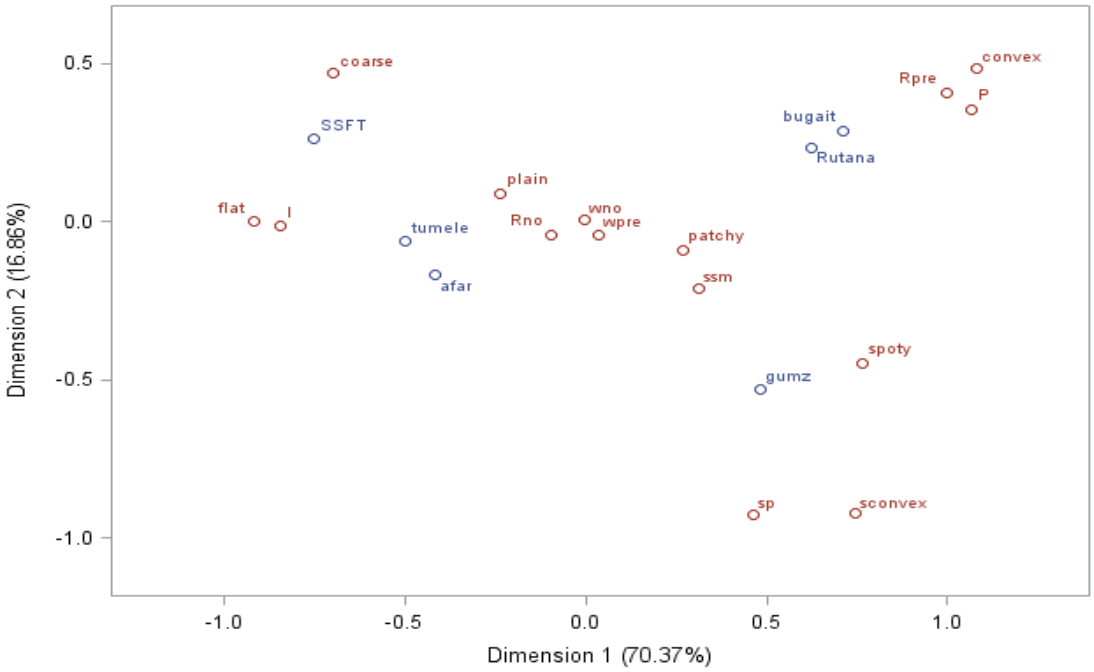

Figure 6. Multiple correspondence analysis that showed the relationship of qualitative traits with populations

The symbol represents: - sp= semi-pendulous, I= lateral, p= pendulous ear formation, ssm= short and smooth hair type, coarse= coarse hair type, Rpre=presence of ruf, Rno= absence of ruf, Wno=absence of wattle, wpre= presence of wattle, and convex= convex head profle, sconvex=semi-convex head profile, flat= flat/straight head profile, patchy= patchy coat color pattern, plain=plain coat color pattern, spotty= spotted coat color pattern.

The fat-tailed groups had flat/straight head profile and lateral ear formation and Afar and Tumele associated with plain coat color pattern with the absence of ruff. The SSFT had coarse hair type with flat /straight head profile and lateral ear formation.

4.4. Description of quantitative traits of the sample population

The coefficient of variation ranges from 5. 16% for rump height to 20.2% for ear length which were the lowest and highest variability, respectively. Ear length, tail length, and body weight had a high coefficient of variation. All variables have shown a significant difference ($P<0.001$) between breeds/populations (Appendix Table 2-7). Body weight had significance ($p<0.05$) difference between breeds in which Rutana sheep population had largest body weight followed by Begayit, and least body weight recorded in Afar breed. Wither and rump height values were highest for Rutana and Begayit sheep and followed by Gumz and SSFT. The least wither and rump height were recorded for Afar breed. Most of the linear body measurements have similar value for Begayit and Rutana sheep except for body weight, tail length, and chest girth. The chest girth was highest for Rutana and least value recorded for Afar sheep. Similarly, tail length was longer for Begayit and shorter for Afar sheep populations. The body weight and other linear body measurements of Tumele sheep similar with SSFT except tail length, chest depth and ear length. The body weight and linear body measurements of Afar sheep breed were low as compared to the other sheep populations (Table 7 and 8).

All traits had a significant difference between age group except tail length, rump height, and ear length (Table 7 and 8). The body weight was higher for the 4PPI age group followed by 3PPI and then 2PPI. The chest depth, body length, wither height and pelvic width value were similar for 3PPI and 4PPI and significantly different ($p<0.001$) form the 2PPI age group (Table 8). The chest girth value was increased as age increases. Gumz and SSFT sheep breed had similar values of chest depth, rump height, and pelvic width.

Table 7. Number of observations, overall mean, CV, significant level and least square mean (± SE) of body weight and linear body measurement of fat-tailed and thin-tailed female sheep populations

		BWT(kg)		TL (cm)		CD (cm)		RH (cm)		RL (cm)
	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)
Overall	659	31.2±0.00	660	33.6±0.00	590	36.3±0.00	590	68.4±0.00	590	21.5±0.00
cv		16.41		15.64		7.6		5.16		9.29
Breed/population		***		***		***		***		***
Afar	111	18.9±0.49^{e}	112	17.3±0.50^{f}	42	27.6±0.43^{d}	42	58.4±0.55^{d}	42	13.8±0.31^{d}
Tumele	122	26.3±0.47^{d}	122	25.8±0.48^{d}	122	34.4±0.25^{c}	122	64.9±0.32^{c}	122	21.1±0.18^{bc}
SSFT	112	24.5±0.49^{d}	112	21.2±0.51^{e}	112	35.2±0.27^{b}	112	64.9±0.34^{bc}	112	21.8±0.19^{b}
Gumz	104	35.9±0.50^{c}	104	38.7±0.52^{c}	104	36.3±0.27^{b}	104	68.8±0.35^{b}	104	20.9±0.20^{c}
Rutana	115	43.1±0.49^{a}	115	49.9±0.50^{b}	115	39.5±0.26^{a}	115	74.3±0.34^{a}	115	23.2±0.19^{a}
Begayit	95	39.7±0.53^{b}	95	52.1±0.54^{a}	95	39.3±0.28^{a}	95	73.7±0.36^{a}	95	23.3±0.21^{a}
Dentation		***		NS		***		NS		*
2PPI	206	29.6±0.36^{c}	206	33.9±0.37	179	34.6±0.22^{b}	179	67.1±0.28	179	20.4±0.16
3PPI	208	31.8±0.36^{b}	209	34.3±0.37	179	35.6±0.21^{a}	179	67.6±0.27	179	20.7±0.15
4PPI	245	32.9±0.33^{a}	245	34.3±0.34	232	36.0±0.19^{a}	232	67.9±0.24	232	21.0±0.14

N=number of observations, CV=Coefficient of variation ***=significant at P<0.001, *= significant at P<0.05 and NS= non-significant, a,b,c,d,e,f means different letters within the same column and class are statistically significant, BWT=body weight, TL=tail length, CD= chest depth, RH=rump height, and RL=rump length; SE= Standard error, 2PPI= two pair of permanent incisors, 3PPI= three pair of permanent incisor and 4PPI= four and above pair of permanent incisors

Table 8. Number of observations, overall mean, CV, significant level and linear body measurements of fat-tailed and thin-tailed female sheep populations

		EL(cm)		BL(cm)		CG(cm)		WH (cm)		PW(cm)
	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)	N	(LSM±SE)
overall	651	10.5±0.00	660	53.2±0.00	660	75.3±0.00	660	67.8±0.00	660	15.5±0.00
cv		20.2		5.25		5.41		5.34		9.09
Breed		***		***		***		***		***
Afar	112	4.4±0.20^{e}	112	46.6±0.27^{d}	112	66.6±0.39^{e}	112	59.6±0.34^{d}	112	13.1±0.13^{c}
Tumele	116	7.4±0.20^{d}	122	51.3±0.26^{c}	122	72.7±0.37^{d}	122	64.1±0.33^{c}	122	15.4±0.13^{b}
SSFT	109	10.2±0.21^{c}	112	51.6±0.27^{c}	112	71.6±0.39^{d}	112	64.6±0.35^{c}	112	15.8±0.14^{b}
Gumz	104	12.6±0.21^{b}	104	54.5±0.25^{b}	104	77.4±0.40^{c}	104	70.0±0.36^{b}	104	15.6±0.14^{b}
Rutana	115	14.8±0.20^{a}	115	58.2±0.27^{a}	115	82.7±0.39^{a}	115	75.0±0.34^{a}	115	16.7±0.13^{a}
Begayit	95	14.5±0.22^{a}	95	57.8±0.29^{a}	95	81.4±0.42^{b}	95	74.7±0.37^{a}	95	16.5±0.15^{a}
Dentation		NS		***		***		***		***
2PPI	204	10.5±0.15	206	52.4±0.20^{b}	206	73.1±0.29^{c}	206	67.2±0.26^{b}	206	15.2±0.10^{b}
3PPI	205	10.8±0.15	209	53.9±0.20^{a}	209	75.9±0.29^{b}	209	68.3±0.25^{a}	209	15.7±0.10^{a}
4PPI	242	10.7±0.14	245	53.8±0.18^{a}	245	77.2±0.27^{a}	245	68.5±0.24^{a}	245	15.6±0.09^{a}

N=number of observations, CV=Coefficient of variation ***=significant at P<0.001 and NS= non-significant, a,b,c,d,e, means different letters within the same column and class are statistically significant, EL=ear length, BL= body length, CG=chest girth, WH=wither height, PW=pelvic width; SE= Standard error, 2PPI= two pair of permanent incisors, 3PPI= three pair of permanent incisor and 4PPI= four and above pair of permanent incisors

The mean body weight of thin-tailed female sheep populations was 43.1±0.49, 39.7±0.53 and 35.9±0.50kg for Rutana, Begayit and Gumz, respectively (Table 7). The mean body weight of fat-tailed female sheep breed was 18.9±0.49, 26.3±0.47, 24.5±0.49kg for Afar, Tumele and SSFT, respectively (Table 7). The higher body length, wither height and chest girth recorded in the thin-tailed sheep population of Rutana and Begayit sheep populations (Table 8).

The number of observations, least-square mean and standard error of litter size for all sheep populations is presented in Table 9. The twin lambing capacity of thin-tailed sheep breed was higher than their counterpart fat-tailed sheep populations. The litter size observed in the present study showed that Rutana sheep breed (1.76) had more lambs per birth followed by Gumz sheep breed (1.47) whereas in the fat-tailed sheep breed single birth was the common phenomena.

The highest litter size was recorded in the Rutana sheep breed and the lower value recorded in Begayit within the thin tailed group (Table 9). While within fat-tailed sheep populations there is no significant difference in litter size value. The litter size was increased as the parity increases. The highest value of litter size was observed in parity six and above whereas the lower value of litter size observed in the first parity.

Table 9. Least mean square and standard error of litter size of fat-tailed and thin-tailed sheep populations of northeastern and northwestern Ethiopia

Traits	N	Min	MAX	Litter size (LSM±SE)
overall	624	1.00		1.23±0.01
Tail type				***
Fat-tailed	332	1.00	2.25	1.02±0.02[b]
Thin-tailed	292	1.00	3.50	1.47±0.02[a]
breed				***
Afar	113	1.00	1.33	1.03±0.03[d]
Tumele	113	1.00	2.25	1.10±0.03[d]
SSFT	106	1.00	2.00	1.04±0.03[d]
Gumz	93	1.00	2.83	1.47±0.04[b]
Rutana	97	1.00	3.50	1.76±0.03[a]
Begayit	102	1.00	2.00	1.26±0.04[c]
parity				***
1	125	1.00	2.00	1.13±0.03[c]
2	145	1.00	3.00	1.22±0.03[b]
3	134	1.00	3.00	1.25±0.03[b]
4	105	1.00	3.50	1.28±0.03[b]
5	72	1.00	3.60	1.25±0.04[b]
>=6	43	1.00	2.83	1.51±0.05[a]

***= significant at P<0.001, different letters with the same column with the same class indicates significant differences

CHAPTER -5

5. Correlation, regression and multivariate analysis

5.1. Correlation of body weight with other linear body measurements

Chest girth, tail length, pelvic width and body length had positive and significant correlation coefficient ($P<0.001$) with body weight for Afar sheep populations. Chest girth, chest depth, tail length and body length had positive and significant correlation ($P<0.001$) with body weight for Tumele sheep. Except for ear length, all linear body measurements had positive and significant correlation coefficient ($P<0.001$) with body weight for SSFT sheep populations. The largest value of the correlation coefficient was observed between body weight and chest girth in all fat-tailed sheep populations (Afar, Tumele and SSFT). Ear length was not associated with body weight in Afar and SSFT female sheep populations. Rump length and pelvic width were not associated with body weight for Tumele sheep populations. The second largest correlation coefficient was observed between body weight and pelvic width for Afar sheep, between body weight and chest depth for Tumele sheep populations and between body weight and body length for SSFT sheep breeds. The correlation coefficient value ranges from $r= 0.11$ for ear length to $r=0.57$ for chest girth, $r=0.04$ for rump height to $r=0.72$ for chest girth and $r=0.18$ for ear length to $r=0.73$ for chest girth for Afar, Tumele and SSFT female sheep, respectively (Table 10).

The correlation coefficient observed in thin-tailed female sheep populations was strongly positive and significant ($P<0.001$) between body weight and other linear body traits except for ear length in the case of Rutana and Begayit (Table 10). The highest positive correlation coefficient in thin-tailed female sheep breed was observed between body weight and chest girth with a value of 0.85, 0.79 and 0.73 for Gumz, Rutana and Begayit, respectively. The second

highest value of the positive correlation coefficient observed between body weight and chest depth for Gumz and Rutana female sheep and between body weight and pelvic width for Begayit sheep breed.

Table 10. Pearson correlation of female body weight with other body linear measurements of fat-tailed and thin-tailed sheep populations.

	Fat-tailed			Thin-tailed		
Traits	Afar	Tumelle	SSFT	Gumz	Rutana	Begayit
N	111	122	112	104	115	95
Tail Length	0.33***	0.38***	0.43***	0.57***	0.33***	0.40***
Chest Depth	0.21*	0.39***	0.58***	0.81***	0.65***	0.55***
Rump Height	0.22*	0.28**	0.41***	0.65***	0.46***	0.51***
Rump Length	0.20*	0.04NS	0.51***	0.51***	0.45***	0.47***
Ear Length	0.11^{NS}	0.21*	0.18^{NS}	0.48***	0.17^{NS}	0.15^{NS}
Body Length	0.31***	0.32***	0.63***	0.74***	0.46***	0.45***
Chest Girth	0.57***	0.72***	0.73***	0.85***	0.79***	0.73***
Wither Height	0.19*	0.28**	0.45***	0.77***	0.55***	0.35***
Pelvic Width	0.38***	0.13NS	0.32***	0.67***	0.48***	0.61***

NS= not significant, *=p<0.05, **=p<0.01 and ***=p<0.001

The correlation coefficient value ranges from r=0.48 for ear length to r=0.85 for chest girth, r=0.17 for ear length to r=0.79 for chest girth and r=0.15 for ear length to r=0.73 for chest girth for Gumz, Rutana and Begayit female sheep populations, respectively.

