BAHIR DAR UNIVERSITY

College of Agriculture and Environmental Sciences

Department of Animal Production and Technology

Phenotypic and Genetic Characterization and Design of Community-Based Breeding Programs for Two Indigenous Goat Populations of Ethiopia

By

Oumer Sheriff Mohammed

May, 2022

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A Dissertation Submitted in Partial Fulfillment of the
Requirements for the Degree of Doctor of Philosophy in
Animal Genetics and Breeding

Principal Supervisor: Kefyalew Alemayehu (Professor)
Co-supervisors: Aynalem Haile (PhD)
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May, 2022
Bahir Dar

DECLARATION

I hereby declare that this Dissertation is my bonafide work and that all sources of materials used for this Dissertation have been duly acknowledged. I have followed all ethical principles of scholarship in the preparation, data collection, data analysis and completion of this Dissertation. All scholarly matter that is included in the Dissertation has been given recognition through citation. Every serious effort has been made to avoid any plagiarism in the preparation of this Dissertation. This Dissertation has been submitted in partial fulfillment of the requirements for PhD degree in Animal Genetics and Breeding (የፍልስፍና ዶክትሬት ዲግሪ በእንስሳት ስነ-ዘረመል እና ዝርያ ማሻሻያ) at Bahir Dar University and is deposited at that University Library to be made available to borrowers under the rules of the library. I solemnly declare that this Dissertation has not been submitted to any other institution anywhere for the award of any academic degree, diploma or certificate. Brief quotations from this Dissertation may be used without special permission provided that accurate and complete acknowledgement of the source is made. Requests for permission for extended quotations from, or reproduction of this Dissertation in whole or in part may be granted by the Head of the School or Department or the Dean/director of the postgraduate Program Directorate when in his or her judgment the proposed use of the material is in the interest of scholarship. In all other instances, however, permission must be obtained from the author of the Dissertation.

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Approval of Dissertation for defense

We hereby certify that we have supervised, read and evaluated this Dissertation titled “Phenotypic and genetic characterization and design of community-based breeding programs for two indigenous goat populations of Ethiopia” by Oumer Sheriff Mohammed prepared under our guidance. We recommend the dissertation be submitted for oral defense.

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Approval of Dissertation Defense Result

As members of the board of examiners, we examined this dissertation entitled "Phenotypic and genetic characterization and design of community-based breeding programs for two indigenous goat populations of Ethiopia" by Oumer Sheriff Mohammed. We hereby certify that the dissertation is accepted for fulfilling the requirements for the award of degree of "Doctor of Philosophy in Animal Genetics and Breeding"

Board of Examiners

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External examiner's name	Signature	Date
Mengistie Taye (PhD)		July 05, 2022
Internal examiner's name	Signature	Date
Asaminew Tassew (PhD)		July 12, 2022
Chair person's name	Signature	Date

DEDICATION

In **memory** of my father, Sheriff Mohammed (1938-1998) and my mother, Alima Adem (1942-2014);

Dedicated to my beloved wife: Dr. Aminat Hussien

,

my Kids: Aehtisham Oumer, Afraz Oumer, Khalid Oumer and Sebiha Oumer

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ABSTRACT

The aim of the dissertation was to undertake phenotypic and genetic characterization and design community-based breeding programs for two indigenous goat populations in Ethiopia, namely Arab and Oromo. The dissertation was based on five manuscripts. Papers I, II, IV and V were based on data generated from production system, morphological characterization and ranking experiments. Paper III was based on whole genome data generated from three indigenous goat populations (Arab, Fellata and Oromo). Genomic data of ten additional goat breeds including four Ethiopian (Abergelle, Gumuz, Keffa, Woiyto-Guji), four African (Kenyan Boran, Morrocan Unknown, Malawian Thyolo, Malian Guera), one Asian (Chinese Tibetan) and one European (French Saanen), obtained from the database, were included for comparison purposes. Reconnaissance survey, focus group discussion and interview with structured questionnaires were used to collect data from 249 households (Paper I). Ten qualitative and nine quantitative traits were recorded/measured from 747 randomly selected goats (Paper II). Genetic diversity metrics within each of three goat populations were assessed and population structure was investigated using principal component analysis (PCA), ADMIXTURE and TREEMIX. Candidate genes underlying strong selection signatures were identified by combining two approaches: pooled hetrozygosity (*Hp*) and population differentiation (*Fst*) (Paper III). Two live animal ranking experiments (own flock and group) were conducted to identify breeding objective traits of Arab and Oromo goat keepers. In the own-flock ranking experiment, a total of 147 households ranked their first, second and third best and the most inferior does in their own flock. In the group-animal ranking experiment, 24 breeding does and bucks were randomly selected and placed into eight groups. Twelve farmers from Arab and Oromo goat keepers, respectively with no knowledge of the experimental animals, ranked the three goats in each group as 1st, 2nd and 3rd, giving reasons for their ranking. After the first round of ranking, the farmers were then provided with the history of each individual goat and asked whether they would reconsider their ranking. This was iterated eight times until a person covered all groups of goats (Paper IV). Four

alternative breeding schemes were simulated and evaluated for the Arab and Oromo goat populations (Paper V). The survey results indicated that goats were kept for a variety of purposes. Income generation (0.40), meat (0.23), and savings (0.16) were the highest priorities, but with different index values between the Arab and Oromo goat keepers. Out of the total flock sizes, breeding does constituted the largest (36.7%) followed by kids (23.7%), young does (20.5%), young bucks (8.5%), bucks (7.3%), and castrates (3.4%), even though there was significant ($p < 0.01$) difference between the two groups of goat keepers. Arab goat keepers owned higher average flock size than Oromo goat keepers. Mating was predominantly uncontrolled mainly due to communal grazing. On average, first kidding occured at the age of 1.2 years, kidding interval at 7.5 months, reproductive life was for about 7.6 years, and produced 10.7 kids per lifetime despite variation between Arab and Oromo goat keepers (Paper I). The qualitative and quantitative data analysis revealed significant ($p < 0.01$) differences between Arab and Oromo goats. White coat color was predominantly observed in Arab goats (33.72%) while brown (deep and light) coat color was the most frequent in Oromo goats (27.81%). Goat population type and age had significant effects on body weight and linear body measurements. When goats of the same age class were compared, Oromo goats were heavier and bigger in size. Positive and highly significant correlations were obtained between body weight and most of the body measurements in both goat populations. The highest correlation was between chest girth and body weight for Arab ($r = 0.95$) and Oromo ($r = 0.92$) (Paper II). The genomic data analysis generated 35,161,094 autosomal biallelic single nucleotide polymorphisms (SNPs) and 3,737,445 insertions and deletions (InDels) from the 13 global goat populations (78 goat genomes). The highest number of SNPs and InDels were detected in Unknown goat while the lowest number of SNPs and InDels were identified in Saanen and Gumuz goats, respectively. Keffa goat demonstrated the lowest level of genetic diversity whereas Woyito-Guji showed the highest. Our results show an inverse relationship between the length and number of runs of homozygosity (ROH). The number of shorter ROHs ($\text{ROH}_{100\text{–}150\text{Kb}}$) category predominated; accounting for 58.18% of the total number of ROHs. The longest ROH category ($\text{ROH}_{>400\text{Kb}}$) was the rarest, wherein the

Gumuz population displayed the highest number of ROH, suggesting recent inbreeding in this population. Principal component analysis (PCA), ADMIXTURE and TREEMIX tools revealed five distinct genetic clusters in the global, three in the African and two in the Ethiopian goat populations. For the selection signature analysis, we used comparative genomics to explore differences between populations that are exposed to different selection pressures (natural versus artificial) and from different geographic zones (tropical semi-arid versus temperate cold) using pooled hetrozygosity (*Hp*) and population differentiation (*Fst*) between the following population pairs: Gumuz versus Saanen and Fellata versus Saanen. By combining the two approaches, candidate genes underlying strong selection signatures including litter size, adaptation to arid environment, coat coloration and body weight were identified (Paper III). The live animal ranking experiments indicated that traits like body size, twining ability, kidding interval and mothering ability were the topmost preferred attributes to select breeding does; whereas body size, libido and growth were the traits used to select breeding bucks in the study area (Paper IV). The four alternative breeding schemes simulated for Arab and Oromo goats resulted in reasonable annual genetic gain (PAGG), especially for six months weight (6 mw). Due to its economic return, Scheme 2 is recommended over other schemes (Paper V). In conclusion, future works should focus on the implementation of CBBP in the study area using Scheme 2. However, care should be taken to ensure the participation of goat keepers from inception through to implementation and include few priority breeding objective traits.

Key words: Breeding objective, Genetic diversity, Morphological characterization, Production system, Selection signature

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ABBREVIATIONS AND ACRONYMS

6 mw	Six Months Weight
AFK	Age at First Kidding
AFLP	Amplified Fragment Length Polymorphism
CBBP	Community Based Breeding Program
CSA	Central Statistical Authority
CV	Cross Validation
DNA	Deoxyribonucleic Acid
EDTA	Ethylene Diamine Tetraacetic Acid
FAO	Food and Agricultural Organization of United Nations
Fst	Population differentiation
He	Expected Heterozygosity or gene diversity
Ho	Observed Hetrozygosity
Hp	Pooled Hetrozygosity
IBC	Institute of Biodiversity and Conservation
IBS	Identical By State
ICARDA	Intonations Center for Agricultural Research in Dry Areas
ILRI	International Livestock Research Institute
KI	Kidding Interval
LBMs	Linear Body Measurments
LSB	Litter Size at Birth
LSM	Least Square Mean
LSW	Litter Size at Weaning
MAF	Minor Allele Frequency
m.a.s.l	Meters Above Sea Level
PA	Peasant Association
PAGG	Predicted Annual Genetic Gain
PCA	Principal Component Analysis
PPI	Pair of Permanent Incisors
PPS	Probability Proportion to Size

QTL	Quantitative Trait Loci
RAPD	Randomly Amplified Polymorphic DNA
ROH	Run of Homozygosity
RFLP	Restricted Fragment Length Polymorphism
SE	Standard Error
SPSS	Statistical Package for Social Sciences
SNP	Single Nucleotide Polymorphism
VEP	Variant Effect Predictor
WGS	Whole Genome Sequence
YBP	Years Before Present

The Dissertation is based on the following five articles/manuscripts, which will be referred in the text by their Roman numerals

I. Production systems and breeding practices of Arab and Oromo goat keepers in northwestern Ethiopia: implications for community-based breeding programs **(Published in Tropical Animal Health and Production, 2018; 52: 1467–1478. https://doi.org/10.1007/s11250-019-02150-3).**

II. Morphological characterization of Arab and Oromo goats in northwestern Ethiopia: implications for community-based breeding programs **(Published in Agriculture and Food Security, 2021; 10 (49) 1–11. https://doi.org/10.1186/s40066-021-00322-9).**

III. Genome-wide Divergence, Candidate Regions and Genes Associated with Important Traits in Ethiopian Indigenous Goat Populations (**To be submitted**)

IV. Phenotypic ranking experiments in identifying breeding objective traits of smallholder farmers in northwestern Ethiopia **(Published in PLoS ONE. 2021; 16(3). e0248779. https://doi.org/10.1371/journal.pone.0248779).**

V. Genetic and economic evaluation of alternative breeding schemes for two indigenous goat populations of Ethiopia **(Published in Journal of Applied Animal Research, 50:1, 80–85. https://doi.org/10.1080/09712119.2021.2023549)**

CHAPTER 1: INTRODUCTION

In Ethiopia, there are more than 52 million heads of goats (CSA, 2021) which are indispensable sources of tangible (cash, milk, meat and manure) and intangible (prestige, saving, insurance, cultural and ceremonial purposes) benefits (Legese et al., 2014). The contribution of this valuable genetic resource to national and household economy is, however, far below their potential (Legese and Fadiga, 2014; Woldu et al., 2016). The current level of productivity of these indigenous goats is also low as a result of many interrelated factors such as biological, environmental and socio-economic; among which lack of systematic breeding is an important constraint (Jembere et al., 2019).

To overcome some of the constraints of smallholder goat production, there have been a few attempts at genetic improvement through crossbreeding of local goats with exotic animals. The noticeable example is the FARM-Africa dairy goat development project in southern and eastern Ethiopia. However, the belief that crossbred genotypes have better overall performance than the indigenous goats led to indiscriminate crossbreeding (Ayalew et al., 2003; Tesfaye, 2004). In fact, there were very few successful goat crossbreeding programs under on-station conditions that produced crossbreds that performed better than the indigenous breeds. Unfortunately, such superiorities were not replicated under on-farm conditions (Ayalew et al., 2003). As a result, the adoption rates of exotic and crossbred genotypes by smallholder farmers were very low (Teressa, 2004; Kosgey et al., 2006) and their number at national level remains insignificant (0.1%) (CSA, 2021). In general, many small ruminant crossbreeding programs in the tropics have not been successful because of incompatibility of the genotypes with the farmers breeding objectives, management methods and the prevailing environment of tropical low input production systems (Ayalew et al., 2003; Kosgey et al., 2006).

The design and implementation of sustainable community-based breeding programs (CBBP) is a promising entry point for low input production systems

(Mueller et al., 2015). Such programs consider the needs, views, decisions and active participation of farmers from inception through to implementation (Haile et al., 2020). In Haile et al. (2011; 2018), the procedures for setting up CBBP for small ruminants is illustrated, and the first step is the description of the production system. The small ruminant production systems in Ethiopia are classified into four: small ruminants in annual crop-based systems located in northern, northwestern, and central highlands; small ruminants in perennial crop-based, mostly found in southern and southwestern highlands; small ruminants in cattle based systems, usually in agropastoral and semi-arid areas; small ruminants dominated systems, found in pastoral and arid areas of eastern and northeastern Ethiopia (Getahun, 2008). The production systems are generally characterized by low inputs and technologies, feed scarcity and disease challenge (Alemayehu, 2006).

The production systems description should be followed by breed characterization. Preliminary identification of breeds or populations involves phenotypic characterization and the first step of it is assessing the variation of qualitative and quantitative traits (Delgado et al., 2001). In Ethiopia, several on-farm and on-station morphological characterization of goats have been undertaken since the onset of goat research in mid-1970s (Aschalew et al., 2000) mainly by universities and research centers.

The morphological characterization need to be complemented by molecular characterization which broadly involves assessment of the level of genetic diversity and population structure (FAO, 2012). The most promising method for molecular characterization is the analysis of genomic DNA variation, which started its journey over decades ago through advances in availability of reference genomes and development of high-throughput genotyping platforms. With whole-genome sequencing (WGS) of different Ethiopian sheep and goat breeds, researchers have provided a comprehensive insight into the genetic basis of adaptive variation of sheep (Wiener et al., 2021) and goats (Berihulay et al., 2019) in different environments. Such studies help the design and implemention of improvement programs in the context of unique quality/ies a population has (Dadi et al., 2008b).

Appropriate definition of smallholder farmers’ breeding objectives is crucial to design and implement suitable breeding programs (Gizaw et al., 2010, Wurzinger et al., 2011). Four different methods have been implemented to identify breeding objective traits. These include semi-structured questionnaire, choice card experiment, focus group discussion and ranking of live animals. While the first three methods were often used by many scholars (Gizaw et al., 2010; Mirkena, 2010; Duguma et al., 2011; Abegaz et al., 2013; Hagos et al., 2018; Oumer et al., 2019), the last method was brought forth by Mirkena (2010). Live animal ranking has two forms: own-flock ranking and group-animal ranking. One can use combination of the methods to determine the breeding objective traits.

Simulation of alternative breeding schemes is very essential before a given breeding program is implemented. To this end, various alternative breeding schemes have been simulated for Ethiopian indigenous goats (Abegaz et al., 2014; Jembere et al., 2019) and sheep (Haile et al., 2011; Mirkena et al., 2012; Gizaw et al., 2014). The simulation process requires input parameters such as population, biological and economic parameters and some other parameters including phenotypic standard deviation, economic weight, genetic correlation, heritability and phenotypic correlation of the breeding objective traits. Comparison among alternative breeding schemes could be done based on the predicted annual genetic gain (PAGG), annual monetary genetic gain (AMGG), discounted returns, discounted profits, generation intervals and selection intensities.

Benishangul Gumuz region, located in northwestern Ethiopia, is home for about 446,323 heads of goats (CSA, 2021) and five goat ecotypes (Agew, Arab, Felata, Gumuz, and Oromo) (Getnet et al., 2005). Agew and Gumuz goats are the most studied. For instance, the production system and morphological characterization of both goat ecotypes has been undertaken (FARM-Africa, 1996; Getnet et al., 2005; Hassen et al., 2012a; Abegaz et al., 2013). Genetic diversities and population structures were also quantified using different molecular techniques (Hassen et al., 2012b; Tarekegn, 2016). However, similar studies were absent in Arab, Felata, and Oromo goat ecotypes and hence the genetic worth of these goat ecotypes remain uncovered till now. As effect, little has been known about their production environment, morphometric characterstics, breeding objective traits, genetic diversity, population structure and major genes associated with important traits. The limited available information so far has been based on on-farm survey and recall interviews (Getnet et al., 2005). The overall objective of the study was, therefore, to undertake phenotypic and genetic characterization and design of community-based breeding programs for two indigenous goat populations, namely Arab and Oromo. The goats are named after the ethnic communities who keep them. In order to achieve the overall objective, the following specific objectives were addressed.

1. Characterization of the production systems of Arab and Oromo goat populations in northwestern Ethiopia
2. Description of the morphological characteristics of the two indigenous goat populations
3. Investigation of genetic diversity, population structure and candidate genome regions and functional genes associated with important traits in Ethiopian indigenous goat populations
4. Identification of goat breeding objectives of smallholder farmers based on participatory live animal ranking approaches
5. Formulation of alternative breeding schemes for two indigenous goat populations in two different agro-ecological zones

CHAPTER 2: LITERATURE REVIEW

2.1. Domestication and Distribution of Goat

Goat is the first ruminant to be domesticated along with their close relative sheep (Melinda et al., 2006) around 12,000 years before present (YBP) in the Fertile Crescent (Hatziminaoglou and Boyazoglu et al., 2004; Zeder, 2008; ; Colli et al., 2018) from a unique wild and still living ancestor, the bezoar *Capra aegagrus* (Naderi et al., 2008). Recent studies are showing mosaic domestication in the Fertile Crescent (Daly et al., 2018). Following patterns of human migration and commercial trade, goats quickly spread worldwide after domestication and adapted to a wide range of environments (Fernandez et al., 2006). To date, the global goat population is estimated to be over one billion heads; classified under 662 breeds (FAO, 2017). Of these, over 90% are distributed in Asia and Africa, followed by the Americas, Europe, and Oceania (Skapetas and Bampidis, 2016). Given its geographical location close to the historical entry points, Ethiopia is believed to have been one of the main gateways of introduction of livestock species including goats into Africa (Gifford-Gonzalez and Hanotte, 2011). The first wave of goats reached Ethiopia from the north between 2000 and 3000 B.C. (Rege and Lebbie, 2000). At present, the country has more than 52 million heads of goats (CSA, 2021) which are characterized by their unique adaptive ability to harsh environments.

2.2. Goat Genetic Resources of Ethiopia

Based on their differences in physical characteristics, Ethiopian goat genetic resources were classified in to twelve local breeds, including Abergelle, Afar, Arsi- Bale, Central Highland, Hararghe Highland, Keffa, Long eared Somali, Nubian, Short-eared Somali, Western Highland, Western Lowland and Woyto-Guji (Kasahun and Solomon, 2009). However, based on microsatellite marker analysis there are only eight distinct breeds (Tesfaye, 2004). Recently, Tarekegn

(2016) evaluated the genome-wide genetic diversity and structure of Ethiopian goat populations using SNP CHIP array and regrouped them into seven.

2.3. Ethiopian Goat Production Systems

In tropical countries, livestock production systems are generally complex by their nature and show variations within and between regions. According to FAO (2012), livestock production systems must be defined, described and put in a geographic context. For example, their integration with crop production, climatic condition, management practice, local resource availability, production objectives of the owners, availability of technologies and government policy should be stated.

Different authors classified Ethiopian livestock/small ruminant production systems based on various criteria. Tibbo (2006) broadly classified the country's production system into "modern" and "traditional". Government ranches and small scale urban production systems are the only few places where the "modern" system is practiced while most of the rural areas experienced the "traditional" system. Based on the degree of integration with crop production, mobility and duration of movement, the traditional livestock production system is sub-divided into mixed crop-livestock, pastoral and agro pastoral systems (Abegaz et al., 2008). Limited number of animals per unit area, low productivity per animal, relatively limited use of improved technology and use of on-farm by-products are generally the common features of the traditional production system.

On the other hand, based on prevalence of agricultural activity, Getahun (2008) classified traditional small ruminant production systems into four subsystems: small ruminant in annual crop-based system located in northern, northwestern, and central highlands; small ruminant in perennial crop-based, mostly found in southern and southwestern highlands; small ruminants in cattle based systems, these systems usually exist in agropastoral and semi-arid areas; small ruminant dominated systems found in pastoral and arid areas of eastern and northeastern Ethiopia, where sheep and goats are the dominant livestock species. In general, it is difficult to generalize about the different types of livestock production systems in Ethiopia due to the fact that the country has diverse topography, climate and culture (Alemayehu, 2006).

2.4. Performance of Indigenous Goats

Understanding the performance of small ruminants is crucial to effectively design sustainable genetic improvement programs (Kosgey and Okeyo, 2007). The most important traits of livestock were broadly classified into two categories: productive and reproductive traits (Abegaz, 2014). Recently, functional and adaptive traits have become important. The traits vary among indigenous goats of Ethiopia due to difference in agro-ecology and management condition (Dereje et al., 2015).

2.4.1. Growth Performance

Growth performance traits are the most important traits for meat production. Abegaz (2014) separated these traits as pre-weaning (birth weight, weaning weight and pre weaning growth rate) and post weaning (six months weight, yearling weight and mature weight). Genetic and non-genetic factors were known to affect growth performance of small ruminants (Haile et al., 2002; Taye et al., 2009; Jembere, 2010). Factors such as parity of doe, birth type of kid, sex of kid and season of birth of kid were known to significantly affect growth performances of goats. For instance, kids from first parity does were lighter than kids from higher parity does (Jembere, 2016). Twin born kids were smaller in weight than their single born counterparts (Dadi et al., 2008a; Deribe and Taye, 2013).

2.4.2. Reproductive performance

Good reproductive performance is a precondition for a successful genetic improvement program as it determines production effectiveness. Reproductive performance of goats depends on various factors including age at first kidding (AFK), kidding interval (KI) and litter size at birth (LSB).

The reported average AFK of most Ethiopian indigenous goats is within the range of 12 and 14 months (Dereje et al., 2015). This variation may be due to various factors such as genotype, nutrition, disease or parasitic burden and year and season of birth in which the doe was born (through their effect on feed availability and quality). In addition, birth type could affect AFK. Kids born for twins had longer age at first kidding than their counterpart single born kids.

KI is another main component of reproductive performance. Available reports show that the average KI for indigenous goat breeds varies within the range of 8.5 to 14 months (Dereje et al., 2015). The difference among indigenous goats may arise due to variations in breed, season (Taye, 2008), year of kidding, nutrition, type of mating, parity of does, post-partum body weight and management practice (Gbangboche et al., 2006). In conditions where good management, adequate nutrition and breeding males are available in the flock for most time of the year, shorter KI can be achieved whereas longer KI are mainly due to the result of controlled breeding, poor management and nutrition.

LSB, a trait largely determined by ovulation rate, is reported to be between 1.07 and 1.5 for indigenous Ethiopian goats (Dereje et al., 2015). Ovulation rate is in turn dependent on age of the dam, level of nutrition, type of breed, season and dam body weight at mating and management system (Mukasa-Mugarwa and Lahlou-Kassi, 1995). LSB is the most variable trait reported for indigenous goats of Ethiopia. This shows the presence of huge opportunity to improve the trait through selection and improved management focusing on breeds having better potential for the trait.

2.5. Goat Breed Characterization

Breed characterization encompasses activities such as identification, qualitative and quantitative description, and documentation of populations and production systems. The initial step in characterization is identification of distinct populations. This could be done using morphological (phenotypic) characters and/or molecular data (Gizaw et al., 2011; FAO, 2012). However, careful selection of the type and number of morphological characters, suitable analysis and most importantly combined analysis of morphological and molecular data has been suggested to reconcile the two approaches and support each other (Gatesy and Arctander, 2000).

2.5.1. Phenotypic/Morphological Characterization

FAO (2012) defined phenotypic characterization as the process of identifying distinct breed populations and describing their external characteristics and production environments, taking in to consideration the "natural" environment, management practices and common uses to which the animals are put, as well as social and economic factors such as market orientation, niche marketing opportunities and gender issues. In other words, phenotypic characterization does mean the description of breeds in terms of external characteristics (like coat color, ear type and shape, horn shape and type), quantitative measurements (such as height at wither, heart girth, body length, ear length), production traits (body weight, milk yield) and reproductive traits (such as age at first kidding, litter size) (Tesfaye, 2004; FAO, 2012).

Phenotypic characterization is a comparatively easy and cheap tool of breed characterization. However, morphological traits are highly affected by natural selection, environmental effects and by sometimes strong genetic and environmental correlations and interaction. Thus, it should be supported by molecular characterization (Gizaw et al., 2011).

2.5.2. Molecular Characterization

Molecular characterization involves describing and classifying of livestock breeds and species at molecular level by measuring frequencies of genotypes and alleles, degrees of polymorphism, allelic diversity (observed and expected hetrozygosity) and genetic distances (Toro et al., 2009; Gizaw et al., 2011). Tools for molecular analysis are broadly classified as biochemical (protein) polymorphisms and molecular DNA. Protein (allozymes) polymorphisms were the first markers used for genetic studies in livestock. However, the number of polymorphic loci that can be assayed, and the level of polymorphisms observed at the loci are often low, which greatly limits their application in genetic diversity studies (Toro et al., 2009). With the development of new technologies, molecular polymorphisms (nuclear DNA) have become the markers of choice for molecular based surveys of genetic variation. Different types of markers were available to detect polymorphisms in nuclear DNA, including randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLP), restriction fragment length polymorphisms (RFLP), microsatellites, single nucleotide polymorphisms (SNPs) and high-throughput sequencing platform (Baumung et al., 2004; Lai et al., 2016; Wang et al., 2021).

2.6. Selection signature analysis

The availability of genome-wide sequence data has enabled the mapping of signatures of selection and discovery of quantitative trait loci (QTL) for various traits (Lai et al., 2016; Guo et al., 2018). In this context, numerous studies of whole genome sequencing have been conducted to identify potential genes/genomic regions associated with important traits including production, reproduction and adaption in various livestock species such as goats (Lai et al., 2016; Lee et al., 2016; Li et al., 2017; Guang-Xin et al., 2019; Tao et al., 2021; Wang et al., 2021), sheep (Yang et al., 2016), cattle (Taye et al., 2017) and pig (Li et al., 2014). However, there are no such studies on the Ethiopian indigenous goats except Berihulay et al. (2019) and Denoyelle et al. (2021). Detail information about genes responsible for economic traits in goat is available (see the review by Siddiki et al., 2020).

2.7. Breeding Goal Definition

Identifying the smallholder farmers’ breeding objective traits is crucial to design appropriate breeding programs (Wurzinger et al., 2011). Four different methods have been implemented to identify the breeding objective traits; for sheep and goats in Ethiopia. These include semi-structured questioner, choice card experiment, group discussion and ranking of live animals. While the first three were often used by many scholars (Mirkena, 2011; Duguma et al., 2011; Abegaz et al., 2013; Hagos et al., 2018; Oumer et al., 2019), the last method was brought forth by (Mirkena, 2011). It has two forms: ranking of own animals with known history and ranking of animals with unknown history. One can use combination of the methods to determine the breeding objective traits for a given breed. In the present study, both methods adapted from (Mirkena, 2011) were applied.

2.8. Goat Genetic improvement strategies in Ethiopia

The most common approach implemented in many developing countries, including Ethiopia, is centralized/on-station crossbreeding program, usually a nucleus breeding unit established at a central station, entirely managed and controlled by governments with minimal, if any, participation by farmers (Haile et al., 2018). To this extent, many crossbreeding programs were undertaken in Ethiopia. For example, on-station crossbreeding between Ethiopian highland goat and Saanen in Adami-Tulu research center (Galal et al., 1982), Adal and Saanen in Melka Werer research center, Hararghe highland and Anglo-Nubian, Somali and Anglo-Nubian, and Hararghe highland and Toggenberg in Haremaya university (the then Alemaya University) and Hawassa university (the then Awassa college of agriculture) were some of the programs. However, the institutions were blamed for not yielding significant impact at farm level (Duguma, 2010; Jembere, 2016). In most cases, the crossbreeding programs were not successful because most of them were done without sufficient pretesting of the suitability and adaptability of the exotic breeds and their resulting crosses to local production systems or conditions, and with no clear strategy concerning what the final genotype would be. Genetic erosion of these local populations and breeds has occurred where indiscriminate crossbreeding with local populations has been practiced (Haile et al., 2018).

A recent alternative approach is community based breeding program (CBBP). It is defined as a program carried out by communities of smallholders, often at subsistence level (Sölkner et al., 1998); and is a design of breeding scheme that is deemed suitable for smallholder farming system (Gizaw et al., 2014). Such programs consider the needs, views, decisions and active participation of farmers from inception through to implementation. Their success is based upon proper consideration of farmers' breeding objectives, available infrastructure, participation and ownership (Sölkner et al., 1998; Wurzinger et al., 2011; Mueller et al., 2015; Haile et al., 2018). In Ethiopia, CBBPs have been established since 2009; for sheep (Gizaw et al., 2009; Duguma et al., 2011; Mirkena et al., 2012) and goats (Abegaz et al., 2014; Alubel, 2015; Zergaw et al., 2016; Jembere et al., 2019).

2.9. Simulation of Alternative Breeding Schemes

There are two methodological approaches, stochastic and deterministic, for simulating alternative breeding schemes. Haile et al. (2011) and Abegaz (2014) gave the pros and cons of the two approaches as follows: a stochastic simulation generates breeding and phenotypic values for each simulated individual while deterministic simulation uses a whole population model. Stochastic simulation is relatively simple, but requires repeated running of a simulated breeding program. Deterministic methods are widely used in livestock breeding plan because of its short computational time requirement and giving more insight into the genetic gain and inbreeding of the breeding programs.

ZPLAN is the most commonly used computer program that uses deterministic method. The first version was developed by Karras (1984) using the gene flow method and selection index. The program is based on comprehensive evaluation of both genetic and economic efficiencies of breeding strategies considering one cycle of selection. Important outcomes of ZPLAN include annual monetary genetic gain (AMGG) for the aggregate genotype, annual genetic gain for individual trait, discounted return and discounted profit for a given investment period. For further information on ZPLAN, see Nitter et al. (1994).