5.2. Multiple regression analysis and models for predicting body weight

These regression models were determined using stepwise multiple regression analysis. All nine body measurements were fitted into the model and through stepwise elimination procedure, five of the body measurements (wither height, rump length, ear length, rump height, and tail length) were observed unfit for the overall models in Rutana sheep breed. Major body measurements that were best fit for the pooled model in Rutana sheep were chest depth, pelvic width, body length and chest girth with a coefficient of determination (R^2) value in the range of 41-53% of the live body weight in Rutana sheep. Chest depth is the first best-fit entry for all prediction equations for overall Rutana breed which has a coefficient of determination value (R^2) 41%. Chest depth is contributed to the largest total variation of the body weight of Rutana female sheep populations as presented in Table 11. This indicated that chest depth is the best variable to predict the body weight of mature Rutana female sheep. The best-fit entry was selected based on the larger value of the coefficient of determination (R^2), a low value of mallow's CP criteria and low value of mean square error (MSE). The best regression model for overall sheep ≥ 2 years age of Rutana female sheep is as follow: $BWT = \alpha + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4$

$$BWT = -44.28 + 0.80CD + 0.84PW + 0.38BL + 0.24CG$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.80)$, $\beta_2(0.84)$, $\beta_3(0.38)$, $\beta_4(0.24)$= the coefficient of chest depth, pelvic width, body length, and chest girth $x_1, x_2, x_3 \, and \, x_4$ = measurement of chest depth, pelvic width, body length and chest girth, respectively.

Body measurements best fit for the model in Gumz sheep were chest girth (CG), body length (BL), ear length (EL) and chest depth (CD with coefficient of determination (R^2) value in the

range of 75-82% of the live body weight in Gumz sheep populations. Body measurements (rump length, rum height, pelvic width, wither height and tail length) were observed unfit for the overall models in Gumz sheep populations. The chest girth is the first variable entered into the model and explained 75% of the total variation of body weight in matured Gumz female sheep breed. This indicated that chest girth alone is the best predictor for the body weight of mature Gumz female sheep. The best regression model for overall mature sheep ≥ 2 years age of Gumz sheep is as follow: $BWT = \alpha + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4$

$$BWT = -74.38 + 0.84CG + 0.50BL + 0.72EL + 0.25CD$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.84)$, $\beta_2(0.50)$, $\beta_3(0.72)$, $and\ \beta_4(0.25)$ = the coefficient of chest girth, body length, ear length, and chest depth and x_1, x_2, x_3, and x_4 = measurement of chest girth, body length, ear length and chest depth, respectively.

Body measurements that were best fitted for the model of Begayit female sheep were chest girth and rump height with the coefficient of determination (R^2) value in ranges from 52% to 58% of the live body weight of Begayit sheep. The majority of the body measurements that were unfit for the models of Begayit sheep were tail length, pelvic width, rump length, ear length, wither height, chest depth and body length. The first variable entered into the model is chest girth and the second-best variable entered into the model is rump height for matured Begayit female sheep. The chest girth alone accounted that 52% of the total variation of body weight of Begayit female sheep. The best regression model for overall mature Begayit sheep is as follow:

$$BWT = \alpha + \beta_1 x_1 + \beta_2 x_2$$

$$BWT = -41.72 + 0.76CG + 1.17RH$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.76)\ and\ \beta_2(1.17)$= the coefficient of chest girth, rump height and $x_1 and\ x_2$ = measurement of chest girth and rump height, respectively.

The regression model for the estimated body weight of thin-tailed sheep breed by age group is presented in Table 12. The regression model for the estimate body weight of 2PPI age group of Rutana sheep had derived two prediction equations which had a coefficient of determination (R^2) value 76% and 84%. The best-fit entry was chest girth and pelvic width. The 3PPI age group also had three regression models derived with a coefficient of determination (R^2) value 61%, 67% and 71%. The variables entered into the models were chest depth, body length and pelvic width. The first variable entered into the model was chest depth and it was explained 61% of the total variation of body weight of Rutana. The age group of 4PPI of Rutana female sheep had only one regression model with a coefficient of determination (R^2) value 55%. The best variable entered into the model was chest girth and accounted for 55% of the total variation of the body weight of the 4PPI age group of Rutana female sheep.

The best entry variables for the regression model of the 2PPI age group of Gumz female sheep breed were chest girth and body length. Best fit entry for 3PPI age group of Gumz female sheep was chest depth and chest girth. Age group 4PPI of Gumz sheep had three regression model which had the best fit entry of chest girth, ear length and chest depth. The value of the coefficient of determination (R^2) in all age groups in the range of 65% to 81%. The first best entry variables for age group 2PPI and 4PPI chest girth which explained 73% and 65% of the total variation of body weight of age group 2PPI and 4PPI of Gumz female sheep populations, respectively. Chest

depth was the first entry for age group 3PPI Gumz female sheep and accounted for 75% of the total variation of body weight of 3PPI age group Gumz female sheep breed.

The Begayit female sheep breed had 2, 1 and 2 regression models for 2PPI, 3PPI and 4PPI age group, respectively. For all age group, chest girth was the first best entry in the regression model. The chest girth was the first best entry in the model and accounted for 72%, 21%, and 73% of the total variation of body weight of age group 2PPI, 3PPI and 4PPI of Begayit female sheep breed, respectively. The second best-fit entry for age group 2PPI and 4PPI was pelvic width. The actual body weight and predicted body weight were almost similar for all thin-tailed sheep populations. The inclusion of variables in the model, increased the coefficient of determination (R^2) and reduce the value of CP criteria and mean square error.

The summary results of stepwise linear regression analysis to predict body weight of fat-tailed sheep populations using the prediction equations developed from linear body measurements is presented in Table 13. The linear body measurements that were best fit for the models of Afar, SSFT and Tumele sheep populations were chest girth, body length, pelvic width, tail length and wither height with a coefficient of determination (R^2) value in ranges of 26%-46%, 52%-64% and 51%-62%, respectively. The chest girth was the first entry and explained 26%, 52% and 51% of the total variation of body weight in the regression model of Afar, SSFT and Tumele female sheep populations. The coefficient of determination value of Afar sheep was lower than 50% compared to the other sheep populations.

Table 11. Stepwise Multiple Linear Regression analysis for Estimation of Live Body Weight, from Body Measurements, Determination Coefficient (R^2), CP, and Least Square Mean of Actual and Predicted Value of thin-tailed Sheep populations.

Populations	step	entered	Prediction equations	ABWT	PBWT	R^2	C(P)	MSE	F-value	Pr>F
Rutana	1	CD	-9.64 + 1.34CD	43.78	39.89	0.41	24.67	23.02	80.38	<0.0001
	2	CD, PW	-24.83 + 1.15CD + 1.37PW		39.56	0.48	10.70	20.51	14.96	0.0002
	3	CD, PW, BL	-37.33 + 1.01CD + 1.22PW + 0.35BL		39.01	0.51	7.18	19.75	5.36	0.0224
	4	CD, PW, BL, CG	-44.28 + 0.80CD + 0.84PW + 0.38BL+ 0.24CG		43.87	0.53	2.91	18.84	6.39	0.0128
Gumz	1	CG	-57.71 + 1.21CG	36.15	35.86	0.75	42.18	18.26	318.42	<.0001
	2	CG, BL	-74.92 +0.94CG + 0.71BL		36.46	0.79	18.25	15.18	22.67	<.0001
	3	CG, BL, EL	-73.76+ 0.93CG + 0.55BL + 0.68EL		36.69	0.81	11.87	14.27	7.80	0.0062
	4	CG, BL, EL, CD	-74.38+ 0.84CG + 0.50BL + 0.72 EL + 0.25CD		36.03	0.82	8.84	13.76	4.85	0.0298
Begayit	1	CG	-37.86 + 0.95CG	39.79	39.63	0.52	17.39	14.78	109.93	<.0001
	2	CG, PW	-41.72 + 0.76CG + 1.17PW		39.64	0.58	6.78	13.30	12.15	0.0007

ABWT=actual body weight, PWBT=predicted body weight

Table 12. Stepwise Multiple Linear Regression analysis for Estimation of Live Body Weight, from linear Body Measurements, Determination Coefficient (R^2), and CP and Predicted Value of thin-tailed female Sheep populations by age group

Populations	dent	Step	Entered	Prediction equations	ABWT	PBWT	R^2	C(P)	MSE	F-value	Pr>F
Rutana	2PPI	1	CG	-57.87+1.22CG	40.53	43.05	0.76	3.28	6.99	47.66	<.0001
		2	CG, PW	-60.87+0.93CG+1.63PW		40.88	0.84	-0.02	5.05	6.76	0.021
	3PPI	1	CD	-14.95+1.48CD		44.54	0.61	8.19	11.92	61.80	<.0001
		2	CD, BL	-34.54+1.35CD+0.42BL	44.71	44.59	0.67	3.38	10.39	6.74	0.0134
		3	CD, BL, PW	-45.66+1.24CD+0.43BL+0.89PW		44.91	0.71	0.62	9.35	5.24	0.0279
	4PPI	1	CG	-48.47+1.10CG	44.07	44.08	0.55	-3.80	21.07	68.15	<.0001
Gumz	2PPI	1	CG	-51.77+1.14CG	31.87	32.09	0.73	17.75	14.27	97.99	<.0001
		2	CG, BL	-71.69+0.79CG+0.86BL		31.85	0.80	4.72	10.49	14.35	0.0006
	3PPI	1	CD	-54.13+2.46CD	36.04	36.17	0.75	4.14	19.83	96.51	<.0001
		2	CD, CG	-66.76+1.61CD+0.56CG		35.89	0.78	1.99	17.98	4.29	0.0467
	4PPI	1	CG	-53.36+1.16CG		40.60	0.65	21.86	17.96	64.52	<.0001
		2	CG, EL	-59.85+1.01CG+1.44EL	40.89	40.66	0.78	5.13	12.07	17.59	0.0002
		3	CG, EL, CD	-60.25+0.68CG+1.44EL+0.73CD		41.23	0.81	1.76	10.54	5.78	0.0222
Begayit	2PPI	1	CG	-55.67+1.18CG	38.31	38.04	0.72	2.28	11.25	70.08	<.0001
		2	CG, PW	-60.77+0.93CG+1.57PW		38.42	0.78	-1.18	9.35	6.49	0.0171
	3PPI	1	CG	-10.69+0.61CG	39.05	38.98	0.21	-2.34	18.55	10.21	0.0028
	4PPI	1	CG	-48.65+1.08CG	42.00	41.68	0.60	17.47	11.18	46.83	<.0001
		2	CG, PW	-48.11+0.79CG+1.42PW		42.02	0.73	4.57	7.87	14.15	0.0007

The second-best entry variable in the regression model of Afar and SSFT female sheep populations was body length and increased the coefficient of determination (R^2) by 11% for Afar by 9% for SSFT sheep populations. Tail length was the second-best entry in the regression model of Tumele female sheep breed/type and improved the coefficient of determination (from r=0.51 to r=0.59) by 8%. Linear body measurements that were best fit for the model in Afar sheep were chest girth (CG), body length (BL) and pelvic width (PW). Linear body measurements (rump length, rum height, tail length, wither height, and chest depth) were observed unfit for the overall models in Afar sheep populations. The best regression model for overall mature Afar sheep is as follow:

$$BWT = \alpha + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3$$

$$BWT = -31.73 + 0.28CG + 0.42BL + 0.94PW$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.28)$, $\beta_2(0.42)$, and $\beta_3(0.94)$ = the coefficient of chest girth, body length and pelvic width and x_1, x_2, and x_3 measurement of chest girth, body length and pelvic width, respectively.

The linear body measurements that best fit in the regression model of SSFT sheep breed were chest girth, body length, and tail length. Traits that did not fit the regression model of SSFT were chest depth, rump height, rump length, pelvic width, wither height and ear length. The best regression model for overall mature SSFT sheep is as follow:

$$BWT = \alpha + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3$$

$$BWT = -44.73 + 0.58CG + 0.47BL + 0.18TL$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.58)$, $\beta_2(0.47), and\ \beta_3(0.18)$ = the coefficient of chest girth, body length, and tail length and x_1, $x_2, and\ x_3$ measurement of chest girth, body length and tail length, respectively.

The best-fit entry for the regression model of Tumele sheep was chest girth, tail length, body length and wither height. The best-fit regression model for overall Tumele sheep is as follow:

$$BWT = \alpha + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4$$

$$BWT = -24.90 + 0.65CG + 0.21TL - 0.24BL + 0.19WH$$

Where BWT= body weight of individual animals, α= the intercept of the best fit straight line, $\beta_1(0.65)$, $\beta_2(0.21)$, $\beta_3(0.24), and\ \beta_4(0.19)$ = the coefficient of chest girth, tail length, body length, and wither height and x_1, x_2, $x_3\ and\ x_4$ measurement of chest girth, tail length, body length and wither height, respectively.

The prediction equations, the body measurements entered to the model, actual body weight and predicted body weight using the equations, coefficient of determination, CP value and mean square error (MSE) value of the regression model of fat-tailed female sheep breed by age group are presented in Table 18. Linear body measurements that best fit in fat-tailed sheep of age group 3PPI were found chest girth as a single variable and explained 25% the total variation of body weight for 3PPI of Afar. Chest girth and body length are the two variables entered into the 4PPI age group of Afar female sheep which described 61% of the total variation of body weight of 4PPI age group Afar sheep.