Depending on the particular situation, in the design and evaluation of a potential breeding program, basic decisions such as defining of tiers in the breeding plan, defining of sexes in the selection group and indication of paths of gene transfer from one group to the other must be taken and selected in ZPLAN (Haile et al., 2011). Then, input parameters (input files) such as population, biological and economic cost parameters are defined by the users. Furthermore, phenotypic and genetic constants are required for modeling alternative breeding plans.

CHAPTER 3: MATERIALS AND METHODS

The dissertation is based on five manuscripts. The general materials and methods followed in the manuscripts are given in this section and the detailed methodologies are available in the specific papers appended herein. **Papers I, II, IV and V** targeted two indigenous goat populations, namely Arab and Oromo while **Paper III** targeted additional Ethiopian indigenous goat populations and goats from Africa, Asia and Europe for comparison purposes.

3.1. Description of the Study Area

The study was conducted in Assosa zone, Benishangul Gumuz region, northwestern Ethiopia (BGR-NWE). Description of the study areas of all manuscripts is almost the same, except **Paper III,** and detailed description is found in **Papers I and III**.

3.2. Sampling Strategies and Data Collection

In this section, sampling strategies and data collection procedures for **Paper I, II, IV and V** will be presented followed by the sampling strategies and data collection procedures for **Paper III**.

To know the distribution of the targeted goat populations and to select representative districts, a focus group discussion was organized with livestock experts working in Assosa zone. This zone is the home tract of both Arab ad Oromo goats (Getinet et al., 2005). Goat population size (based on the available data from the districts' agricultural offices), presence of communal grazing lands, access to market and road, relative significance of goats to the livelihood of the communities and willingness of the farmers to participate in CBBP were the criteria used to select the districts.

Based on the outcome of the discussion, two representative districts (Bambasi and Homosha) were selected. Oromo goat population predominates in Bambasi district whereas Arab goat population prevails in Homosha district. Field visits and additional discussions with livestock experts and key informants in the respective districts were made and then four peasant associations (PAs)—the lowest administrative units in Ethiopia, were selected from each district based on the same criteria used to select districts. The selected PAs were Bambasi 02, Mutsa 01, Shebora, and Womba-selama from Bambasi and Gumu-Abush, Sherkole, Tumet, and Tsore-almetema from Homosha. Probability proportional to size (PPS) sampling technique was employed to select target households from each PA. The calculated numbers of households following the PPS sampling technique were 59 (Mutsa 01), 42 (Bambasi 02), 33 (Shebora), and 29 (Womba-selama) from Bambasi and 22 (Gumu-Abushu), 25 (Sherkole), 21 (Tumet), 18 (Tsore-almetema) from Homosha. In general, a total of 249 households, out of which 163 from Bambasi and 86 from Homosha, were selected for questionnaire data collection/interviewing (**Paper I**). Only households who had a minimum of three adult goats were included in the study.

For the morphological characterization study, three goats per household, a total of 747 goats (258 Arab goats and 489 Oromo goats) were evaluated. Ten qualitative variables and nine morphometric measurements were recorded from each goat in the morning before they were released for grazing. The records and measurements were taken as described by FAO (2012) (**Paper II**).

In the phenotypic ranking experiments (**Paper IV**), we collected data from two PAs in each district. The same criteria that we used to select the districts were applied here to select PAs. The selected PAs and the number of households in brackets were Mutsa 01 (59) and Bambasi 02 (42) from Bambasi and Sherkole (25) and Tumet (21) from Homosha. In the own-flock ranking experiment, the goat keepers were asked to choose their 1st, 2nd and 3rd best and the most inferior does among the breeding does in their flock. Reasons for the ranking and life history of the ranked does were recorded. In the group-animal ranking experiment, twelve breeding does and twelve breeding bucks from the Arab goats and the same number of does and bucks from the Oromo goats were randomly selected and marked. Animals of same sex were randomly assigned to four groups in Arab (three animals each) and the same was applied in Oromo. Twelve farmers from the Arab goat keepers and the same number of Oromo goat keepers, who have not known the selected animals, were then invited to rank the animals. Each farmer was asked to rank the three animals in each group as 1st, 2nd and 3rd, and the reasons for ranking. The farmers were then provided with the history of each individual animal and asked whether they would re-rank the animals or not. This procedure was continued eight times until a farmer covered all groups of the animals (**Paper IV**).

For the simulation study (**Paper V**), the results of two papers, **Papers I and IV,** were used to determine breeding objective traits. Based on results of the two papers, three measurable breeding objective traits were selected for each population. The traits were: i) body size, twinning ability and kidding interval for Arab goat; and ii) body size, twinning and mothering abilities for Oromo goat. The selection criteria were six-month weight (6mw), litter size at birth (LSB), litter size at weaning (LSW) and KI for body size, twinning ability, mothering ability and reproduction performance, respectively.

The selection groups were breeding bucks (BB), breeding does (BD) and production does (PD). The defined selection paths were: 1) bucks to produce breeding bucks (BB > BB), 2) bucks to produce breeding does (BB > BD), 3) does to produce breeding bucks (BD > BB), 4) does to produce breeding does (BD > BD, 5) bucks to produce production does (BB > PD) and 6) does to produce production does (PD > PD). The flocks from 60 households with an average of 7 breeding does per household were considered as one breeding unit for Arab while the flocks from 60 households with an average of 6 breeding does per household were considered as one breeding unit for Oromo. The period for which breeding does and bucks remain in the flock were adopted from previous study on indigenous sheep breeds in Ethiopia (Mirkena et al., 2012). Conception rate, kidding rate and kid survival to six month of age were based on published literature. The kidding interval and kid size at birth were obtained from monitoring data generated on the two goat populations. The rest biological parameters were derived from **papers I** and **IV.**

Regarding the cost parameters, only costs of additional activities to the normal management practices were considered (Nitter et al., 1994). These were enumerator salary, cost of items for animal identification, cost of stationary materials and cost of drugs. The costs were computed as of late March 2019 (1 EURO = 1.1374 USD, 1 USD = 28.8439 Ethiopian birr and 1 EURO = 32.8070 Ethiopian birr) when all the information were gathered and compiled from the study area. The phenotypic standard deviations were obtained from the respective data generated on the two goat populations. Economic weight for each trait was computed using indices from goat keepers' trait preference (**Paper I**). Indices of the selected breeding objective traits were scaled to unity and inversely weighted by additive genetic standard deviation (σ_a) of each trait. Similar approach was recommended by FAO (2010, page 73) when only few socio-economic data are available as in the present case. Genetic parameters are lacking for Arab and Oromo goat populations. Hence, published reports on goats (Abegaz et al., 2014; Jembere et al., 2017) and sheep (Mirkena et al., 2012) were consulted to estimate these parameters.

3.3. Blood Sample Collection and DNA extraction

A total of 30 unrelated individual goats representing three Ethiopian indigenous goat populations (Arab, Felata and Oromo) were used for the molecular study. Whole blood samples were collected by puncturing the jugular vein using EDTA coated vacutainer tubes. We extracted genomic DNA at the International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, using DNeasy® Blood and Tissue kit (https://www.QIAGEN.com) following the manufacturer's protocol. The quality and quantity of the isolated DNA were evaluated using a NanoDrop2000 spectrophotometer (Thermo Fisher Scientific, Wilmington, DE) and 1.5% gel electrophoresis, respectively. The construction of the sequencing libraries and actual sequencing were performed on the Illumina high-throughput sequencing platform NovaSeq 6000^{TM} by Tianjin Noozhiyuan Technology Co., Ltd (**Paper III**).

Genotype data of 60 animals including four populations from Ethiopia (Abergelle, Keffa, Gumuz and Woyito-Guji), four populations from East (Kenya: Boran), north (Morroco: Unknown), south (Malawi: Thyolo) and west (Mali: Guera) Africa, one population from Europe (France: Saanen), and one population from Asia (China: Tibetan) obtained from VarGoats project (available in the European Nucleotide Archive (ENA project number PRJEB37507) in FASTQ format and from which we extracted filtered genotyping data were included to assess the genetic variation and history of Ethiopian goat populations at national, continental and global levels (**Paper III**).

3.4. Data Analyses

Survey data (**Paper I**) were analyzed using Statistical Package for Social Sciences version 22 (SPSS, 2013). Indices were calculated to provide ranking of (a) the purposes of keeping goats and (b) the trait preference and selection criteria of goat keepers in reference to the formula: Index = Sum of [3 for rank 1 + 2 for rank 2 + 1 for rank 3] given for an individual reason divided by the sum of [3 for rank 1 + 2 for rank 2 + 1 for rank 3] for overall reasons.

The data collected in **Paper II** were analyzed using R statistical software version 3.5.2 (R Core Team, 2018). We used ‘gmodels package’ (Gregory et al., 2018) to analyze qualitative data, ‘lsmeans package’ (Russell, 2016) to analyze quantitative data, ‘dplyr package’ (Hadley et al., 2020) to compute Pearson’s correlation coefficient (r) between BW and LBM. The model used to analyze the effect of age and goat type on linear body measurements (LBMs) and the regression equation used to regress live body weight (BW) on linear body measurments (LBMs) are found in **Paper II.**

The molecular data (**Paper III**) were analyzed by employing various software. The VCFtools (v.0.1.15) (Danecek et al., 2011) was used to estimate population genetic diversity metrics such as expected (*He*) and observed (*Ho*) heterozygosity, nucleotide diversity (π), inbreeding coefficient (*F*), heterozygous/homozygous (*het/hom*) ratio and Polymorphic SNPs (*Pn*) in each population. We performed principal component analyses (PCA; Jolliffe, 2002) with Plink 1.9 (Purcell et al., 2007) and admixture analysis with ADMIXTURE v.1.3 software (Alexander et al., 2009) to determine population structure. We also used the maximum likelihood tree-based approach implemented in TreeMix (Pickrell and Pritchard, 2012) to evaluate historical relationships and interactions (gene flow) within and between the goat populations (**Paper III**). Within-group pooled heterozygosity (*Hp*) (Rubin et al., 2010) and genetic differentiation based on *F*st (Weir and Cockerham, 1984) were used for selection signature analysis. We annotated the candidate regions on the Caprine reference genome (ARS1) assembly with the *Ensembl BioMart* tool (http://www.ensembl.org/biomart) and performed functional enrichment analysis of the annotated genes using DAVID v6.8 (Huang et al., 2009) (**Paper III**).

The phenotypic ranking experiment data (**Paper IV**) were analyzed with R (R Core Team, 2020). We used ‘gmodels package’ (Gregory et al., 2018) to analyze the proportion of breeding doe and buck traits preferred by goat keepers in both experiments and rank proportions before and after provision of life history information in group-animal ranking experiment. Similarly, we used the ‘lsmeans package’ (Russell, 2016) to analyze the Mean ± SE values for age and some production and reproduction traits fitting the rank as fixed effects in the model.

The computer program ZPLAN (Willam et al., 2008) was used to simulate alternative breeding programs (**Paper V**). In the study area, there was no distinction between the breeding and production tiers, i.e., the farmers are both breeders and producers. In this extent, we considered community based one-tier selection scheme as the optimal breeding program for both populations. Thus, the following four alternative schemes were simulated: 1) Scheme 1 (SCM1): 2 years of buck use and 10% selection proportion, 2) Scheme 2 (SCM2): 2 years of buck use and 15% selection proportion, 3) Scheme 3 (SCM3): 3 years of buck use and

10% selection proportion, and 4) Scheme 4 (SCM4): 3 years of buck use and 15% selection proportion.

CHAPTER 4: RESULTS

4.1. Indigenous goat production system and breeding practices

While 38.6% of households in the Oromo goat keepers had some level of formal education (primary, secondary, adult education), a significantly ($p < 0.01$) lower proportion (22.1%) of respondents among the Arab goat keepers were literate. Complete absence of record keeping and identification of goats was observed among the interviewed households. There was a significant difference ($P < 0.01$) in the average number of goats per household. Higher numbers were observed amongst Arab goat keepers (12.5 ± 4.0). Breeding does and kids constitute about 60% of the flocks. Income generation, meat production and saving were the most frequently stated reasons of keeping goats. None of the interviewed households in this study kept goats for milk production. Body size, twining ability, coat color and kid growth, in that order, were considered the most important traits in selecting breeding does whereas body size, growth rate, coat color and libido were found to be the most important attributes for selection of breeding bucks. Mating of goats was predominantly uncontrolled. Communal grazing areas and lack of awareness about the deleterious effects of inbreeding were the main reasons mentioned by the goat keepers. Own flock, bucks borrowed from neighbors or communal bucks and purchased bucks were the main sources of breeding bucks. Castration was a common phenomenon in the study area and fattening was found to be the most common reason for castration, followed by prevention of unwanted mating by bucks with undesirable traits including bad temperament. However, during the focus group discussions, it was revealed that bucks with good body conformation that can potentially be fattened were subjected to castration (**Paper I**).

4.2. Morphological diversity

The chi-square test revealed that all categorical variables, except wattle presence, showed significant ($P < 0.001$) difference between the Arab and Oromo goat populations. White in Arab goats (33.72%) and brown in Oromo goats (27.81%)

were found to be the most dominant coat color types while black was the least frequent in both populations. Amongst the mixed coat colors, white and black with white dominant is the foremost coat color observed in both Arab and Oromo goats. Considering other categorical variables, most of the Arab and Oromo goats were characterized by straight head, straight horn oriented backward, lateral ear, absence of wattle and ruff and short and smooth hair. Pair wise mean comparisons between the two goat populations showed significant differences for all quantitative variables except horn length and ear length. Oromo goats have significantly ($p < 0.001$) higher average measurements for body weight, chest girth, body length, wither height and pelvic width than Arab goats (**Paper II**).

The correlation analysis between body weight (BW) and linear body measurements (LBMs) showed that BW had positive and highly significant ($p < 0.001$) correlations with all LBMs except with EL in the Arab goats. The strongest correlation was between BW and CG ($r = 0.95$ in Arab goats and 0.92 in Oromo goats). In the multiple stepwise regression analyses, we found seven parameters (CG, BL, RH, PW, HL, WH and EL) for Arab goats and five parameters (CG, EL, CW, BL and HL) for Oromo goats to be significant ($p < 0.05$) in predicting BW from LBMs. In the present study, high coefficient of determination (R^2) that ranged between (90–96%) in Arab goats and (85–86%) in Oromo goats and low residual mean square (MSE) values between 2.11 to 5.00 in Arab goats and 2.72 to 3.04 in Oromo goats were recorded using the regression analyses (**Paper II**).

4.3. Genetic Diversity, Population structure and Selection Signature

We obtained 38.89 million high quality variants, including 90.39% SNPs and 9.61% InDels, in 13 populations ($n = 78$ individuals) (**Paper III**). The highest number of SNPs (18,266,925) and InDels (2,033,758) were detected in Unknown goat; while the lowest number of SNPs (14,389,837) and InDels (1,739,360) were identified in Saanen and Gumuz goats, respectively. The proportions of polymorphic SNPs (*Pn*) ranged from 90.5% to 96%. Keffa goat had the lowest observed hetrozygosity (0.254 ± 0.115) and nucleotide diversity (0.0017 ± 0.001), but the highest rate of inbreeding (0.261 ± 0.326), Woyto-Guji goat showed the highest observed hetrozygosity (0.335 ± 0.009) and nucleotide diversity (0.0023 ± 0.001), but the lowest level of inbreeding (F = 0.016 ± 0.027). Our results show an inverse relationship between runs of homozygosity (ROH) length and number. The number of shorter ROHs ($\mathrm{ROH}_{100–150\mathrm{Kb}}$) category predominated; the number of these ROHs accounted for 58.18% of the total number of ROHs. However, the frequency of ROHs in this major category varied between populations. Thyolo had the highest number (5897) whereas Saanen had the lowest number (664). The longest ROH category ($\mathrm{ROH}_{>400\mathrm{Kb}}$) was the rarest, wherein the Gumuz population displayed the highest number of ROH while Saanen showed the lowest number of ROH compared with other breeds.

In the PCA, we had classified the analysis into three different categories: global, African and Ethiopian. Results from the PCA plot incorporating the 13 global goat populations distinguished the goats into five groups (East and South African; North African; West African; Asian and European). When the PCA was performed for African goat populations, the result revealed three genetic clusters (East African; North and West African; and South African). When we further ran the PCA with only Ethiopian goats, we found three genetic entities (Fellata; Gumuz and Woiyto-Guji; and Abergelle, Arab, Keffa and Oromo) (**Paper III**).

The population ADMIXTURE analysis revealed the least cross-validation (CV) error at K = 5 suggesting this to be the most optimal number of clusters. Increasing K above 5 did not reveal any detectable population substructure and the population clusters remained the same. At this K, five gene pools were observed. These are designated East African group 1 (EA-G1), East African group 2 (EA-G2), north, west and south African (NWSA), European (EU) and Asian (AS). EA-G1 comprised Arab, Fellata, Oromo, Abergelle and Keffa and EA-G2 included Gumuz, Woyto-Guji and Boran. The NWSA consisted of

Unknown, Guera and Thyolo while AS and EU gene pools are exclusive to Tibetan and Saanen breeds, respectively (**Paper III**).

The Phylogenetic network generated with TREEMIX mirrors the PCA results. While each of North African, West African, European and Asian goat population formed separate cluster, East African (Ethiopian and Kenyan) populations clustered very close to South African goat population. Overall, in the TREEMIX plot, the goats were positioned between French Saanen and Chinese Tibetan and it revealed extensive gene flow between the study populations, which most likely reflect the current and historical intermixing of goat following human socio-cultural and economic interactions. This appears to be a common feature in Ethiopia and most likely the Northeast and eastern Africa region (**Paper III**).

For the selection signature analysis, we used comparative genomics based on the results of PCA, ADMIXTURE and TREEMIX. Here, we explored differences between populations that are exposed to different selection pressures (natural versus artificial) and from different geographic zones (tropical semi-arid versus temperate cold) using two selection signature approaches (*Hp* and *Fst*) between the following population pairs: Gumuz versus Saanen and Fellata versus Saanen. The top windows which passed the significance threshold, for each method ($ZHp \leq -4.0$, $ZFst \geq 4.0$) were used to define the candidate regions under selection. The two methods, separately, identified multiple regions under selection. However, we focused only on the regions that overlapped between the two approaches. For Fellata, the methods, in combination, identified 25 candidate regions spanning 73 genes. Similarly, a total of 142 genes were identified across 39 candidate regions in Gumuz using the two analytical approaches. We performed gene ontology (GO) enrichment analysis for the candidate genes revealed in each population. The five topmost GO terms associated with the candidate genes in Fellata goat include cellular nitrogen compound biosynthetic process (GO:0044271), macromolecule metabolic process (GO:0043170), protein metabolic process (GO:0019538), cellular biosynthetic process (GO:0044249) and gene expression (GO:0010467). The top GO terms associated with the Gumuz candidate genes include osteoclast differentiation (GO:0030316), nuclear division (GO:0000280), amelogenesis (GO:0097186), odontogenesis (GO:0042476) and reproductive process (GO:0022414).

4.4. Doe and Buck Breeding Objective Traits

In the own-flock ranking experiment, doe traits like mothering ability, kid growth, body size, and twinning rate were reported to be the most preferred traits by both Arab and Oromo goat keepers. None of the goat keepers in this study reported the use of goat milk (**Paper IV**). When the body measurement results obtained from the 1st, 2nd and 3rd best and the most inferior does were compared, we obtained reasonable differences. For example, comparing the body weight of 1st best and inferior does, we obtained 2.2 kg difference in Arab goats and 2.66 kg difference in Oromo goats. Similarly, the difference between the two groups (1st best versus inferior) in the number of kids born and kids weaned were 1.83 and 1.70, respectively for Arab. For the same comparison and criteria, the results obtained for Oromo goats were 1.62 and 1.79, respectively.

In the group animal ranking experiment, coat color, body size and body conformation were found to be the most important traits in both Arab and Oromo doe-ranking experiment, but with varying order. Likewise, in the ranking of bucks, coat color, body size, body conformation and body length were the four most important phenotypic traits mentioned by Arab and Oromo goat keepers, but with varying order (**Paper IV**).

After provision of the life history of ranked does, the farmers re-ranked the animals. Of does that ranked as first, second, and third prior to provision of life history, 70.8%, 68.8% and 72.9% of the farmers retained their ranking, respectively. The corresponding values for Oromo goats were 52.1%, 47.9% and 50%. Unlike does, life history information only minimally altered respondents' decision in buck-group ranking. For example, in Arab goats, only 6.2% and 2.1%

of the respondents revised their ranks from 1st to 2nd and 1st to 3rd, respectively. The corresponding values in Oromo goats were 4.2% and 0% (**Paper IV**).

4.5. Predicted Annual Genetic Gains and Breeding Costs

Four breeding schemes were simulated for the two indigenous goat populations (Arab and Oromo) in Ethiopia. The schemes were compared based on predicted annual genetic gains (PAGGs) and profitability. For both populations, PAGG in 6 months weight (6 mw) (kg) were highest in SCM2 followed by SCM1, SCM4 and SCM3, respectively. For all schemes, the 6 mw ranged from 288 to 322 g in Arab and from 342 to 382 g in Oromo flocks. The same sequence of superiority of PAGGs in LSB for both populations and LSW for Oromo goats was observed (SCM2>SCM1>SCM4>SCM3) as in 6 mw, though the values in these traits were relatively small. SCM3 had the best PAGG in KI for Arab goats (**Paper V**).

Among the schemes, SCM2 resulted in the highest marginal profits, followed by SCM1, SCM4 and SCM3. The alternative breeding schemes for Arab were more profitable than for Oromo goat population. The values (1 EURO = 32.8070 Ethiopian birr on late March 2019) ranged from 0.75 to 0.91 in Arab and 0.37 to 0.46 Euro in Oromo. The higher profitability in Arab was due to the fact that the number of initial does and calculated number of candidate males was higher as compared to the Oromo (**Paper V**).

CHAPTER 5: DISCUSSION

Characterization of farm animal genetic resources encompasses all activities associated with the production system, identification, qualitative and quantitative description and documentation of breeds/populations (FAO, 2012). The present study characterized production systems, described morphological characteristics, assessed genetic diversity and population structure, identified breeding objective traits and evaluated alternative breeding schemes for two indigenous goat populations (Arab and Oromo). To this end, whole genome data generated from Fellata goat and genomic data of ten goat breeds accessed from the database were included for comparison purposes. Candidate genes underlying strong selection signatures in Fellata and Gumuz goat populations were identified by combining two approaches: pooled hetrozygosity (*Hp*) and population differentiation (*Fst*).

In **Paper I**, the production systems and breeding practices of Arab and Oromo goat keepers were explicitly described as a first step towards setting up community-based breeding programs in the selected areas of Northwestern Ethiopia. The engagement of young and middle-aged adults in goat farming, as in the present study, might be a good indicator for successful implementation of new approaches such as CBBP. However, complete absence of identification and recording would make the implementation of CBBP challenging. Thus, awareness should be created among goat keepers and simple recording format should be developed. Here, the guidelines developed by Haile et al. (2011) can be adopted for goats in the study areas.

Generation of income was the overriding reason for keeping goats and the same reason was reported elsewhere (Kosgey et al., 2008; Okeno et al., 2011; Abegazetal et al., 2013; Onzima et al., 2018). Consumption of goat milk was considered a cultural taboo by Arab and Oromo goat keepers; goat milk production was thus not mentioned as a trait of importance.

The average number of goats per household is relatively low and hence it is difficult to make selection at the household level. In Haile et al. (2011), it was underlined that the minimum number of breeding female animals should be > 500 for one to undertake selection. This calls for design and implementation of CBBP, where selection takes place within the community flocks. Prioritization of body size, twining ability, growth rate, and coat color among others in selecting breeding males and females in the current study may be related to various reasons. Due emphasis on body size, growth rate and color may be related to observed market conditions—the larger the goat, the higher the price; fast growing goats reach market weight sooner; black colored goats have low market price. Preference for twining ability indicates the genetic potential of Arab and Oromo goats for multiple births.

During the focus group discussions, it was revealed that good-looking and fast-growing males, potentially the “best” breeders, were sold at early age when the goat keepers need money for various economic and social activities. This may result in negative selection. Awareness creation about better performing animals, through the extension service, should be in place. Strategies should be also designed to retain males that have good potential for breeding. One of such strategies is organizing the goat keepers in cooperatives and facilitates credit service, with minimum interest, when they need money. In addition, it is necessary to castrate mediocre males at the recommended age. Alemu (2009) suggested castration of male goats as soon as the testicles descend into the scrotum, i.e., from a few days of age to 3 weeks. For the study area, castration should be done before the males can serve (i.e., before they reach age at first mating). This can be, on average, as early as 6–8 months of age. In CBBP, it was recommended that selection of breeding males shall be made twice; at three and six months of age (Haile et al., 2011).

The age at first mating for male and female and the age at first kidding of Arab and Oromo goats, respectively, were within the reported ranges of 7–15 and 12–20 months for indigenous goats of Ethiopia (Solomon et al., 2014). The kidding interval also falls within the range of 6–10 months reported for tropical goat breeds (Banerjee et al., 2000). This indicates that the reproductive performance of both Arab and Oromo goat populations is fairly good and in the short term, reproductive traits may not be a priority for intervention. CBBPs implemented in the study area should be directed towards production traits.

The study goats were characterized by wide ranges of coat color patterns and types, among which white in Arab and light brown in Oromo were the predominant colors. In areas such as the study area, which is characterized by intense solar radiation in most times of the year, having high proportion of light coat color is a means of adaptation and is an indication that the study goats were not thermally stressed and hence their productivity not compromised. They are also characterized by smooth hair has an advantage to adapt the hot environment as it permits conventional heat loss from the animal surface and also ensure easy disposal of dirt (Yakubu et al., 2010).

On the basis of wither height, adult goats can be classified as large (> 65 cm), small to medium (51–65 cm) and dwarf (< 50 cm) (Devendra et al., 1983). Accordingly, both Arab and Oromo goats can be considered as small to medium sized breeds.

Positive and highly significant correlations were obtained among quantitative traits with the highest correlation between body weight and chest girth in both goat populations (r = 0.95 in Arab and 0.92 in Oromo goats). Similar findings were reported elsewhere in Ethiopia (Hassen et al., 2012a; Gebreyesus et al., 2013; Ahmed et al., 2016; Zergaw et al., 2016). The correlation results indicate the following important things: i) CG could be the best trait in predicting BW of Arab and Oromo goats, ii) The goat populations have harmonious body conformation and balanced physical growth, and iii) the morphometric traits in the present study are under the same genetic influence due to additive genetic effect and hence selection for one or more traits may consistently improve other traits.

In the regression analysis, seven and five traits in Arab Oromo, respectively were identified to predict BW with high coefficients of determination indicating the strong association and success of LBMs in describing variation in BW. Nevertheless, CG was found to be the most appropriate variable to explain variation in body weights. Hence, BW could be predicted from CG measurement using the regression equation $y = -33.65 + 0.89x$ for Arab and $y = -37.55 + 0.94x$ for Oromo goats, where y and x are BW and CG measurements, respectively (**Paper II**). This is helpful for goat keepers to make selection with better accuracy to avoid errors of visual determination. However, realistically, it may be difficult for farmers to use these equiations given our findings of the level of literacy in the study areas. Hence, it would be better to use these equations to calibrate a weighband for the two breeds which is easier and straightforward to use.

Genetic diversity within the 13 global goat populations is high, as evidenced from the overall average observed and expected hetrozygosity (*Ho* and He) values that exceeded 0.300. This suggests high levels of genome diversitis and the values for most of the individual populations are close to previous studies in Sudanese (Rahmatalla et al., 2017) and Pakistani (Kumar et al., 2018) goats and Egyptian Barki breed (Kim et al., 2016). High genetic diversity within a population that could be attributed to uncontrolled mating is characteristic of large communal populations (Lauvergne et al., 2000). Within population selection may benefit from the within population variation. It can also complement goat community based breeding program (CBBP) in Ethiopia. CBBP, in which selection within a population is exercised, provides a good framework for the implementation of genomic selection in smallholder production systems (Mrode et al., 2018). Among the 13 global goat populations, Keffa demonstrated the lowest level of genetic diversity. This suggests high inbreeding in this goat population which might be due to extensive use of few breeding bucks within flocks. This result is consistent with previous finding that was arrived at using Caprine 52KSNP genotype data (Tarekegn et al., 2021) who reported Keffa is the least diverse among 13 Ethiopian indigenous goat populations. Attention should be paid to this goat population to prevent a loss of goat genetic resources (**Paper III**).

Runs of homozygosities (ROHs) are continuous homozygous genomic segments, at the individual and population levels. The length and frequency of ROH may describe past and recent population history and may also reveal the level of inbreeding within populations, recent population bottlenecks or signatures of positive selection (Szmatola et al., 2019; Ceballos et al., 2018). This is particularly important for African indigenous livestock which is characterized by lack of pedigree record data (Kosgey et al., 2006). In the absence of such data, ROH can be used to describe population history (Zavarez et al., 2015). In the present study, all of the 13 global populations showed their majority of ROH in the short (100–150 Kb) length category, which is in agreement with the results obtained for other goats (Guo et al., 2018; Onzima et al., 2018; Islam et al., 2019). Different ROH distribution patterns were noted for Gumuz and Unknown goat populations, which displayed higher number of ROH than other populations in the long (> 400 Kb) length category. The accumulations of long ROHs in the genome of the two populations enable them to carry deleterious mutations in homozygous form (Szpiech et al., 2013) and is indicative of demographic decline and recent inbreeding (Manunza et al., 2016). The highest number of short ROH in the Thyolo population indicates ancient inbreeding and/or small founder effect (Manunza et al., 2016) (**Paper III**).

A combination of PCA, ADMIXTURE (K = 5) and TREEMIX tools revealed the underlying genetic structure in the global, East African and Ethiopian goat populations. The tools revealed five distinct genetic clusters in the global goat populations. The East African goats, represented here by Ethiopian and Kenyan goats, formed two distinct groups: EA-G1 and EA-G2. Our finding on the sub-grouping of East African goats into two groups accords with previous findings of Tarekegn et al. (2018) and Kibegwa et al. (2016), who performed mtDNA analyses of Ethiopian and Kenyan goats respectively and identified two haplogroups (A and G), suggesting the presence of two genetic groups of goats in East Africa. However, based on the current dataset, it is difficult to infer whether EA-G1 and EA-G2 arrived together or independently. Indeed, the geographic locations of the two goat groups give indirect insights. The fact that EA-G1 populations are found in areas close to the Red sea and Mediterranean coast compared to EA-G2 populations indicate that the ancestors of the two groups have arrived independently, with the arrival of EA-G2 preceding EA-G1. The tools also identified two genetic clusters in the Ethiopian goat populations. Cluster 1: Gumuz and Woyto-Guji; and cluster 2: Abergelle, Arab, Fellata, Keffa and Oromo. Home tracts of Arab, Fellata and Oromo goat populations are very tied up that may facilitate ease of flock exchange between farmers and favored gene flow between goat populations. However, given the geographical isolation between Gumuz and Woyto-Guji, they appeared in one cluster. Likewise, Abergelle and Keffa are far apart yet found very close in the PCA (**Paper III**).

In selection signature analysis, we used two approaches (*Hp* and *Fst*). The methods are based on different algorithms and assumptions and thus if common signatures are detected by two of the methods it suggests good reliability of the results while reducing the likelihood of interpreting false positives. The *Hp* approach is a variability indicator based on allele counts across sliding windows and *Fst* indicates the same but based on an increase or decrease in allele frequency differentiation between populations/breeds. The methods are based on different algorithms and assumptions and thus if common signatures are detected by two of the methods it suggests good reliability of the results while reducing the likelihood of interpreting false positives. In this study, we used both methods to detect the signatures of selection across the autosomes of two distinct Ethiopian indigenous goat populations, including Fellata and Gumuz. The approaches identified overlapping regions that spanned genes associated with litter size (*FLT1, AMHR2, IGF2B2*), coat coloration (*KIT*, *KITLG*, *MITF*), adaptation to arid environments (*ZBTB46*, *ARFRP1*, *STMN3*, *GMEB2*) and body weight (*IGF2BP, MAPK7*) traits in Fellata and Gumuz goats (**Paper III**).

In the phenotypic ranking experiments (**Paper IV**), two experiments were conducted: own-flock ranking and group animal ranking. We observed a general tendency of Arab and Oromo goat keepers towards productive and reproductive traits during the own-flock ranking while they focused on observable physical traits like coat color, body size and body conformation during group animal ranking.

The own-flock ranking results show that Arab and Oromo does generally have good growth and reproductive performance. Based on index values (**Paper I**), body size and twinning ability were found to be the first two most important trait in selecting Arab and Oromo does. Among other traits, Arab goat keepers also mentioned drought tolerance as important trait in selecting breeding animals but this trait was not mentioned at all by the Oromo goat keepers. This finding is clearly associated with agro-ecology. Arab goats are found in semi-arid while Oromo goats inhabit sub-humid areas. The home tract of Arab population is harsher in terms of feed and water shortage in most parts of the year. Similar findings on preference of drought tolerance of goats and sheep in comparable environments were also reported in Ethiopia (Mirkena, 2010; Duguma et al., 2011; Gebreyesus et al., 2013; Abegaz, 2014).

The results obtained from the comparisons made among 1st, 2nd and 3rd best and the most inferior does (**Paper IV**) indicated that farmers' choices of does were precise as confirmed by the objective measurements. This shows that the farmers' indigenous knowledge have significant contribution in selecting the best breeding does. This approach is even more plausible in areas such as the study area, where record keeping is not practiced.

During the group animal ranking, the participants were asked if they change their ranking after provision of the life history information of the ranked bucks. Nearly 92% of Arab farmers and 96% of Oromo farmers maintained their position. The situation was, however, a bit different during doe ranking. Only 70% of Arab farmers and 50% of Oromo farmers did not change their ranking. The likely reason for this is that keepers tended to judge and select female animals based on their reproductive performance apart from physical appearance. The same findings were reported in group-animal ranking for sheep (Mirkena, 2010) and goats in Ethiopia (Abegaz, 2014) and Ankole cattle in Uganda (Ndumu et al., 2008) (**Paper IV**).

The four alternative breeding schemes simulated for Arab and Oromo goats resulted in realistic PAGGs, especially for 6 mw and were comparable with the findings of Abegaz et al. (2014) for 6 mw in Abergelle goat and Dagnew et al. (2018) for yearling weight in Gumuz sheep. On the contrary, Mirkena et al. (2012) reported much higher results for yearling weights of three sheep breeds though it is less realistic to achieve these much gains under on-farm condition. The PAGGs for the rest of the selection criteria were not remarkable implying adequate management actions should be part of the breeding activity (**Paper V)**.

CHAPTER 6: CONCLUSIONS AND RECOMMENDATIONS

Breeding programs aimed at genetic improvement of Arab and Oromo goats need to consider the multiple functions of goats and goat keepers' trait preference. Given large number of traits identified in the present study, it would be useful to include only few priority traits to keep the breeding programs as simple as possible and for easy implementation under smallholders' circumstances. Based on the results of **papers I, IV and V,** body size, twining ability, kidding interval and mothering ability were the topmost preferred attributes to select breeding does; whereas body size, libido and growth were the traits used to select breeding bucks in the study area.

Besides to production traits, observable physical attributes like presence of horn and wattle, short and smooth hair (**Paper II**), conformation, coat color and some adaptive traits of breeding does and bucks should be considered in decision making. However, the studies identified pertinent constraints such as absence of record keeping, negative selection, small flock size and utilization of breeding bucks born within the flock. Training and awareness creation about identification, record keeping and negative selection, strengthening the extension service, mixing of household flocks in communal grazing areas and involvement of the goat keepers from inception through to implementation of the CBBP are some of the actions needed.

Compared to Arab goats, Oromo goats were on average wider, bigger and heavier in size and also show considerably higher variation in body size (**Paper II**). This indicates that there would be a good opportunity to select best young breeding males for genetic improvement aimed at increase meat production (improve growth rate and conformation) of goats in the study area. The correlation analysis has showed that chest girth had the highest association with body weight and hence it can be used to estimate weight using regression equations.

High genetic diversity was recorded within the indigenous Ethiopian goat populations (**Paper III**). This can complement goat community based breeding program (CBBP) in Ethiopia as CBBP provides a good framework for the implementation of genomic selection in areas such as the study area where smallholder production systems prevails.

In general, design and implementation of the CBBP using SCM2 had an advantage over other schemes. To this end, participation of local goat keepers from inception through to implementation should be ensured and their needs and views should be addressed. Furthermore, the CBBP should target only few priority breeding objective traits to make the programs simple and sustainable.

CHAPTER 7: SCOPE FOR FUTURE WORKS

- The attention given to Fellata goat, in the goat research endeavors of Ethiopia, is minimal. In the present study, only molecular characterization was undertaken on this goat population. Future works shall focus on production system, morphological characterization and simulation studies so that design and implementation of appropriate CBBP is possible for Fellata itself.

- Benishangul Gumuz region is one of the hotspot areas for Trypanosomiasis and many livestock species, including goats, found in this area is highly threatened with the disease. In connection to this, it has been postulated that some Ethiopian indigenous goat breeds, particularly goats in north-west, west, and south-west Ethiopia have some level of trypano-tolerance. Hence, the association between the uniform genetic background of Gumuz goat population and reduced susceptibility to this parasitic disease needs further study.

- In the present work, SCM2 was recommended over other schemes. Future works should focus on design and implementation of CBBP for Arab and Oromo goats using this scheme.

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CHAPTER 9: PAPERS

Paper I: Production systems and breeding practices of Arab and Oromo goat keepers in northwestern Ethiopia: implications for community-based breeding programs

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Abstract

We conducted a household survey in the semi-arid and sub-humid parts of Benishangul Gumuz region in northwestern Ethiopia to better understand and describe production systems and breeding practices of Arab and Oromo goat keepers. Multi-stage random sampling was employed to select peasant associations, while probability proportional to size sampling was used to select households. Data were collected from 249 households, out of which 86 were Arab and 163 were Oromo goat keepers that live in semi-arid and sub-humid agroecologies respectively. Personal observations, focus group discussions and structured questionnaires were used to collect data. Data were analyzed using SPSS and results were presented using descriptive statistics and indices. Ninety two percent of Arab and 86% of Oromo goat keepers indicated crop and livestock production as their main occupation. Goats were kept for a variety of purposes. Income generation, meat and savings were the highest priorities. The average flock size owned by Arab goat keepers (12.5 ± 4.0) was significantly ($p < 0.01$) higher than that of Oromo goat keepers (9.9 ± 3.8). Breeding does constituted the largest average flock size followed by kids, young does and young bucks. Body size, twining ability, coat color and kid growth were considered important in selecting breeding does, while body size, growth rate, coat color and libido were the most preferred traits for buck selection. Mating was predominantly uncontrolled mainly due to communal grazing lands. Castration of bucks was significantly ($p < 0.01$) more frequent in Arab goat keepers than in Oromo goat keepers. Arab goats have better reproductive performance than Oromo goats. On average, female goats in the study areas gave first births at the age of 1.2 years, kidded every 7.5 months, stayed on reproduction for about 7.6 years and produced 10.7 kids per lifetime. Compared to Arab goats, Oromo goats had significantly ($p < 0.01$) higher average age at first mating, age at first kidding, kidding interval and reproductive lifetime, but produced lower average number of kids per lifetime. Nucleus breeding schemes are recommended to optimize the limited available resources in the study areas. A single nucleus could serve both Arab and Oromo goat keepers. In conclusion, breeding programs that aim to implement in the study areas should consider the production systems and breeding practices of Arab and Oromo goat keepers appropriately.

Keywords Arab goats, Breeding practices, Oromo goats, Production systems, Traits

Introduction

The goat population of Ethiopia is currently estimated to be 30,200,226 heads (CSA 2017). Based on morphological characterization, the country is endowed with 11 goat populations (Awgichew and Abegaz 2008), even though, the recent molecular study regrouped them in to 7 genetic entities (Mekuriaw 2016). The majority of this goat population is found in large flocks in arid and semi-arid lowlands, while goats in the highlands are widely distributed with very small flock sizes (Solomon et al. 2014). Estimates indicate that the great majority (99.97%) of the goat population in Ethiopia belongs to indigenous breeds (CSA 2017) which are characterized by good adaptation to adverse climatic conditions, resistance to a wide range of diseases and parasitic loads, and ability to better utilize poor quality feeds (Gizaw 2009). Under prevailing and hostile environments, indigenous goats provide their owners with tangible (cash, milk, meat, fiber and manure) and intangible benefits (prestige, saving, insurance, cultural and ceremonial purposes) (Legese et al. 2014).

Despite the large population size, high genetic diversity and multiple functions of goats in the country, present level of productivity is generally very low with minimal contribution to the national economy (Legese and Fadiga 2014). For instance, in 2013, goats contributed only 11% of the total annual national meat production and 1.4% of the milk production (FAOSTAT 2016). There is need to improve goat productivity to meet the protein demand of the ever-increasing human population and alleviate poverty among rural farmers. However, there are some key limiting factors that contribute to low productivity of indigenous goats. Among these constraints, lack of feasible and sustainable breeding programs is an important barrier (Hagos et al. 2018).

Cognizant of this fact, crossbreeding indigenous goats with imported exotic breeds such as Anglo-Nubian, Boer, Saanen and Toggenburg was implemented in the past four decades (Solomon et al. 2014). Even though successful goat crossbreeding programs and developed specialized breeds are available worldwide, attempts to adopt such breeding programs and large size breeds have not been successful in Ethiopia (Ayalew et al. 2003). Recently, community-based breeding programs, born from the previous lessons, are being advocated (Haile et al. 2011; Abegaz et al. 2013; Gizaw et al. 2014). However, design and implementation of such breeding programs require precise description of the husbandry practices (Haile et al. 2011; Wurzinger et al. 2011).

Benishangul Gumuz region, located in northwestern Ethiopia, is home for about 440,719 heads of goats (CSA 2015) and five goat ecotypes (Agew, Arab, Felata, Gumuz and Oromo) (Getinet et al. 2005). Among these ecotypes, Agew and Gumuz goat populations are the most studied. For instance, FARM-Africa (1996), Getinet et al. (2005), Halima et al. (2012a) and Abegaz et al. (2013) undertook on-farm phenotypic characterizations and described the production systems and breeding practices of both goat ecotypes. Their genetic diversity was also quantified using different molecular techniques (Halima et al. 2012b; Mekuriaw 2016). However, the production environments and breeding practices of Arab, Felata and Oromo goat ecotypes were neglected in goat research and development activities of the country. The limited information about the three goat populations so far has been based on on-farm survey and recall interviews (Getinet et al. 2005). Analysis of the husbandry practices, with full participation of the community, are prerequisites to develop sustainable improvement and conservation programs at smallholder levels (Kohler-Rollefson and Rathore 2006; Kosgey et al. 2006). Therefore, the objective of the current study was to describe the production systems and breeding practices of Arab and Oromo goat keepers as a first step towards setting up community-based breeding programs in the selected areas of Benishangul Gumuz region in northwestern Ethiopia.

Materials and methods

Description of the study areas

The study was carried out from December 2017 to February 2018 in the Homosha and Bambasi districts of Assosa zone, Benishangul Gumuz region. The region is located in northwestern Ethiopia and is divided into three zones—Assosa, Kamashi and Metekel (Negasa 2017). The Assosa zone was selected because it is the breeding tract of both Arab and Oromo goat populations (Getinet et al. 2005).

Homosha and Bambasi districts were selected purposively to address the production systems and breeding practices in two different agroecologies, farming systems and goat populations.

The Homosha district is located in a semi-arid agroecological zone of the region bordered by Assosa in the south, Kurmuk in the northwest and Menge in the east (Homosha BoARD 2018). The district extends from 6° 44` to 6° 84` north latitude and from 37° 92’ to 38° 6’ east longitude at an average latitude of 1,373 masl (elevationmap.net 2018). The rainfall pattern is erratic and uneven with a mean annual range of 700–1,200 mm; most rainfall occurs between May and September with the highest rainfall in July or August. The temperature ranges from 20–30°C. The district covers an estimated area of 645.78 km^2, comprising 14 rural and one urban peasant associations (PAs)—the lowest administrative units in Ethiopia. The production systems are mixed crop-livestock and agro-pastoral. The district is known for its limited crop production due to poor soil fertility and unreliable rainfall (Homosha BoARD 2018). Traditional goat production and breeding is practiced in the area.

The second study area, Bambasi district, named after the highest point in Assosa zone (mount Bambasi), is situated in the sub-humid agroecology of the region. It is bordered by OdaBildigilu in the north, Begi and Mao-komo in the south, Menesibu in the east and Assosa in the west. The district is positioned at 9° 45′ north latitude and 34° 44′ east longitude with an elevation of 1,668 masl (Latitude.to, maps, geolocated articles, latitude longitude coordinate conversion 2018). The mean annual rainfall ranges from 900–1,500 mm and the average temperature is 28^{o}C. Dabus river originates in this district and can irrigate up to 51,000 ha of land (Merkorewos 2008). The total area coverage of the district is 2,210.16 km^2, encompassing 41 rural and two urban peasant associations. A mixed crop-livestock system is the dominant production system. Maize, sorghum, finger millet, teff, haricot bean and sesame are among the crops produced in the area; while goat, cattle, sheep, mule, donkey and poultry are the livestock species kept by households (Bambasi BoARD 2018).

Description of goats in the study areas

The Arab goat, named after the Berta/Arab ethnic group, predominates in the Homosha district. It is raised by sedentary agriculturalists and agro-pastoralists and considered dual purpose (used for meat and milk production). The average adult weight of this goat ecotype was estimated to be 38 kg (Getinet et al. 2005). The percentages of qualitative variables observed in the Arab goat ecotype were straight (53%) or straight concave head (29%); horizontal and lobbed ear (86%); straight (36%) or curved (31%) or spiral horn (23%) oriented upward (40%) or backward (34%); patchy pattern (56%) coat and smooth (69%) or white (14%) or black hair (11%). Beard was present in 42% and wattle was present in 30% of the goats. The average measurements of chest girth and height at withers were reported to be 70.9 cm and 68.2 cm, respectively (Getinet et al. 2005). On the other hand, the Oromo goat, named after the Oromo community, is the predominant type of goat in Bambasi district. It is raised by sedentary agriculturalists. This goat ecotype was considered as meat type with an average adult weight of 42 kg (Getinet et al. 2005). The percentages of qualitative variables observed in the Oromo goat ecotype were straight (53%) or curved head (26%); erect ear (64%); straight (40%) and backward horn (47%); patchy coat (54%); short smooth (53%) or coarse (47%) and white and black (23%) or roam hair (11%). The presence of beard (59%) and wattle (56%) were also the features of Oromo goat. The average measurements of chest girth and height at withers were reported to be 73.6 cm and 70.5 cm, respectively (Getinet et al. 2005).

Sampling techniques and sample size

A group discussion was organized with livestock experts working in Assosa zone in order to know the distribution of the targeted goat populations and to select representative districts. Based on the outcome of the discussion, two districts (Homosha and Bambasi) were purposively selected for this study to address goat production systems and breeding practices in two different agroecologies, farming systems and goat populations. After field visits and additional discussions with six livestock experts and five key informants in the respective districts, four PAs were selected from Homosha (Gumu-Abush, Sherkole, Tumet and Tsore-almetema) and Bambasi (Bambasi 02, Mutsa 01, Shebora and Womba-selama). This means, out of a total of 58 PAs in the two districts (Bambasi BoARD 2018; Homosha BoARD 2018), about 14% of the districts were covered by the sampling procedure. Goat population size (based on the available data from the respective districts' agricultural offices), presence of communal grazing areas, relative significance of goats to the livelihood of the communities, access to market and road were the criteria used when selecting the PAs. Eight meetings were held with the communities in the selected PAs in order to clarify the objectives and possible outcomes of the research.

The number of sampled households was determined following the recommended formula (Arsham 2007): $N = 0.25/(SE)^2$; where: N = sample size and SE = standard error. To make the size of the sample selected from each PA proportional to the size of the corresponding PA, the probability proportional to size (PPS) sampling technique was employed as: $W = [A/B] \times N$ (Yadeta et al. 2016); where: W = number of households to be calculated from each selected PA; A = number of households in each selected PA; B = total number of households in all eight selected PAs and N = the calculated sample size.

Accordingly, assuming SE of 3.17% (determined after a pilot study) and 95% confidence level, the calculated sample size (N) was 249. Based on the information obtained from the districts, the number of households living in the selected PAs were 315 (Gumu-Abush), 357 (Sherkole), 301 (Tumet), 259 (Tsore-almetema), 854 (Mutsa 01), 601 (Bambasi 02), 470 (Shebora) and 420 (Womba-selama) (Bambasi BoARD 2018; Homosha BoARD 2018). Therefore, the calculated number of households following the PPS sampling technique were 22 (Gumu-Abushu), 25 (Sherkole), 21 (Tumet), 18 (Tsore-almetema), 59 (Mutsa 01), 42 (Bambasi 02), 33 (Shebora) and 29 (Womba-selama). In general, a total of 86 respondents from Homosha district and 163 respondents from Bambasi district were selected for interviewing.

Finally, households who owned at least four adult goats with a minimum of one year experience in goat husbandry and willing to participate in community-based breeding programs were identified. The list was prepared in each selected PA with the help of data collectors. Respondents were selected from the prepared list using systematic random sampling technique until the calculated sample size of each PA was maintained.

Data collection

Semi-structured questionnaires and formal interviews were used to gather information from the selected households. Data on socioeconomic characteristics, purposes of keeping goats, flock size and composition, trait preferences and selection criteria, mating systems, source of breeding bucks, castration and reproductive characteristics were collected by eight trained enumerators from the PAs with close supervision by the researchers. The questionnaire was tested before the actual survey to ensure that all questions were of sufficient clarity for the interviewees. To generate additional information and validate the data collected from individual farmer interviews, participatory focus group discussions were made. Three elders, one village leader, two women goat owners, two youngsters, one veterinarian and one goat trader participated within the group of 10 participants from each of the selected PA.

Data management and analysis

Data collected from the districts were encoded and fed into MS-Excel (2010) for further analysis using Statistical Package for Social Sciences version 22 (SPSS 2013). Preliminary data analysis like homogeneity test, normality test and screening of outliers was employed before conducting the main data analysis. Chi-square test was employed when required to test the independence of categories or to assess the statistical significance. Indices were calculated to provide ranking of (a) the purposes of keeping goats and (b) the trait preference and selection criteria of goat keepers in reference to the formula:

Index = Sum of [3 for rank 1 + 2 for rank 2 + 1 for rank 3] given for an individual reason divided by the sum of [3 for rank 1 + 2 for rank 2 + 1 for rank 3] for overall reasons.

The rate of inbreeding coefficient (ΔF) was calculated from effective population size (N_e) as: $\Delta F = 1/(2N_e)$. The N_e for a randomly mated population was calculated as: $N_e = (4N_m N_f) / (N_m + N_f)$ (Falconer and Mackay 1996), where, N_e = effective population size, N_m = number of breeding males and N_f = number of breeding females.

Results

General household characteristics

Out of the total of 249 interviewed households, 34.5% kept Arab and 65.5% kept Oromo goats. The overall majority (88.2%) of the household heads were male. The average ± SD age of respondents was 47.1 ± 13.0 years in Arab and 45.1 ± 9.7 years in Oromo goat keepers. While 38.6% of households in the Oromo goat keepers attended primary, secondary and adult education, a significantly ($p < 0.01$) lower proportion (22.1%) of respondents among the Arab goat keepers were literate. Complete absence of record keeping and identification of goats was observed among the interviewed households. The overall average family size of households was 7.94 ± 4.2. The Arab goat keepers have had significantly ($p < 0.05$) higher family size (8.8 ± 3.0) than the Oromo goat keepers (7.5 ± 4.4). The marital status among the Arab and Oromo goat keepers varied significantly ($p < 0.05$). In Arab goat keepers, 98.8% were married and 1.2% were divorced; whereas married and divorced goat keepers represented 89% and 1.6% of the Oromo goat keepers respectively. The rest of the Oromo goat keepers were widowed (6.1%) and single (3.1%). The average privately owned land per household was 2.3 ± 1.8 for Arab and 1.9 ± 1.6 ha for Oromo goat keepers. The private lands were used mainly for crop production and communal areas were available for grazing.

The Arab goat keepers were mainly crop and livestock producers (92%), traders (6%) and civil servants (2%). Likewise, crop and livestock production

(86%), civil service (8%) and trade (6%) were important for Oromo as for Arab goat keepers. Herding of goats was mostly by children (86% of boys vs. 9% of girls) and women (5%) in Arab goat keepers, while hired labor (84%) and children (13% of boys vs. 3% of girls) were responsible for herding in Oromo goat keepers. Goats were herded only during the wet season in Arab and both in dry and wet seasons in Oromo goat keepers. Participation of women in decision making on the goat farming systems varied significantly ($p < 0.05$) among keepers. Women in Arab goat keeping communities participated more frequently than those in Oromo goat keeping communities in purchasing and selling of goats (40% vs. 24%), slaughtering (28% vs. 20%), breeding (36% vs. 22%) and animal health (37% vs. 24%). Overall, the characteristics of the households mentioned above do not seem to be related to animal breeding directly but are important sources of information on the socioeconomic features of the households.

Purposes of keeping goats

Table 1 presents ranks and indices of purposes of keeping goats. Goats were kept for multifunctional roles in the study areas, but the most frequently reported purposes of keeping goats were income generation from sale of live animals (0.40) followed distantly by meat production for home consumption (0.23) and saving (using goats as storage of capital or ‘village bank’) (0.17). While the indices for other purposes were relatively small, keeping goats as a sign of wealth status among the Arab goat keepers (0.12) and for manure production among the Oromo goat keepers (0.10) were of some importance. None of the interviewed households in this study kept goats for milk production.

Table 1: Ranks and indices of purposes for keeping goats

Purpose	**Arab goat keepers (N=86)**				**Oromo goat keepers (N=163)**				**Overall Index**
	Rank			**Index**	**Rank**			**Index**	
	1st	**2nd**	**3rd**		**1st**	**2nd**	**3rd**		
Income	55	17	7	0.40	100	33	14	0.39	0.40
Meat	9	27	17	0.19	24	79	30	0.27	0.23

Milk	0	0	0	0.00	0	0	0	0.00	0.00
Saving	12	15	22	0.17	18	24	53	0.16	0.16
Wealth status	1	19	19	0.12	4	11	26	0.06	0.09
Manure	5	6	18	0.09	16	10	30	0.10	0.10
Skin	4	2	3	0.03	1	6	10	0.03	0.03

N = Number of households

Flock size and composition

The average flock size and composition of goats kept by the households are presented in Table 2. The overall average flock size obtained in the study areas was 11.2 ± 4.0 heads of goats. Arab goat keepers owned significantly ($p < 0.01$) higher average flock size (12.5 ± 4.0) than Oromo goat keepers (9.9 ± 3.8). Breeding does (females above 1 year) constitute the largest overall proportion of the flock (36.7%), followed distantly by kids (males and females less than 6 months) (23.7%), young does (females between 6-12 months) (20.5%), young bucks (males between 6-12 months) (8.5%), bucks (males above 1 year) (7.3%) and castrates (3.4%).

Table 2: Descriptive statistics for Arab and Oromo flocks of goats by age class

Age class	**Arab goat keepers (N=86)**			**Oromo goat keepers (N=163)**			**p-value**
	Mean ± SD	**Range**	**%**	**Mean ± SD**	**Range**	**%**	
Flock size	12.5 ± 4.0	7–28	100	9.9 ± 3.8	3–27	100	**
Flock composition							
Does	4.7 ± 1.6	1–11	37.5	3.6 ± 1.6	0–12	35.9	**
Bucks	0.9 ± 0.7	0–2	7.2	0.7 ± 0.7	0–3	7.3	*
Young does	2.5 ± 1.5	0–11	20.3	2.0 ± 1.3	0–5	20.6	**
Young bucks	1.1 ± 1.0	0–3	8.6	0.8 ± 1.0	0–4	8.4	NS
Kids	2.8 ± 1.2	0–6	22.6	2.5 ± 1.3	0–8	24.8	*
Castrates	0.5 ± 0.8	0–4	3.8	0.3 ± 0.6	0–5	3.0	*

*N = Number of households, SD = Standard deviation, NS = Non-significant, *$p < 0.05$, **$p < 0.01$*

Trait preference and selection criteria

Table 3 summarizes the relative importance of different traits as ranked by the goat keepers for selecting breeding does and bucks. It was found that traits like body size (index = 0.29), twining ability (0.27), coat color (0.17) and kid growth (0.10) were all considered important at both sites and given due emphasis in selecting breeding does. On the other hand, body conformation (wide chest, long body and up right stance) (0.30), growth rate (0.24), coat color (0.20) and libido (0.08) were found to be the most important attributes for selection of breeding bucks. However, divergence among the selection criteria and their indices was observed, indicating that goat keepers have different selection goals depending on their breeding skills and socioeconomic needs. For instance, body size was ranked first (0.35), followed by twining ability (0.21) and coat color (0.17) among Arab goat keepers in selecting breeding does; whereas twining ability was the most featured attribute (0.33), followed by body size (0.23) and coat color (0.17) in Oromo goat keepers. Traits such as kidding frequency, age at puberty, kid survival and mothering ability in does and adaptability, ability to walk long distance, horns, age at puberty, character and pedigree in bucks were mentioned as selection criteria but with lower ranking.

Table 3: Ranks and indices for trait preference in breeding does and bucks

Traits	**Arab goat keepers (N=86)**				**Oromo goat keepers (N=163)**				**Overall Index**
	Rank			**Index**	**Rank**			**Index**	
	1st	**2nd**	**3rd**		**1st**	**2nd**	**3rd**		
Traits for does									
Body size	42	21	11	0.35	44	34	29	0.23	0.29
Coat color	8	20	24	0.17	9	53	36	0.17	0.17
Kid growth	9	11	9	0.11	13	13	23	0.09	0.10
Kid survival	3	9	6	0.06	3	4	8	0.03	0.05
kidding frequency	0	2	5	0.02	0	1	13	0.02	0.02
Twining ability	18	21	14	0.21	71	42	21	0.33	0.27
Mothering ability	5	2	12	0.06	11	13	21	0.08	0.07
Milk yield	0	0	0	0.00	0	0	0	0.00	0.00
Age at puberty	1	0	5	0.02	12	3	12	0.06	0.04
Traits for bucks									
Body conformation	39	14	17	0.31	68	28	26	0.29	0.30
Coat color	14	17	18	0.18	25	47	34	0.21	0.20
Horns	0	3	4	0.02	0	5	1	0.01	0.01

Character	1	4	12	0.04	4	13	21	0.06	0.05
Growth rate	20	24	14	0.24	43	43	29	0.25	0.24
Libido	5	15	11	0.11	1	9	14	0.04	0.08
Ability to walk long distance	0	1	1	0.01	0	0	1	0.001	0.01
Age at puberty	3	2	3	0.03	14	1	15	0.06	0.05
Pedigree	3	5	3	0.04	8	16	11	0.07	0.06
Adaptability	1	1	3	0.02	0	1	11	0.01	0.01

N = Number of households

Breeding practices

Mating system and sources of breeding bucks

Mating of goats was predominantly uncontrolled. For instance, the majority of Arab (69.8%) and Oromo goat keepers (92%) practiced uncontrolled mating (Table 4). Communal grazing areas were the main reason for the absence of controlled mating in 81.7% of Arab goat keepers and 92.1% of Oromo goat keepers. Lack of awareness about the harmful effects of inbreeding was also the reason mentioned by 18.3% of Arab goat keepers and 7.3% of Oromo goat keepers. Most of the Arab (95.3%) and Oromo goat keepers (80.4%) practiced mixing of their flocks during grazing on average with five other flocks in Arab goat keepers and three other flocks in Oromo goat keepers. When goat flocks of households were not mixed and mating was random, average inbreeding rates of 16.6% and 21.4% were estimated for Arab and Oromo goats respectively. On the contrary, when goat flocks were mixed, the estimated change in inbreeding rates were 2.8% and 5.3% for Arab and Oromo goats respectively.

Own flock was the main source of breeding bucks in the study areas. Yet, utilization of breeding bucks born from own flock was significantly ($p < 0.05$) lower in Arab (65.1%) than Oromo goat keepers (81%). When breeding bucks were not reared on the farm, goat keepers used bucks borrowed from neighbors or communal bucks. When breeding bucks were neither reared nor borrowed, keepers purchased bucks from nearby markets. The main reasons for keeping bucks were mating and fattening, or both. Artificial insemination was not used in any of the flocks surveyed. The average service year of a buck was reported to be 3.8 ± 1.5 years in Arab and 4.1 ± 1.3 years in Oromo goat flocks. Subsequently, bucks are usually castrated and fattened for sale or slaughter. The average replacement age for breeding bucks in the Arab group appeared to be relatively better for the prevention of inbreeding.