Table 13. Stepwise Multiple Linear Regression analysis for Estimation of Live Body Weight, from Body Measurements, Determination Coefficient (R^2), CP, and Least Square Mean of Actual and Predicted Value of thin-tailed female Sheep populations

breed	stp	entered	Prediction equations	ABWT	PBWT	R^2	C(P)	MSE	F-value	Pr>F
Afar	1	CG	-3.71 + 0.35CG		20.12	0.26	10.40	3.35	12.93	0.0009
	2	CG, BL	-22.04 + 0.32CG + 0.43BL	19.77	19.99	0.37	5.92	2.95	6.00	0.0193
	3	CG, BL, PW	-31.73+0.28CG+0.42BL+0.94PW		19.74	0.46	2.32	2.60	5.88	0.0206
SSFT	1	CG	-35.01 + 0.83CG		24.65	0.52	38.39	10.22	113.73	<0.0001
	2	CG, BL	-46.24 + 0.62CG + 0.51BL		24.62	0.61	12.77	8.33	25.28	<0.0001
	3	CG, BL, TL	-44.73 + 0.58CG + 0.47BL + 0.18TL	24.71	25.02	0.64	7.11	7.85	7.45	0.0074
Tumele	1	CG	-22.19 + 0.67CG		26.19	0.51	36.99	8.42	124.32	<.0001
	2	CG, TL	-23.78 + 0.62CG + 0.20TL		26.11	0.59	14.78	7.17	22.03	<.0001
	3	CG, TL, BL	-18.38 + 0.68CG+0.19TL-0.19BL	25.91	25.85	0.60	12.33	6.97	4.16	0.0435
	4	CG, TL, BL, WH	-24.90+0.65CG+0.21TL-0.24BL+0.19WH		27.26	0.62	8.41	6.71	5.75	0.0181

ABWT=actual body weight, PWBT=predicted body weight

Table 14. Stepwise Multiple Linear Regression analysis for Estimation of Live Body Weight, from Body Measurements, Determination Coefficient (R^2), CP, and Least Square Mean of Actual and Predicted Value of thin-tailed female Sheep populations

populations	step		Entered	Prediction equations	BWT	EBWT	R^2	C(P)	MSE	F-value	Pr>F
Afar	3PPI	1	CG	1.40+027CG	19.68	19.46	0.25	0.41	4.28	4.65	0.049
	4PPI	1	CG	-34.43+0.79CG	19.97	20.11	0.47	3.70	2.37	16.56	0.0007
		2	CG, BL	-46.83+0.68CG+0.42BL		19.82	0.61	0.29	1.84	6.39	0.0211
SSFT	2PPI	1	BL	-27.25+1.01BL	23.78	23.93	0.44	14.08	12.21	27.91	<.0001
		2	BL, CG	-41.16+0.72BL+0.41CG		24.19	0.54	8.02	10.42	7.03	0.0121
	3PPI	1	CD	-27.30+1.47CD	25.25	25.03	0.67	0.40	11.50	22.59	0.0006
	4PPI	1	CG	-39.46+0.89CG	25.29	25.33	0.59	18.01	7.58	80.89	<.0001
		2	CG, BL	-48.82+0.76CG+0.37BL		25.69	0.64	10.50	6.71	8.39	0.0054
		3	CG, BL, TL	-44.07+0.65CG+0.34BL+0.21TL		25.25	0.67	7.07	6.25	5.24	0.0273
Tumele	2PPI	1	CG	-10.81+0.50CG	24.33	24.24	0.30	7.44	6.68	23.69	<.0001
		2	CG, TL	-10.85+0.45CG+0.15TL		24.54	0.35	4.45	6.25	4.86	0.0317
	3PPI	1	CG	-33.40+0.82CG	27.47	27.30	0.56	12.72	10.01	46.42	<.0001
		2	CG, TL	-28.90+0.67CG+0.27TL		27.78	0.65	5.57	8.28	8.52	0.0061
	4PPI	1	CG	-16.47+0.59CG	27.24	27.27	0.44	12.86	9.75	18.88	0.0002
		2	CG, TL	-22.68+0.60CG+0.22TL		27.24	0.59	5.81	7.53	8.06	0.0093
		3	CG, TL, RL	-35.22+0.64CG+0.19TL+0.49RL		27.24	0.69	1.53	5.96	7.07	0.0143

Body length was the first entry for the 2PPI age group of SSFT which explained alone 44% of the total variation of body weight in the model. The second-best entry variable in the 2PPI age group of SSFT sheep breed was chest girth and improved the coefficient of determination (R^2) to 54%. A regression model that had a large value coefficient of determination (R^2), a low value of mallow's C(P) and mean square error selected as best models. The actual body weight and estimated body weight in each breed and age group had a closely similar value.

5.3. Multivariate analysis of quantitative traits

The principal component analysis has shown that the first two PC explained more than 83 % of the total variation (Table 15). The first principal component accounted for 75% of the total variation and the second PC explained 8% of the total variation. All traits were contributing to PC1 and had a positive value. Rump length, pelvic width and chest depth were the most contributing traits to PC2 and had a positive value. The PC1 separates the northwestern thin-tailed sheep from the northeastern fat-tailed sheep population and within a thin-tailed sheep population more intermixing was observed. Within fat-tailed, the PCA analysis showed Afar sheep population had minimum level of intermixing but Tumele and SSFT had high level of intermixing.

Table 15. Eigenvalue, the proportion of variance, eigenvectors and cumulative variance of qualitative traits of the northeastern and northwestern sheep population

Variable	PC1	PC2
Body weight	0.34	-0.22
Tail Length	0.33	-0.3
Chest depth	0.33	0.24
Rump Height	0.33	-0.03
Rump Length	0.27	0.58
Ear Length	0.31	-0.27
Body Length	0.33	-0.01
Chest Girth	0.34	-0.15
Height at Wither	0.34	-0.17
Pelvic Width	0.25	0.59
Eigenvalue	7.50	0.84
Proportion of variance	0.75	0.08
Cumulative	0.75	0.83

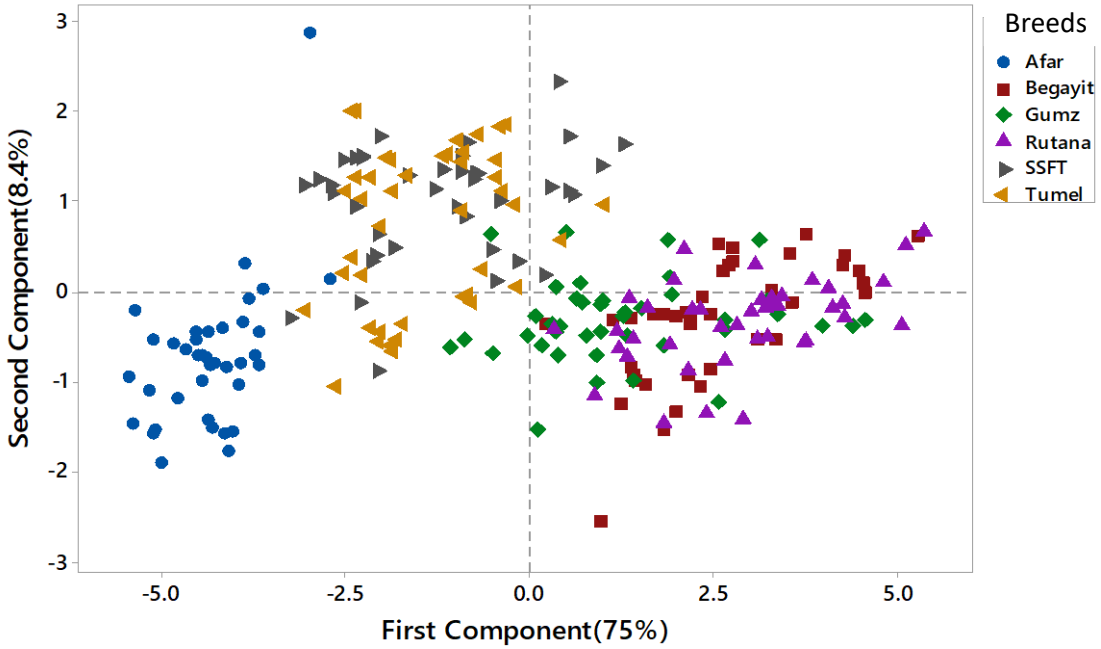

Figure 7. Score plot of quantitative traits northeastern fat-tailed and northwestern thin-tailed sheep populations

The analysis of variance revealed that there were significant differences ($p<0.001$) in morphometric measurements among sheep populations studied. Out of ten variables subjected to the analysis, eight were selected by the stepwise discriminant procedure.

The summary result of the stepwise discriminant analysis is shown in Table 16. The variables pelvic width and body length had not showed significance difference ($P>0.05$) among the studied sheep populations. The stepwise discriminant analysis was significant at ($P<0.01$) for all traits, except rump height. Tail length, rump length, ear length, and body weight were the most discriminating variables among the studied sheep populations. Their respective partial R^2 were 0.84, 0.44, 0.34, and 0.13 and F values 640.52, 91.18, 60.01, and 17.02 with high significant values ($P < 0.0001$). The four morphological variables (tail length, rump length, ear length, and body weight) obtained in the present study are more important and informative and could assign the studied sheep populations into distinct populations.

Table 16. Summary of a stepwise selection of traits

Step	Entered	Partial R-Square	F Value	Pr > F	Wilks' Lambda	Pr < Lambda	Average Squared Canonical Correlation	Pr >ASCC
1	TL	0.84	640.52	<.0001	0.16	<.0001	0.17	<.0001
2	RL	0.44	91.18	<.0001	0.09	<.0001	0.26	<.0001
3	EL	0.34	60.01	<.0001	0.06	<.0001	0.30	<.0001
4	BWT	0.13	17.02	<.0001	0.05	<.0001	0.32	<.0001
5	CD	0.03	3.92	0.002	0.05	<.0001	0.32	<.0001
6	CG	0.03	3.29	0.006	0.05	<.0001	0.33	<.0001
7	RH	0.02	2.48	0.031	0.05	<.0001	0.33	<.0001
8	WH	0.03	3.11	0.009	0.05	<.0001	0.34	<.0001

TL=tail-length, RL=rump length, EL=ear length, BWT=body weight, CD=chest depth, CG=chest girth, RH=rump height, and WH=wither height

The result obtained from the discriminant analysis has shown that the pairwise Mahalanobis distances matrix between populations are shown in Table 17. The

pairwise distance between populations was highly significant (P < 0.001). The greatest Mahalanobis distance was observed between Afar and Begayit (58.24) and followed by between Afar and Rutana (57.44). The least Mahalanobis distance was observed between Rutana and Begayit (1.08) and between small short fat-tailed (SSFT) and "Tumele" sheep populations (3.15).

Table 17. Mahalanobis distance between fat-tailed and thin-tailed sheep populations

Populations	Thin-tailed			Fat-tailed		
	Begayit	Gumz	Rutana	Afar	SSFT	Tumele
Begayit		6.62	1.08	58.24	33.86	30.65
Gumz	***		5.16	29.44	12.97	11.45
Rutana	***	***		57.44	32.16	29.84
Afar	***	***	***		10.24	5.16
SSFT	***	***	***	***		3.15
Tumele	***	***	***	***	***	

***=Significant at 0.001

The number of observation and proportion of correct classification and misclassification of the cross-validated observations were recorded as shown in Table 18. The proportion of the cross-validation classification results in 60.8%, 62.4%, 51.7%, 88%, 76.8%, and 68.5% of Begayit, Gumz, Rutana, Afar, SSFT, and Tumele population were correctly assigned into their source of genetic group. The value morphological distance between the fat-tailed populations and thin-tailed population coupled with a value correct assignment to source genetic groups indicates that they belong to different populations.

Table 18. Cross validation table that shows the number of observations and percent of individual sheep classified into their own source of breeds/ populations

Breeds/ Populations	Fat-tailed			Thin-tailed			Total
	Afar	SSFT	Tumele	Begayit	Gumz	Rutana	
Rutana	0(0.00)	0(0.00)	0(0.00)	34(29.31)	22(18.97)	60(51.72)	116(100)
SSFT	8(7.14)	86(76.79)	15(13.39)	0(0.00)	3(2.68)	0(0.00)	112(100)
Afar	103(88.03)	6(5.13)	8(6.84)	0(0.00)	0(0.00)	0(0.00)	117(100)
Begayit	0(0.00)	0(0.00)	0(0.00)	62(60.78)	7(6.86)	33(32.35)	102(100)
Gumz	0(0.00)	2(1.83)	11(10.09)	7(6.42)	68(62.39)	21(19.27)	109(100)
Tumele	7(5.51)	23(18.11)	87(68.50)	0(0.00)	10(7.87)	0(0.00)	127(100)
Total	118(17.28)	117(17.13)	121(17.72)	103(15.08)	110(16.11)	114(16.69)	683(100)
Error rate	0.12	0.23	0.32	0.39	0.38	0.48	0.32
Priors	0.1713	0.1640	0.1859	0.1493	0.1596	0.1698	

The scatter plot of the six populations built based on the morphometric measurements using multivariate discriminant analysis was showed two main clusters. The first one was formed by fat-tailed sheep and the second one by thin-tailed sheep populations. The first group further classified into two groups and Afar sheep purely isolated from fat-tailed group while SSFT and Tumele had some intermix. Similarly, from thin-tailed group Gumz sheep isolated with few intermix with Rutana. Rutana and Begayit sheep were highly intermixed as shown in Figure 8. This result similar to the result of multiple correspondence analyses using qualitative traits in the previous section except for Afar and Tumele closer than SSFT and Tumele in the correspondence analysis.

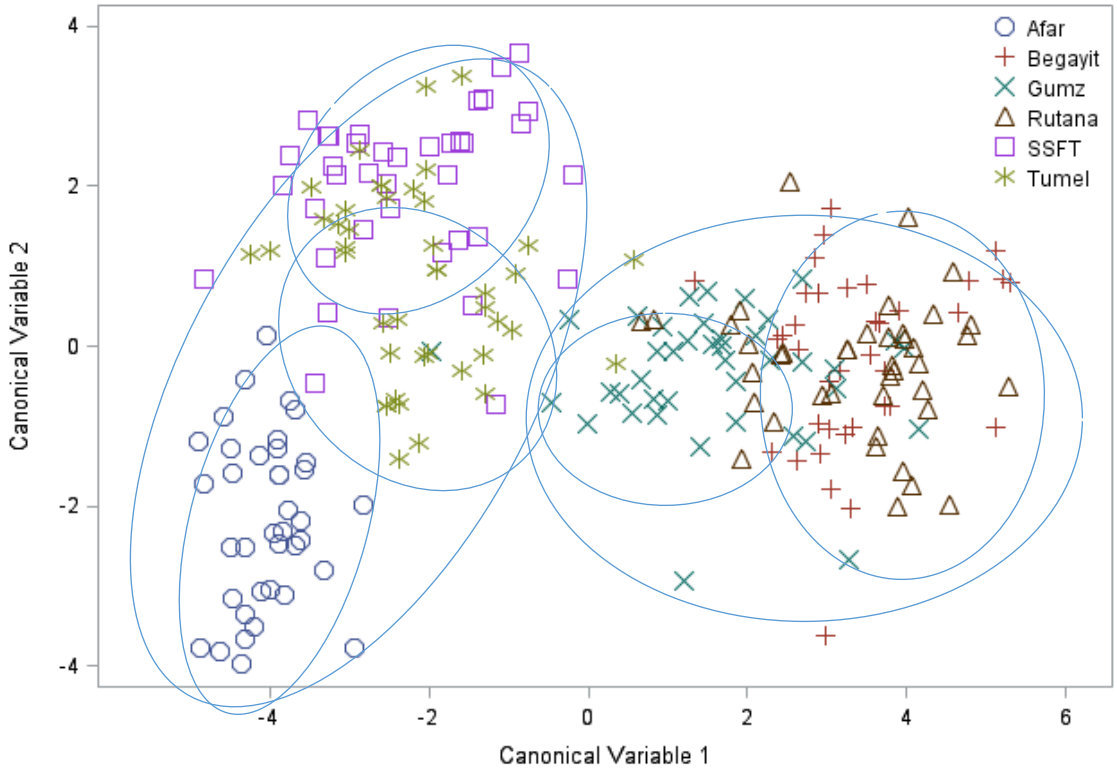

Figure 8. The scattered plot showed the classification of sheep populations based on the discriminant analysis of quantitative traits of fat-tailed and thin-tailed sheep populations.