Table 4: Mating system and sources of breeding bucks

Descriptor	**Arab goat keepers (N=86) (%)**	**Oromo goat keepers (N=163) (%)**	χ^2	**p-value**
Mating system			21.11	**
Controlled	26 (30.2)	13 (8)		
Uncontrolled	60 (69.8)	150 (92)		
Reasons for uncontrolled mating			7.13	**
Communal grazing land	49 (81.7)	139 (92.1)		
Lack of awareness	11 (18.3)	11 (7.3)		
Mixing of individual flocks			10.2	**
Yes	82 (95.3)	131 (80.4)		
No	4 (4.7)	32 (19.6)		
Source of breeding buck			12.5	*
Own flock	56 (65.1)	132 (81)		
Neighbor/communal	24 (27.9)	17 (10.4)		
Purchased from market	6 (7)	14 (8.6)		
Purpose of keeping breeding bucks			7.14	**
Mating	58 (67.4)	134 (82.2)		
Fattening	16 (18.6)	15 (9.2)		
Mating and fattening	12 (14)	14 (8.6)		
Service year of a buck (Mean ± SD)	3.8 ± 1.54	4.1 ± 1.31		NS
Number of households mixing their flocks (Mean ± SD)	5.6 ± 2.9	4.1 ± 2.5		**

*N = Number of households; SD = Standard deviation, NS=Non-significant, *p < 0.05, **P < 0.01,* χ^2 *= Chi-square*

Castration Practice

Castration of bucks was a common phenomenon in both study sites, but it was significantly ($p < 0.01$) more frequent in the Arab (97.7%) than in the Oromo goat keepers (60.1%) (Table 5). Irrespective of keepers, fattening was found to be the most common reason for castration, followed by prevention of unwanted mating by bucks with undesirable traits including bad temperament. However, during the focus group discussions, it was revealed that bucks with good body conformation that can potentially be fattened were subjected to castration. Castration methods differed significantly ($p < 0.05$) between the two groups of goat keepers.

Households who used modern castration method were proportionally more numerous in Arab (45.3%) than in Oromo goat keepers (36.2%). In contrast, households who used traditional castration method represented 54.7% of the respondents in Arab against 63.8% in Oromo. The traditional castration method involves crushing the vas deferens using a smooth and round stone locally known as ‘alello’ followed by bandaging the testes until they wither from lack of blood flow. Goat keepers who used modern castration took their male goats to a nearby veterinary clinic to use burdizzo, a device used to castrate male animals by crushing the epididymal cord and associated blood vessels leading to the testicles (Kristy et al. 2016). Age at castration ranged from 1.3 to 3.3 years with an average age of 1.9 ± 0.6 years in Arab goat keepers and 2.2 ± 1.1 years in Oromo goat keepers.

Table 5: Summary of castration

Descriptor	**Arab goat keepers N=86 (%)**	**Oromo goat keepers N=163 (%)**	χ^2	**p-value**
Practice of castration			40.36	**
Yes	84 (97.7)	98 (60.1)		
No	2 (2.3)	65 (39.9)		
Reason for castration			1.82	NS
Fattening	70 (83.3)	84 (85.7)		
Control mating	10 (11.9)	7 (7.1)		
Better temperament	4 (4.8)	7 (7.1)		
Castration methods			1.98	*
Traditional	47 (54.7)	104 (63.8)		*
Modern	39 (45.3)	59 (36.2)		
Age at castration (year) (Mean ± SD)	1.9 ± 0.6	2.2 ± 1.1		*

N = Number of households; SD = Standard deviation, NS=Non-significant, *p < 0.05, **p < 0.01, χ^2 _= Chi-square_

Reproductive performance

The results obtained for reproductive performance of Arab and Oromo goat populations are presented in Table 6. There were significant ($p < 0.01$) differences between the two goat populations in their reproductive performance. On average, male Arab goats reached age at first mating earlier than male Oromo goats. Similarly, female Arab goats reached age at first mating earlier and gave first births sooner than female Oromo goats. Additionally, female Arab goats have had shorter kidding interval and reproductive lifetime, but produced more number of kids per lifetime than female Oromo goats.

Table 6: Average reproductive performance of goats as estimated by respondents

Parameters	**Arab goat keepers (N=86)**		**Oromo goat keepers (N=163)**		**p-value**
	Mean ± SD	**Range**	**Mean ± SD**	**Range**	
Age at 1st mating of male goats (months)	7.0 ± 1.0	6–12	7.6 ± 0.9	6–12	**
Age at 1st mating of female goats (months)	7.9 ± 0.9	6–12	8.3 ± 0.7	6–12	**
Age at 1st kidding (months)	13.9 ± 1.7	12–18	14.9 ± 2.4	12–18	**
Kidding interval (months)	7.2 ± 1.8	5–12	7.8 ± 1.1	5–12	**
Reproductive lifetime of does (year)	7.2 ± 2.0	4–15	7.9 ± 1.9	4–15	**
Number of kids born/lifetime/doe	10.7 ± 2.5	5–20	9.7 ± 1.6	5–20	**

*N = Number of households, SD = Standard deviation, **p < 0.01*

Discussion

Young and middle-aged adults were more likely engaged in goat farming. This observation agrees with the report from Dossa et al (2015) who indicated that small ruminant keepers were mainly people of middle age. This might indicate that new approaches such as community-based breeding programs can be successfully implemented given that younger people are generally more receptive to innovations and new technologies than older ones (Adesina et al. 2000). In the present study, women played a significant role in goat production and breeding. Thus, in order to develop sustainable breeding programs, their role has to be properly spelled out. Women need to be involved from inception to implementation. The literacy level of surveyed households was generally low, but the remarkably higher proportion of literate people in the Oromo goat keepers, as discussed by Kosgey and Okeyo (2007), could be an opportunity to implement goat improvement programs that would improve performance and pedigree recording. However, complete absence of recording and identification of goats would make the implementation quite challenging (Haile et al. 2013). There is thus a need to create awareness among goat keepers on the importance of record keeping and individual animal identification. Appropriate, simple and cost-effective recording systems should be developed and provided for them. The recording formats developed by Haile et al. (2011) for ewes and lambs, and the methodologies implemented by Mirkena (2010) and Duguma (2010) can be adopted for the study areas. Both authors developed recording formats and provided a weighing scale with 100 kg capacity and accuracy of 200 g, plain and printed ear tags, and permanent markers to the community.

Income generation was considered the overriding reason of keeping goats. This finding is consistent with earlier studies in developing countries that emphasize the importance of livestock in generating income (Kosgey et al. 2008; Okeno et al. 2011; Abegaz et al. 2013; Onzima et al. 2018). However, milk production from goats was not the objective in the present study. The consumption of goat milk is generally considered as cultural taboo and goat milk is unpopular among keepers. This concurs with the findings in the highland areas of Ethiopia (Abegaz et al. 2013; Legese et al. 2014) and West Africa (Dubeuf 2010; Dossa et al. 2015), but contradicts with studies in pastoral communities of Ethiopia (Hassen and Tesfaye 2014; Biruh et al. 2017; Hagos et al. 2018) and Kenya (Kosgey et al. 2008) that unequivocally showed milk to be the primary reason for keeping goats. Lack of awareness about its nutritional and medicinal values is probably a likely explanation for the low preference and acceptance of goat milk in Ethiopia in general and the study areas in particular. The present study also indicated the intangible benefits of keeping goats. These benefits are often forgotten in conventional evaluation methods used to define breeding objectives which is particularly true in most genetic improvement programs attempted in the tropics (Mirkena 2010). In general, the importance that keepers attach to the multiple functions of goats suggests that community-based breeding programs could, if carefully planned, have good chances of success in the study areas.

The average flock size obtained in the present study is comparable with 10.8 goats per household in Metema (Abegaz et al. 2013). On the other hand, large flock sizes were reported in Benatsemay (54.7), Hamer (63.2) and Dasenech

(37.1) (Biruh et al. 2017) and Abergelle (48.5) (Abegaz et al. 2013). The observed variations in flock size are probably related to the differences in production systems and agroecologies, the role of livestock as a major source of livelihood and availability of land and feed (Solomon et al. 2014). Small flock sizes as in the present study are recognized as one of the limiting factors in applying selection at the household level. This calls for design and implementation of community-based breeding programs, where selection takes place within the community flocks in order to increase selection intensity and effectiveness. The high proportion of breeding females obtained in the present study could imply the practice of retaining female goats for breeding purposes and production of kids. In contrast, breeding males were proportionally lower which could imply the removal of male goats for sale or home consumption, nevertheless, the ratio of breeding males to breeding females was about 1:5, which is much lower than the recommended ratio of 1:25 for tropical traditional production systems (Wilson and Durkin 1988). So, sufficient numbers of male goats were kept in the flock for breeding purposes. Castrated goats represented the lowest share of the flocks.

Goat keepers in the study areas ranked body size/conformation, twining ability, growth rate and coat color as the most important traits in the choice of breeding males and females. Body size and twinning ability were the most preferred traits of breeding does in western Tigray (Hagos et al. 2018). High emphasis on body size/conformation and growth rate in both sexes may be related to observed market conditions—the larger the goat, the higher the price; and fast growing goats reach market weight sooner. However, during the focus group discussions, it was revealed that good looking and fast growing males, potentially the 'best' breeders, were sold at early age while mediocre males were retained. This may result in negative selection for growth rate and body conformation. Goat keepers should be made aware and convinced of the importance of better genotypes for their respective traits of interest. Furthermore, mechanisms should be designed to retain males that have good potential for breeding. In this regard, community level selection of ‘best’ males and using them effectively before they are sold off is suggested. Yet, the selection should be done based on recorded data (own and maternal performance) for the set of agreed traits (Haile et al. 2011). For good reasons, it is important to cull undesirable males before they can serve (i.e., before they reach age at first mating). This can be, on average, as early as 6–8 months of age (Table 6). The preference of goat keepers for twining ability indicates the genetic potential of Arab and Oromo goats for multiple births and the interest of keepers to increase flock size and overall flock productivity. Similarly, coat color preference specifies the importance of this trait in selecting breeding males and females. Plain black was the least preferred, while white and brown were the most preferred coat colors. The preference of white and brown over black is due to the effect of coat color on goat marketing value. For instance, due to cultural taboo, goats with full black coat are not preferred for slaughtering for home meat consumption. Similar observations on the aversion of black coat were reported in Ethiopia by Halima et al. (2012a).

Overall, it would be possible to select for fast growth, large size/conformation, good twining ability (multiple births) and white/brown coat color within Arab and Oromo goats whilst at the same time maintaining their adaptability in the study areas. However, care should be taken when deciding on what trait to improve. Traits that represent a comprehensive breeding goal are mostly complex with components of production and reproduction, e.g., meat production (Kosgey 2004). Recording of such trait and individual animal identification would be, in many cases, difficult in the study areas. Furthermore, the difficulty to measure and value intangible benefits of goats, such as savings and wealth status, presents more complications (Roeleveld 1996). Strategies for genetic improvement that overcome these problems need to be designed. Open nucleus scheme is proposed as a strategy for genetic improvement of goats in the study areas. A single nucleus could serve both Arab and Oromo goat keepers (Mueller et al. 2002).

The predominance of uncontrolled mating and small flock sizes, as discussed by Seleka (2001), increases the rate of inbreeding. However, communal herding, which appears to have been a common practice among keepers in the present study, can minimize inbreeding (Jaitner et al. 2001; Kosgey 2004). For example, when the goat keepers practiced mixing of their flocks, the levels of inbreeding in both sites are minimized below the maximum acceptable level of 6.3% (Armstrong 2006). Community-based breeding programs are the most appropriate to implement in situations where livestock keepers already run their animals together, such as in communal grazing areas (Gizaw et al. 2010a; Gizaw et al. 2011; Haile et al. 2013). However, some breeding male goats were kept up to five years of age in the current study. This is not sound production practice, especially if they are allowed to mate their own offspring (Kosgey 2004). To be successful in community-based breeding programs, unselected, mediocre males should be castrated through agreement of the community sharing the grazing areas (Haile et al. 2011). The mean age of castration in the study areas seems to contradict with what was recommended by Alemu (2009). The same author suggested castration of male goats as soon as the testicles descend into the scrotum, i.e., from a few days of age to three weeks.

Results of reproductive performance demonstrated that the current findings of age at first mating (in both sexes) and age at first kidding were within the ranges of 7–15 and 12–20 months respectively for indigenous goats of Ethiopia (Solomon et al. 2014). Similarly, the kidding interval falls within the range of 180–300 days reported for tropical goat breeds (Banerjee et al. 2000). This indicates that the reproductive performance of both Arab and Oromo goat populations are fairly good. However, the inverse relation of average reproductive lifetime of a doe and number of kids born per lifetime of a doe showed that Arab goats had better reproductive performance than Oromo goats. Arab goats predominate in semi-arid areas whereas Oromo goats are found in sub-humid zones of Benishangul Gumuz region (Getinet et al. 2005). As elucidated by Solomon et al. (2014), the highest values for most reproductive traits in the Ethiopian indigenous goat breeds, except kidding interval and average number of kids born, were observed in goats from arid and semi-arid areas. The average service year of male and female goats obtained in the present study is higher than the Kenyan goats (Kosgey et al. 2008). The same authors reported average service year of male and female goats to be 2–3 and 4–5 years respectively. In general, the reproductive performance of both Arab and Oromo goats is fairly good and in the short term, this parameter may not be a priority for intervention. Community-based breeding programs that aim to implement in the study areas should be directed towards production traits.

Conclusion

Breeding programs aimed at genetic improvement of Arab and Oromo goats need to incorporate the multifunctional roles that goats play in these production systems and focus on those traits that are identified as the most important. Body size/conformation, twining ability and coat color were the most preferred attributes for selecting breeding does and bucks. As an input for setting up community-based breeding programs in the study areas, the study identified constraints such as absence of record keeping, disposal of fast-growing and good-looking bucks through selling or castration, small flock sizes and using breeding bucks born within the flock. All these constraints suggest that action is needed. To start record keeping practices in the study areas, the traditional goat husbandry practices should be improved through training. Strong extension services are vital to create interest and convince the goat keepers about the benefits of better genotypes. Considering the small flock sizes in both study areas, strengthening the existing practice of mixing different goat flocks is suggested. The use of open nucleus breeding scheme is proposed to improve growth rate of goats in the study areas. To start the nucleus, apparently superior male and female foundation animals have to be screened from the base populations. To minimize inbreeding, efforts would be made to have widely distributed base flocks to enable selection of bucks from flocks that do not contribute does. Overall, vital for success and sustainability of community-based breeding programs are the support of national development policy and involvement of the goat keepers at every stage in the planning and operation of the breeding program, while at the same time incorporating their needs, views, willingness, indigenous knowledge, experience and decisions.

Declarations

Ethics approval and consent to participate

The paper meets all applicable standards with regard to ethics and integrity. The corresponding author along with the co-authors submitted this paper with full responsibility and following due ethical procedure. There are no duplicate publications, fraud or plagiarism. Furthermore, the manuscript does not contain clinical studies or patient data.

Consent for publication

Not applicable

Contribution of authors

Oumer Sheriff drafted and organized the manuscript while Kefyalew Alemayehu and Aynalem Haile participated in coordination and drafting the manuscript. All the authors read and approved the final manuscript.

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Competing interests

The authors declare that they have no competing interests.

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Paper 2: Morphological characterization of Arab and Oromo goats in northwestern Ethiopia

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Abstract

Background: An exploratory field research was conducted in Northwestern Ethiopia, to characterize the morphological features of Arab and Oromo goat populations as an input to design community-based breeding programs. Ten qualitative and nine quantitative traits were considered from 747 randomly selected goats. All data collected during the study period were analyzed using R statistical software.

Results: Plain white coat color was predominantly observed in Arab goats (33.72%) while plain brown (deep and light) coat color was the most frequent in Oromo goats (27.81%). The morphometric measurements indicated that Oromo goats have significantly higher body weight and linear body measurements than Arab goats. Positive, strong and highly significant correlations were obtained between body weight and most of the body measurements in both goat populations. The highest correlation coefficients of chest girth with body weight for Arab ($r = 0.95$) and Oromo ($r = 0.92$) goat populations demonstrated a strong association between these variables. Live body weight could be predicted with regression equations of $y = – 33.65 + 0.89\ x$ for Arab goats ($R^2 = 90$) and $y = – 37.55 + 0.94\ x$ for Oromo goats ($R^2 = 85$), where y and x are body weight and chest girth, respectively, in these goat types.

Conclusions: The morphological variations obtained in this study could be complemented by performance data and molecular characterization using DNA markers to guide the overall goat conservation and formulation of appropriate breeding and selection strategies.

Keywords: Body weight, Body measurements, Ethiopia, Indigenous goats, Qualitative variable

Background

In developing countries, goat farming is one of the largest agricultural sectors, and about 35% of the world goat population (heads) is found in Africa [1]. In Ethiopia, the population of goats is estimated at 36.81 million heads [2]. Indigenous goats play vital roles in ensuring food and economic security and cultural benefits of resource-poor households [3]. The productivity of these genetic resources is, however, very low and hence their contribution to the national economy is far below potential [4]. Many interrelated factors including absence of sustainable goat genetic improvement program are identified as important constraints [5]. To plan such program, a good understanding of physical characteristics of goats under their production systems is required [6].

In Ethiopia, morphological characterization of indigenous goats dated back to the mid-1970s [7]. The first attempt was made by the Ministry of Agriculture in 1975 and classified Ethiopian goats into five major groups: Nubian, Highland, Afar, Somali and Long Tailed Gishe [8]. Later, FARM-Africa characterized Ethiopian and Eritrean goats and shown the presence of 14 different goat types [9]. Since then, several on-farm and on-station morphological characterization of goats have been undertaken mainly by Universities and research centers.

Benishangul Gumuz region (BGR), located in northwestern Ethiopia, is home for about 411,503 heads of goats [10] and five goat populations (Agew, Arab, Felata, Gumuz and Oromo) [11]. Among these, Agew and Gumuz goat populations are the most studied. For instance, 2 decades ago, [9] described the morphological characteristics of Gumuz goats. Later, the genetic diversity of this goat type was investigated by [12] using microsatellite DNA markers. Subsequently, [13, 14] undertook phenotypic and molecular characterization of Gumuz and Agew goats. [15] also characterized Gumuz goats using high density SNP CHIPs array. Very recently, [16] investigated the genetic diversity of Gumuz goats using *Caprine* SNP CHIPs array. In general, among the five goat populations found in BGR, most of the goat characterization efforts focused exclusively on Gumuz and/or Agew goat populations. However, Arab and Oromo goats, like many others, deserve to be characterized.

The Arab goats, named after the dominant tribe that generally owns this goat population, are more adaptable to semi-arid areas, trypano tolerant and considered as dual purpose (used for meat and milk production) [11]. On the other hand, the Oromo goats, named after Oromo community, inhabit the sub-humid agro-ecology and known as meat type [11]. Both goat populations provide their owners with tangible and intangible benefits such as cash, meat, manure, prestige, saving, insurance, cultural and ceremonial purposes. However, they are neglected in goat research and development endeavors of the country. The limited available information about the two goat populations, so far, has been based on on-farm survey and recall interviews. The objective of the current study was, therefore, to undertake morphological characterization of Arab and Oromo goat populations and suggest sustainable breeding program in the selected areas of BGR in northwestern Ethiopia.

Materials and Methods

Description of the study area

This study was carried out in two districts of BGR from December 2017 to April 2018. The districts, Homosha and Bambasi (Figure 1), were selected purposively because they are believed to be breeding tracts of Arab and Oromo goats, respectively. Homosha is located in semiarid agro-ecology. It extends from 6° 44′ to 6° 84′ north latitude and from 37° 92′ to 38° 6′ east longitude [17] with an average altitude of 1,373 masl [18]. The temperature ranges from 20–30°C and the mean annual rainfall is 700–1,200 mm. The Arab goats predominate in this district. The second study area, Bambasi, is situated in the sub-humid agroecology and it is positioned at 9°45′ north latitude and 34° 44′ east longitude with an elevation of 1,668 masl [19]. The mean annual rainfall ranges from 900–1,500 mm and the average temperature is 28°C. The Oromo goats are predominant in Bambasi district.

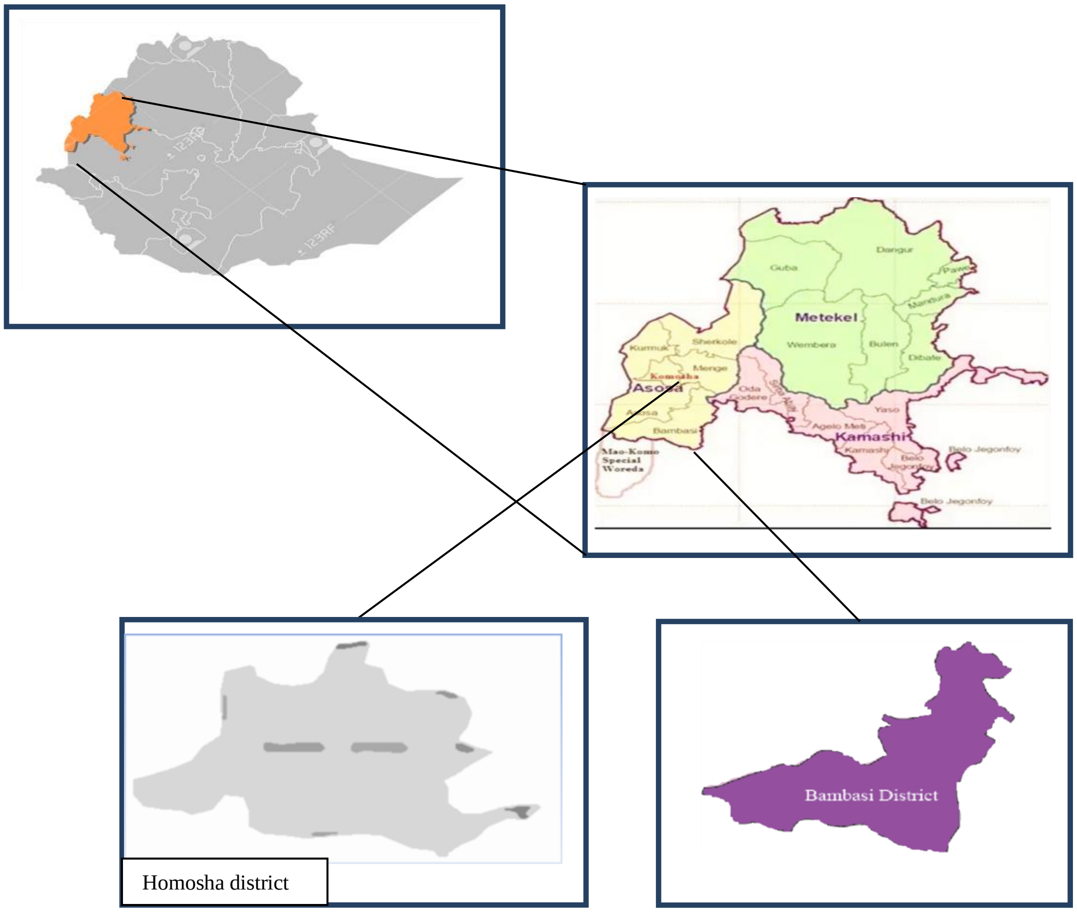

Figure 1: Map of the study area

Sampling techniques and sample size

Two districts (Homosha and Bambasi) were purposively selected for this study. Subsequently, four peasant associations (PAs)—the lowest administrative units in Ethiopia—were selected from each district. The number of sampled households in each PA was determined following the recommended formula [20]: $N = 0.25/(SE)^2$; where: N = sample size and SE = standard error. To make the number of the sampled households from each PA proportional to the size of the corresponding PA, the probability proportional to size (PPS) sampling technique was employed. The PPS was based on the formula: $W = [A/B] \times N$ [21]; where: W = number of households to be calculated from each selected PA; A = number of households in each selected PA; B = total number of households in all eight selected PAs and N = the calculated sample size. Detailed information on the sampling technique and the number of sampled households is given in [22]. Overall, a total of 86 households from Homosha district and 163 households from Bambasi district were selected following the steps in [20] and [21]. Finally, three goats per household were sampled for qualitative records and quantitative measurements. This gives a total of 747 goats (258 Arab and 489 Oromo goats). The goats were classified into six age groups based on their dentition, i.e., kids (< 6 months), young (6–12 months), 1 pair of permanent incisors (1PPI) (1 year), 2PPI (2 years), 3PPI (3 years) and 4PPI (≥ 4 years) [23]. The kids and young goats were differentiated by asking the age of goats from owners while the goats in 1, 2, 3 and 4 and above years were differentiated by observing their dentition. From the total sample size, 629 (84.2%) were female goats. Pregnant does were excluded from measurement to avoid over estimation of body weight (BW) and linear body measurements (LBMs). In the current study, quantitative traits, except BW, are generally named as LBMs.

Data collection

Ten qualitative variables (coat color pattern, coat color type, head profile, horn presence, horn shape, horn orientation, ear orientation, wattle presence, ruff presence and hair type) were recorded by using the standard format adapted from [6] breed descriptor list.

Nine morphometric measurements were also taken from each goat early in the morning before they were released for grazing. The measurements were taken as described by [6]. They included body weight (BW), (the fasted live body weight (in kg)); chest girth (CG), (circumference of the body (in cm) immediately behind the shoulder blades and perpendicular to the body axis); body length (BL), (horizontal distance (in cm) from the point of shoulder to the pin bone); wither height (WH), (vertical height (in cm) from the bottom of the front foot to the highest point of the shoulder); rump height (RH), (vertical height from the bottom of the back foot to the highest point of the rump); chest width (CW), (width (in cm) of the chest between the briskets); pelvic width (PW), (horizontal distance (in cm) between the extreme lateral points of the hook bone of the pelvis); horn length

(HL), (length of the horn (in cm) on its exterior side from its root at the poll to the tip; and ear length (EL), (length (in cm) of the external ear from its root on the poll to the tip). Body weight (kg) measurements were recorded using suspended spring balance in kg with a precision of 0.2 kg. The height measurements (cm) were taken using a graduated measuring stick while the length, width and circumference measurements (cm) were measured with plastic measuring tape. All measurements were taken after restraining and holding the goats in their natural position.

Statistical analyses

All the data collected during the study period were encoded and fed into MS-Excel (2010) and analyzed using R statistical software version 3.5.2, 2018 [24]. However, based on the nature of data, different R packages were used.

During the qualitative data analysis, 'gmodels package' [25] was used to calculate the frequency and percent of qualitative characteristics observed in the two goat populations. On the other hand, the quantitative data were analyzed using the 'lsmeans package' [26]. Tukey's comparison test was used to compare the sub-factors that brought significant differences.

The statistical model used was: $Y_{ijk} = \mu + A_i + G_j + (A \times G)_{ij} + e_{ijk}$

Where, Y_{ijk} = the recorded k (body weight and linear body measurements) in the ith age and jth goat population; μ = overall mean; A_i = fixed effect of ith age (i = 1, 2, 3 and 4; 1 = 1PPI, 2 = 2PPI, 3 = 3PPI, and 4 = 4PPI); G_j = fixed effect of jth goat population (j = 1 and 2; 1 = Arab and 2 = Oromo); $(A \times G)_{ij}$ = interaction effect of age with goat population; and e_{ijk} = effect of random residual error. Due to the fact that only a few male goats at older age classes (3PPI and 4PPI) were available in the study area, male animals were excluded from the model in the analysis of BW and LBMs.

Pearson's correlation coefficient (r) values were computed to assess the relationship between BW and LBM using 'dplyr package' [27]. Live BW was regressed on LBMs using stepwise multiple linear regression analysis. The coefficient of determination (R^2) was used to assess the accuracy of prediction equations between BW and LBMs. Furthermore, MSE (mean square of error) was calculated from each fitted regression equation. In the first step, all LBMs were entered together into the equation for each goat population. Then, a group of variables having the maximum R^2 and minimum MSE were selected. In addition, Akaike’s information criteria (AIC) and the Bayesian information criteria (BIC) were considered. In the second step, the variables which were selected by maximum R^2 and minimum MSE were entered together into the model to find the best fitted regression equation.

$$Yi = \beta 0 + \beta 1X1 + \beta 2X2 + \beta 3X3 + \beta 4X4 + \beta 5X5 + \beta 6X6 + ei$$

Where, Yi = dependent variable (BW); $\beta 0$ = intercept; $X1, \ldots, X6$ = independent variables (CG, BL, WH, PW, HL and EL); $\beta 1, \ldots, \beta 6$ = regression coefficients of the variables $X1, \ldots, X6$; and ei = residual random error.

Results

Qualitative characteristics

The frequency and percent of qualitative characteristics observed in male and female goats of the two populations are presented in Tables 1 and 2. The results of the study showed that plain, patchy and spotted coat color patterns were observed in both goat populations, with maximum incidence in Arab goats (66.28% plain) and minimum incidence in Oromo goats (9.41% spotted). Thirteen types of coat colors were observed in the sampled goats, of which white in Arab (33.72%) and brown in Oromo (27.81%) goat populations were the most frequently observed coat colors followed by brown (16.67%) and white (21.27%) in Arab and Oromo goats, respectively. Plain black coat color was less frequent than plain white, brown or gray ones. However, amongst the mixed goat coat colors, a mixture of white and black with white dominant is the predominant coat color observed in both goat populations.

Variations between the two goat populations were also observed in other qualitative characteristics. For instance, 61.63% of Arab and 95.5% of Oromo goats were characterized by straight head. The horned goats accounted for about 97.67% and 87.93% of Arab and Oromo goats, respectively. More than two-thirds of Arab and almost all of Oromo goat populations have straight horn shape oriented backward in 96.51% of Arab and 85.28% of Oromo goats. Some characteristics, such as presence of droopy ear orientation, are also shared by roughly half of the total population in Arab goats whilst majorities (62.99%) of Oromo goats have lateral ears. Wattles were found in Arab (14.34%) and Oromo goats (12.07%). It was also found that 88.76% of Arab and 86.50% of Oromo goats have no ruff. Most of Arab (90.70%) and Oromo goat populations (92.23%) have short and smooth hair while the rest of goats were characterized by short and course hair. In general, results of the present study showed the presence of clear morphological variations between and within Arab and Oromo goat populations.

Table 1: Coat color pattern and color type of Arab and Oromo goat populations by sex

Characters and attributes	**Goat population**						**P-value**
	Arab			**Oromo**			
	Male **N (%)**	**Female** **N (%)**	**Total** **N (%)**	**Male** **N (%)**	**Female** **N (%)**	**Total** **N (%)**	
Coat Color pattern							***
Plain	21 (50.00)	150 (69.44)	171 (66.28)	37 (48.68)	232 (56.17)	269 (55.01)	
Patchy	18 (42.86)	42 (19.44)	60 (23.26)	35 (46.05)	139 (33.66)	174 (35.58)	
Spotted	3 (7.14)	24 (11.11)	27 (10.47)	4 (5.26)	42 (10.17)	46 (9.41)	
Coat color type							***
White	10 (23.81)	77 (35.65)	87 (33.72)	10 (13.16)	94 (22.76)	104 (21.27)	
Brown	7 (16.67)	36 (16.67)	43 (16.67)	32 (42.11)	104 (25.18)	136 (27.81)	
Black	1 (2.38)	9 (4.17)	10 (3.88)	-	6 (1.45)	6 (1.23)	
Gray	3 (7.14)	16 (7.40)	19 (7.36)	10 (13.16)	48 (11.62)	58 (11.86)	
White + brown	5 (11.9)	17 (7.87)	22 (8.53)	2 (2.63)	24 (5.81)	26 (5.32)	
White + black	6 (14.29)	30 (13.89)	36 (13.95)	16 (21.05)	84 (20.34)	100 (20.45)	
Brown + black	2 (4.76)	5 (2.32)	7 (2.71)	2 (2.63)	10 (2.42)	12 (2.45)	
Brown + gray	3 (7.14)	4 (1.85)	7 (2.71)	-	-	-	
Gray + black	1 (2.38)	3 (1.39)	4 (1.55)	-	-	-	
White + brown + black	3 (7.14)	9 (4.17)	12 (4.65)	-	31 (7.51)	31 (6.34)	
White + brown + gray	-	4 (1.85)	4 (1.55)	-	4 (0.97)	4 (0.82)	
White + gray + black	1 (2.38)	1 (0.46)	2 (0.78)	-	-	-	
Brown + black + gray	-	5 (2.32)	5 (1.94)	4 (5.26)	8 (1.94)	12 (2.45)	

N= Number of goats; ***P ≤ 0.001

Table 2: Some qualitative features of Arab and Oromo goat populations by sex

Characters and attributes	Goat population						P-value
	Arab			Oromo			
	Male N (%)	Female N (%)	Total N (%)	Male N (%)	Female N (%)	Total N (%)	
Head Profile							***
Straight	16 (38.10)	143 (66.20)	159 (61.63)	70 (92.11)	397 (96.13)	467 (95.50)	
Slight concave	26 (61.90)	73 (33.80)	99 (38.37)	6 (7.89)	16 (3.87)	22 (4.50)	
Horn presence							***
Horned	40 (95.24)	212 (98.15)	252 (97.67)	56 (73.68)	374 (90.56)	430 (87.93)	
Polled	2 (4.76)	4 (1.85)	6 (2.33)	20 (26.32)	39 (9.44)	59 (12.07)	
Horn shape							***
Straight	26 (61.90)	153 (70.83)	179 (69.38)	76 (100)	405 (98.06)	481 (98.36)	
Curved	16 (38.10)	63 (29.17)	79 (30.62)	-	8 (1.94)	8 (1.64)	
Horn orientation							***
Obliquely upward	2 (4.76)	4 (1.85)	6 (2.33)	20 (26.32)	39 (9.44)	59 (12.07)	
Front	-	3 (1.39)	3 (1.16)	-	13 (3.15)	13 (2.66)	
Backward	40 (95.24)	209 (96.76)	249 (96.51)	56 (73.68)	361 (87.40)	417 (85.28)	
Ear orientation							***
Forward	5 (11.9)	19 (8.80)	24 (9.30)	7 (9.21)	26 (6.30)	33 (6.75)	
Lateral	18 (42.86)	85 (39.35)	103 (39.92)	46 (60.52)	262 (63.44)	308 (62.99)	
Droopy	19 (45.24)	112 (51.85)	131 (50.78)	23 (30.26)	125 (30.27)	148 (30.27)	
Wattle presence							
Present	4 (9.52)	33 (15.28)	37 (14.34)	4 (5.26)	55 (13.32)	59 (12.07)	
Absent	38 (90.48)	183 (84.72)	221 (85.66	72 (94.74)	358 (86.68)	430 (87.93)	
Ruff presence							***
Present	18 (42.86)	11 (5.09)	29 (11.24)	30 (39.47)	36 (8.72)	66 (13.50)	
Absent	24 (57.14)	205 (94.91)	229 (88.76)	46 (60.53)	377 (91.28)	423 (86.50)	
Hair type							***
Short and smooth	36 (85.71)	198 (91.67)	234 (90.70)	62 (81.58)	389(94.19)	451 (92.23)	
Short and course	6 (14.29)	18 (8.33)	24 (9.30)	14 (18.42)	24 (5.81)	38 (7.77)	

N= Number of goats; ***P ≤ 0.001

Body weight and linear body measurements

Goat type effect: Least-square means and standard error (LSM ± SE) for main effect of goat type on body weight and linear measurements is given in Table 3. Oromo goats have significantly ($p < 0.001$) higher average body weight, chest girth, body length, wither height and pelvic width measurements than Arab goats.

Age effect: The LSM for BW and LBMs were significantly ($p < 0.01$) influenced by age groups. Except for age classes of 2PPI and 3PPI, there were significant increases in BW and other LBMs as the age increased from the youngest (kid) to the oldest (4PPI) age group (Table 3). Results clearly indicate that BW and LBMs increase proportionately with the advancement of age. This situation is however expected since the size and shape of animals change as the age increases. Maximum gain on BW and LBMs was observed between 6 to 12 months of age.

Interaction effect: The interaction effect of age with goat type significantly ($p < 0.001$) affected BW, CG, BL and WH, but it affected PW and HL moderately ($p < 0.05$). When same age class Arab and Oromo goats were compared to each other, Oromo goats had significantly ($p < 0.001$) higher measurements in most of the variables. In general, 4PPI Oromo goats had the highest measurements; whereas Arab kids had the lowest measurement in all variables.

Table 3: Least squares means and standard error for body quantitative traits for different goat population and age groups

Effects and levels	**N**	**BW (kg)**	**CG (cm)**	**BL (cm)**	**WH (cm)**	**RH (cm)**	**CW (cm)**	**PW (cm)**	**HL (cm)**	**EL (cm)**
		LSM ± SE	**LSM± SE**	**LSM ± SE**	**LSM ± SE**	**LSM ± SE**	**LSM± SE**	**LSM ± SE**	**LSM ± SE**	**LSM ± SE**
Overall		24.7 ± 0.2	65.4 ± 0.3	55.5 ± 0.4	61.8 ± 0.4	63.5 ± 0.5	15.9 ± 0.1	13.9 ± 0.1	11.3 ± 0.4	13.9 ± 0.1
CV percent		22.69	9.10	10.66	9.50	9.65	6.58	6.05	23.72	5.60
Goat type		***	***	***	***	***	***	***	NS	NS
Arab	216	22.9 ± 0.4	63.3 ± 0.4	53.5 ± 0.4	60.1 ± 0.4	61.5 ± 0.4	15.6 ± 0.1	13.6 ± 0.1	11.0 ± 0.2	13.8 ± 0.1
Oromo	413	26.4 ± 0.3	67.9 ± 0.3	57.3 ± 0.3	64.4 ± 0.3	66.1 ± 0.3	16.1 ± 0.1	13.9 ± 0.1	11.3 ± 0.1	13.9 ± 0.1
Age		***	***	***	***	***	***	***	***	***
Kids	88	11.6 ± 0.3^{a}	51.6 ± 0.4^{a}	42.0 ± 0.5^{a}	48.4 ± 0.4^{a}	49.8 ± 0.5^{a}	14.5 ± 0.1^{a}	12.6 ± 0.1^{a}	8.6 ± 0.3^{a}	12.9 ± 0.1^{a}
Young	126	19.6 ± 0.2^{b}	62.2 ± 0.3^{b}	52.4 ± 0.3^{b}	59.3 ± 0.3^{b}	60.9 ± 0.3^{b}	15.6 ± 0.1^{b}	13.3 ± 0.1^{b}	9.8 ± 0.2^{b}	13.2 ± 0.1^{a}
1PPI	50	25.8 ± 0.2^{c}	66.5 ± 0.2^{c}	56.2 ± 0.3^{c}	63.3 ± 0.2^{c}	64.8 ± 0.3^{c}	15.7 ± 0.1^{b}	13.7 ± 0.1^{c}	11.3 ± 0.2^{c}	13.7 ± 0.1^{b}
2PPI	63	28.1 ± 0.2^{d}	69.8 ± 0.2^{d}	58.6 ± 0.2^{d}	66.4 ± 0.2^{d}	67.9 ± 0.2^{d}	16.2 ± 0.1^{c}	14.2 ± 0.1^{d}	12.0 ± 0.2^{d}	14.1 ± 0.1^{b}
3PPI	82	30.7 ± 0.2^{e}	70.9 ± 0.3^{de}	60.8 ± 0.3^{e}	66.5 ± 0.3^{de}	68.5 ± 0.4^{de}	16.7 ± 0.1^{d}	14.4 ± 0.1^{d}	12.1 ± 0.3^{d}	14.6 ± 0.1^{d}
4PPI	220	32.8 ± 0.4^{f}	72.4 ± 0.7^{e}	63.3 ± 0.7^{f}	67.9 ± 0.7^{f}	70.3 ± 0.8^{f}	16.9 ± 0.2^{d}	15.1 ± 0.1^{e}	13.8 ± 0.5^{e}	15.5 ± 0.1^{e}
Age x Goat type		***	***	***	***	***	***	*	*	NS
Kid x Arab	30	9.4 ± 0.2^{a}	49.4 ± 0.3^{a}	40.0 ± 0.5^{a}	46.2 ± 0.5^{a}	48.4 ± 0.5^{a}	14.0 ± 0.2^{a}	12.4 ± 0.1^{a}	8.8 ± 0.4^{b}	12.8 ± 0.1
Kid x Oromo	58	14.4 ± 0.2^{b}	54.3 ± 0.4^{b}	44.4 ± 0.5^{b}	50.9 ± 0.5^{b}	51.6 ± 0.6^{b}	15.1 ± 0.2^{b}	12.8 ± 0.1^{b}	8.4 ± 0.5^{a}	13.0 ± 0.1
Young x Arab	43	16.1 ± 0.2^{c}	56.2 ± 0.3^{c}	46.8 ± 0.5^{c}	53.4 ± 0.4^{c}	54.2 ± 0.5^{c}	15.2 ± 0.1^{b}	13.0 ± 0.1^{b}	10.3 ± 0.4^{d}	12.9 ± 0.1
Young x Oromo	82	21.1 ± 0.1^{d}	64.8 ± 0.2^{d}	54.8 ± 0.3^{d}	61.9 ± 0.3^{d}	63.8 ± 0.3^{e}	15.7 ± 0.1^{cd}	13.5 ± 0.1^{c}	9.5 ± 0.3^{c}	13.3 ± 0.1
1PPI x Arab	17	22.8 ± 0.2^{e}	63.9 ± 0.3^{d}	53.9 ± 0.4^{d}	61.8 ± 0.4^{d}	62.4 ± 0.5^{d}	15.5 ± 0.1^{c}	13.5 ± 0.1^{c}	10.4 ± 0.4^{d}	13.7 ± 0.1
1PPI x Oromo	33	26.6 ± 0.1^{f}	67.2 ± 0.2^{e}	56.8 ± 0.2^{e}	63.7 ± 0.2^{e}	65.4 ± 0.2^{ef}	15.8 ± 0.1^{d}	13.7 ± 0.1^{cd}	11.5 ± 0.2^{e}	13.7 ± 0.1
2 PPI x Arab	22	25.9 ± 0.1^{f}	66.5 ± 0.3^{e}	56.3 ± 0.4^{e}	63.8 ± 0.4^{e}	64.9 ± 0.4^{e}	15.8 ± 0.1^{d}	13.9 ± 0.1^{d}	11.8 ± 0.4^{e}	14.0 ± 0.1
2PPI x Oromo	41	28.7 ± 0.1^{g}	70.7 ± 0.1^{fg}	59.2 ± 0.2^{f}	67.0 ± 0.2^{g}	68.7 ± 0.2^{h}	16.3 ± 0.1^{e}	14.3 ± 0.1^{e}	12.1 ± 0.2^{f}	14.1 ± 0.1
3PPI x Arab	28	29.3 ± 0.1^{g}	69.7 ± 0.2^{f}	59.7 ± 0.3^{f}	65.4 ± 0.3^{f}	67.4 ± 0.4^{g}	16.2 ± 0.1^{e}	14.3 ± 0.1^{e}	11.9 ± 0.3^{ef}	14.5 ± 0.1
3PPI x Oromo	54	32.8 ± 0.2^{h}	72.7 ± 0.3^{h}	62.5 ± 0.4^{g}	68.3 ± 0.4^{h}	70.2 ± 0.5^{i}	17.4 ± 0.1^{g}	14.3 ± 0.1^{e}	12.3 ± 0.4^{f}	14.7 ± 0.1
4PPI x Arab	76	31.7 ± 0.2^{h}	71.1 ± 0.5^{g}	61.6 ± 0.7^{g}	66.7 ± 0.6^{g}	69.3 ± 0.7^{hi}	16.6 ± 0.2^{f}	14.8 ± 0.1^{f}	13.3 ± 0.6^{g}	15.3 ± 0.1
4PPI x Oromo	145	37.0 ± 0.5^{i}	77.0 ± 0.9^{i}	69.5 ± 1.3^{h}	72.2 ± 1.2^{i}	74.0 ± 1.4^{j}	18.2 ± 0.4^{h}	16.2 ± 0.3^{g}	15.8 ± 1.2^{h}	16.0 ± 0.3

Column means within each sub-class with different superscript letter are statistically different. NS, non-significant; *$p \leq 0.05$; ***$p \leq 0.001$; BW, body weight; CG, chest girth; BL, body length; WH, wither height; RH, rump height; CW, chest width; PW, pelvic width; HL, horn length; EL, ear length; PPI=pair of permanent incisors; SE, standard error

Correlation between BW and LBMs

In both Arab and Oromo goat populations, BW had positive and highly significant ($p < 0.001$) correlations with all LBMs except with EL in Arab goats (Table 4). Similarly, most of the quantitative traits in both goat populations showed positive and highly significant ($P < 0.001$) associations with one another. The strongest positive and highly significant correlation was between BW and CG in both goat populations (r = 0.95 in Arab goats and 0.92 in Oromo goats).

Table 4: Coefficient of correlation between body weight and linear body measurements (above diagonal for Arab and below diagonal for Oromo goat populations)

	BW	CG	BL	WH	RH	CW	PW	HL	EL
BW		0.95***	0.93***	0.89***	0.89***	0.65***	0.75***	0.38***	0.10^{NS}
CG	0.92***		0.88***	0.86***	0.86***	0.60***	0.70***	0.36***	0.05^{NS}
BL	0.82***	0.87***		0.86***	0.86***	0.62***	0.69***	0.31***	0.13*
WH	0.83***	0.90***	0.78***		0.85***	0.62***	0.67***	0.32***	0.03^{NS}
RH	0.81***	0.89***	0.77***	0.85***		0.59***	0.65***	0.24***	0.11^{NS}
CD	0.44***	0.42***	0.30***	0.39***	0.40***		0.81***	0.21***	0.13^{NS}
PW	0.58***	0.56***	0.53***	0.52***	0.51***	0.76***		0.27***	0.16*
HL	0.40***	0.37***	0.31***	0.32***	0.35***	0.19***	0.25***		-0.29***
EL	0.35***	0.32***	0.25***	0.29***	0.28***	0.15***	0.20***	0.12*	

NS, non-significant; *$p \leq 0.05$; ***$p \leq 0.001$; BW, body weight; CG, chest girth; BL, body length; WH, wither height; RH, rump height; CW, chest width; PW, pelvic width; HL, horn length; EL, ear length; PPI=pair of permanent incisors; SE, standard error

Prediction of BW from LBMs

Equations predicting BW from LBM of Arab and Oromo goats are presented in Table 5. In the prediction of BW, the multiple stepwise regressions found seven parameters (CG, BL, RH, PW, HL, WH and EL) to be significant ($p < 0.05$) for Arab goats and five parameters (CG, EL, CW, BL and HL) to be significant ($p < 0.05$) for Oromo goats. In the present study, high coefficient of determination (R^2) that ranged between 90–96% in Arab goats and 85–86% in Oromo goats and low residual mean square (MSE) values between 2.11 to 5.00 in Arab goats and 2.72 to 3.04 in Oromo goats were recorded using the regression analyses.

Table 5: Multiple regression analysis of live BW on different body measurements of Arab and Oromo goats in all age groups

Breed	**Model**	**Parameters**								**Adj. R^2**	**AIC**	**BIC**	**MSE**
		β0	**β1**	**β2**	**β3**	**β4**	**β5**	**β6**	**β7**				
Arab	CG	-33.65	0.89							0.90	922.15	932.14	5.00
	CG + BL	-33.09	0.54	0.41						0.94	809.18	822.49	2.86
	CG + BL + RH	-34.03	0.47	0.34	0.14					0.95	791.72	808.36	2.60
	CG + BL + RH + PW	-40.16	0.44	0.32	0.14	0.73				0.95	776.47	796.43	2.39
	CG + BL + RH + PW + HL	-40.74	0.41	0.31	0.16	0.70	0.18			0.96	764.88	788.18	2.24
	CG + BL + RH + PW + HL + WH	-40.84	0.39	0.28	0.13	0.66	0.17	0.09		0.96	758.55	785.17	2.15
	CG + BL + RH + PW + HL + WH + EL	-42.13	0.39	0.27	0.12	0.60	0.21	0.10	0.12	0.96	756.51	786.46	2.11
Oromo	CG	-37.55	0.94							0.85	1676.19	1688.34	3.04
	CG + EL	-42.52	0.92	0.47						0.85	1665.31	1681.50	2.95
	CG + EL + CW	-45.32	0.89	0.46	0.30					0.86	1656.16	1676.39	2.87
	CG + EL + CW+ BL	-45.41	0.77	0.48	0.35	0.13				0.86	1645.29	1669.57	2.78
	CG + EL + CW + BL + HL	-44.76	0.74	0.48	0.34	0.13	0.09			0.86	1637.51	1665.84	2.72

CG, chest girth; BL, body length; RH, rump height; PW, pelvic width; HL, horn length; WH, wither height; EL, ear length and CW, chest width;R^2, coefficient of determination; AIC, Alkaike's information criteria; SBC (BIC), Bayesian information criteria and MSE, mean square error

Discussion

This study was exclusively based on qualitative records and quantitative measurements to characterize and identify the morphological features of Arab and Oromo goat populations of BGR in northwestern Ethiopia.

The result revealed the presence of relatively more number of female goats sampled than male goats. This could be attributed to the fact that female goats are normally retained in flocks for reproduction while the males are more frequently put up for sale and more importantly slaughtered for food more often [22]. Indigenous goats thus make an important contribution in ensuring food security and alleviating poverty by providing animal source foods directly or from sale indirectly. [28] documented that goats contribute to food security through direct access to animal source foods and providing cash income from sales, which can be used to purchase food.

Regarding coat color, the sampled goats were characterized by wide ranges of coat color patterns and types. Yet, white color in Arab and light brown color in Oromo goats were the predominant colors and they are reflections of the goats' adaptability to the study area (which is relatively warm and humid during most parts of the year). As reported by [29], animals with higher percentage of light color, such as white and brown, have better resistance to heat in areas characterized by higher solar radiation. In other words, the relatively high proportion of light colors observed in the two goat populations is an indication that the goats were not thermal stressed and their productivity could not be compromised. Horn presence is an advantage for self-defense, thermoregulation [30] and better reproductive performance [31]. Majority of the goats sampled were horned (Table 2), an indication of their ability to defend themselves, fight competitors for feed and water and even for does during mating. Likewise, presence of wattle is associated with thermoregulatory function, milk yield and reproductive performance such as higher prolificacy, litter size, fertility and conception rate [32] and higher body measurements [33]. Hair type is also an important economic trait in that smooth hair has an advantage as it permits conventional heat loss from the animal surface and also ensure easy disposal of dirt [34]. Overall, in order to set up sustainable genetic improvement strategies such as community-based breeding programs (CBBPs) in the study area, qualitative traits such as coat color pattern and type, presence of horn and wattle, and hair type should be part of the selection criteria of breeding males and females.

[35] reported that on the basis of wither height; adult goats can be classified as large (> 65 cm), small to medium (51–65 cm) and dwarf (< 50 cm). According to the current results, both Arab and Oromo goats can be grouped under small to medium sized breeds. However, Oromo goats had significantly higher averages of BW and LBMs, showing that animals belonging to this population have better body conformation for meat production than animals in Arab goat population. The variation between the two goat populations could arise due to difference in genetic characteristics and/or environmental conditions that may affect phenotypic variance [34]. The relatively harsher environment, in terms of feed and water shortage and high environmental temperature, under which the Arab goats are raised could have been largely responsible for their lower body dimensions. Because these stress factors could have prevented the Arab goats from expressing their genetic potential. This is in line with what has been reported by [36]. The authors documented that temporal and spatial variation in weather, plant productivity and subsequent nutrition could have major impacts on physical growth of animals. However, at the scope of the present study, it is difficult to associate body size, shape and conformation to any genetic background. Future studies could look in to genetic differences of the two goat populations. The coefficients of variation (CV) obtained for quantitative traits such as BW, CG, BL, WH, RH and HL were relatively higher. This could be due to absence of systematic selection, or the body parts are affected more by the environment than others [37].

Investigation on the effect of age on quantitative measurements of goats indicated that BW and LBMs increase proportionately with the advancement of age. Similar findings were reported by [38] for goats found in western Ethiopia. However, the maximum body gain was observed between 6 months to 12 months. This may be due to natural increase in dry matter intake after the goats reached age at puberty. Study by [39] also found maximum body gain at 9 months of age for Rohilkhand goats in India. The current average body measurements of goats in different age classes are higher than previous findings from similar age western lowland goats reported by [15].

The correlations among quantitative traits were generally positive and highly significant that ranged from 13–95% in Arab and 12–92% in Oromo goats with the highest correlation between BW and CG in both goat populations (r = 0.95 in Arab and 0.92 in Oromo goats). In agreement with this finding, several authors [13, 38, 40, 41] reported the highest correlation between BW and CG for some Ethiopian goats. This specifies that CG could be the best trait in predicting BW.

The positive and significant correlations among quantitative traits obtained in this study also indicate that both goat populations have harmonious body conformation, reflecting balanced physical growth. Furthermore, it shows that the traits are under the same genetic influence due to additive genetic effect [42]. This implies selection for one or more of these traits may consistently increase other traits that have positive association with the selected trait/s. In addition, selection of positively correlated traits would have paramount importance in designing breeding programs in that the selection will lead to significant improvement of body weight and other body measurements that are of economic importance [37].

The regression analyses of BW with LBMs in the present study identified seven traits in Arab and five traits in Oromo goats to predict BW. Similarly, [38] found seven traits in female (R^2 = 83%) and five traits in male (R^2 = 88%) to predict BW of western Ethiopian goats. [41] also reported five traits to estimate BW of Woyto-Guji and Central Highland goats with R^2 values of 84% and 79%, respectively. Nevertheless, CG was found to be the most appropriate variable to explain more variation in both Arab (adjusted R^2 = 90%) and Oromo goat populations (adjusted R^2 = 85%). The high coefficients of determination (R^2) in the current study indicated the strong association and success of LBMs in describing more variation in BW. This may be helpful for local goat keepers to make selection and cull decisions as it can be relatively low cost, high accuracy and consistency [43]. Body measurements in some cases can be more reliable than modern weighing machines as the latter can give biased results caused by gut fullness [44]. As shown in table 5, addition of a new variable to the model did not always increase the adjusted R^2. However, AIC, BIC and MSE decreased as a new variable was added with little or no influence on the adjusted R^2. On the other hand, addition of unnecessary variables to the model may increase the error. Therefore, addition of other LBMs to CG did not result in significant increase in adjusted R^2, though it improved the accuracy of prediction by decreasing the error.

In the study area, where formal breed data recording schemes are not well established [22] and goat keepers could not easily access weighing scales and understand complex formula, BW could be predicted from the regression equation y = -33.65 + 0.89x for Arab goats and y = -37.55 + 0.94x for Oromo goats, where y and x are BW and CG measurements, respectively. These formulas indicate that an increase of one cm of CG would result in an increase of 0.89 and 0.94 kg of BW in Arab and Oromo goat populations, respectively, which is comparable with the findings on goats elsewhere in Ethiopia [13, 38, 41]. The possibility of using simple body measurements that can easily be measured in the field to predict important economic traits have been demonstrated by [45, 46]. Overall, assessment of BW and LBMs in both goat populations based on the expressed regression equations remains very important for avoiding errors of visual determination of animal weights in the study area where weighing balance cannot be easily accessed.

Conclusion and recommendation

The significance of morphological characterization of indigenous goat genetic resources cannot be over emphasized. The present study is based on qualitative records and quantitative measurements of Arab and Oromo goat populations. The results revealed the presence of morphological variations within and between the goat populations in the studied agroecological zones of BGR in northwestern Ethiopia. It was also found that the goat populations in the study area have developed diverse qualitative traits such as white and brown coat colors, presence of horn and wattle, and short and smooth hair. Compared to Arab goats, Oromo goats are on average not only wider and bigger in size but also show considerably higher variation in body size. This indicates that there would be a good opportunity to select best young breeding males for genetic improvement of goats in the study area. The correlation analysis has shown that chest girth had the highest association with body weight and hence it can be used as a marker to estimate weight using regression equations. Overall, it would be useful if the present characterization work is supported by performance data to understand which genotype has comparative advantage within an agro-ecological zone. Furthermore, an investigation on the molecular characterization using molecular markers like SNP will complement the results obtained from morphometric differentiation and also be helpful in high resolution characterization, conservation and formulation of breeding and selection strategies.

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Authors' contributions

OS performed the data collection and analysis and wrote this paper. KA and AH participated in coordination and helped to draft the manuscript. All the authors read and approved the final manuscript.

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Availability of data and materials

All data generated or analyzed during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

The paper meets all applicable standards with regard to ethics and integrity. The corresponding author along with the co-authors submitted this paper with full responsibility and following due ethical procedure. There are no duplicate publications, fraud or plagiarism. Furthermore, the manuscript does not contain clinical studies or patient data.

Consent for publication

Not applicable.

Competing Interests

The authors declare that they have no competing interests.

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Paper 3: Genome-wide Diversity, Population Structure and Selective Sweep Analyses in Three Ethiopian Indigenous Goat Populations

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To be submitted

Abstract

Due to its geographical location near to entry points of livestock species including goats into Africa, Ethiopia is believed to be a corridor for genetic diversity. To date, the country has more than 52 million heads of goats that inhabit areas ranging from hot arid lowlands to cool humid highlands. Natural and human driven forces shaped the genomes of Ethiopian indigenous goat populations and resulted in marked phenotypic variations. Here, we investigated autosomal genome-wide profiles of three Ethiopian indigenous goat populations, such as Arab, Fellata and Oromo, using Illumina high-throughput sequencing. Genotype data of ten goat breeds including four Ethiopian (Abergelle, Gumuz, Keffa, Woiyto-Guji), four African (Kenyan Boran, Morrocan Unknown, Malawian Thyolo, Malian Guera), one Asian (Chinese Tibetan) and one European (French Saanen), obtained from the database, were included in this study to address history of Ethiopian goats at global level. We generated 35,161,094 autosomal biallelic single nucleotide polymorphisms (SNPs) and 3,737,445 insertions and deletions (InDels) from 78 goat genomes. The highest number of SNPs and InDels were detected in Unknown goat while the lowest number of SNPs and InDels were identified in Saanen and Gumuz goats, respectively. Keffa goat demonstrated the lowest level of genetic diversity whereas Woyito-Guji showed the highest. Our results show an inverse relationship between the length and number of runs of homozygosity (ROH). The number of shorter ROHs ($ROH_{100–150Kb}$) category predominated; accounting for 58.18% of the total number of ROHs. The longest ROH category ($ROH_{>400Kb}$) was the rarest, wherein the Gumuz population displayed the highest number of ROH, suggesting recent inbreeding in this population. Principal component analysis (PCA), ADMIXTURE and TREEMIX tools revealed five distinct genetic clusters in the global, three in the African and two in the Ethiopian goat populations. For the selection signature analysis, we used comparative genomics to explore differences between populations that are exposed to different selection pressures (natural versus artificial) and from different geographic zones (tropical semi-arid versus temperate cold) using pooled hetrozygosity (*Hp)* and population differentiation *(Fst)* between the following population pairs: Gumuz versus Saanen and Fellata versus Saanen. By combining the two approaches, candidate genes underlying strong selection signatures including litter size, adaptation to arid environment, coat coloration and body were identified. Our findings suggest that Ethiopian Fellata and Gumuz represent unique gene pools that present important resource for understanding the genetic basis of important traits. This may need to be considered in designing goat breeding programs and genome-wide association studies.

Keywords: Africa, Capra hircus, diversity, pooled hetrozygosity, population differentiation, selection signatures

INTRODUCTION

Goats (*Capra hircus*) are of economic, nutritional and cultural significance to humankind. It was domesticated around 12,000 years ago in the Fertile Crescent (Hatziminaoglou and Boyazoglu et al., 2004; Zeder, 2008; Colli et al., 2018) from a unique wild and still living progenitor, the bezoar *Capra aegagrus* (Naderi et al., 2008). Recent studies are showing mosaic domestication in the Fertile Crescent (Daly et al., 2018). Since its domestication, goats have dispersed across the globe following patterns of human migration and commercial trade and adapted to diverse environments.

Ethiopia is considered as a gateway of livestock species including goats into Africa (Hanotte et al., 2002; Gifford-Gonzalez and Hanotte, 2011). Today, the country is home to ~52 million heads of goats (CSA, 2021), a great majority of which are indigenous types and are kept by pastoralists in large flocks while very small flock sizes are widely distributed in the highland areas (Abegaz et al., 2014). Ethiopian indigenous goats are classified into 13 populations based on their physical characteristics (FARM-Africa, 1996) and are mainly named after their geographic location or associated ethnic communities. This type of classification, however, might have considered genetically similar goat populations as phenotypically different groups.

Systematic studies on genetic diversity and population structure of farm animals would be necessary to develop sustainable breed improvement strategies (Groeneveld et al., 2010). To this end, efforts have been made to characterize genetic diversity and structure of Ethiopian indigenous goat populations using microsatellite markers (Tesfaye, 2004; Hassen et al., 2012) and medium density SNP chip panel (Abegaz, 2014; Tarekegn, 2016) and revealed high level of genetic diversity but weak population structure. Furthermore, Berihulay et al. (2021) identify the genes under selection in Ethiopian indigenous goat populations. Nevertheless, the studies did not include goat populations such as Arab, Fellata and Oromo and hence the genetic diversity and population structure and positively selected genes remain uncovered till now. Genomic characterization of the three goat populations using state of the art genomic tool is of paramount importance to ensure conservation and genetic improvement of these goat populations. Recently developed high-throughput genotyping technology has provided an opportunity to study genetic diversity and population structure at high resolution, and search genomic regions that may have undergone selection (Guo et al., 2018; Wang et al., 2021). Here, using whole-genome sequence (WGS) data, we investigated the (i) genetic diversity and population structure of the three Ethiopian indigenous goat populations and (ii) identified candidate genome regions and genes associated with important traits.