The dendrogram based on seven quantitative traits of body length, chest girth, tail length, rump height, rump length, pelvic width and chest depth shown in Figure 10. The cluster analysis based on quantitative traits showed two major clusters that isolated fat-tailed and thin-tailed sheep populations. Both fat-tailed and thin-tailed clusters was further divided into two clusters and the first cluster includes SSFT sheep breed and the second includes the fat-tailed grouped (Afar and Tumele), Similarly, Gumz sheep breed was separated from the thin-tailed sheep populations (Rutana and Begayit). The cluster analysis of qualitative traits and correspondence analysis of qualitative traits are varied from cluster analysis based on quantitative traits, discriminant analysis and PC analysis of quantitative traits in which Tumele sheep closer to Afar but in the quantitative traits cluster analysis, discriminant and PC analysis Tumele population closer to SSFT breed.

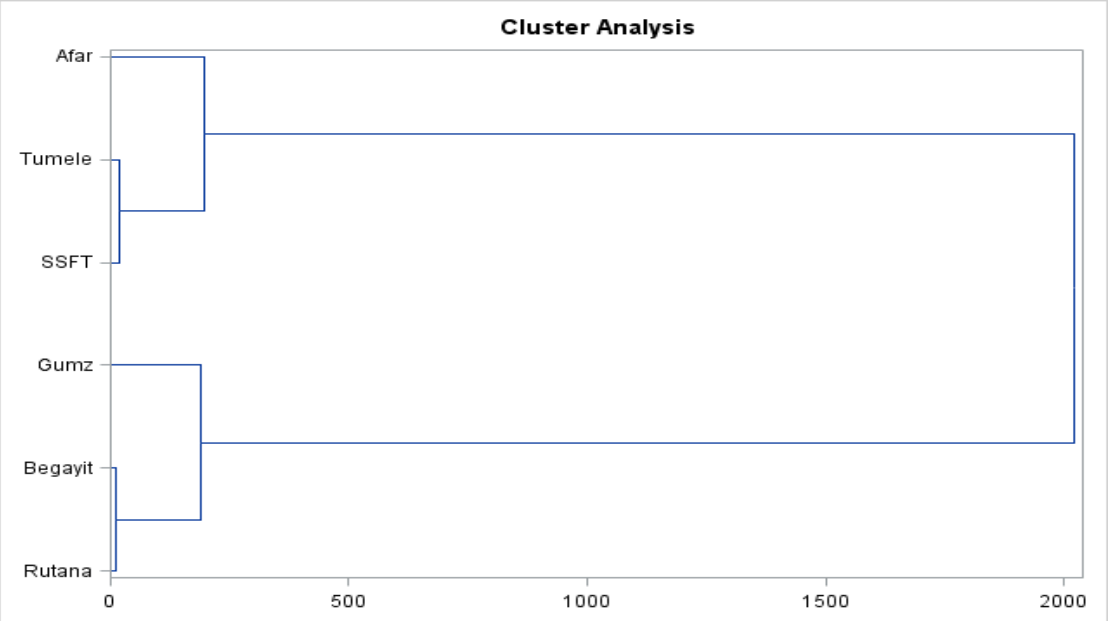

Figure 9. Dendrogram built based on seven quantitative traits of hierarchical clustering of fat-tailed and thin-tailed sheep populations of Ethiopia

CHAPTER-6

6. Genetic diversity and population structure

6.1. Genetic variation within populations

Sample-based quality control resulted in the exclusion of 28 samples due to their poor genotyping call rate. The excluded samples from the fat-tailed group were: 3 Afar, 3 Tumele, and 6 SSFT, and 5 Begayit, 7 Gumz and 4 Rutana from thin-tailed group. A genotyping call rate range from 96.2% to 99.8% for the rest of the sample. Minor allele frequency (MAF) analysis for all the sheep populations were ranged from 0.00 to 0.258 (Table 19). The distribution and percent of SNPs of the minor allele frequency of fat-tailed and thin-tailed sheep populations show that about 15% of the SNPs across all populations had low variability (MAF <0.1) and above 46% of SNPs are highly variable (MAF>0.3). The highest variability of SNPs was observed in Rutana sheep (50.79%) and the lowest variability was observed in SSFT (45.9%).

Genetic diversity within each of the six populations was assessed by estimating the percentage of polymorphic SNPs (pn), the observed and expected heterozygosity. The proportion of polymorphic loci within a breed ranged from 0.94 for (Afar and SSFT) to 0. 96 (Tumele and Rutana), with a mean of 0.95. The average relatedness between individual pairs, based on the proportion IBD was calculated as 0.8%, 0.7%, 3.5%, 0.5%, 0.8% and 0.5% for Afar, Tumele, SSFT, Gumz, Rutana and Begayit populations, respectively.

Table 19. Distribution and SNP proportion (%) of minor allelic frequency of the studied sheep populations of Ethiopia

MAF	Afar	Tumele	SSFT	Gumz	Rutana	Begayit	Overall mean
0	3.11	1.39	5.74	1.94	1.26	2.34	2.63
>0≤0.05	4.99	5.76	6.36	6.1	4.27	5.69	5.53
>0.05≤0.1	8.01	7.21	6.35	6.52	7.47	6.22	6.96
>0.1≤0.2	17.7	16.61	16.07	17.57	17.41	17.19	17.09
>0.2≤0.3	18.59	20.33	19.58	18.66	18.8	21	19.49
>0.3≤0.4	23.65	24.54	20.88	24.56	25.01	23.76	23.73
>0.4≤0.5	23.95	24.16	25.02	24.65	25.78	23.8	24.56

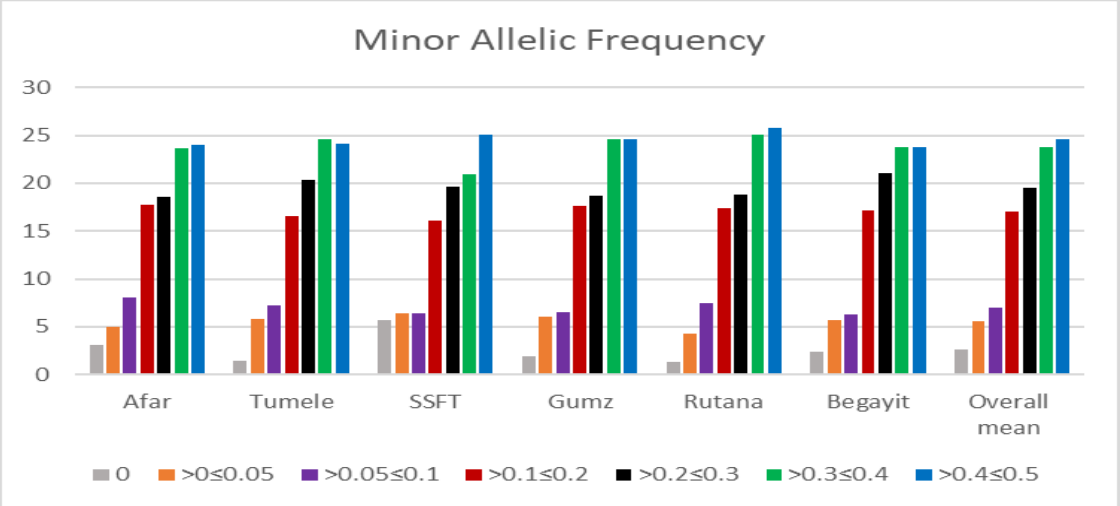

Figure 10. Graphical presentation of the distribution of minor allelic frequency of fat-tailed and thin-tailed sheep breed of Ethiopia.

Mean number of gene copies/haplotype per locus, observed heterozygosity, expected heterozygosity, relatedness (PI_HAT), and inbreeding coefficient of the studied sheep populations calculated are presented in Table 20. The results of proportion of

polymorphic SNPs in each population, observed heterozygosity and expected heterozygosity showed variation among the populations. The highest haplotype or number of gene copy was recorded in Tumele and the lowest in SSFT. The observed heterozygosity was 0.36 ± 0.15 for Begayit and Gumz, and 0.37 ± 0.15 for Rutana, Afar, Tumele and SSFT. The expected heterozygosity values were 0.37 ± 0.14 for Begayit, Gumz, Afar and SSFT and 0.38 ± 0.14 for Rutana and Tumele. The expected heterozygosity slightly higher than the observed heterozygosity for Begayit, Rutana, Gumz and Tumele sheep population but the value of observed heterozygosity and expected heterozygosity for Afar and SSFT sheep breeds similar. All populations demonstrated positive FIS values and slightly higher in thin-tailed sheep. The FIS value ranged from 0.004 (Afar) to 0.032 (Begayit).

Table 20. Proportion of polymorphic SNPs (PN), mean number of gene copies (H), observed heterozygosity (Ho), expected heterozygosity (He), and inbreeding coefficient (FIS) of the studied populations

Breed/	N	PN	H (M±STD)	Ho (M±STD)	He (M±STD)	PI-HAT	FIS
Begayit	34	95	67.95±0.623	0.36±0.15	0.37±0.14	0.005	0.032
Gumz	33	95	69.68±1.141	0.36±0.15	0.37±0.14	0.005	0.022
Rutana	40	96	75.84±0.85	0.37±0.15	0.38±0.14	0.008	0.029
Afar	38	94	75.98 ±0.20	0.37±0.16	0.37±0.14	0.008	0.004
Tumele	40	96	81.92±0.77	0.37±0.15	0.38±0.13	0.007	0.017
SSFT	32	94	63.89±0.74	0.37±0.15	0.37±0.14	0.035	0.01
Overall Mean	217	95	72.54±0.72	0.37±0.15	0.37±0.14	0.007	0.019

M=mean and STD=standard deviation

6.2. Genetic variation between populations

The results of molecular variance analysis revealed that the greatest variation existed within individuals across the whole populations (93.37%) as presented in Table 21. Molecular variance among individuals within populations, among populations within groups and among groups were low (1.83%, 2.63%, and 2.17%), respectively.

Table 21. Analysis of molecular variance of Ethiopian sheep populations grouped based on tail phenotype from analysis of SNPs analysis.

Source of variation	d.f.	Variance components	Percentage of variation
Among Group (fat-tailed and thin-tailed)	1	60.07	2.17
Among populations within groups	4	72.99	2.63
Among individuals within populations	211	50.69	1.83
Among individuals within across the whole population	217	2589.17	93.37
Total	433	2772.91	

The degree of genetic differentiation between pairs of populations is shown in Table 22. F_{ST} values for all pairs of populations were also significantly different from zero ($P<0.001$). The highest F_{ST} values were observed between Begayit and Afar (F_{ST} = 0.062) followed by between Begayit and SSFT (F_{ST}=0.059) populations, while the lowest value was observed between Afar and Tumele populations (F_{ST} = 0.015). Tumele sheep population had closer distance with Afar sheep breed (F_{ST}=0.015). Similarly, in the thin-tailed sheep populations, the highest genetic differentiation value was between Begayit and Gumz (F_{ST}=0.035) and the lowest between Gumz and Rutana (F_{ST}=0.022).

Table 22. Pairwise genetic differentiation ($F_{ST)}$ between studied fat-tailed and thin tailed sheep populations. (F_{ST} value below diagonal and significant level above diagonal)

Populations	Fat-tailed			Thin-tailed		
	Afar	Tumele	SSFT	Begayit	Gumz	Rutana
Afar	0.00	***	***	***	***	***
Tumele	0.015	0.00	***	***	***	***
SSFT	0.053	0.017	0.00	***	***	***
Begayit	0.062	0.046	0.059	0.00	***	***
Gumz	0.056	0.038	0.048	0.035	0.00	***
Rutana	0.049	0.034	0.047	0.025	0.022	0.00

*** = significance at P<0.001

6.3. Population structure and admixture

The first principal component axis shows the separation of thin-tailed and fat-tailed sheep and a substantial overlap within each group. PC1 explains 5 % of the total variation in the sample, whereas the second principal component accounted for 3.3% of the total variation. The PCA result shows a considerable intermixing within the thin-tailed and fat-tailed population. The first three principal components explained 10.7% of the total variation (Figure 11). Mixed population in the PCA plot key represented Tumele sheep populations.

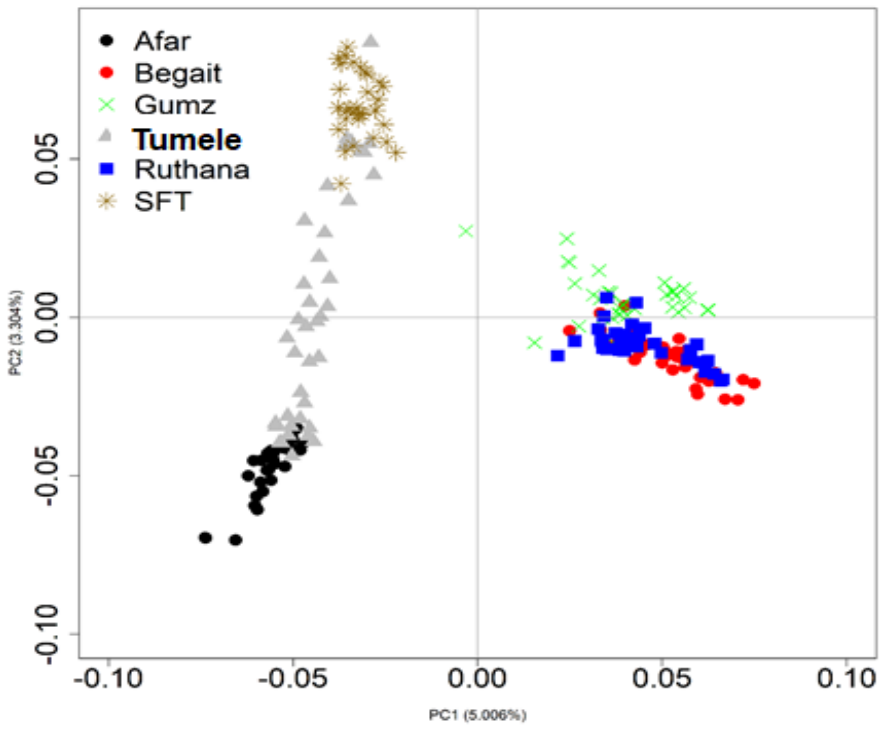

Figure 11. Principal component analysis (PCA) of six sheep populations based on LD bead chips SNPs

The best fitting number of subpopulations present in the total sample was five (Figure 12). A graphic presentation of the estimated membership coefficients to the clusters is shown in Figure 14, where model-based clustering partitioned the genome of each sample into a predefined number of components. Proportion of membership of each of the six-predefined populations in each of the five-inferred populations obtained from admixture analysis indicated that Afar breed 89.3% and SSFT sheep breed 89% were pure and they are the only populations with the minimal level of admixture while thin-tailed Northwestern sheep population and Tumele sheep in the northeastern region has shown a higher level of admixture which is consistent with its crossing with other populations.