MATERIALS AND METHODS

Animals and whole-genome sequencing

A total of 18 unrelated animals representing three Ethiopian indigenous goat populations (Arab (ARB), Felata (FEL) and Oromo (ORO)) were analyzed in the present study. Whole blood was collected by puncturing the jugular vein using EDTA coated vacutainer tubes. We followed the recommendations of the Ministry of Livestock and Fisheries of the Federal Democratic Republic of Ethiopia concerning animal care. No ethical approvals were required at the time. Efforts were made to avoid sampling of closely related animals. Genomic DNA was extracted from whole blood using DNeasy® Blood and Tissue kit (https://www.QIAGEN.com) following the manufacturer's protocol with a few modifications. The quality and quantity of the isolated DNA were evaluated using a NanoDrop2000 spectrophotometer (Thermo Fisher Scientific, Wilmington, DE) and 1.5% agarose gel electrophoresis, respectively. Sequencing was done with Illumina high-throughput sequencing platform NovaSeq 6000^{TM} at Tianjin Noozhiyuan Technology Co., Ltd.

To assess the genetic variation and history of Ethiopian goat populations at national, continental and global levels, we included data of 60 animals representing ten goat populations, including four from Ethiopia (Abergelle (ABR); Keffa (KEF); Gumuz (GUM) and Woyito-Guji (WGU)), four from Africa (East (Kenya: Boran (BOR)), North (Morroco: Unknown (UNK)), South (Malawi: Thyolo (THY)) and West (Mali: Guera (GUE)) Africa), one from Europe (France: Saanen (SAN)), and one from Asia (China: Tibetan (TIB))) obtained from VarGoats project (available in the European Nucleotide Archive (ENA) as project number PRJEB37507) in FASTQ format and from which we extracted filtered genotype data. Detail description of the environmental characteristics of the study goat populations is given (see **Chapter 10 supplementary Table 1**).

Read alignment and variant calling

Prior to mapping, sequence read qualities were evaluated using FastQc v0.11.5 and adapter reads were trimmed with Trimmomatic v0.36 (Bolger et al., 2014) based on the following criteria: Slidingwindow:4:15, Leading:3,Trailing:3 and Minlen:36. The clean reads were mapped to the latest goat reference genome (assembly ARS1) (Genbank accession number GCA_001704415.1) (Bickhart et al., 2017) using BWA-MEM v0.7.17 software (Li, 2013) with default parameters except for "-t 8 -M" and "-R" to add read groups. Each resulting sequence alignment map (SAM) (Li and Durbin, 2009) was sorted and converted to binary alignment map (BAM) (Li and Durbin, 2009) using Picard (https://broadinstitute.github.io/picard/) 'SortSam' v2.22.8. Using the same software, duplicate reads were marked with 'MarkDuplicates'. Each BAM file was indexed using 'BuildBamIndex' and read groups were added using 'AddOrReplaceReadGroups' of Picard v2.22.8. GATK (McKenna et al., 2010) (Genome Analysis Toolkit) BaseRecalibrator and ApplyBQSR v4.1.7.0 were run per sample for base quality score recalibration. The "known-sites" file that is necessary for BQSR step was computed for each individual. GATK HaplotypeCaller v4.1.7.0 (Poplin et al., 2018) was run, to call the variants in each individual, in GVCF (Genomic Variant Call Format) mode using the parameter –ERC GVCF on the pre-processed BAM files. GATK's CombineGVCFs v4.1.7.0 was then used to aggregate all GVCF files per scaffold. GenotypeGVCFs v4.1.7.0 of GATK was used to perform joint genotyping and output multi-sample raw variant call format (VCF) (Danecek et al., 2011) per chromosome/scaffold.

Filtering process

The multi-sample raw VCF of each goat population was filtered by VariantRecalibrator v4.1.7.0 of GATK. Two training resources, one with true sites ("known=false,training=true,truth=true,prior=15.0") and the other with non-true sites ("known=true,training=false,truth=false,prior=2.0") used for recalibration were dbSNP variants obtained from Ensembl v105. The variant call annotations (for SNPs and InDels)

DepthOfCoverage (DP), QualByDepth (QD), RMSMappingQuality (MQ), MappingQualityRankSumTest (MQRankSum), ReadPosRankSumTest (ReadPosRankSum), FisherStrand (FS) and StrandOddsRatio (SOR) were used for VariantRecalibrator. Based on the "SNPs. tranches" (see **Chapter 10 Supplementary Figure 1**), no false-positive variants were observed in the 90 tranche. Therefore, the 99 tranche was included to increase the sensitivity of variant discovery. We considered the highest tranche (99.9 to 100) as a false positive and excluded it. The remaining variants (SNPs and InDels) were then recalibrated at the truth sensitivity filter level (tranche) of 99 using ApplyVQSR v4.1.7.0 of GATK. In general, the entire filtration process resulted in a high confidence set of 35,161,094 autosomal biallelic SNPs and 3,737,445 InDels. The final set of SNPs were annotated using variant effect predictor (VEP) v104.3.

Genetic diversity analyses

We estimated the levels of genetic diversity for each population. The VCFtools v.0.1.15 (Danecek et al., 2011) was used to derive expected (*He*) and observed (*Ho*) heterozygosity, nucleotide diversity (π), inbreeding coefficient (*F*), heterozygous/homozygous (*het/hom*) ratio and proportion of polymorphic SNPs (*Pn*) for each population. *Pn* - the fraction of total SNPs that displayed both alleles - were calculated as the proportion of SNPs with minor allele frequency (MAF) greater than 1%. MAF is the frequency estimate of the least common allele per population.

The average pairwise genetic distance (D_{ST}) between individuals within a population was calculated in PLINK v1.9 (Purcell et al., 2007). The average proportion of alleles shared between two individuals was calculated using the "--genome" command line in PLINK v1.9 as:

$$\boldsymbol{D_{ST}} = \frac{\boldsymbol{IBS_2 + (0.5\ X\ IBS_1)}}{\boldsymbol{N}}$$

IBS_1 and IBS_2 represent the number of loci which share either 1 or 2 alleles that are identical by state (IBS) in pairwise comparisons between individuals, respectively, and N is the number of loci tested. The genetic distance between all pair-wise combinations of individuals was calculated as: $D = 1 - D_{ST}$.

The run of hemozigosity (*ROH*) was estimated with PLINK v1.9 by invoking "--homozyg" option. The parameters used to detect *ROH* were: (i) minimum number of SNPs in ROH or in sliding window = 50, (ii) minimum length of ROH = 100 Kb, (iii) minimum number of missing SNP in the ROH = 1, (iv) minimum allowed density of SNPs within a run = 1 SNP/100 Kb, (v) minimum number of heterozygous SNPs in each ROH = 1, and (vi) maximum gap between consecutive homozygous SNPs = 1Mb. We estimated the *ROH*-derived genomic inbreeding coefficient (F_{ROH}) following McQuillan et al. (2008) as:

$$\boldsymbol{F_{ROH} = \frac{L_{ROH}}{L_{AUTO}}}$$

Where L_{ROH} is the total length of *ROH* of each individual in the genome and L_{AUTO} is the length of the goat autosomal genome (~2400 Mb) (Kumar et al., 2018). To compare the ROH length between populations, four length categories were allocated: 100–150, >150–250, >250–400 and >400 Kb (classified as $\mathrm{ROH}_{100–150\mathrm{Kb}}$, $\mathrm{ROH}_{150–250\mathrm{Kb}}$, $\mathrm{ROH}_{250–400\mathrm{Kb}}$ and $\mathrm{ROH}_{>400\mathrm{Kb},}$ respectively).

Population genetic structure analyses

To investigate population structure, we did principal component analyses with the "--pca" command line in Plink v1.9 (Purcell et al., 2007). To summarize the relationship among individuals, we plotted the first two eigenvectors. Here, we filtered out SNPs with minor allele frequency (MAF) < 0.01 and hence we used 27,728,833 SNPs.

We investigated the proportion of the genome arising from common ancestry using ADMIXTURE v.1.3 software (Alexander et al., 2009). For admixture analysis, we used 8,344,942 autosomal SNPs that were retained after we prunned the 27,728,833 SNPs used in PCA, for linkage disequilibrium (LD). We implemented the block relaxation algorithm with the Kinship (*K*) values set from 2 to 8; five runs were performed for each *K*. A five-fold cross-validation (CV) procedure was used to determine the optimal number of ancestral genomes (*K*) and the proportion of ADMIXTURE. The PCA and ADMIXTURE results were visualized with GENESIS (Buchmann and Hazelhurst, 2014).

We also evaluated historical relationships and interactions (gene flow) between populations using the maximum likelihood tree-based approach implemented in TreeMix (Pickrell and Pritchard, 2012) and included the Saanen goat as an out-group. The number of migration events (m) varied between 1 and 13; migration between two and all the populations, respectively. The number of migration events that best fitted the data was identified using the fraction of the variance in the sample covariance matrix explained by the model covariance matrix (Pickrell and Pritchard, 2012). Each analysis was run with 1000 bootstrap replicates in order to verify the consistency of the trees' edges and nodes. Furthermore, to test for admixture among breeds and to assess the statistical significance of migration events, the THREEPOP and FOURPOP functions (implemented in TreeMix) were run to calculate the f3 and f4 statistics, respectively (Ahbara et al., 2019). In the f3 test, the putative admixture of a target population (A) is tested against two source populations (B, C). A significant negative value of the resulting f3 score indicates A being the result of admixture of B and C. Similarly, the f4 test investigates the tree topology of four populations, with resulting f4 scores significantly different from 0 in cases of a distorted topology likely being due to admixture. Extreme positive scores suggest gene flow between A and C and/or D and B that surpasses any gene flow between A and D and/or B and C, whereas extreme negative scores suggest gene flow between A and D and/or B and C that surpasses that between A and C and/or B and D.

Detection of signatures of selection

Combining alternative approaches to detect selection signatures has been suggested as a way of increasing the reliability of selection signature studies (Simianer, 2014). Therefore, we implemented two methods: i) within-group pooled heterozygosity (*Hp*) (Rubin et al., 2010) and, ii) genetic differentiation based on *F*st (Weir and Cockerham, 1984). A sliding window approach was used to perform the *Hp* and *Fst* analyses with

VCFtools v.0.1.15 using a 100 kb window size and a 50 kb sliding step following the equations:

$$\boldsymbol{Hp} = \frac{2\sum nMaj\sum nMin}{(\sum nMaj+\sum nMin)^2} \qquad (1)$$

Where $\sum n_{\mathrm{Maj}}$ and $\sum n_{\mathrm{Min}}$ are the sums of major and minor allele frequencies, respectively for all the SNPs in the 100 kb window. The values for the *Hp* calculated for each window size were then Z-transformed using the equation:

$$\boldsymbol{ZHp} = \frac{Hp - \mu(Hp)}{\sigma(Hp)} \qquad (2)$$

Where μ is the mean and σ is the standard deviation of H_p.

A genome-wide score of $ZHp \leq -4.0$ was taken as the threshold after examining the distribution plot of the *ZHp* values (**Chapter 10 Supplementary Figure 4**). The windows which passed the significance threshold were used to define candidate regions under selection.

The *Fst* (Weir and Cockerham, 1984) values were estimated for each SNP in each window between test groups using a window size of 100 kb and a sliding step size of 50 kb with the formulae:

$$\boldsymbol{Fst} = 1 - \frac{p1q1+p2q2}{2prqr} \qquad (3)$$

Where p1, p2 and q1, q2 are the frequencies of alleles A and a in the first and second group of the test populations, respectively, and pr and qr are the frequencies of alleles A and a, respectively, across the tested groups (Zhi et al., 2018). The *Fst* values were standardized into Z-scores as follows:

$$\boldsymbol{ZFst} = \frac{Fst - \mu(Fst)}{\sigma(Fst)} \qquad (4)$$

Where μ is the mean and σ is the standard deviation of *Fst* derived from all the windows tested between test groups. A genome-wide score of $ZFst \leq -2.0$ was taken as the threshold after examining the distribution plot of the *ZFst* values (**Chapter 10 Supplementary Figure 5**).

Functional annotation

Based on genome annotation, a gene was deemed to show evidence of being under selection if it overlapped with an outlier genomic window based on both *ZHp* and *ZFst.* Hence, we annotated the candidate regions using the Caprine reference genome (ARS1) assembly with the *Ensembl BioMart* tool (http://www.ensembl.org/biomart). Using *Capra hircus* as a background species, we performed functional enrichment analysis of all the annotated genes using DAVID v6.8 (Huang et al., 2009). To infer gene functions, we consulted the NCBI database (http://www.ncbi.nlm.nih.gov) and review of literatures.

RESULTS

Genome Sequence Mapping and SNP Calling

We compared the sequence reads obtained from the present study to the recent goat reference genome (assembly ARS1: https:// p.ncbi.nih.gov/snp/organisms/goat_9925/VCF/). We obtained 38.89 million high quality variants, including 90.39% SNPs and 9.61% InDels, in 13 populations (n = 78 goats). The SNPs and InDels summary statistics of the sequence parameters for each population are shown (**Chapter 10 Supplementary Table 2** and **Supplementary Table 3**). The highest number of SNPs (18,266,925) and InDels (2,033,758) were detected in Unknown (UNK) goat; while the lowest number of SNPs (14,389,837) and InDels (1,739,360) were identified in Saanen (SAN) and Gumuz (GUM) goats, respectively. At the sample level, the average number of SNPs ranged from 6,591,579 Keffa (KEF) to 8,866,137 Woyito-Guji (WGU) and the InDels ranged from 660,074 Keffa (KEF) to 976,619 Abergelle (ABR). The hetrozygosity to homozygosity (*het/hom*) ratio ranged from 1.03 Keffa (KEF) to 1.62 Unknown (UNK). Comparison with *C. hircus* dbSNP database revealed that 29 to 35% of SNPs and 78 to 82% of InDels were not present in the database. In general, out of a total of 35,161,094 SNPs generated in this study, 33.03% are located within genes (intronic = 31.80% + exonic = 0.74% + UTRs = 0.42% + splicing = 0.07%) and the rest are found outside genes (intergenic = 60.1% and up/downstream = 6.71%) (**Chapter 10 Supplementary Table 4** and **Supplementary Figure 2**). SNPs in exonic regions are further classified as synonymous (51.84%), non-synonymous (47.12%) and stop gain or loss (1.04%) polymorphisms.

Genetic Diversity

Genetic diversity metrics (mean ± standard deviation (*SD*); **Table 1**) within each of the 13 goat populations were assessed by estimating the proportion of polymorphic SNPs (*Pn)*, observed and expected hetrozygosity *(Ho*, *He)*, inbreeding coefficient (*F)*, runs of homozygosity (*ROH*), F_{ROH}, nucleotide diversity (π) and average pairwise genetic distance (D_{ST}). The proportion of polymorphic SNPs ranged from 90.5% to 96%, with the highest *Pn* found in Unknown breed from Morocco and the lowest in Thylo breed from Malawi. Keffa goat had the lowest observed hetrozygosity (0.254 ± 0.115) and nucleotide diversity (0.0017 ± 0.001), but it had the highest rate of inbreeding (0.261 ± 0.326), Woyito-Guji goat showed the highest observed hetrozygosity (0.335 ± 0.009) and nucleotide diversity (0.0023 ± 0.001), but the lowest level of inbreeding (F = 0.016 ± 0.027) and genetic distance (D_{ST} = 0.264 ± 0.001). Gumuz goat had on average the longest length of *ROH* (0.193 ± 0.138) while Saanen had on average the shortest (0.140 ± 0.048). Saanen also had the lowest F_{RoH} (0.053), while Thyolo had the highest (0.790).

The number of ROHs for the four genome length categories ($ROH_{100–150Kb}$, $ROH_{150–250Kb}$, $ROH_{250–400Kb}$ and $ROH_{>400Kb}$) is shown in **Figure 1**. Our results show an inverse relationship between ROH length and number. The number of shorter ROHs ($ROH_{100–150Kb}$) category predominated; the number of these ROHs accounted for 58.18% of the total number of ROHs. However, the frequency of ROHs in this major category varied between populations. Thyolo had the highest number (5897) whereas Saanen had the lowest number (664). The longest ROH category ($ROH_{>400Kb}$) was the rarest, wherein the Gumuz population displayed the highest number of ROH while Saanen showed the lowest number of ROH compared with other breeds.

Table 1: Estimates of genetic diversity parameters for each of the 13 populations analyzed in this study

Population	**Pn**	**Ho**	**He**	**F**	**ROH size (Mb)**	**F_{ROH}**	**π**	**D_{ST}**
		Mean ± SD	**Mean ± SD**	**Mean ± SD**	**Mean ± SD**	**Mean ± SD**	**Mean ± SD**	**Mean ± SD**
Arab	0.928	0.310 ± 0.010	0.347 ± 4.35e-05	0.105 ± 0.030	0.169 ± 0.096	0.351	0.0020 ± 0.01	0.280 ± 0.033
Fellata	0.944	0.288 ± 0.005	0.334 ± 0.0001	0.137 ± 0.016	0.150 ± 0.062	0.196	0.0021 ± 0.001	0.281 ± 0.005
Oromo	0.930	0.306 ± 0.012	0.345 ± 0.0002	0.112 ± 0.034	0.155 ± 0.070	0.266	0.0020 ± 0.001	0.281 ± 0.016
Abergelle	0.933	0.299 ± 0.074	0.340 ± 0.003	0.121 ± 0.210	0.160 ± 0.084	0.181	0.0019 ± 0.001	0.280 ± 0.004
Keffa	0.924	0.254 ± 0.115	0.342 ± 0.004	0.261 ± 0.326	0.165 ± 0.090	0.119	0.0017 ± 0.001	0.296 ± 0.017
Gumuz	0.932	0.334 ± 0.025	0.345 ± 8.80e-05	0.032 ± 0.072	0.193 ± 0.138	0.560	0.0022 ± 0.001	0.269 ± 0.005
Woyto-Guji	0.939	0.335 ± 0.009	0.339 ± 9.06e-05	0.016 ± 0.027	0.173 ± 0.115	0.410	0.0023 ± 0.001	0.264 ± 0.001
Boran	0.941	0.330 ± 0.011	0.337 ± 0.0002	0.020 ± 0.032	0.151 ± 0.064	0.252	0.0022 ± 0.001	0.265 ± 0.002
Unknown	0.960	0.304 ± 0.023	0.328 ± 5.15e-05	0.072 ± 0.071	0.192 ± 0.128	0.411	0.0022 ± 0.001	0.272 ± 0.007
Thyolo	0.905	0.332 ± 0.048	0.357 ± 7.30e-05	0.068 ± 0.135	0.172 ± 0.086	0.790	0.0019 ± 0.001	0.274 ± 0.009
Guera	0.934	0.322 ± 0.029	0.346 ± 0.0007	0.069 ± 0.084	0.186 ± 0.143	0.357	0.0020 ± 0.001	0.278 ± 0.016
Saanen	0.915	0.331 ± 0.038	0.369 ± 0.0011	0.174 ± 0.101	0.140 ± 0.048	0.053	0.0018 ± 0.001	0.306 ± 0.012
Tibetan	0.932	0.330 ± 0.026	0.334 ± 0.0006	0.117 ± 0.077	0.151 ± 0.061	0.186	0.0021 ± 0.001	0.275 ± 0.025

Pn: polymorphic SNPs; Ho: Observed hetrozygosity; He: Expected hetrozygosity; F: Inbreeding coefficient; ROH: Run of homozygosity; π: Nucleotide diversity and D_{ST}: Pairwise genetic distance

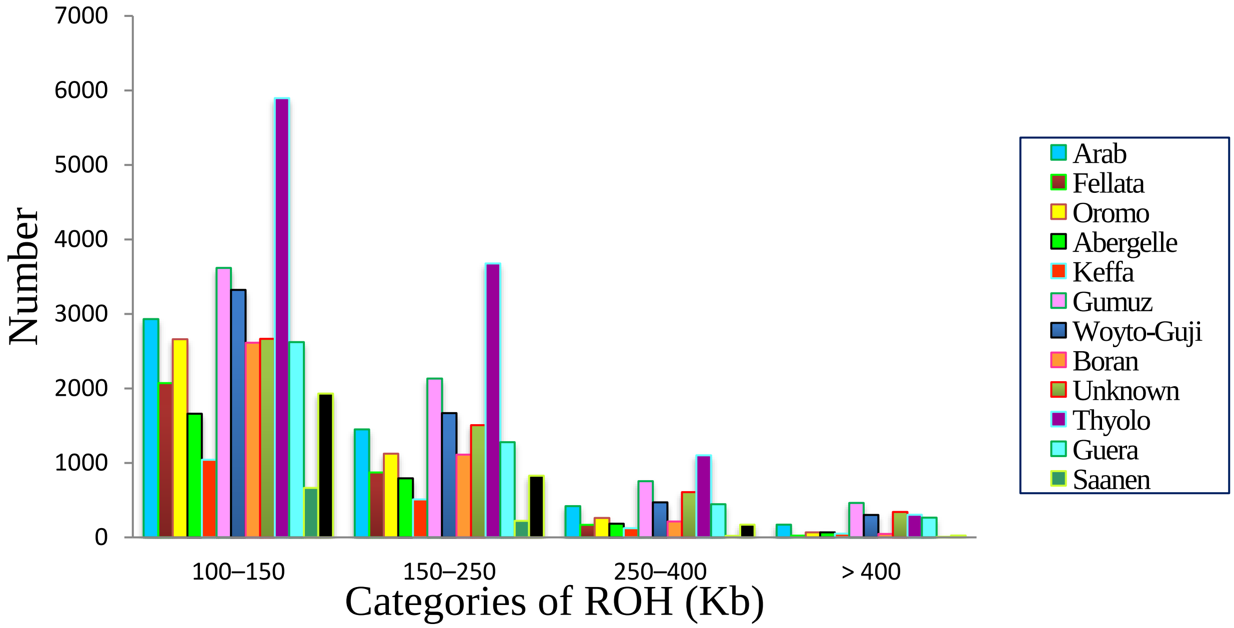

Figure 1: Number of ROH for the four genome length categories ($\mathrm{ROH}_{100–150\mathrm{Kb}}$, $\mathrm{ROH}_{150–250\mathrm{Kb}}$, $\mathrm{ROH}_{250–400\mathrm{Kb}}$ and $\mathrm{ROH}_{>400\mathrm{Kb}}$) of the study goat populations

Population structure

The genetic relationship between individuals was analyzed by principal component analysis (PCA). Here, we had classified the analysis into three different categories: global, African and Ethiopian. Results from the PCA plot incorporating the 13 global goat populations distinguished the goats into five groups showing a marked concordance with geographic origin (East and South African; North African; West African; Asian and European). In this PCA, PC1 and PC2 explained 13.32% and 10.66%, respectively of the total genetic variation (**Figure 2A**).

To investigate the clustering pattern and obtain a clearer picture of the genetic variation among African populations, we performed the PCA but excluding Asian and European populations (**Figure 2B**) and resulted in three genetic clusters (East African; North and West African; and South African).

To further illustrate the distribution of genetic variation among Ethiopian populations, we performed the PCA with only the Ethiopian goats (**Figure 3**) and found three genetic entities (Fellata; Gumuz and Woiyto-Guji; and Abergelle, Arab, Keffa and Oromo).

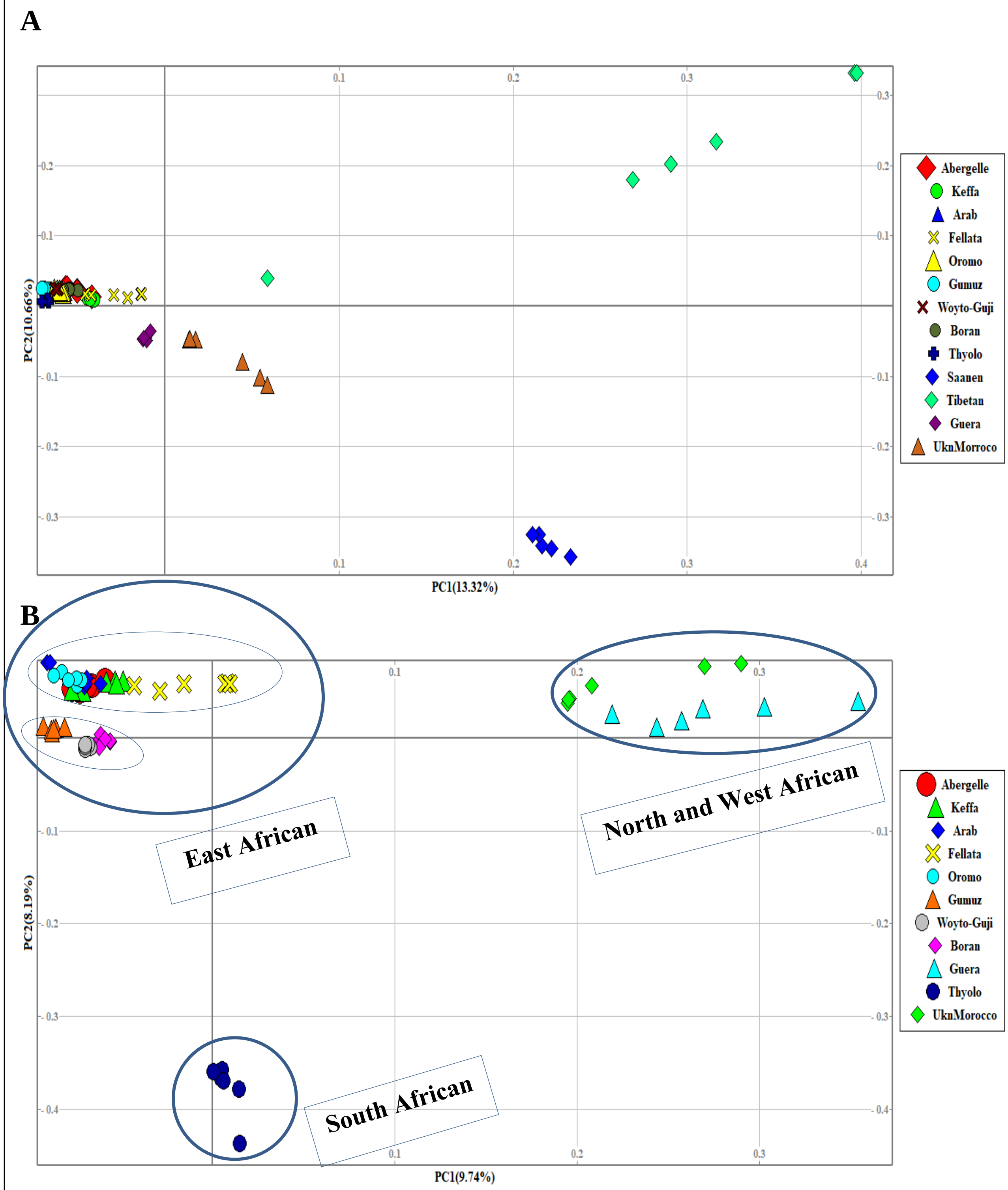

Figure 2: PCA plots for the first two components (PC1 and PC2, the respective variation explained in brackets) **(A)** for the global goat populations and **(B)** for African goats

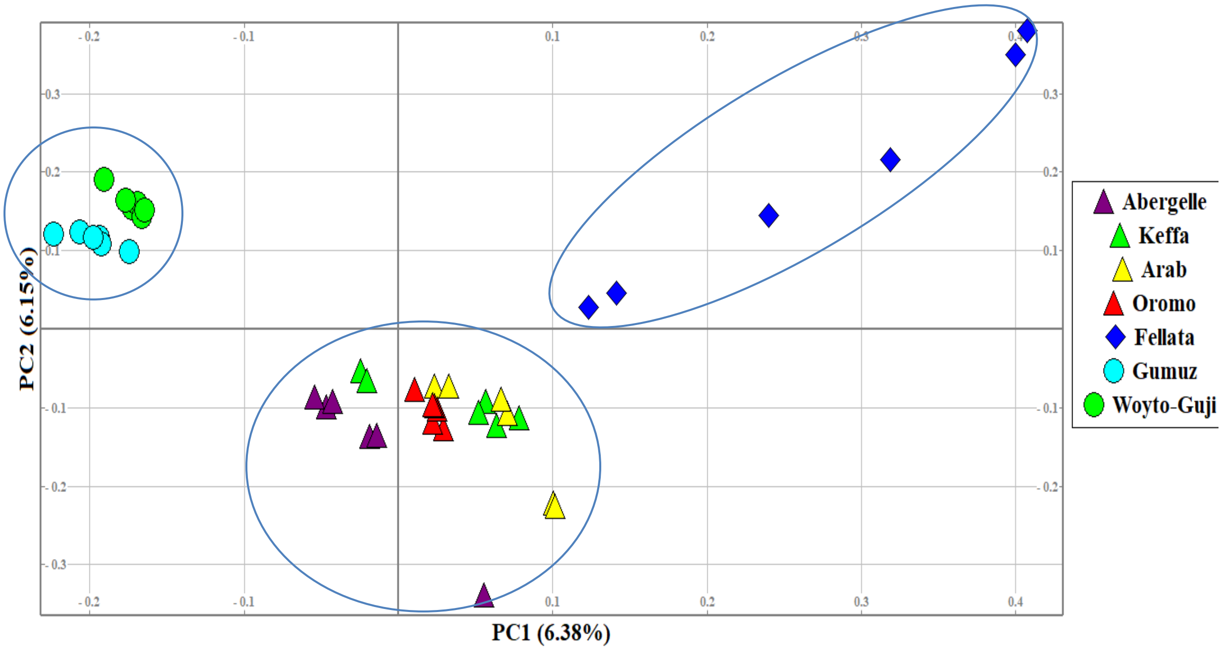

Figure 3: PCA plots for the first two components (PC1 and PC2, the respective variation explained in brackets) for the Ethiopian goats

We used the ADMIXTURE to investigate genome architecture. The ADMIXTURE results for K = 2 to K = 8 are presented in **Figure 4**. The cross-validation (CV) error recorded the least value at K = 5 (**Chapter 10 Supplementary Figure 3**) suggesting this to be the most optimal number of clusters explaining the variation in the 13 global goat populations. Increasing K above 5 did not reveal any detectable population substructure and the population clusters remained the same. At this K, five gene pools were observed. These are designated East African group 1 (EA-G1), East African group 2 (EA-G2), North, West and South African (NWSA), European (EU) and Asian (AS). EA-G1 comprised Arab, Fellata, Oromo, Abergelle and Keffa and EA-G2 included Gumuz, Woyito-Guji and Boran. The NWSA consisted of Unknown, Guera and Thyolo while AS and EU gene pools are exclusive to Tibetan and Saanen breeds, respectively.