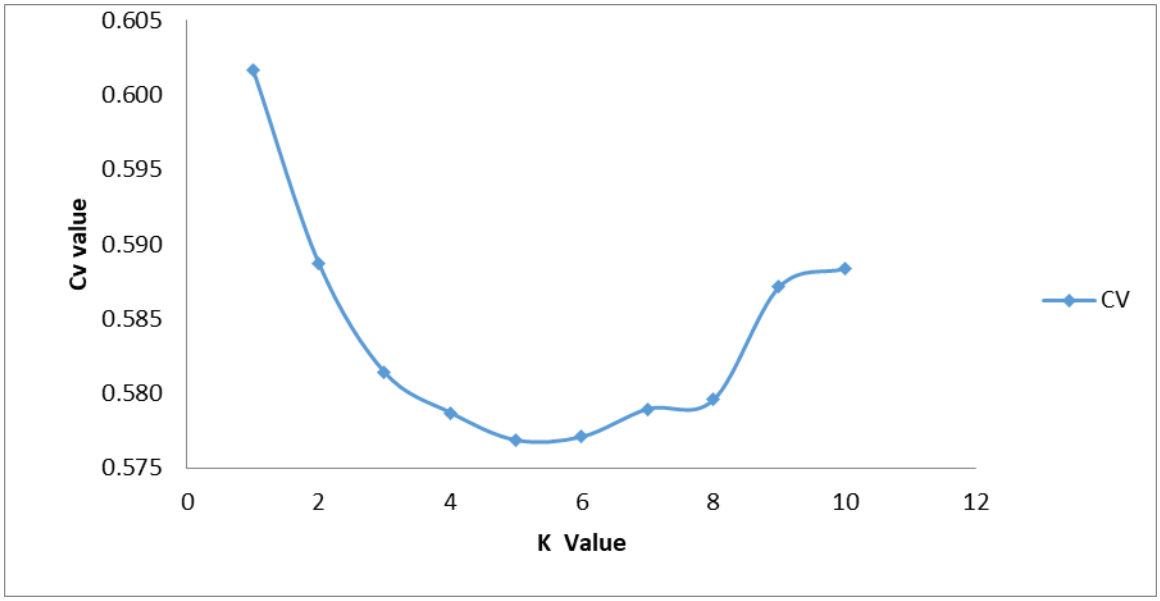

Figure 12. Cross-validation error plot indicating the K value for the optimum inferred populations

Genetic structure of Tumele sheep showed 48.9% admixture with Afar and 45.7% from SSFT at K=5. This indicates that Tumele sheep is hybrid of Afar and SSFT populations. Most thin-tailed sheep populations showed high admixture with some pure individual populations are present in each group. The proportion of membership in Table 23 indicates that Gumz sheep admixture of Rutana (12.9%,) Begayit (12.1%) and SSFT (13.8%). Similarly, Rutana sheep breed is intermixed 17.8% with Begayit, 18.2% with Gumz and nearly 10% with SSFT and Afar sheep. The Begayit population is over 38% intermixed with Rutana and Gumz.

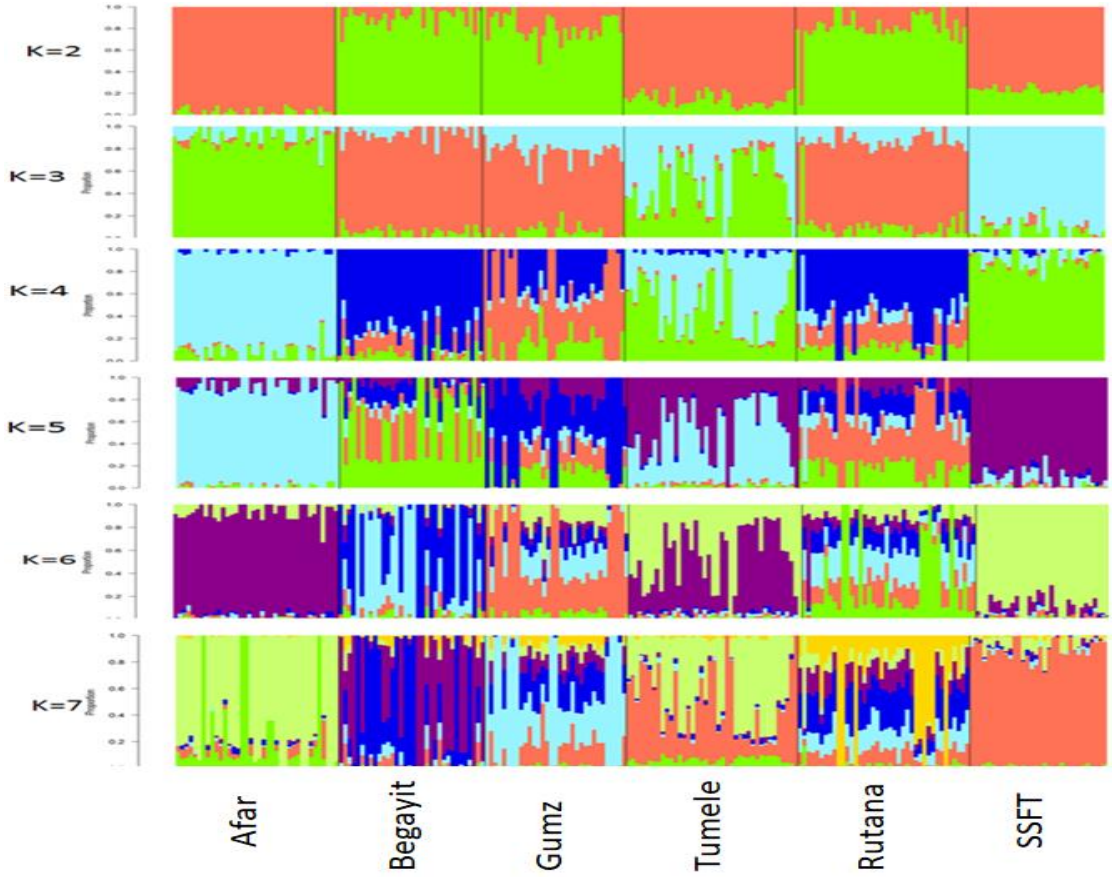

Figure 13. Graphs presenting the genetic structure of sheep populations of fat-tailed and thin-tailed sheep populations of Ethiopia.

Table 23. The proportion of membership of each of the six-predefined populations in each of the five-inferred populations obtained from admixture analysis.

Predefined populations	**Inferred populations**				
	1	**2**	**3**	**4**	**5**
Afar	0.007	0.015	**0.893**	0.010	0.073
Tumele	0.014	0.019	**0.489**	0.018	**0.457**
SSFT	0.014	0.010	0.068	0.017	**0.890**
Gumz	**0.129**	**0.121**	0.055	**0.557**	**0.138**
Rutana	**0.442**	**0.178**	0.098	**0.182**	0.099
Begayit	**0.211**	**0.571**	0.045	**0.123**	0.050

CHAPTER-7

7. Discussion

7.1. Description of morphological traits of the studied sheep populations

Knowing morphological character and their variations among and within sheep populations is an alternative tool in conservation and breeding programs (Carneiro *et al.*, 2010; FAO, 2012). Ogah *et al.* (2011) defines phenotypic variability as the observable variation in a population, this includes both genotypic and environmental components. The morphological trait analysis of fat-tailed sheep populations in the present study had plain followed by patchy coat color pattern. The coat color pattern in SSFT sheep breed in the present study is in agreement with the previous result reported for Menz sheep by Tesfaye Getachew (2008). Tassew Mohammed *et al.* (2014) also studied the sheep population of Gubalafto district and found that plain dominate coat color pattern followed by patchy. Farata sheep categorized within small short fat-tailed sheep breed had plain (54.9%), spotted (29.5%) and patchy (15.6%) coat color patterns (Tewodros Bimerow *et al.*, 2011). The dominant coat colors observed in SSFT female sheep found in the current study is similar with previous report on Menz sheep by (Tesfaye Getachew, 2008). On the contrary, the previous study on Wollo Tikur sheep which is sheep population categorized in SSFT breed, reported by Tassew Mohammed *et al.* (2014) deviated from the current results. Farata sheep categorized within the same breed also have many color types to which white coat color was relatively frequent in both males and females (Tewodros Bimerow *et al.*, 2011).

Coarse hair type observed in SSFT sheep breed is in agreement with the hair type reported for Farta sheep (96.6%) and Menz sheep (98.8%) (Solomon Gizaw *et al.*,

2008b; Tesfaye Getachew, 2008; Tewodros Bimerow *et al.*, 2011). But it varies from the Afar and thin-tailed sheep in the current study. These variations might be explained by the fact that SSFT sheep are characterized by long fleece with coarse wool type having small body size which are known to be more adapted to cold environments (Solomon Gizaw *et al.*, 2008b; Tesfaye Getachew *et al.*, 2010). Hair type of Afar sheep breed had similar results with the previous result on the same populations (Solomon Gizaw *et al.*, 2008b; Tesfaye Getachew, 2008). Similarly, Begayit sheep population showed similar result with the previous result on the same populations reported by Bewketu Amare *et al.*, (2012). The current study showed that hair type is mostly influenced by the environment where the populations living, populations that found in the cool highland area and middle altitude have coarse hair types and populations live in hot arid and the semi-arid area had short and smooth hair type. Tumele sheep population had both short and smooth and coarse hair type. This might be due to the breeding tract of Tumele found in mid altitude of North and South Wollo and North Shewa zones.

The coat color type observed in Tumele female sheep similar with the previous study on the same breed in Habru Woreda reported by Tassew Mohammed *et.al.* (2014). They found that plain brown and brown dominant patches coat color was the most frequent in female sheep. Koseniuk *et al.* (2018) explained that a large coat color variation in animals is due to both genetic and environmental backgrounds. The preference of farmers for a particular coat color might be associated with socio-cultural practices and market demand (Bosenu Abera *et al.*, 2014).

The current finding on coat color pattern of Afar sheep breed varies with the previous study in the same populations by Tesfaye Getachew (2008) who found that 58.1% patchy, plain 40.6% and rarely spotty (1.3%). This might be due to the variation of specific sampling area, intermixing, difference of farmers' preference for coat color pattern. Moreover, the Afar breed showed minimum intermixing in the current results, this might be contributed to uniform coat color pattern. A breed reared by Afar community may be isolated from other breeds because of isolation of communities due to cultural barriers. The frequent coat color type observed in Afar female sheep varies from the previous report by Tesfaye Getachew (2008) that shows coat color type of the breed was white with red patch along the back (41.9%), plain light red (30.9%), plain white (17.2%) and plain dark red (7%). The coat color type of sheep is changed through time based on farmers' preference and market coat color demand and due to climate change, adaptation, agro-ecology and elevation of the sample site that is why the present observed coat color did not match with previously reported coat color type for the same breed.

The previous study on Gumz sheep by Solomon Abegaz *et al.* (2011) showed similar coat color patterns with the current study for the same populations. The color type observed in Gumz and Rutana sheep similar with the previous study in Gumz sheep breed by Solomon Abegaz *et al.* (2011). Farmers preferred red and brown coat color types in the Abra Jira area due to red and brown coat colors preferred in the marketplace. According to Bosenu Abera *et al.* (2014) the preference of farmers for a particular coat color might be associated with socio-cultural practices and market demand. Dominant coat color could reflect strong selection for animals to meet the preference of market demand. In this area, the majority of the farmers kept pure

Rutana sheep due to farmer's assumption that pure Rutana sheep had a capacity of twining birth rate and fast growth rate. The observed coat color type of Begayit female sheep is in agreement with the previous results reported by Bewketu Amare *et al.* (2012). Coat color diversity observed could be associated with ecological variation, climatic and vegetation differences, thus the findings were in agreement with a suggestion made by Solomon Gizaw *et al.* (2007).

The correspondence analysis of five qualitative traits of the studied populations was used to detect the relationship of breeds. Correspondence analysis is an exploratory data analysis technique for the graphical display multivariate categorical data (Hoffman and Franke, 1986). The current study result showed that strong difference between thin-tailed and fat-tailed sheep breeds. Thin-tailed sheep populations of Begayit and Rutana female sheep was associated with a marked convex head profile and pendulous ear formation. Gumz sheep breed also associated with semi-pendulous ear formation and semi-convex head profile.

The fat-tailed sheep populations were associated with a straight head profile and lateral ear formation. The head profile observed in fat-tailed sheep populations (Afar, Tumele and SSFT) were comparable to the previously reported results on the same animals (Solomon Gizaw *et al.*, 2008b; Tesfaye Getachew, 2008). Tesfaye Getachew (2008) was reported a straight head profile for Afar sheep and Menz sheep which had 98% straight and slightly concave head profile. Solomon Gizaw *et al.* (2008b) also reported a straight head profile for Menz sheep. Contrary to the current result, Tassew Mohammed *et al.* (2014) reported straight (37.3%), concave (51.9%) and convex (10.7%) head profile for Gubalafto sheep populations and straight (33.8%),

concave (57.6%) and convex (8.6%) head profile for Habru Woreda sheep populations. This result also deviates from the current results for the same breed.

Description of the physical characteristics of livestock populations is very important for developing a breeding strategy in a particular production system. Body size parameters of sheep can reflect its growth development, production performance and genetic characteristics (Zhang *et al.*, 2018). According to Afolayan *et al.* (2006) growth usually defined as the increase in size or body weight at a given age is one of the important selection criteria for the improvement of meat animals such as sheep. Size and body conformation are critically important traits to most sheep producing farmers and are probably under strong selection in most breeds (Haren *et al.*, 2018). The value of body weight and linear body measurements of fat-tailed and thin-tailed sheep showed significant ($P<0.05$) variation between populations.

The body weight and linear body measurement of fat-tailed female sheep lower than the thin-tailed sheep breed in the current study. The body weight of female Tumele sheep in the current study was similar to SSFT and higher than Afar breed and lower than thin tailed sheep populations. The value was higher than the value reported for Menz, Afar and Farta sheep (Tesfaye Getachew *et al*., 2010 and Shigdaf Mekuriaw *et al.*, 2013). The current value of body weight of SSFT and Tumele female sheep were lower than the value reported for sheep populations of Sidama-Gedeo (27.6±2.3kg), Kenbata, Tembaro-Hadiya (27.5±6.0kg) Gamogofa (28.0±4.0kg), Wolaita (32.0±5.3kg) and Gurage-Silte (30.8±4.5kg) and (Aberra Melesse *et al.*, 2013) and the value reported for Washera (Shigdaf Mekuriaw *et al.*, 2013).

The current results of Afar sheep lower than the value reported for the same breed (Tesfaye Getachew *et al.*, 2010), for Habru and Gubalafto sheep population{Tassew Mohammed, 2014 #58}, and for sheep population of North Shewa zone of Selale area (Bosenu Abera *et al.*, 2014). It is also lower than the value reported for Menz sheep (20.6±0.15kg) (Tesfaye Getachew, 2008) and the value reported for yearling Farta sheep (20.08±0.73kg) (Shigdaf Mekuriaw *et al.*, 2013). These variations might be explained by the differences of sheep type and management and/or production environments in which the animals were kept and might

The value of body length similar for SSFT and Tumele and lower than the value reported for thin-tailed sheep population and higher than Afar sheep breed in the current study. It was also lower than the value of the body weight reported for Gubalafto and Habru sheep population (Tassew Mohammed *et al.*, 2014) and Gumz breed (Solomon Gizaw *et al.*, 2008b; Solomon Abegaz *et al.*, 2011), Washera (Solomon Gizaw *et al.*, 2008b), Farta (Solomon Gizaw *et al.*, 2008b; Tewodros Bimerow *et al.*, 2011; Shigdaf Mekuriaw *et al.*, 2013), Menz, Afar, and Tikur sheep (Solomon Gizaw *et al.*, 2008b). The value of body length in the present study in Afar sheep was lower than the value reported for the same breed and for Menz sheep (Solomon Gizaw *et al.*, 2008b; Tesfaye Getachew, 2008). It was also less than the value reported for the sheep population of the southern regional state (Sidama-Gedeo, Kenbata, Tembaro-Hadiya, Gamogofa, Wolaita and Gurage-Silte) (Aberra Melesse *et al.*, 2013). The body size and shape are most dominant morphological characteristics influencing adaptation of animals in harsh environment (Berihulay *et al.*, 2019). Animals with longer leg have higher kinetic capacity being more adapted to plain and long tracks with bodies further from the ground to avoid heat radiation

and animals' body close to the ground which may correspond to its adaptations to mountain terrain.