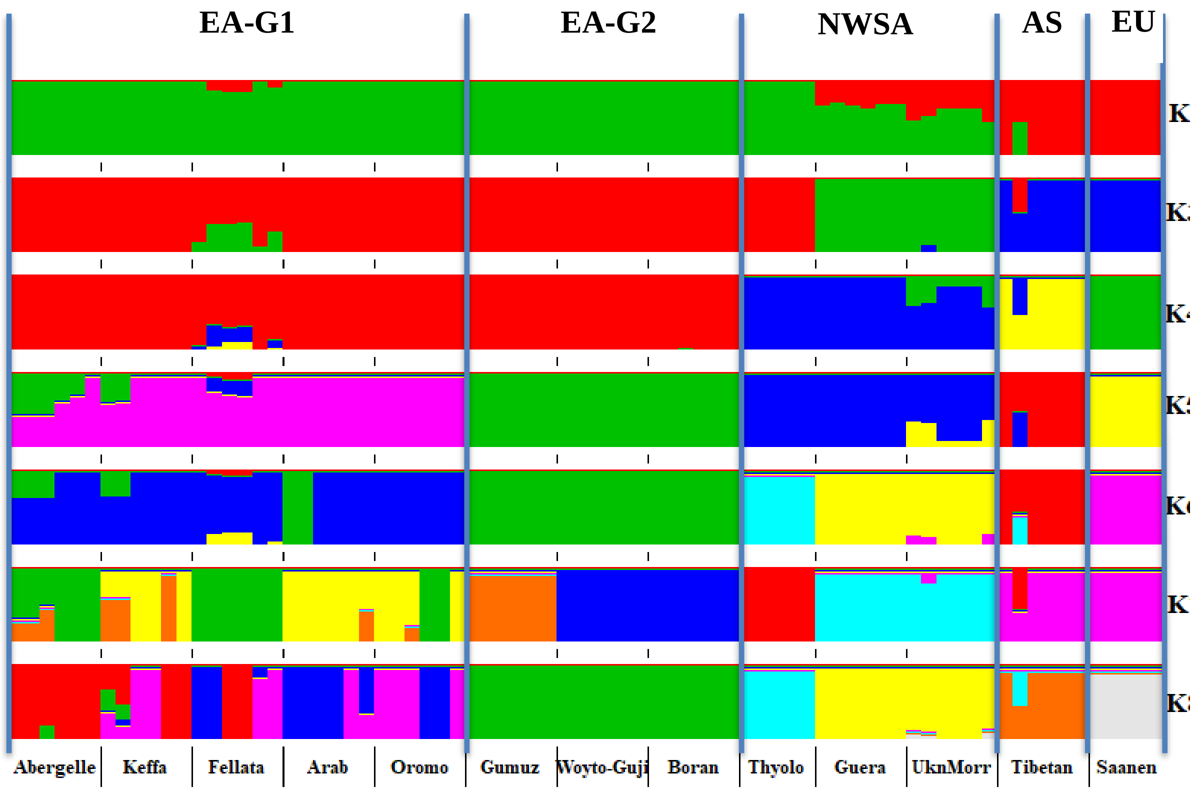

Figure 4: ADMIXTURE plot of the studied goat populations in a global context for 2 ≤ K ≤ 8 (**EA-G1**: East African Group 1; **EA-G2**: East African Group 2; **NWSA**: North, West and South African; **AS**: Asian and **EU**: European)

The Phylogenetic network generated with TREEMIX mirrors the PCA results. While each of North African, West African, European and Asian goat population formed separate cluster, East African (Ethiopian and Kenyan) populations clustered very close to South African goat population. Overall, the goats were positioned between French Saanen and Chinese Tibetan. Furthermore, it revealed extensive gene flow between the study populations, which most likely reflect the current and historical intermixing of goat following human socio-cultural and economic interactions. This appears to be a common feature in Ethiopia and most likely the Northeast and eastern Africa region.

The f4-statistics highlighted possibilities of gene flow among various populations. The highest Z values (>|54|) were observed between Boran and Abergelle and Unknown and Saanen (**Chapter 10 Supplementary Table 6**). The f3-statistics however, did not reveal any likelihood of gene-flow between the populations analyzed (**Chapter 10**

Supplementary Table 5). This could be due to a complex pattern of gene-flow between the study populations, which may not be accounted for by a three-way model.

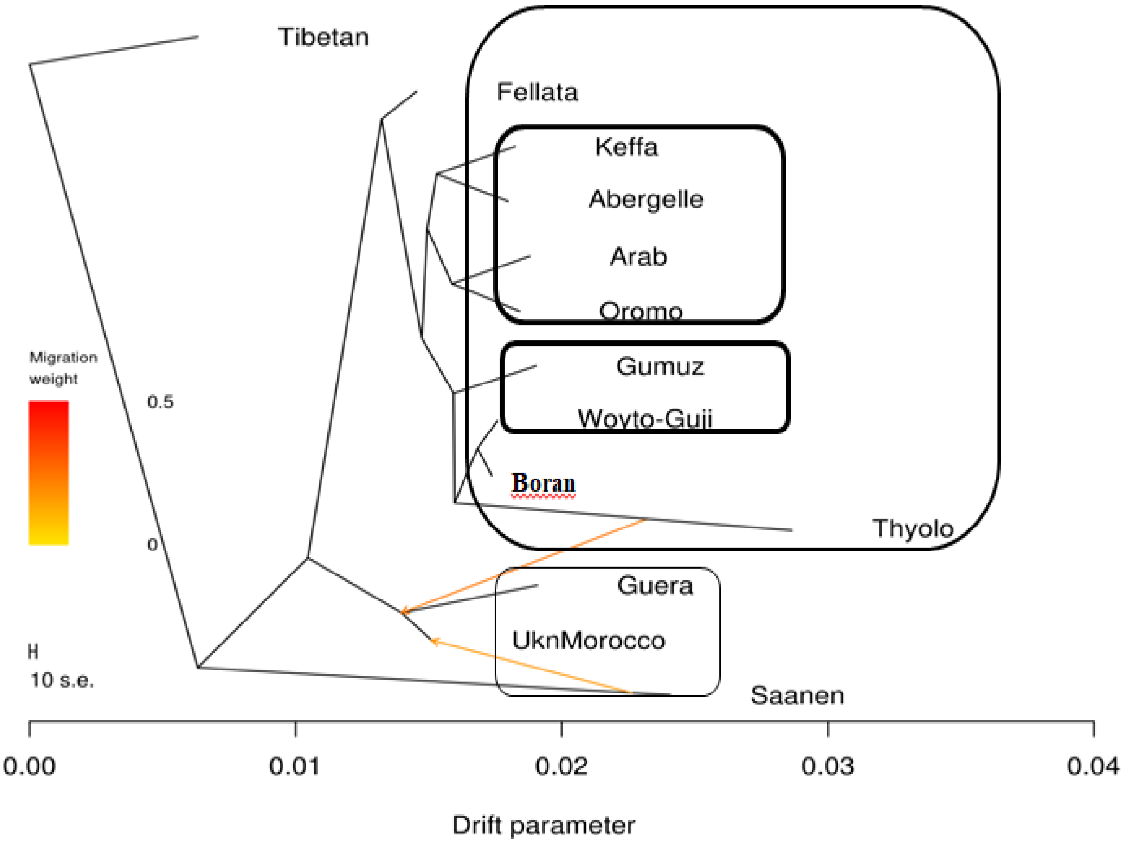

Figure 5: Tree-mix plot. Phylogenetic network inferred by Tree-mix of the relationships between global goat populations. Thirteen migration edges between populations are shown with arrows pointing in the direction toward the recipient group and colored according to the ancestry percentage received from the donor.

pressures (natural versus artificial) and from different geographic zones (tropical semi-arid versus temperate cold) using two selection signature approaches (*Hp* and *Fst*) between the following population pairs: Gumuz versus Saanen and Fellata versus Saanen. The top windows (**Chapter 10 Supplementary Tables 7–10**), which passed the significance threshold, for each method ($ZHp \leq -4.0$, $ZFst \geq 4.0$) were used to define the candidate regions under selection.

The two methods, separately, identified multiple regions under selection (**Figure 6** and **Figure 7**). Here, we focused only on the regions that overlapped between the two approaches. For Fellata, the methods, in combination, identified 25 candidate regions spanning 73 genes (**Table 2**). Similarly, a total of 142 genes were identified across 39 candidate regions (**Table 3**) in Gumuz using the two analytical approaches.

We performed gene ontology (GO) enrichment analysis for the candidate genes revealed in each population (**Chapter 10 Supplementary Table 11**). The five topmost GO terms associated with the candidate genes in Fellata goat include cellular nitrogen compound biosynthetic process (GO:0044271), macromolecule metabolic process (GO:0043170), protein metabolic process (GO:0019538), cellular biosynthetic process (GO:0044249) and gene expression (GO:0010467). The top GO terms associated with the Gumuz candidate genes include osteoclast differentiation (GO:0030316), nuclear division (GO:0000280), amelogenesis (GO:0097186), odontogenesis (GO:0042476) and reproductive process (GO:0022414).

Table 2: Candidate regions and genes identified to be under selection by a combination of two methods (*ZHp*ZFst*) in the Fellata vs. Saanen goats

Chr	Overlapping region	Gene location	Method	Gene name	Gene description
3	46600001-46850000	46724858-46740710	*ZHp*ZFst*	ZRANB2	zinc finger RANBP2-type containing 2
		46727417-46727502		chi-mir-186	chi-mir-186
		46664272-46705573	*ZHp*ZFst*	PTGER3	prostaglandin E receptor 3
6	114550001-114650000	114463897-114630702	*ZHp*ZFst*	ABLIM2	actin binding LIM protein family member 2
	34150001-39150000	33914901-35024825	*ZHp*ZFst*	CCSER1	coiled-coil serine rich protein 1
	70650001-70850000	70711312-70794841	*ZHp*ZFst*	KIT	KIT proto-onco, receptor tyrosine kinase
	44450001-44550000	44554179-44609024	*ZHp*ZFst*	DHX15	DEAH-box helicase 15
7	58950001-59100000	58990844-59062428	*ZHp*ZFst*	PFDN1	prefoldin subunit 1
	66750001-66950000	66767776-66769468		FAM174C	family with sequence similarity 174 member C
		66898830-66902627		POLR2E	RNA polymerase II, I and III subunit E
		66783596-66793493		MIDN	midnolin
		66804620-66810585		CBARP	CACN subunit beta associated regulatory protein
		66772818-66774019		CIRBP	cold inducible RNA binding protein
		66813220-66827946		STK11	serine/threonine kinase 11
		66891741-66893843		GPX4	glutathione peroxidase 4
		66862306-66891766		SBNO2	strawberry notch homolog 2
		66745282-66760161		EFNA2	ephrin A2
		66798216-66799857		ATP5F1D	ATP synthase F1 subunit delta
8	43300001-43400000	43381242-43381358	*ZHp*ZFst*	5S_rRNA	5S ribosomal RNA
9	86100001-86300000	86121330-86272172	*ZHp*ZFst*	QKI	QKI, KH domain containing RNA binding
10	51500001-51850000	51717760-51717866	*ZHp*ZFst*	U6	U6 spliceosomal RNA
		51487996-51622546		ADAM10	ADAM metallopeptidase domain 10
		51644920-51722918		MINDY2	MINDY lysine 48 deubiquitinase 2
		51773327-51817738		SLTM	SAFB like transcription modulator
11	38350001-39000000	38444352-38663454	*ZHp*ZFst*	CCDC85A	coiled-coil domain containing 85A
12	54750001-54900000	54770699-54892292	*ZHp*ZFst*	PAN3	poly(A) specific ribonuclease subunit PAN3
		54897606-55105184		FLT1	fms related receptor tyrosine kinase 1
13	39950001-40050000	39971065-40038312	*ZHp*ZFst*	XRN2	5'-3' exoribonuclease 2
		40043705-40045163		NKX2-4	NK2 homeobox 4
	53300001-53400000	53370062-53375182	*ZHp*ZFst*	ARFRP1	ADP ribosylation factor related protein 1
		53423910-53436635		GMEB2	glucocorticoid modulatory element binding protein 2
		53439544-53440545		FNDC11	fibronectin type III domain containing 11
		53352694-53355776		SLC2A4RG	SLC2A4 regulator
		53443336-53449093		SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites

		53376904-53378283		TNFRSF6B	TNF receptor superfamily member 6b
		53407247-53409735		STMN3	stathmin 3
		53359706-53368860		ZGPAT	zinc finger CCCH-type and G-patch domain containing
		53321214-53349353		ZBTB46	zinc finger and BTB domain containing 46
15	1-100000	9017-69513	*ZHp*ZFst*	NCAPD3	non-SMC condensin II complex subunit D3
18	15950001-16050000	15951720-15955104	*ZHp*ZFst*	CHMP1A	charged multivesicular body protein 1A
		15968206-15974866		CDK10	cyclin dependent kinase 10
		15975821-15979637		SPATA2L	spermatogenesis associated 2 like
		15983075-15992098		VPS9D1	VPS9 domain containing 1
		15992855-16006910		ZNF276	zinc finger protein 276
		16007189-16043896		FANCA	FA complementation group A
	26850001-27100000	26840087-26861817	*ZHp*ZFst*	CCDC102A	coiled-coil domain containing 102A
		26875088-26902276		ADGRG5	adhesion G protein-coupled receptor G5
		26966612-26991056		ADGRG1	adhesion G protein-coupled receptor G1
		26993583-27020617		ADGRG3	adhesion G protein-coupled receptor G3
		27024863-27048291		DRC7	dynein regulatory complex subunit 7
		27049391-27067420		KATNB1	katanin regulatory subunit B1
	55250001-55400000	55204669-55266425	*ZHp*ZFst*	SAE1	SUMO1 activating enzyme subunit 1
		55270566-55274583		BBC3	BCL2 binding component 3
		55302640-55311312		CCDC9	coiled-coil domain containing 9
		55314452-55314889		INAFM1	InaF motif containing 1
		55346343-55362018		C5AR1	complement C5a receptor 1
19	13300001-13400000	13318403-13330489	*ZHp*ZFst*	C17orf78	chromosome 17 open reading frame 78
	33600001-33700000	33614694-33627722	*ZHp*ZFst*	CARD6	caspase recruitment domain family member 6
20		33645923-33647842		RPL37	ribosomal protein L37
		33647611-33647690		SNORD72	small nucleolar RNA, C/D box 72
		33665566-33690885		PRKAA1	protein kinase AMP-activated catalytic subunit alpha 1
21	56450001-56550000	56485353-56665103	*ZHp*ZFst*	SLC24A4	solute carrier family 24 member 4
22	56450001-56550000	56454088-56516884	*ZHp*ZFst*	RAF1	Raf-1 proto-oncogene, serine/threonine kinase
		56518780-56561374		MKRN2	makorin ring finger protein 2
25	3000001-3100000	2913691-2964110	*ZHp*ZFst*	TRAP1	TNF receptor associated protein 1
		2970849-3091059		CREBBP	CREB binding protein
	3650001-3800000	3661107-3665199	*ZHp*ZFst*	UBALD1	UBA like domain containing 1
		3670857-3704883		MGRN1	mahogunin ring finger 1
		3713917-3719705		NUDT16L1	nudix hydrolase 16 like 1
		3716969-3730681		ANKS3	ankyrin repeat and sterile alpha motif domain containing 3
		3778183-3787801		SEPTIN12	septin 12
		3796634-3801937		ROGDI	rogdi atypical leucine zipper
28	15550001-15650000	15079519-15623232	*ZHp*ZFst*	ADK	adenosine kinase

Table 3: Candidate regions and genes identified to be under selection by a combination of two methods (*ZHp*ZFst*) in the Gumuz vs. Saanen goats

Chr	Overlapping region	Gene location	Method	Gene name	Gene description
1	81150001-81400000	81080594-81243253	*ZHp*ZFst*	IGF2BP2	insulin like growth factor 2 mRNA binding protein 2
		81306056-81356307		LIPH	lipase H
2	16050001-16150000	15749601-16107764	*ZHp*ZFst*	DIS3L2	DIS3 like 3'-5' exoribonuclease 2
		16087126-16087259		SNORA62	Small nucleolar RNA SNORA62/SNORA6 family
		16143978-16149196		NPPC	natriuretic peptide C
	83650001-83750000	83533429-83920207	*ZHp*ZFst*	GTDC1	glycosyltransferase like domain containing 1
3	16800001-16900000	16769226-16898198	*ZHp*ZFst*	FOXJ3	forkhead box J3
	103650001-103750000	103647594-103659139	*ZHp*ZFst*	DENND4B	DENN domain containing 4B
		103663129-103672236		CRTC2	CREB regulated transcription coactivator 2
		103673826-103676095		SLC39A1	solute carrier family 39 member 1
		103680814-103685105		CREB3L4	cAMP responsive element binding protein 3 like 4
		103701073-103790482		NUP210L	nucleoporin 210 like
4	14900001-15000000	14907380-14907661	*ZHp*ZFst*	TRBV3-1	T cell receptor beta variable 3-1
		14972872-14979328		PRSS58	serine protease 58
	26600001-26700000	26563963-26642527	*ZHp*ZFst*	NRF1	nuclear respiratory factor 1
5	17750001-18100000	17951263-18151736	*ZHp*ZFst*	KITLG	KIT ligand
	26300001-26750000	26424191-26432938	*ZHp*ZFst*	SP7	Sp7 transcription factor
		26284172-26302607		PCBP2	poly(rC) binding protein 2
		26300669-26300775		U6	U6 spliceosomal RNA
		26332993-26338873		AMHR2	anti-Mullerian hormone receptor type 2
		26350346-26383816		SP1	Sp1 transcription factor
		26436332-26450350		AAAS	aladin WD repeat nucleoporin
6	45600001-45700000	45605882-45619150	*ZHp*ZFst*	SLC34A2	solute carrier family 34 member 2
		45658612-45769098		SEL1L3	SEL1L family member 3
7	17450001-17550000	17492003-17500941	*ZHp*ZFst*	NR2F1	nuclear receptor subfamily 2 group F member 1
	51350001-56250000	51416609-51425884	*ZHp*ZFst*	SPINK1	serine peptidase inhibitor Kazal type 1
		56060015-56169881		NR3C1	nuclear receptor subfamily 3 group C member 1
	66500001-66750000	66519753-66527003	*ZHp*ZFst*	MBD3	methyl-CpG binding domain protein 3
		66533422-66541829		MEX3D	mex-3 RNA binding family member D
		66585598-66586900		REEP6	receptor accessory protein 6
		66591573-66598065		PCSK4	proprotein convertase subtilisin/kexin type 4
		66603174-66606676		C19orf25	chromosome 19 open reading frame 25
		66609852-66625867		APC2	APC regulator of WNT signaling pathway 2
		66641582-66653537		DAZAP1	DAZ associated protein 1
		66667014-66669783		GAMT	guanidinoacetate N-methyltransferase
		66670469-66674670		NDUFS7	NADH:ubiquinone oxidoreductase core subunit S7
		66679294-66695691		PWWP3A	PWWP domain containing 3A, DNA repair factor

		66745282-66760161		EFNA2	ephrin A2
		66767776-66769468		FAM174C	family with sequence similarity 174 member C
		66772818-66774019		CIRBP	cold inducible RNA binding protein
		66783596-66793493		MIDN	midnolin
		66798216-66799857	*ZHp*ZFst*	ATP5F1D	ATP synthase F1 subunit delta
	66800001-67000000	66804620-66810585		CBARP	CACN subunit beta associated regulatory protein
		66813220-66827946		STK11	serine/threonine kinase 11
		66862306-66891766		SBNO2	strawberry notch homolog 2
		66891741-66893843		GPX4	glutathione peroxidase 4
		66898830-66902627		POLR2E	RNA polymerase II, I and III subunit E
		66906700-66918974		ARHGAP45	Rho GTPase activating protein 45
		66920634-66937537		ABCA7	ATP binding cassette subfamily A member 7
		66952810-66962129		TMEM259	transmembrane protein 259
		66969003-66978955		WDR18	WD repeat domain 18
		66981853-67013587		ARID3A	AT-rich interaction domain 3A
	67100001-67200000	67094581-67104141	*ZHp*ZFst*	PLPPR3	phospholipid phosphatase related 3
		67102342-67115014		PTBP1	polypyrimidine tract binding protein 1
		67146345-67151195		MISP	mitotic spindle positioning
		67157958-67170570		PALM	paralemmin
		67187674-67194868		PRSS57	serine protease 57
		67194703-67200206		FSTL3	follistatin like 3
		67209174-67216701		RNF126	ring finger protein 126
		67218307-67220955		FGF22	fibroblast growth factor 22
		67230939-67244120		POLRMT	RNA polymerase mitochondrial
		67244855-67264548		HCN2	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2
8	43350001-43550000	43381242-43381358	*ZHp*ZFst*	5S_rRNA	5S ribosomal RNA
		43411349-43424869		DMRT3	doublesex and mab-3 related transcription factor 3
		43431658-43524941		DMRT1	doublesex and mab-3 related transcription factor 1
10	46350001-46450000	46420405-46610471	*ZHp*ZFst*	WDR72	WD repeat domain 72
11	69500001-70750000	70658980-70670864	*ZHp*ZFst*	TRMT61B	tRNA methyltransferase 61B
		70671040-70702909		SPDYA	speedy/RINGO cell cycle regulator family member A
		70716899-70749413		PPP1CB	protein phosphatase 1 catalytic subunit beta
13	60500001-60900000	60722858-60771784	*ZHp*ZFst*	TTLL9	tubulin tyrosine ligase like 9
		60774603-60780307		PDRG1	p53 and DNA damage regulated 1
		60796444-60821549		XKR7	XK related 7
		60834727-60853093		CCM2L	CCM2 like scaffold protein
14	54000001-54100000	54022025-54053306	*ZHp*ZFst*	TTPA	alpha tocopherol transfer protein
		54059977-54089686		GGH	gamma-glutamyl hydrolase
	88750001-90300000	88768841-88768947	*ZHp*ZFst*	U6	U6 spliceosomal RNA

		90147751-90291047		LMBRD1	LMBR1 domain containing 1
		90388846-90389146		7SK	7SK RNA
15	39600001-44400000	39485068-39983128	*ZHp*ZFst*	SBF2	SET binding factor 2
16	62250001-62350000	62171995-62226824	*ZHp*ZFst*	RGSL1	regulator of G protein signaling like 1
		62247654-62262178		RNASEL	ribonuclease L
		62275420-62281737		RGS16	regulator of G protein signaling 16
18	15900001-16050000	15902497-15913971	*ZHp*ZFst*	CPNE7	copine 7
		15936405-15942118		DPEP1	dipeptidase 1
		15951720-15955104		CHMP1A	charged multivesicular body protein 1A
		15975821-15979637		SPATA2L	spermatogenesis associated 2 like
		15983075-15992098		VPS9D1	VPS9 domain containing 1
		15992855-16006910		ZNF276	zinc finger protein 276
		16007189-16043896		FANCA	FA complementation group A
	26150001-27100000	26158111-26261951	*ZHp*ZFst*	NUP93	nucleoporin 93
		26273622-26273704		MIR138-2	microRNA 138-2
		26277672-26316261		SLC12A3	solute carrier family 12 member 3
		26840087-26861817		CCDC102A	coiled-coil domain containing 102A
		26875088-26902276		ADGRG5	adhesion G protein-coupled receptor G5
		26966612-26991056		ADGRG1	adhesion G protein-coupled receptor G1
		26993583-27020617		ADGRG3	adhesion G protein-coupled receptor G3
		27024863-27048291		DRC7	dynein regulatory complex subunit 7
		27049391-27067420		KATNB1	katanin regulatory subunit B1
	36650001-36750000	36663068-36676147	*ZHp*ZFst*	PSKH1	protein serine kinase H1
		36682628-36685030		PSMB10	proteasome 20S subunit beta 10
		36686615-36690928		LCAT	lecithin-cholesterol acyltransferase
		36690545-36712359		SLC12A4	solute carrier family 12 member 4
		36718454-36722463		DPEP3	dipeptidase 3
		36724741-36729232		DPEP2	dipeptidase 2
		36742896-36744533		DDX28	DEAD-box helicase 28
		36748685-36776337		DUS2	dihydrouridine synthase 2
		36782715-36872679		NFATC3	nuclear factor of activated T cells 3
		36859911-36860018		U6	U6 spliceosomal RNA
		36876400-36881911		ESRP2	epithelial splicing regulatory protein 2
		36888559-36900932		PLA2G15	phospholipase A2 group XV
		36914669-36934459		SLC7A6	solute carrier family 7 member 6
		36938284-36944006		SLC7A6OS	solute carrier family 7 member 6 opposite strand
		36947431-36982624		PRMT7	protein arginine methyltransferase 7
		36986634-37010350		SMPD3	sphingomyelin phosphodiesterase 3
19	13300001-13400000	13318403-13330489	*ZHp*ZFst*	C17orf78	chromosome 17 open reading frame 78
	13300000-18500000	18279378-18526212	*ZHp*ZFst*	NF1	neurofibromin 1

	29350001-29450000	29384700-29389588	*ZHp*ZFst*	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent
		29392508-29407859		TMEM220	transmembrane protein 220
		29489115-29489522		PIRT	phosphoinositide interacting regulator of transient receptor potential channels
	33750001-34450000	33749216-33750820	*ZHp*ZFst*	MFAP4	microfibril associated protein 4
		33751874-33756381		MAPK7	mitogen-activated protein kinase 7
		33773312-33781322		B9D1	B9 domain containing 1
		33784485-33835720		EPN2	epsin 2
		34297613-34401427		RAI1	retinoic acid induced 1
20	6750001-6900000	6753922-6798997	*ZHp*ZFst*	FAM169A	family with sequence similarity 169 member A
		6818105-6861599		GFM2	GTP dependent ribosome recycling factor mitochondrial 2
21	56450001-56550000	56485353-56665103	*ZHp*ZFst*	SLC24A4	solute carrier family 24 member 4
22	31550001-31700000	31527873-31755428	*ZHp*ZFst*	MITF	melanocyte inducing transcription factor
23	1000001-1100000	788570-1217296	*ZHp*ZFst*	GMDS	GDP-mannose 4,6-dehydratase
24	25100001-25400000	25006472-25238535	*ZHp*ZFst*	GAREM1	GRB2 associated regulator of MAPK1 subtype 1
		25293755-25328374		MEP1B	meprin A subunit beta
		25387398-25426069		RNF138	ring finger protein 138
25	3650001-370000	3661107-3665199	*ZHp*ZFst*	UBALD1	UBA like domain containing 1
		3670857-3704883		MGRN1	mahogunin ring finger 1
		3713917-3719705		NUDT16L1	nudix hydrolase 16 like 1
		3716969-3730681		ANKS3	ankyrin repeat and sterile alpha motif domain containing 3
26	30350001-30500000	30404780-30415917	*ZHp*ZFst*	SCD	stearoyl-CoA desaturase
		30438562-30483527		PKD2L1	polycystin 2 like 1, transient receptor potential cation channel
27	25750001-25900000	25769588-25834074	*ZHp*ZFst*	SLC7A2	solute carrier family 7 member 2
		25844297-25928982		PDGFRL	platelet derived growth factor receptor like
29	46600001-46700000	46612922-46622157	*ZHp*ZFst*	TCIRG1	T cell immune regulator 1, ATPase H+ transporting V0 subunit a3
		46620698-46681876		CHKA	choline kinase alpha

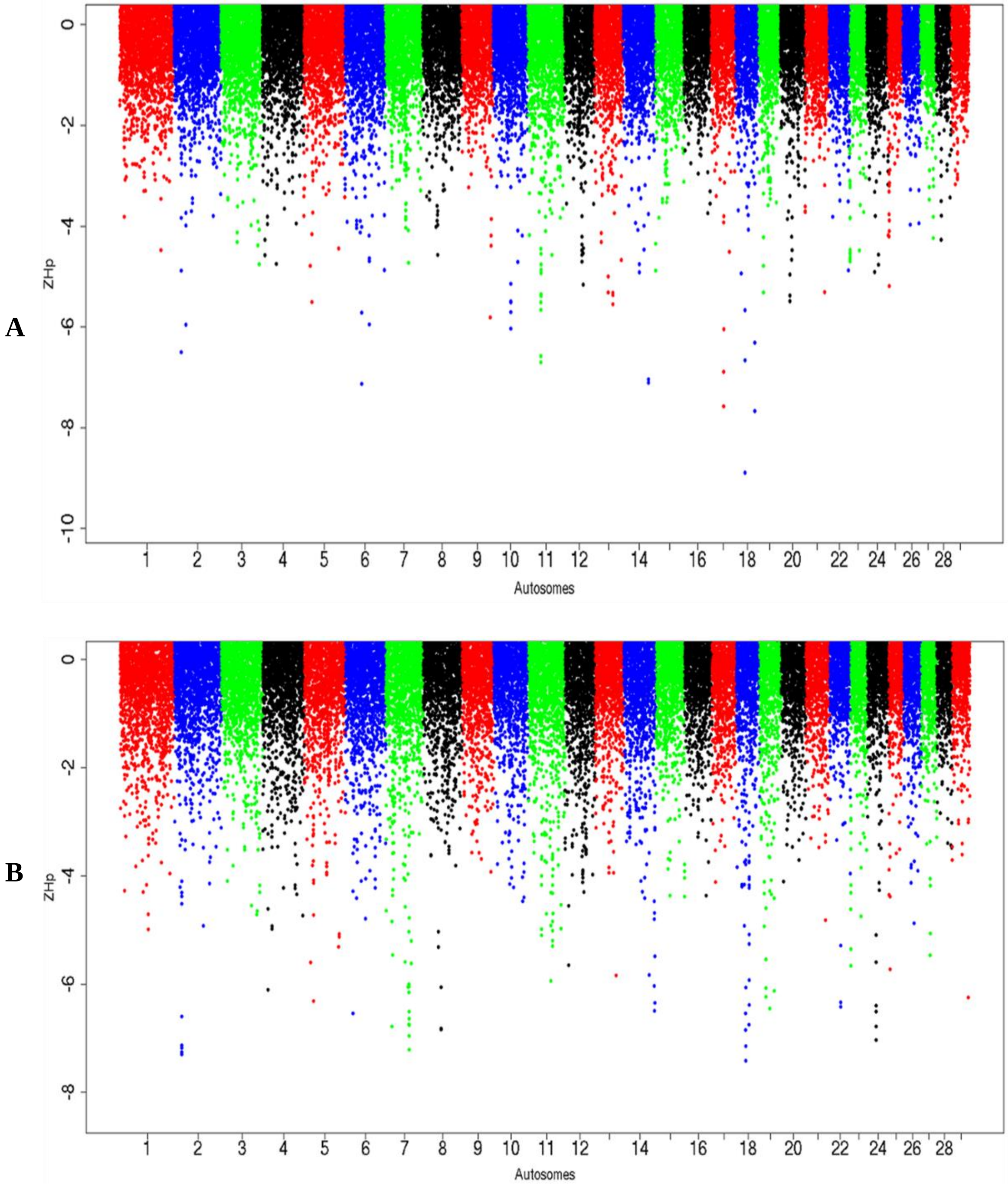

Figure 6: Manhantan plots for selection sweep analysis of **(A)** Fellata and **(B)** Gumuz goat populations performed using the standardized pool heterozygosity (ZHp) approach. The horizontal line represents the arbitrary threshold for $ZHp \leq -4.0$.