The chest girth value of Afar sheep was lower than SSFT and Tumele sheep in the present study and also lower than previous study for the same breed by Solomon Gizaw *et al.* (2008b) and comparable to the value reported for the same breed by (Tesfaye Getachew *et al.*, 2010). It was lower than the value reported for sheep populations of Gubalafto (Tassew Mohammed *et al.*, 2014). The chest girth value of SSFT and Tumele sheep were slightly lower than the value reported for Washera, Farta and sheep populations of Selale area (Shigdaf Mekuriaw *et al.*, 2013; Bosenu Abera *et al.*, 2014) and higher than the value reported for sheep population of Habru and Gubalafto (Tassew Mohammed *et al.*, 2014), the value reported for Washera, Gumz, Menz, Afar, Tikur and Wollo by (Solomon Gizaw *et al.*, 2008b).

The value of body weight, chest depth, wither height and chest girth of Begayit sheep were higher than the previous result reported by Bewketu Amare *et al.* (2012) for the same breed. But the value of the body length and pelvic width were lower than the previous report. This might be related to the age difference of animals used for data collection and sample size. The value reported for the present study was analyzed from adult animals' ≥2 years of age but the value reported by Bewketu Amare *et al.* (2012) analyzed from animals of 0PPI to 4PPI age group.

The value of body weight of Gumz sheep was higher than the value reported for the same breed (Solomon Gizaw *et al.*, 2008b; Solomon Abegaz *et al.*, 2011) and the value reported for Begayit sheep (Bewketu Amare *et al.*, 2012). But the value of body

length was lower than the result of the previous study. The value of wither height was comparable with the value reported for Washera sheep and higher than the value reported for the same breed by earlier studies (Solomon Gizaw *et al.,* 2008b; Solomon Abegaz *et al.*, 2011) and the value reported for Begayit sheep (Bewketu Amare *et al.*, 2012). The chest girth of Gumz was comparable with the result reported for the same breed (Solomon Abegaz *et al.*, 2011)(Solomon Abegaz *et al.*, 2011) and higher than the result reported for the same breed by (Solomon Gizaw *et al.,* 2008b) and Begayit sheep (Bewketu Amare *et al.*, 2012). Body linear measurement of Gumz sheep has deviated from Begayit and Rutana.

Litter size is defined as the number of offspring born per parturition. It is one of the most important reproductive parameters affecting the productivity of a dam and thereby the profitability of a farm. Litter size varies significantly ($P<0.001$) between fat-tailed and thin-tailed sheep. Fat-tailed sheep had litter size lower than the thin-tailed sheep populations. The litter size of SSFT sheep found in the ranges of the result reported for the same breed by Solomon Gizaw *et al.* (2008b) and it is in agreement with the result reported for Menz sheep by Niftalem Dibessa (1990). The Litter size of Afar sheep breed found in the present study is in agreement with the result reported for sheep populations in pastoral and agro-pastoral production systems by (Wilson, 1986). The lower litter size of fat-tailed sheep might be related to difference of sheep type, production environment and agro-ecology evolved.

The litter size of Gumz sheep found in the current study were higher than the result reported for the same populations by Solomon Gizaw *et al.* (2008b) and Solomon Abegaz *et al.*, (2011). The litter size found in thin-tailed sheep populations was higher

than the result reported for Menz (1.14±0.01) and Horro (1.16±0.01) sheep populations by Berhan and Van Arendonk (2006). Parity had effects on the mean litter size. There was a general increasing trend in litter size with increasing parity of ewe. This might be explained that the lower litter size of younger ewes might be associated with an underdeveloped state of the reproductive futures required successive litter bearing compared with older ewes that have reached physiological maturity.

7.2. Predicting body weight of fat-tailed and thin-tailed sheep populations from linear body measurements

The correlation matrix of body weight and other linear body measurements of female sheep populations of fat-tailed and thin-tailed sheep breed showed positive and significant ($P<0.05$) relationship in most variables. Body weight had a positive and significant ($P<0.05$) correlation coefficient with linear body measurements except for ear length for Afar and SSFT and rump length and pelvic width for Tumele. The observed positive correlations between weight and other body measurements suggested that either of these variables or their combination could provide a good estimate for predicting body weight. Chest girth had positive and highest correlation coefficient with the body weight indicating chest girth is best predictor variables for body weight. Selecting animals for one of these morphological variables, simultaneously improves other variables that have high correlation with it (Kefena Effa *et al.*, 2012). The correlation coefficient of body weight with other linear body measurements of thin-tailed sheep populations showed a positive and strong association except for ear length for Rutana and Begayit sheep. The highest association was observed between body weight and chest girth with r-value of 0.85 for Gumz, 0.79 for Rutana and 0.73 for Begayit sheep breed. The higher association

of body weight with chest girth was possibly due to relatively larger contribution in body weight by chest girth consisting of bones, muscles, and viscera (Thiruvenkadan, 2005) and it can be indicated that chest girth is the best variable for predict the body weight than other linear body measurements. Many scholars reported chest girth was highly associated with body weight in sheep (Tesfaye Getachew *et al.*, 2010; Shigdaf Mekuriaw *et al.*, 2013; Tassew Mohammed *et al.*, 2014).

The correlation coefficient between body weight and other linear body measurements of Afar sheep also ranges from r=0.12 for tail length to r=0.81 for chest girth and for Menz sheep also ranges from r=0.27 for tail length to r=0.82 for chest girth as reported by Tesfaye Getachew (2010). The correlation coefficient between body weight and other linear body measurements of North Wollo sheep populations ranges from r=0.32 rump height to r=0.94 chest girth in female sheep as reported by Tassew Mohammed *et al.,* (2014). Similarly, Shigdaf Mekuriaw *et al.* (2013) also reported correlation coefficient between body weight and other linear body measurements of Washera and Farta local sheep populations and found that r=0.31 for ear length to r=0.85 for chest girth for Washera and r=0.13 for ear length to r=0.80 for chest girth for Farta sheep.

Different prediction models for fat-tailed and thin tailed female sheep populations by age group and pooled were developed using stepwise regression analysis. The best model was identified using the coefficient of determination (R^2), CP criteria and mean square error (MSE). The coefficient of determination (R^2) represents the proportion of the total variability explained by the model. The highest value of the coefficient of determination (R^2), and lower value of CP criteria and mean square error (MSE) were

selected as the best prediction model to estimate body weight of the animals. Developing prediction models to estimate body weight from body linear measurement is of particular significance in livestock breeding, particularly under village breeding programs where measuring live weight is difficult (Solomon Gizaw *et al.*, 2008a). Chest girth was the first variable to explain more variation in fat-tailed sheep populations than other variables. It accounted for 26%, 52% and 51% of the highest variation in body weight for the pooled data for Afar, SSFT and Tumele sheep populations, respectively. Chest girth was also the first entry variable in the models of thin-tailed sheep populations for Begayit and Gumz for the pooled prediction model. But the first variable entered to the model for pooled mature Rutana sheep breed was chest depth. Most authors reported that chest girth was the first variable to explain more variation in the regression models of different sheep populations (Shigdaf et al., 2013, Tesfaye Getachew et al., 2010, Tassew Mohammed et al., 2014, Solomon Abegaz et al., 20ll). In all cases, the inclusion of variables in the model, increased the value of the coefficient of determination and reduce the value of mean square error and increased precision of prediction of body weight. But the inclusion of more variables in the models might be making complexity, time-consuming and financially not feasible at on-farm conditions. Similarly, (Zewdu Edea *et al.*, 2012) on Bonga and Horro sheep and Tesfaye Getachew *et al.* (2010) on Menz and Afar sheep indicated that inclusion of more linear body measurement in the prediction equation has improved prediction accuracy but increase the number of variables in the model, it might be cause complexity under farmer's level.

Chest girth was the best single predictor and accounted alone for 55%, 21% of the variation in body weight of age group 4PPI of Rutana and 3PPI of Begayit female

sheep populations, respectively. Similarly, chest girth was the best single predictor for age group 3PPI of Afar sheep and explained alone for 25% of the variation of body weight. Chest depth was also the best single predictor for the age group of 3PPI of SSFT sheep breed and accounted for 67% of the variation of body weight. The presence of muscle and bone around the heart region was responsible for the relatively higher and positive relationship between body weight and chest girth when compared to other linear traits (Bello, 2012).

7.3 . Multivariate analysis of quantitative traits

We have found only two PCs which explained 83% of a total variation. The first PCs accounted for 75% of a total variation was associated with the loading of all morphological traits. The second PCs explained 8% of a total variation was associated with loading of rump length, pelvic width. These may be related to the different associations of each measurement with bone, environmental components. According to Jolliffe (2003), the first PC almost always has positive coefficients for all variables and simply reflects overall ‘size’ of the individuals but the later PCs usually contrast some of the measurements with others, and can often be interpreted as defining certain aspects of ‘shape’ that are important for the populations. Yakubu (2013) found that first factor explained 57.03% of the generalized variance and 11% of the total variance was explained by the second factor for Yankasa sheep age group between 15.5 to 28.3 months. According to Yakubu (2013), the grouping of conformation traits into PCs might be related to the different associations of each measurement with skeletal growth, environmental influence. Similarly, Mavule *et al.* (2013) extracted two components with a total variance of 66.85% in young sheep and four components in adult sheep which explained a total variance of 62.13% using morphometric traits

and explained that the first factor (PC1) in each case had high loadings for variables relating to body size, whilst PC2 had high association with traits reflecting body shape. Salako (2006) also found that the first and second principal components explained 67.6 and 11.03% of the generalized variance in body measurements and gave approximately equal emphasis to each variable. The plot of principal components showed that PC1 classified thin tailed sheep populations from fat-tailed sheep populations. And further sub-classification within fat-tailed and thin-tailed sheep were observed. More overlap was observed in thin-tailed sheep populations indicated that the presence of a high level of admixture between populations within groups. The Afar sheep breed had a low level of admixture in the fat-tailed sheep breeds. This indicated that gene flow from other populations of the nearby areas is low. The importance of PCA as a multivariate statistical tool was evident in the reduction of a large number of explanatory variables into components that gave a better description of size and shape (Yakubu, 2013).

Discriminant analysis is one of the multivariate techniques commonly used for examining many variables simultaneously. The discriminant analysis encompasses procedures for classifying observations into groups and describing the relative importance of variables for distinguishing among groups (Lix and Sajobi, 2010). The discriminant analysis is used to reduce the number of original traits and allow the discrimination and classification of the populations. Multifactorial discriminant analyses are more suitable in assessing variation within a population and can discriminate different population types when all measured morphological variables are considered jointly (Yakubu, 2011). The present study revealed that tail length chronologically followed by rump length, ear length and body weight were the most

discriminating variables in separating the studied sheep populations. Similarly reports from the stepwise discriminant analysis indicated tail length, rump height, chest girth, ear length and chest depth as the most discriminating variables for classification of indigenous sheep as examined by (Agaviezor *et al.*, 2012). Also, Yakubu *et al.* (2010) selected seven morphometric traits including rump height, body length, horn length, face length, chest girth, neck circumference and head width based on linear discriminant analysis for separating two goat populations. Ebegbulem *et al.* (2011) also discovered six variables rump height (RH), body weight, chest girth, body length, and foreleg length as the major determinants of classification by discriminant analysis approach. The tail length, rump height, ear length and body weight are more important in differentiating between the sheep population than acquiring numerous additional measurements.

All pairwise distances were significant ($P<0.0001$) that showed the populations had different measurements value and distinct genetic group. The largest pairwise Mahalanobis distance (58.24) was recorded between Begayit and Afar sheep while the smallest distance (1.08) was recorded for Begayit and Rutana sheep followed by between Rutana and Afar sheep. The largest distance between Begayit and Afar sheep and between Rutana and Afar sheep might be geographically distance, differences in management practices, agroclimatic conditions, and biophysical resources. According to Kefena Effa *et al.* (2012) and Yadav *et al.* (2013) phenotypic divergence between populations might be partly associated with the differences in management practices, biophysical resources and relative breeding objectives practiced between populations. Yakubu (2012) also described that the significant differences in the distance indicated that differences among sheep breed populations are important for classification. The

smallest distance observed between Begayit and Rutana possibly due to high gene flow between two populations due to the proximity of their breeding tract and have common gene pool.

Classification of sheep populations into their correct source genetic group under field conditions is important for their effective management and conservation. The overall error level recorded was 0.32 that indicated 68% of the population assigned correctly into their genetic groups. The lower error rate (0.12) was observed in Afar sheep populations while the highest error rate (0.48) observed in the Rutana sheep breed. The lower error rate in Afar breed reared by afar community might be isolated from other breeds because of isolation of communities due to cultural barriers. But in Rutana sheep breed the high error rate indicates the presence of gene flow with neighboring sheep populations. Many authors used discriminant analysis for classification of breeds and measure of level of admixture using morphological data (Traoré *et al.* (2008) observed that most (61%) of the Sudanese (Djallonke) individuals were classified as being Sudan Sahel (Mossi) individuals but most (89.5%) Burkina-Sahel individuals were classified into their correct environmental area. After applying, Ebegbulem *et al.* (2011) also identified 83.5% of the goats they studied were correctly classified into their source breed. Dossa *et al.* (2007) were able to correctly allocate more than 70% of individual goats into their different groups. The higher error rate observed in thin-tailed sheep indicates the presence of intermixing between neighboring sheep population.

7.4. Genetic diversity within populations

Heterozygosity measures the level of genetic variation within a population with higher values indicating greater genetic variability (Kaur *et al.*, 2014) . The observed heterozygosity value found in the current study is higher than the result reported by Zewdu Edea *et al.* (2017) for long fat-tailed sheep, short fat-tailed and fat-rumped sheep based on high-density SNP markers and similar with an overall mean value reported for various goat populations by Brito *et al.* (2017) based on genome-wide association analysis. It is also comparable to the value reported for local Awassi (0.36) and higher than the value reported for Menz (0.32), Wollo and improved Awassi sheep populations (Tesfaye Getachew 2015). This is might be due to the 15K SNP chip has developed by selected higher polymorphic SNPs as compared to high density 50K SNP chips.

The expected heterozygosity values found in the current study is higher than the value reported by Zewdu Edea *et al.* (2017) for long fat-tailed, short fat-tailed and fat-rumped sheep populations and it is found in the range of the values reported by Deniskova *et al.* (2018) for Russian sheep populations based on Ovine SNP 50K Bead Chip. It is also within the value reported for the world's sheep breed analyzed based on ovine SNP50K bead chip (Kijas *et al.*, 2012). The result of the current study is within the range of the value that reported for Welsh populations (mean = 0.349, range = 0.306–0.380) (Beynon *et al.*, 2015) and lower than the value reported for Zandi sheep (0.393) by Mohammadi *et al.* (2018). The studied populations have shown a high level of genetic variability. This is due to the fact that the local populations were not under selection.

The inbreeding coefficient is a key parameter to understand the amount of mating that has taken place between related individuals in a population. The inbreeding coefficient (F_{IS}) value in the current study is ranging from 0.004 (Afar) to 0.032 (Begayit) with an overall inbreeding coefficient of 0.019. The latter value is lower than the overall value (0.06) estimated by Zewdu Edea *et al.* (2017) for long fat-tailed, short fat-tailed and fat-rumped sheep breed. A low to moderate inbreeding coefficient was observed in the current study. Fat-tailed northeastern sheep had a low inbreeding coefficient than their counterpart in thin-tailed sheep populations (Begayit, Rutana, and Gumz). A low inbreeding coefficient indicates the presence of more genetic variability. But the thin-tailed sheep breed had higher inbreeding coefficient implies that the thin-tailed sheep had low genetic variability. Inbreeding leads to an increase in homozygosity, which, in turn, reduces the performance of production traits (inbreeding depression), reduces fitness and compromises the long-term viability of the population (Pérez-Tris *et al.*, 2019). Therefore, control of inbreeding is itself an objective in animal production or conservation genetics. The Begayit sheep had sensible inbreeding coefficient. Creation of awareness of the current status of their gene pool including estimation of levels of inbreeding and an evaluation of possible admixture patterns are crucial for both the management of the sheep populations and the conservation of their unique traits.

7.5. Genetic variation between populations

The result of the analysis of molecular variance revealed that the largest variation exists within individuals across overall sheep populations (93.37%). The highest variation within across overall individual sheep populations could be explained by the presence of uncontrolled mating together in the absence of selection and movement of

animals through various market routes and agricultural extension systems (Solomon Gizaw *et al.*, 2008b). This variation is important to exploit unique traits for the improvement of the sheep within populations. Similarly, Zewdu Edea *et al.* (2017) reported that 94.62% of the genetic variation was attributable to differences within populations.

The degree of genetic differentiation between pair of populations is ranging from 0.015 between Afar and Tumele to 0.062 between Begayit and Afar. This value is comparable with the value reported by Zewdu Edea *et al.* (2017) who found genetic differentiation among populations ranging from 0.02 to 0.07 in long fat-tailed, short fat-tailed and long fat-rumped Ethiopian sheep populations. Considering pairwise F_{ST} among all populations, Begayit was the most distant population from compared breeds. The high F_{ST} value was observed between Begayit and Afar populations (F_{ST}=0.062) followed by between Begayit and SSFT (F_{ST}=0.059), while the lowest was observed between Afar and Tumele populations (F_{ST}=0.015). The high F_{ST} values for Begayit and Afar, and Begayit and SSFT are because of these populations found in different geographical area, production system and agro-ecology that limit the cross breeding among the deems.

The genetic relatedness between Afar and Tumele sheep populations might be explained by considering that they are characterized by a common breeding system and geographical location, and husbandry practice, which might have led to gene flow between them. Similarly, Gumz and Rutana sheep breeds found in a northwestern part of the country had a low pairwise F_{ST} (0.022). This implies that there is genetic flow between these breeds. This might be explained by the fact that two populations are

found in the same breeding area and most of the smallholder and commercial farmers in the area rear both populations together, except few commercial farmers in Abra Jira who prefer keeping pure Rutana sheep. The genetic distance between Afar and Tumele and between Tumele and SSFT showed low and significant that implies the presence of shared gene between them. Thus, Tumele sheep had close genetic relation with Afar and SSFT sheep breeds.

7.6. Population structure and admixture

Population structure of the studied sheep populations was assessed through principal component analysis (PCA) and admixture analysis. PCA is commonly used to discover and display patterns, especially to elucidate population structure (Gauch *et al.*, 2018). The PC1 shows the separation of thin-tailed and fat-tailed sheep and there was although substantial overlap within each group. It might have been due to gene flow through the migration of individuals that usually occurred in the same regions.

The first three principal components explained 10.7% of the total variation. PC1 explains 5 %, PC2 3.3% and PC3 2.4% of the total variation in the sample. The PCA result shows low variation within fat and thin-tailed sheep population indicating that the sheep population had a close genetic relationship. The variation explained by the three principal components in the current study, PC1 (5%), PC2 (3.3%) and PC3 (2.4%) were higher than the value reported for world sheep populations PC1 (2.98%), PC2 (1.44%) and PC2 (1.19%) (Kijas *et al.*, 2012).

The genetic structure analysis done on model-based clustering partitioned the genome of each sample into a predefined number of components. The six sheep populations

based on the least cross-validation error, identified as K = 5 was the optimal number of subpopulations. Similar to the results from PCA, admixture analysis at K = 2 separated thin and fat-tailed sheep populations. Afar and SSFT sheep are distinct populations and had low level of admixture at k=5. The northeastern sheep populations of Tumele had a high level of admixture with Afar and SSFT sheep as expected which indicates that the population is the hybrid of the two populations since it is found between the highland sheep SSFT populations and arid lowland fat rumped Afar sheep populations. There is gene flow between these populations at the border region.

The northwestern sheep populations, Gumz, Rutana and Begayit sheep populations showed high level of admixture with each other and a few individual sheep show pure line from all populations. The PCA also has shown a high overlap in this thin-tailed sheep group. The sheep populations in the northwestern region are intermixing with each other and the pure breed individuals of Gumz sheep reduced because of crossing with the adjacent sheep populations and farmers in the region rear both Gumz and Rutana sheep populations together. Gumz sheep one of indigenous prolific and fast growth sheep breeds in the northwestern part of the country (Solomon Abegaz *et al.*, 2011). Thus, conserving this breed should be an urgent for protecting from further dilution that might be result in a loss of adaptable genes.

Mean value and frequency of quantitative and qualitative traits, discriminant analysis result indicated that variation in body size, qualitative traits and level of admixture between populations. The pairwise mahalanobis distance and Pairwise genetic differentiation (F_{ST}) value showed similar results that the highest distance found

between Begayit and Afar. But the least distance found between Tumele and SSFT based on pairwise mahalanobis distance and between Afar and Tumele based on genetic differentiation (F_{ST}) value. Both PCA analysis using morphological traits and molecular analysis separated the studied sheep based on their tail type.

CHAPTER-8

8. Conclusion and Recommendation

8.1. Conclusion

This study conducted on the fat-tailed and thin-tailed sheep populations northeastern and northwestern part of Ethiopia focused on of morphological and low-density SNPs markers.

There was genetic variation between and within fat and thin tailed populations in the study area. There is a morphological variation (coat color pattern, coat color type, hair type, head profile, ear formation and body size) between the studied sheep populations. Fat-tailed female sheep populations dominated by plain followed by patchy coat color pattern with foremost straight head profile and lateral ear formation. Whereas, the thin-tailed female sheep breed mainly dominated by patchy coat color pattern except Rutana sheep, with mainly convex and semi-convex head profile and pendulous and semi-pendulous ear formation.

Morphological traits were showed a significant variation between populations and age groups. The larger variability was observed in ear length, tail length and body weight and lower variability was observed in rump height. The thin-tailed sheep breed had larger body size as compared to fat-tailed sheep populations. Rutana and Begayit sheep had a similar body measurement except body weight, chest girth and tail length. The lower body weight and linear body measurements was recorded for Afar sheep breed. Tumele sheep body weight and body linear measurements similar with SSFT than Afar sheep but the genetic relationship closer to Afar than SSFT.

Correlation and regression analysis revealed that most of the linear body measurements had positive and significant correlation coefficient with body weight of both fat-tailed and thin-tailed sheep populations. The largest value of the correlation coefficient was observed between body weight and chest girth in both groups implies that the chest girth is could be the best body weight predictor for both populations. Chest girth was the primary variable to explain more variation in fat-tailed and thin-tailed sheep populations than other variables.

Discriminant analysis of variance revealed that tail length, rump length, ear length and body were the most important and informative discriminating variables and could assign the studied sheep populations into distinct populations. All pairwise mahalanobis distances and pairwise genetic differentiation were significant ($P<0.0001$) that showed the populations had different measurements value and distinct genetic group. Populations that were found in the similar geographical region had low pairwise Mahalanobis and genetic distance. While populations that are geographically isolated had larger pairwise Mahalanobis and genetic distance.

PCA analysis using both morphological traits and molecular data revealed two PCs isolated based on tailed type indicated that sheep populations had larger genetic distance between fat-tailed population and thin-tailed sheep populations than within fat-tailed or thin-tailed group.

The inbreeding coefficient across all populations was positive and had low to moderate value. There was high variation within individuals across all populations of fat-tailed and thin-tailed sheep populations.

The admixture result indicates that Tumele sheep is as expected intermixed population with Afar and SSFT sheep breeds. The Afar and SSFT sheep populations were the only populations with the minimal case of admixture at all level while thin-tailed northwestern sheep populations and Tumele sheep in the northeastern region had high level of admixture. The genetic differentiation indicated that the Rutana and Begayit sheep population genetically distinct but both populations had high level of intermixing results and low genetic variation. The genetic variation within fat-tailed and thin-tailed sheep was low but the genetic variation between fat-tailed and thin-tailed populations substantial.

8.2. Recommendations

Therefore, the following recommendations were forwarded from the key finding and discussions of the research conducted in this study: -

- Lager values of inbreeding coefficient (F_{IS}) observed in thin-tailed sheep population and Tumele sheep in the present studies needs to considered for future breeding program.
- The high level of admixture observed in thin-tailed sheep in the present study indicated the needs conservation for sustainable utilization of the genetic resources.
- Low level of genetic admixture in Afar and SSFT sheep breeds would create an opportunity for future genetic improvement in line with conserving the pure breed in the study area.
- The inbreeding coefficient (F_{IS}), genetic differentiation (F_{ST}) population pattern and level of admixture found in this study will have paramount

importance for future breeding plan for conservation and improvement of the studied sheep populations.

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Appendixes

Details of modified salting-out methods

One mL EDTA anticoagulant blood sample was placed in 3mL glass tubes. Then 1.6 mL of lysis buffer (0.3 M sucrose, 0.01 M Tris-HCl, pH 7.5, 5 mM $MgCl_2$, 1% Triton X100) was added to the tube. The tube was centrifuged for 5 min at 2,500 g. The supernatant was discarded and 60 µl of 10 mM Tris-HCl, pH 8, was added to the pellet.

The pellets were released from the bottom of the tubes and transferred quickly to fresh microfuge tubes. The sediment was suspended by vigorous vortexing, and the product was centrifuged for 1 min at 700 g. After the supernatant was discarded, 66 µL of 10 mM Tris-HCl, pH 8; 66 µL of laundry powder solution (concentrations 30 mg/mL); and a glass bead were added to each tube.

The samples were vortexed for 1 min, 50 µL of 6M NaCl was added, and they were vortexed again for 20 sec. Then the tubes were spun down for 5 min at 15,000g. The supernatant was transferred to fresh tubes (about 150 µL) and DNA was precipitated by adding 150 µL of 96% ethanol. DNA precipitate was retrieved using a heat-sealed, thin-end glass pipette, washed twice in 0.1 mL of 70% ethanol, and finally dissolved in 20 µL of 10 mM Tris-HCl, pH 8. The precipitate was dissolved by incubation at 70 ^{0}C for 5 min.

Appendix Table 1. Body measurements were made using measuring tape calibrated in centimeters (cm)

Traits	Description
Body length (BL)	It was measured as the diagonal distance from the tip of the sternum to the base of the tail
Chest girth (CG)	It was taken as the circumference of the body immediately behind the shoulder blades in a vertical plane perpendicular to the long axis of the body
Chest depth (CD)	The distance measured from the backbone at the shoulder to the brisket between the front legs (cm).
Rump height (RH)	Height from ground to the spina illiaca (cm).
Rump length (RL)	Distance from the anterior point to the posterior extremity of the pin bone (cm).
Wither height (WH)	It was measured from the bottom of the front foot to the highest point of the shoulder between the withers
Pelvic width (PW)	It was measured as the distance between pelvic bones across the dorsum
Tail length (TL)	It was taken as the distance from the base to the tip of the tail on the outer side of the tail

Appendix Table 2. Analysis of variance of body weight of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F-Value	Pr > F
Model	7	42323.24	6046.178	197.11	<.0001
pop	5	39266.54	7853.308	256.03	<.0001
den	2	1437.656	718.8278	23.43	<.0001
Error	602	18465.73	30.67397		
Corrected Total	609	60788.97			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 3. Analysis of variance of Tail length of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F-Value	Pr > F
Model	7	102372.8	14624.69	472.48	<.0001
breed	5	100584.1	20116.82	649.92	<.0001
dent	2	32.8974	16.4487	0.53	0.588
Error	603	18664.56	30.9528		
Corrected Total	610	121037.4			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 4. Analysis of variance of chest depth of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	6323.79	903.40	96	<.0001
breed	5	6121.33	1224.27	130.1	<.0001
dent	2	155.25	77.63	8.25	0.0003
Error	603	5674.40	9.41		
Corrected Total	610	11998.19			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 5. Analysis of variance of rump height of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	14623.62	2089.088	161.38	<.0001
breed	5	14330.67	2866.134	221.41	<.0001
dent	2	71.32142	35.66071	2.75	0.0644
Error	603	7805.876	12.94507		
Corrected Total	610	22429.5			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 6. Analysis of variance of rump length of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F Value	Pr > F
Model	7	3349.516	478.5023	107.96	<.0001
breed	5	3324.974	664.9948	150.04	<.0001
dent	2	44.44518	22.22259	5.01	0.0069
Error	603	2672.62	4.432206		
Corrected Total	610	6022.137			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 7. Analysis of variance of body length of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	8211.581	1173.083	129.7	<.0001
breed	5	7626.735	1525.347	168.64	<.0001
dent	2	288.4095	144.2048	15.94	<.0001
Error	603	5454.055	9.04487		
Corrected Total	610	13665.64			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 8. Analysis of variance of chest girth of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	17482.62	2497.516	124.58	<.0001
breed	5	14836.95	2967.39	148.02	<.0001
dent	2	1802.101	901.0503	44.95	<.0001
Error	603	12088.19	20.04675		
Corrected Total	610	29570.8			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 9. Analysis of variance of wither height of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	15746.71	2249.53	3.56	0.0009
breed	5	15564.1	3112.82	4.93	0.0002
dent	2	675.017	337.5085	0.53	0.586
Error	603	380504.4	631.019		
Corrected Total	610	396251.1			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 10. Analysis of variance of pelvic width of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F- Value	Pr > F
Model	7	476.2652	68.03789	24.67	<.0001
breed	5	439.9205	87.98411	31.91	<.0001
dent	2	29.08423	14.54212	5.27	0.0054
Error	603	1662.847	2.757623		
Corrected Total	610	2139.112			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 11. Analysis of variance of pelvic width of fat-tailed and thin-tailed female sheep by breed and dentition

Source	DF	SS	MS	F Value	Pr > F
Model	7	6759.67	965.67	204.76	<.0001
breed	5	6654.64	1330.93	282.22	<.0001
dent	2	12.91	6.45	1.37	0.2554
Error	594	2801.31	4.72		
Corrected Total	601	9560.98			

DF=degree of freedom, SS= sum of square, MS= mean of square, and dent=dentition

Appendix Table 12**.** Population structure of inferred subpopulation of Northeastern and Northwestern sheep populations

Predefined populations	Q1	Q2	Q3	Q4	Q5
Rutana	0.53	0.14	0.03	0.21	0.09
Rutana	0.53	0.14	0.03	0.21	0.09
Rutana	0.65	0.10	0.07	0.12	0.06
Rutana	0.84	0.06	0.01	0.05	0.05
Rutana	0.88	0.05	0.00	0.03	0.05
Rutana	0.74	0.13	0.03	0.09	0.01
Rutana	0.81	0.08	0.01	0.11	0.00
Rutana	1.00	0.00	0.00	0.00	0.00
Rutana	1.00	0.00	0.00	0.00	0.00
Rutana	1.00	0.00	0.00	0.00	0.00
Rutana	1.00	0.00	0.00	0.00	0.00
Rutana	1.00	0.00	0.00	0.00	0.00
Begayit	0.12	0.63	0.04	0.12	0.09
Begayit	0.05	0.76	0.00	0.10	0.08
Begayit	0.17	0.60	0.00	0.16	0.07
Begayit	0.13	0.69	0.05	0.08	0.05
Begayit	0.05	0.85	0.00	0.07	0.03
Begayit	0.08	0.78	0.00	0.12	0.03
Begayit	0.10	0.84	0.02	0.03	0.02
Begayit	0.12	0.81	0.05	0.00	0.01
Begayit	0.02	0.91	0.02	0.05	0.00
Begayit	0.09	0.81	0.00	0.10	0.00
Begayit	0.02	0.93	0.00	0.05	0.00
Begayit	0.00	0.93	0.03	0.04	0.00
Begayit	0.01	0.96	0.00	0.03	0.00
Begayit	0.00	1.00	0.00	0.00	0.00
Begayit	0.00	1.00	0.00	0.00	0.00
Begayit	0.00	1.00	0.00	0.00	0.00
Begayit	0.00	1.00	0.00	0.00	0.00
Begayit	0.00	1.00	0.00	0.00	0.00
Tumele	0.01	0.01	0.51	0.01	0.46
Tumele	0.03	0.02	0.50	0.00	0.44

Predefined populations	Q1	Q2	Q3	Q4	Q5
Tumele	0.02	0.01	0.53	0.03	0.42
Tumele	0.01	0.00	0.55	0.03	0.41
Tumele	0.02	0.04	0.54	0.00	0.41
Tumele	0.00	0.03	0.56	0.01	0.40
Tumele	0.00	0.00	0.60	0.01	0.39
Afar	0.00	0.00	0.63	0.03	0.34
Tumele	0.05	0.01	0.62	0.00	0.32
Tumele	0.03	0.02	0.60	0.03	0.32
Tumele	0.02	0.02	0.69	0.03	0.25
Tumele	0.02	0.04	0.71	0.01	0.22
Tumele	0.03	0.01	0.76	0.01	0.19
Tumele	0.03	0.05	0.73	0.00	0.18
Tumele	0.00	0.02	0.79	0.01	0.18
Tumele	0.00	0.01	0.78	0.03	0.18
Tumele	0.02	0.02	0.78	0.02	0.16
Tumele	0.04	0.02	0.76	0.02	0.16
Afar	0.01	0.05	0.77	0.02	0.15
Tumele	0.00	0.02	0.81	0.03	0.15
Tumele	0.03	0.03	0.75	0.04	0.14
Afar	0.02	0.02	0.79	0.02	0.14
Afar	0.00	0.04	0.83	0.00	0.13
Afar	0.01	0.03	0.81	0.01	0.13
Afar	0.02	0.01	0.81	0.02	0.13
Afar	0.03	0.04	0.78	0.02	0.13
Tumele	0.04	0.05	0.77	0.02	0.13
Tumele	0.00	0.03	0.80	0.05	0.12
Afar	0.02	0.02	0.83	0.00	0.12
Afar	0.00	0.02	0.83	0.03	0.12
Tumele	0.02	0.03	0.81	0.02	0.12
Afar	0.03	0.03	0.80	0.02	0.12
Afar	0.00	0.03	0.85	0.01	0.11
Tumele	0.05	0.03	0.78	0.03	0.11
Afar	0.00	0.04	0.83	0.02	0.11
Afar	0.00	0.02	0.85	0.02	0.11
Afar	0.05	0.00	0.79	0.06	0.10

Predefined populations	Q1	Q2	Q3	Q4	Q5
Afar	0.01	0.03	0.84	0.01	0.10
Afar	0.01	0.03	0.87	0.00	0.09
Afar	0.00	0.02	0.86	0.03	0.09
Afar	0.03	0.00	0.88	0.00	0.09
Afar	0.00	0.01	0.90	0.00	0.09
Rutana	0.02	0.04	0.82	0.03	0.09
Afar	0.00	0.00	0.89	0.04	0.07
Afar	0.00	0.00	0.95	0.00	0.05
Afar	0.00	0.00	0.95	0.00	0.05
Afar	0.00	0.00	0.95	0.00	0.05
Afar	0.00	0.00	0.95	0.01	0.04
Afar	0.01	0.01	0.95	0.00	0.03
Afar	0.00	0.06	0.91	0.00	0.03
Afar	0.00	0.06	0.91	0.00	0.03
Afar	0.00	0.00	0.98	0.00	0.02
Afar	0.00	0.00	0.98	0.00	0.02
Afar	0.01	0.00	0.97	0.02	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Afar	0.00	0.00	1.00	0.00	0.00
Gumz	0.01	0.00	0.00	0.97	0.02
Gumz	0.06	0.07	0.00	0.86	0.01
Gumz	0.00	0.00	0.00	0.99	0.01
Gumz	0.04	0.00	0.00	0.96	0.00
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.00	0.00	0.00	1.00	0.00

Predefined populations	Q1	Q2	Q3	Q4	Q5
Gumz	0.00	0.00	0.00	1.00	0.00
Gumz	0.05	0.03	0.00	0.92	0.00
Tumele	0.00	0.00	0.00	0.00	1.00
Tumele	0.00	0.00	0.00	0.00	1.00
SSFT	0.00	0.00	0.00	0.00	1.00
SSFT	0.00	0.00	0.00	0.00	1.00
SSFT	0.00	0.00	0.00	0.00	1.00
SSFT	0.00	0.01	0.00	0.00	0.99
SSFT	0.00	0.00	0.00	0.01	0.99
SSFT	0.02	0.01	0.00	0.00	0.97
SSFT	0.00	0.03	0.01	0.00	0.96
SSFT	0.03	0.01	0.00	0.01	0.96
SSFT	0.00	0.02	0.02	0.00	0.95
SSFT	0.00	0.01	0.00	0.04	0.95
SSFT	0.00	0.00	0.03	0.03	0.93
SSFT	0.00	0.00	0.04	0.03	0.93
SSFT	0.01	0.00	0.06	0.00	0.93
SSFT	0.00	0.00	0.09	0.00	0.91
SSFT	0.03	0.04	0.01	0.02	0.91
SSFT	0.00	0.00	0.10	0.00	0.90
SSFT	0.01	0.00	0.09	0.00	0.90
SSFT	0.00	0.06	0.03	0.02	0.89
SSFT	0.01	0.00	0.09	0.02	0.88
SSFT	0.00	0.00	0.08	0.05	0.86
SSFT	0.01	0.01	0.11	0.01	0.86
SSFT	0.04	0.01	0.09	0.00	0.86
SSFT	0.03	0.01	0.09	0.02	0.85
SSFT	0.00	0.01	0.11	0.04	0.84
SSFT	0.02	0.00	0.15	0.00	0.83
SSFT	0.02	0.01	0.08	0.07	0.82
Tumele	0.02	0.02	0.15	0.00	0.80
SSFT	0.02	0.00	0.17	0.00	0.80
SSFT	0.02	0.03	0.11	0.03	0.80
Tumele	0.00	0.01	0.15	0.04	0.80
Tumele	0.05	0.03	0.12	0.00	0.80

Predefined populations	Q1	Q2	Q3	Q4	Q5
Tumele	0.03	0.00	0.16	0.01	0.80
Tumele	0.03	0.00	0.16	0.02	0.80
SSFT	0.03	0.00	0.16	0.02	0.79
Tumele	0.01	0.04	0.15	0.02	0.78
SSFT	0.05	0.01	0.11	0.05	0.77
Tumele	0.00	0.04	0.16	0.03	0.77
SSFT	0.04	0.04	0.11	0.06	0.75
Tumele	0.03	0.02	0.18	0.06	0.71
SSFT	0.05	0.00	0.24	0.00	0.71
Tumele	0.01	0.00	0.27	0.02	0.70
Tumele	0.03	0.03	0.26	0.04	0.65
Tumele	0.00	0.00	0.36	0.00	0.64
Tumele	0.00	0.01	0.36	0.02	0.61
Tumele	0.00	0.03	0.41	0.00	0.56
Tumele	0.00	0.01	0.48	0.00	0.50
Tumele	0.03	0.01	0.44	0.02	0.49
Gumz	0.11	0.08	0.15	0.17	0.48
Gumz	0.15	0.13	0.03	0.35	0.35
Gumz	0.15	0.17	0.07	0.31	0.30
Gumz	0.17	0.13	0.06	0.34	0.30
Gumz	0.22	0.24	0.09	0.17	0.29
Gumz	0.16	0.19	0.03	0.36	0.26
Bega	0.26	0.25	0.09	0.19	0.22
Gumz	0.19	0.18	0.07	0.35	0.21
Gumz	0.19	0.17	0.10	0.34	0.20
Gumz	0.18	0.17	0.10	0.35	0.20
Gumz	0.22	0.17	0.05	0.37	0.19
Begayit	0.25	0.21	0.17	0.19	0.19
Rutana	0.22	0.17	0.08	0.34	0.19
Rutana	0.23	0.24	0.06	0.29	0.18
Gumz	0.24	0.23	0.05	0.30	0.18
Gumz	0.20	0.21	0.15	0.26	0.18
Rutana	0.23	0.23	0.04	0.32	0.17
Rutana	0.22	0.23	0.11	0.28	0.17
Begayit	0.24	0.28	0.12	0.20	0.17

Predefined populations	Q1	Q2	Q3	Q4	Q5
Rutana	0.30	0.24	0.12	0.18	0.16
Gumz	0.22	0.20	0.05	0.36	0.16
Gumz	0.17	0.15	0.24	0.28	0.16
Gumz	0.21	0.22	0.11	0.30	0.16
Gumz	0.20	0.18	0.08	0.39	0.16
Gumz	0.22	0.21	0.05	0.36	0.16
Gumz	0.21	0.24	0.05	0.34	0.15
Rutana	0.24	0.28	0.13	0.19	0.15
Rutana	0.28	0.27	0.11	0.18	0.15
Gumz	0.23	0.19	0.10	0.33	0.15
Rutana	0.24	0.21	0.06	0.35	0.15
Rutana	0.25	0.29	0.10	0.22	0.14
Gumz	0.21	0.22	0.09	0.34	0.14
Rutana	0.22	0.21	0.19	0.24	0.14
Rutana	0.29	0.26	0.11	0.20	0.14
Rutana	0.30	0.27	0.11	0.19	0.13
Rutana	0.27	0.25	0.06	0.30	0.13
Rutana	0.44	0.16	0.09	0.19	0.13
Rutana	0.28	0.25	0.13	0.21	0.13
Rutana	0.41	0.19	0.07	0.19	0.13
Begayit	0.27	0.27	0.09	0.24	0.13
Begayit	0.36	0.23	0.12	0.17	0.12
Rutana	0.36	0.28	0.05	0.19	0.12
Rutana	0.35	0.24	0.07	0.21	0.12
Rutana	0.28	0.24	0.15	0.20	0.12
Gumz	0.25	0.23	0.08	0.32	0.12
Rutana	0.18	0.20	0.24	0.26	0.11
Rutana	0.31	0.23	0.13	0.22	0.11
Rutana	0.28	0.22	0.15	0.24	0.11
Rutana	0.30	0.25	0.11	0.23	0.10
Rutana	0.33	0.24	0.11	0.22	0.10
Begayit	0.40	0.23	0.08	0.18	0.10
Rutana	0.28	0.25	0.13	0.24	0.10
Begayit	0.40	0.22	0.12	0.19	0.07
Begayit	0.40	0.22	0.10	0.21	0.07

Predefined populations	Q1	Q2	Q3	Q4	Q5
Begayit	0.42	0.26	0.05	0.20	0.07
Rutana	0.30	0.24	0.11	0.28	0.06
Rutana	0.30	0.24	0.11	0.28	0.06
Begayit	0.43	0.24	0.07	0.21	0.06
Begayit	0.45	0.23	0.04	0.22	0.05
Begayit	0.46	0.25	0.06	0.19	0.03
Begayit	0.48	0.26	0.05	0.18	0.02
Begayit	0.45	0.25	0.07	0.22	0.02
Begayit	0.47	0.26	0.04	0.24	0.00
Begayit	0.48	0.25	0.06	0.21	0.00

Appendix Table 13. Chromosome number, frequency and percent of SNP removed due to HWE < 0.0001

CHR	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	5	5.56	5	5.56
2	7	7.78	12	13.33
3	4	4.44	16	17.78
4	2	2.22	18	20.00
5	2	2.22	20	22.22
6	23	25.56	43	47.78
7	4	4.44	47	52.22
9	6	6.67	53	58.89
10	4	4.44	57	63.33
11	1	1.11	58	64.44
12	5	5.56	63	70.00
13	5	5.56	68	75.56
14	3	3.33	71	78.89
16	2	2.22	73	81.11
17	5	5.56	78	86.67

CHR	Frequency	Percent	Cumulative Frequency	Cumulative Percent
18	4	4.44	82	91.11
19	3	3.33	85	94.44
20	1	1.11	86	95.56
23	2	2.22	88	97.78
25	1	1.11	89	98.89
26	1	1.11	90	100.00

Appendix Table 14. Sheep linear body measurement and physical description data collection format

Region_____ Zone_____ District_____ Site_____ PA___

IDNo	Flock No	sex	castration	origin	Body weight	Body condition	Coat color		Hair type	Head profile	wattle	ruff	Tail length	Chest depth	Rump height	Rump length
							pattern	*color*								
1																
2																
3																
4																
5																

Ser. no	Age	Dentation	ear		horn			body length	chest girth	Height at wither	pelvic width	Scortum circumference	parity	No of lambs born
			formation	*length*	*shape*	*orientation*	*length*							
1														
2														
3														
4														
5														
6														
7														

Shows Rutana sheep flocks at their homestead

Begayit sheep flock

Afar sheep flock at Mile and at Chifra

Wollo sheep flock grazing at Wollo Tebasie

Appendix Figure 1. Pictures of studied sheep frock in their homestead