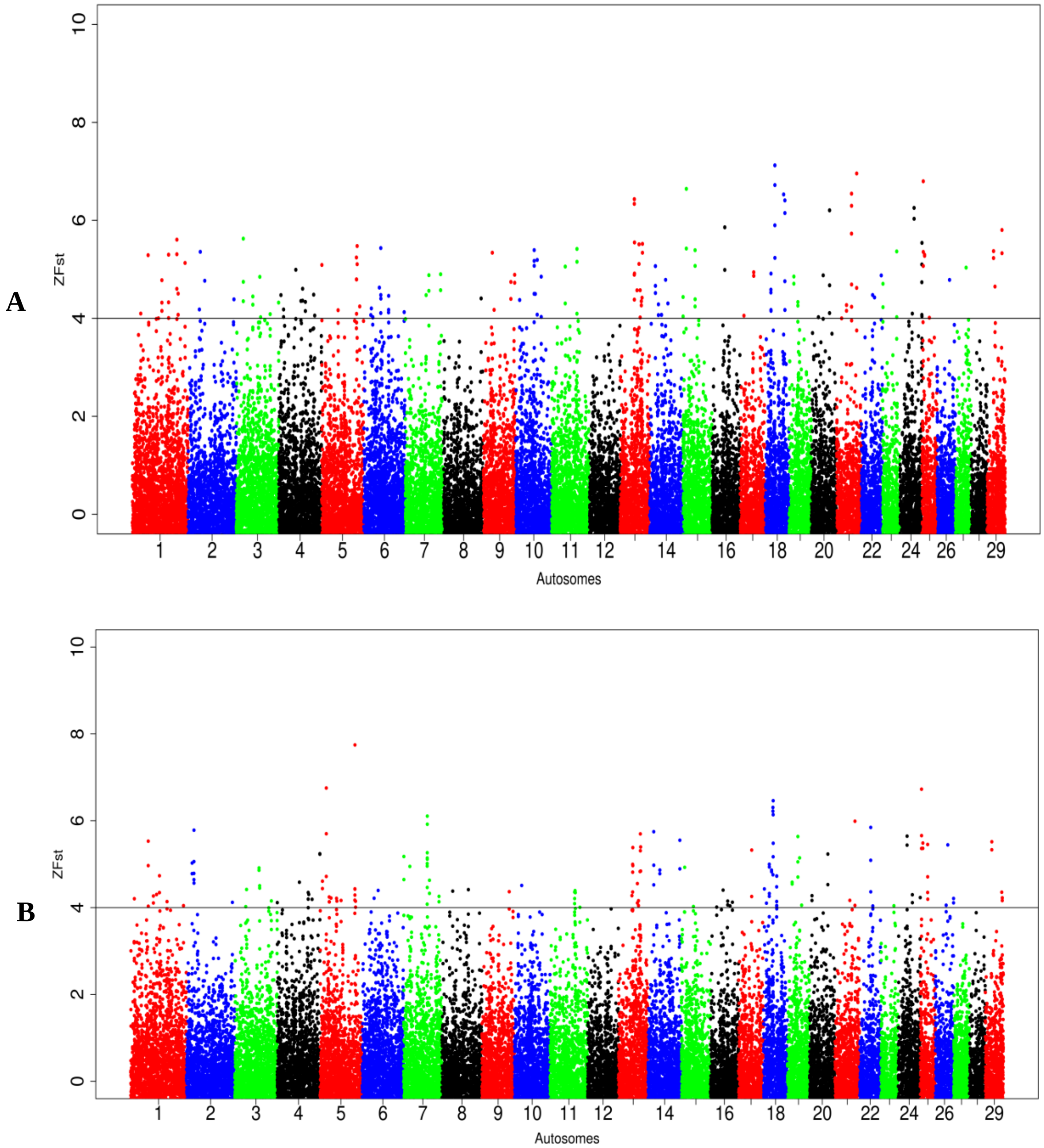

Figure 7: Manhantan plots for selection sweep analysis **(A)** between Fellata vs Saanen and **(B)** between Gumuz vs Saanen goat populations performed using the standardized pool heterozygosity (ZHp) approach. The horizontal line represents the arbitrary threshold for $ZFst \geq 4.0$.

DISCUSSION

Due to its proximity to the historical entry points of domestic plant and animal species into and out of the African continent, altitudinal gradients that ranges from 125 m below sea level to 4,500 m above sea level, ethnic diversity of ancient origin associated with diverse livestock husbandry practice and migrations of people and animals due to recurrent drought, flood and war, Ethiopia is considered a reservoir of genetic diversity. Such variations in environmental, climatic, socio-anthropological and production conditions might have shaped the genomic architecture of indigenous goats. Here, we investigated the genome architecture of three (Arab, Fellata and Oromo) indigenous Ethiopian goat populations. The overall average *Ho* and *He* exceeded 0.300, suggesting high levels of genome diversity and the values for most of the individual populations are close to previous studies in Sudanese (Rahmatalla et al., 2017) and Pakistani (Kumar et al., 2018) goats and Egyptian Barki breed (Kim et al., 2016). High genetic diversity within a population that could be attributed to uncontrolled mating is characteristic of large communal populations (Lauvergne et al., 2000). Within population selection may benefit from the within population variation. It can also complement goat community based breeding program (CBBP) in Ethiopia. CBBP, in which selection within a population is exercised, provides a good framework for the implementation of genomic selection in smallholder production systems (Mrode et al., 2018). Although the within breed genetic diversity estimates for the three goat populations are high, they are slightly lower than Chinese Tibetan and French Saanen populations. Deliberate avoidance of inbreeding in the Tibetan and Saanen breeds could explain this result. Among the 13 global goat populations, Keffa demonstrated the lowest level of genetic diversity. This suggests high inbreeding in this goat population which might be due to extensive use of few breeding bucks within flocks. This result is consistent with previous finding that was arrived at using Caprine 52KSNP genotype data (Tarekegn et al., 2021) who reported Keffa is the least diverse among 13 Ethiopian indigenous goat populations. Attention should be paid to this goat population to prevent a loss of goat genetic resources.

Runs of homozygosities (ROHs) are continuous homozygous genomic segments, at the individual and population levels. The length and frequency of ROH may describe past and recent population history and may also reveal the level of inbreeding within populations, recent population bottlenecks or signatures of positive selection (Szmatola et al., 2019; Ceballos et al., 2018). This is particularly important for African indigenous livestock which is characterized by lack of pedigree record data (Kosgey et al., 2006). In the absence of such data, ROH can be used to describe population history (Zavarez et al., 2015). In the present study, all of the 13 global populations showed their majority of ROH in the short (100–150 Kb) length category, which is in agreement with the results obtained for other goats (Guo et al., 2018; Onzima et al., 2018; Islam et al., 2019). Different ROH distribution patterns were noted for Gumuz and Unknown goat populations, which displayed higher number of ROH than other populations in the long (> 400 Kb) length category. The accumulations of long ROHs in the genome of the two populations enable them to carry deleterious mutations in homozygous form [Szpiech et al., 2013] and is indicative of demographic decline and recent inbreeding (Manunza et al., 2016). The highest number of short ROH in the Thyolo population indicates ancient inbreeding and/or small founder effect (Manunza et al., 2016).

A combination of PCA, ADMIXTURE (K = 5) and TREEMIX tools revealed the underlying genetic structure in the global, East African and Ethiopian goat populations. The tools revealed five distinct genetic clusters in the global goat populations. The East African goats, represented here by Ethiopian and Kenyan goats, formed two distinct groups: EA-G1 and EA-G2. Our finding on the sub-grouping of East African goats into two groups accords with previous findings of Tarekegn et al. (2018) and Kibegwa et al. (2016), who performed mtDNA analyses of Ethiopian and Kenyan goats respectively and identified two haplogroups (A and G), suggesting the presence of two genetic groups of goats in East Africa. However, based on the current dataset, it is difficult to infer whether EA-G1 and EA-G2 arrived together or independently. Indeed, the geographic locations of the two goat groups give indirect insights. The fact that EA-G1 populations are found in areas close to the Red sea and Mediterranean coast compared to EA-G2 populations indicate that the ancestors of the two groups have arrived independently, with the arrival of EA-G2 preceding EA-G1. The tools also identified two genetic clusters in the Ethiopian goat populations. Cluster 1: Gumuz and Woyto-Guji; and cluster 2: Abergelle, Arab, Fellata, Keffa and Oromo. Home tracts of Arab, Fellata and Oromo goat populations are very tied up that may facilitate ease of flock exchange between farmers and favored gene flow between goat populations. However, given the geographical isolation between Gumuz and Woyto-Guji, they appeared in one cluster. Likewise, Abergelle and Keffa are far apart yet found very close in the PCA.

In selection signature analysis, we used two approaches (*Hp* and *Fst*). The *Hp* approach is a variability indicator based on allele counts across sliding windows and *Fst* indicates the same but based on an increase or decrease in allele frequency differentiation between populations/breeds. The methods are based on different algorithms and assumptions and thus if common signatures are detected by two of the methods it suggests good reliability of the results while reducing the likelihood of interpreting false positives. In this study, we used both methods to detect the signatures of selection across the autosomes of two distinct Ethiopian indigenous goat populations, including Fellata and Gumuz. The populations are considered to be adapted to their production environments and they represent an important model species for investigating and enhancing our knowledge on the genome profiles of litter size, environmental adaptation, coat coloration and body weight.

Candidate genes associated with litter size

Litter size is an important economic trait that appears to be controlled by multiple genes and factors like ovarian follicular development, oocyte maturation, ovulation, fertilization, embryogenesis, embryo implantation and uterine receptivity (Feng et al., 2015). The development of high-tech molecular tools enabled animal geneticists to identify major and minor genes associated with litter size in goats (e.g., Lai, et al., 2016; Guang-Xin et al., 2019; Tao et al., 2021; Wang et al., 2021). Our selective sweep mapping involving Fellata and Gumuz goats identified fecundity genes. In the earlier, we identified *FLT1* (Fms related receptor tyrosine kinase 1) (CHI12) and in the later we found *AMHR2* (Anti-Mullerian hormone receptor type 2) (CHI5) and *IGF2BP2* (insulin like growth factor 2 mRNA binding protein 2) (CHI1). These genes comprised the three most significant GO terms, "reproductive process" (GO:0022414), "macromolecule metabolic process" (GO:0043170) and protein metabolic process (GO:0019538) suggesting these genes may underlie reproductive changes. Indeed, *FLT1* is associated with female reproduction in Arsi-Bale goat breed (Tarekegn et al., 2021), bovines (Kfir et al., 2018) and chicken (Sun et al., 2015; Shen et al., 2017). It is also a candidate region under selection in Finn and Texel sheep breeds (Xu et al., 2018), swine (Ding et al., 2006), Spanish Holstein dairy cattle (Sassi et al., 2016) and humans (Tal et al., 2014). The *AMRH2* gene is significantly associated with litter size as evidenced from association study on high fecundity Chinese Laoshan dairy goats (Lai et al., 2016). A study by Monniaux et al. (2011) identified *AMRH2* as a predictive endocrine marker for embryo production in the French goat. Similarly, it was found to be a highly reliable endocrine marker of the size of the ovarian pool of growing follicles in humans (Visser and Themmen, 2005), mice (Kevenaar et al., 2006) and cows (Rico et al., 2009). *IGF2BP2* plays an essential role in the development and maturation of germ cells and embryos and is a candidate gene for goat litter size (Xin et al., 2021). By using WGS analysis in Dazu Black goat, the gene *IGF2BP2* has been identified as a candidate gene associated with litter size (E et al., 2019). Additionally, *IGF2BP2* expression has been detected in both resting and growing oocytes and granulocytes in mature mouse and human ovaries (Hammer et al., 2005). It also promotes myoblast growth and it is a key regulator of skeletal muscle development (Li et al., 2012).

Genome targets for adaptation to arid environments

High ambient temperature resulting in thermal stress presents the physiological challenge to organisms residing in hot environments. It may affect livestock production and reproduction performance. Our results provided insights on possible mechanisms underlying adaptation to hot environments. Among the genes identified in Fellata goats (CHI13) were *ZBTB46* (Zinc finger and BTB domain containing 46), *ARFRP1* (ADP ribosylation factor related protein 1), *STMN3* (stathmin 3) and *GMEB2* (glucocorticoid modulatory element binding protein 2). Tarekegn et al. (2021) and Liu et al. (2016) also identified *ZBTB46*, *ARFRP1*, *STMN3* and *GMEB2* genes in Nubian goats that are adapted to hot arid environments and in Mongolian sheep sampled from different ecoregions, respectively.

Candidate regions associated with coat color

Apart from its aesthetic appeal, color can affect an animal's temperature because all else being equal, dark color absorb more solar energy than do light color and that energy is converted into heat (Stuart-Fox et al., 2017). Though the genes responsible for the coat color are pleiotropic in their effect (Bhat et al., 2019), the coat color of an animal is mainly determined by the distribution and activity of melanocytes in the body. In our study, we identified coat coloration genes like *KIT* (KIT proto-onco, receptor tyrosine kinase) (CHI6) in Fellata and *KITLG* (KIT ligand) (CHI5) and *MITF* (melanocyte inducing transcription factor) (CHI22) in Gumuz. *KIT* is ascribed for white color pigmentation in cattle (Brenig et al., 2013), goats (Nazari-Ghadikolaei et al., 2018; Bhat et al., 2019) and domestic cats (Cooper et al., 2006). Similarly, *MITF* gene is implicated in controlling white spotting in dogs (Rothschild et al., 2006), Holstein cattle (Liu et al., 2009) and Geese (Wang et al., 2014). Experimental evidence stated that *KITLG* has positive influence on melanocyte proliferation and melanin distribution and activates keratinocytes (Cario-André et al., 2006). The pigmentation loci, KIT and KITLG, are the shared signals in Neolithic goat populations (Daly et al., 2018) and are the common signals in the modern livestock (Kijas et al., 2012; Alberto et al., 2018). The presence of genes responsible for white coat color in Fellata and Gumuz goats could be an adaptive response to intense solar radiation. The predominance of white coat color in Fellata goat was observed by the first author during sampling.

Candidate genes associated with body weight

Body weight is an economically important trait in goat production. Thus, it is vitally important to investigate the underlying molecular mechanisms behind this trait and identify the important functional genes that influence it. Here, we identified candidate genes including *IGF2BP2* on (CHI1) and *MAPK7* (CHI19) in Gumuz goat. *IGF2BP2* (insulin like growth factor 2 mRNA binding protein 2) promotes myoblast growth and it is a key regulator of skeletal muscle development (Li et al., 2012). *MAPK7* (Mitogen-activated protein kinase 7) has been found to play crucial role in myocyte proliferation and differentiation (Glass, 2005).

CONCLUSION

We used whole genome sequence data to investigate signatures of selection in Ethiopian indigenous goat populations. This genomic data identified several potential candidate genes possibly under selection, including disease resistance genes (*DIS3L2, TRPM2*) in Keffa goat, body weight genes (*IGF2B2, MAPK7*) in Gumuz goat, litter size related genes (*FLT1*, *AMHR2*) and coat color associated genes (*KIT*, *KITLG*, *MITF*) in Fellata and Gumuz goats. To the best of our knowledge, we are the first to report these candidate genes in Ethiopian indigenous goat populations. Our results provide a foundation for future studies to investigate the genome architectures in different ruminant species coexisting in a similar environment.

DATA ACCESSIBILITY

Genotypic data of 30 animals representing three Ethiopian goat populations are deposited and available at (……)

ETHICS STATEMENT

Before we collected blood samples from each individual animal, we informed the farmers about the objectives of the study to make informed decisions. During the blood sample collection, animal welfare and health regulations were observed. No further specific permissions were required from the Ethics Committee of the Bahir Dar or Assosa Universities, Ethiopia at the time of the sampling.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

OS, AH, JM, and KA conceived and designed the study. OS collected the blood samples, extracted the DNA with the help of JM, analyzed the data with inputs from AbA and JM and wrote the manuscript. JM revised the manuscript. JLH and JM contributed to sequencing and mapping data of the three Ethiopian goat populations. All authors read and approved the final manuscript.

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Paper 4: Phenotypic ranking experiments in identifying breeding objective traits of smallholder farmers in northwestern Ethiopia

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Abstract

We executed two live animal ranking experiments, own-flock and group-animal ranking, to identify the breeding objectives of Arab and Oromo goat keepers in northwestern Ethiopia as a preliminary step towards designing sustainable breeding programs for two goat populations. In the own-flock ranking experiment, a total of 147 households, out of which 46 were Arab and 101 were Oromo goat keepers that live in semi-arid and sub-humid agroecologies respectively, were visited at their homesteads and were asked to choose their first best, second best, third best and the most inferior does from their own flock. The reasons of ranking and life history of the does (age, previous production and reproduction information) were inquired and recorded; live body weight and some linear body measurements were taken. In the group-animal ranking experiment, 12 breeding does and 12 breeding bucks from Arab goats and the same number of animals from Oromo goats were randomly selected. Life history of selected does and bucks (age, birth type, libido and temperament) were inquired from the owners. The selected animals were randomly grouped into four in Arab goats (three animals per group) and the same was applied in Oromo goats. Twelve farmers for Arab goats and the same number of farmers for Oromo goats who have not known the experimental animals were invited to do the ranking. Each person ranked the three animals in each group as 1st, 2nd and 3rd, giving reasons of ranking. After a first round of ranking, s/he was then provided with the history of each individual animal and asked whether s/he would consider re-ranking them. This procedure was continued eight times until a person covered all groups of does and bucks. It was found out that in own-flock ranking experiment, keepers focus on productive, reproductive and behavioral traits (such as body size, mothering ability, twinning rate, kidding interval and temperament) while in group-animal ranking experiment, there was a general tendency to focus on observable physical traits like coat color, body size and body conformation. Simultaneous use of both own-flock and group-animal ranking experiments is advisable to identify breeding objective traits in production systems where record keeping is absent.

Keywords: Breeding objectives; Goats; Group-animal ranking; Own-flock ranking

Introduction

There are about 36.81 million goat populations in Ethiopia, of which 99.97% are local breeds [1]. Most of them are found in large flocks in arid and semi-arid lowlands while very small flock sizes are widely distributed in the highlands [2]. Goats play an important role in the smallholders' farming systems, for instance, they provide tangible (cash, milk, meat, fiber and manure) and intangible benefits (prestige, saving, insurance, cultural and ceremonial purposes) [3].

Given the presence of large number of goats and their diverse functions, the productivity of this valuable genetic resource is generally low. For instance, in the years (1999-2008), the average carcass weight produced from a yearling goat was only 8 kg; one of the lowest compared to the world average (12 kg) [4]. Likewise, the dressing percentage (DP) at one year of age is also very low (42–45%) [5]. The causes for poor performance of indigenous goats could be attributed to various interrelated factors [6, 7]. Among them, lack of suitable breeding programs is an important constraint.

Identifying the smallholder farmers' breeding objective traits is crucial to design appropriate breeding programs [8, 9]. Four different methods have been implemented to identify the breeding objective traits; for sheep and goats in Ethiopia. These include semi-structured questioner, choice card experiment, group discussion and ranking of live animals. While the first three were often used by many scholars [8, 10, 11, 12, 13, 14), the last method was brought forth by [10]. It has two forms: ranking of own animals with known history and ranking of animals with unknown history. One can use combination of the methods to determine the breeding objective traits for a given breed. Detailed descriptions of the methods are given elsewhere [10, 15].

Benishangul Gumuz region, our study area, is found in the northwestern lowlands of Ethiopia. The region is among the major goat production areas in the country, where Arab and Oromo goat populations and their crosses with other indigenous goats are widely distributed [16, 17]. The official census recorded 440,719 goats in 2015 [18] which are mostly produced in small familial units (on average eleven goats/household) for sale, own consumption, saving and cultural importance [13]. It can be said that the goat populations, including the study area, are untapped resources with very little research efforts. The breeding objective traits of the local goat keepers were not empirically identified and defined. Farmers simply select animals based on morphological features and production characteristics. This as it is, the local goat populations are noted for their low productivity [19]. The present study was therefore aimed at identifying breeding objective traits of Arab and Oromo goat keepers in northwestern Ethiopia, using own-flock and group-animal ranking approaches, as a preliminary step towards designing sustainable breeding.

Materials and Methods

Description of the study area

Ethics approval and consent to participate

The current study and the proposed parent study were approved by Bahir Dar University College of Agriculture and Environmental Studies (BDUCAES) and Bahir Dar University Biotechnology Research Institute (BDUBRI). Following endorsement by the BDUCAES and BDUBRI, Assosa University (AsU) was informed about the objectives of the study through a support letter (Ref. 1/2241/134 dated back to November 13, 2017) from BDUCAES. After reviewing the proposal, AsU wrote a permission and support letter to agricultural and rural development offices of Bambasi and Homosha districts. Then, the corresponding author of this paper and four development agents from the two districts selected the goat owners for the present study. Finally, the goat owners were informed about the research and asked for verbal consent to confirm us to take the morphometric measurements on the selected goats. Four independent peasant association administrators acted as witnesses for voluntary informed decision making of the goat owners.

Description of the study area

Detailed descriptions of the study areas and the goat populations found in the study areas were given elsewhere [13, 16]. In brief, the study was conducted in Bambasi and Homosha districts of Benishangul Gumuz region, northwestern Ethiopia. The districts were purposively selected to represent two different agroecologies, farming systems and goat populations. In each district, two peasant associations (PAs)—the lowest administrative units in Ethiopia, (Tumet and Sherkole from Homosha district and Bambasi 02 and Mutsa 01 from Bambasi district) were selected based on goat population size, presence of communal grazing areas, relative significance of goats to the livelihood of the communities, access to market and road. The number of sampled households was determined following [13]. Accordingly, the calculated number of households were 25 (Sherkole), 21 (Tumet), 42 (Bambasi 02) and 59 (Mutsa 01). This makes the total number of households covered in this study to be 147 (i.e., 46 from Homosha district and 101 from Bambasi district). Finally, households who owned at least four adult goats with a minimum of one year experience in goat husbandry and willing to participate in community-based breeding programs were identified. The list was prepared in each selected PA with the help of development agents. Respondents were selected from the prepared list using systematic random sampling technique until the calculated sample size of each PA was maintained.

Communities in Bambasi are mainly sedentary agriculturalists who keep Oromo goats – named after the Oromo community. These goats are meat type and are adapted to sub-humid agroecology. Maize, sorghum, finger millet, teff, haricot bean and sesame are among the crops produced in the area. Homosha is semi-arid area characterized by limited crop production due to poor soil fertility and unreliable rainfall. The Arab goats – named after the Arab/Berta community – predominate in the area.

Own-flock ranking experiments

The data for this study were collected from January to February 2019. During the data collection, goat keepers were visited early in the morning at their homestead before their goats were let out for grazing. The goat keepers were asked to choose their 1st, 2nd and 3rd best and the most inferior does among the breeding does in their flock. Reasons for the ranking and life history of the ranked does (age, number of kidding, twinning ability, number of kids born per kidding and number of kids weaned) were inquired and recorded. As there are no records kept by the goat keepers in the study areas, family members who had participated in the ranking exercises were reminding each other about the history of their animals.

Body weight (BW) and linear body measurements (LBMs) such as body length (BL), chest girth (CG), wither height (WH) and rump height (RH) were taken from each animal as described by FAO (2012). BW is the fasted live body weight (in kg); BL is the horizontal distance (in cm) from the point of shoulder to the pin bone; CG is the circumference of the body (in cm) immediately behind the shoulder blades and perpendicular to the body axis; WH is the vertical height (in cm) from the bottom of the front foot to the highest point of the shoulder and RH is the vertical height from the bottom of the back foot to the highest point of the rump.

BW (kg) was recorded using suspended spring balance with 50 kg capacity and a precision of 200 g. Weighing sacks were used to lift goats during the BW measurements. The height measurements (cm) were taken using a graduated measuring stick while the length, width and circumference measurements (cm) were measured with plastic measuring tape (1.50 m long with the precision of 2 cm). All measurements were taken after restraining and holding the goats in their natural position and before they were released for grazing to avoid the effect of feeding and watering on the goats' size and conformation [20].

Group-animal ranking experiments

In these experiments, twelve breeding does and twelve breeding bucks from the Arab goats and the same number of does and bucks from the Oromo goats were randomly selected and marked. To avoid repeated measurements, the does were chosen from the own-flock ranking experiments covering all ranks. The information previously obtained from the owner (age, number of kidding, twinning ability, number of kids born per kidding and number of kids weaned) and the phenotypic measurements recorded during the own-flock experiments were used as life history for each selected doe. Similarly, the life history of the selected bucks (age, birth type, libido and temperament) and body weight measurements were inquired and recorded.

The selected animals were brought to a central place in each district and randomly assigned into groups. Animals of same sex were randomly assigned to four groups in Arab goats (three animals each) and the same was applied in Oromo goats. Twelve farmers for Arab goats and 12 farmers for Oromo goats, who have not known the selected animals, were then invited to rank the animals. Each farmer was inquired to rank the three animals in each group as 1st, 2nd and 3rd, and the reasons of ranking. The farmers were then provided with the history of each individual animal and asked whether they would re-rank the animals or not. This procedure was continued eight times until a farmer covered all groups of the animals.

Data management and analysis

The data collected from the study area were arranged, coded and managed in Microsoft-Excel spread sheet for further analysis. Since the responses of the goat keepers for both own-flock and group-animal ranking experiments were open ended, reasons for ranking were first checked one by one to determine the trait levels and then coded. Based on the nature of data, different types of statistical analyses were used. The statistical software R [21] was used to analyze the data from the own-flock and group-animal ranking experiments. The frequency and proportion of breeding doe and buck traits preferred by the goat keepers in both experiments and rank proportions before and after provision of life history information in group-animal ranking experiment were analyzed by the ‘gmodels package’ of R, version 4.0.3 using the ‘CrossTable function’. Similarly, the Mean ± SE values for dentition and some production and reproduction traits were analyzed using ‘LSM (least squares mean) package version 3.5.2’ of R [21] fitting the rank as fixed effects in the model.

Results and discussions

Doe traits in own-flock ranking experiments

The lists of preferred doe traits from the own-flock ranking experiments are summarized in Table 1. Although no organized breeding program is in place in the study area, goat keepers, however, select breeding does based on own memory and various attributes of the animal. Application of similar selection strategy for breeding does was also reported in Ethiopia [6, 12, 13] and elsewhere in Africa [22, 23, 24]. Mothering ability, kid growth, body size, twinning rate, coat color and body conformation were found to be the most important doe traits, in that order, influencing keepers’ preference in Arab. They accounted for 56.05% of the total proportions of mentioned traits. On the other hand, twinning rate, mothering ability, kid growth, kid size at birth and body size, in that order of importance, together contributed 64.75% of the total proportions of doe traits mentioned by Oromo goat keepers. Other important traits include kidding interval (7.01%), kid size at birth (6.37%) and drought tolerance (5.10%) in Arab and coat color (7.47%), kidding interval (4.79%) and pedigree (4.21%) in Oromo. In general, the breeding objective traits preferred by the goat keepers reflected what traits of Arab and Oromo does were appreciated by owners.

Table 1: List of doe traits in own-flock ranking experiment

Traits		Arab		Oromo	
		Freq	**%**	**Freq**	**%**
1.	Body size	29	9.24	44	8.43
2.	Kid growth	33	10.51	72	13.79
3.	Kid size at birth	20	6.37	71	13.60
4.	Mothering ability	38	12.10	74	14.18
5.	Twinning rate	29	9.24	77	14.75
6.	Kidding interval	22	7.01	25	4.79

7.	Coat color	24	7.64	39	7.47
8.	Body condition	10	3.18	19	3.64
9.	Drought tolerance	16	5.10	-	-
10.	Body conformation	23	7.32	21	4.02
11.	Body length	9	2.87	6	1.15
12.	Temperament	12	3.82	10	1.92
13.	Sex of kid	11	3.50	12	2.30
14.	Age at puberty	11	3.50	20	3.83
15.	Pedigree	14	4.46	22	4.21
16.	Foraging ability	4	1.27	10	1.92
17.	Body width	9	2.87	-	-
	Sum	314		522	

In the present study, we observed that both Arab and Oromo goat keepers generally focus on kid quality (such as kid growth and kid size at birth) and related reproductive traits (like twinning rate and mothering ability). However, there was noticeable difference in preference for some of these and other traits between the two goat keepers. For instance, in Arab goat keepers, drought tolerance and body width were mentioned as important traits but these traits were not mentioned at all by the Oromo goat keepers. This result is clearly associated with agro-ecology and breeding objective of the breeders. Arab goat keepers, who dwell in the semi-arid areas, were opted for does with better drought tolerance due to the harsher environment, in terms of feed and water shortage and prevalence of moisture stress in most parts of the year. They also associated wide bodied does with higher twinning rate, better mothering ability and high carcass yield. Similar findings on preference of drought tolerance and body width for goats and sheep in comparable environments were also reported in Ethiopia [6, 10, 11, 25].

The preference of big body size and fast kid growth as important traits in both study areas are expected when the main purpose of keeping goats is for cash income. In most of the time, goats with big body size have high market demand and fast growing goats reach market weight sooner. Oromo goat keepers mentioned kid size at birth quite frequently (13.60%) than Arab goat keepers.

This may be due to the reason that Oromo does have significantly bigger body sizes than Arab does [16] so that their kids might be bigger at birth. In relation to this, [26] and [27] elucidated that maternal body size positively influences the weight of their progeny at birth. Similarly, a relatively higher twinning rate (14.75%) as the preferred trait of Oromo goat keepers might be due to the availability of adequate feed throughout the year that can support many animals compared to the dry semi-arid area of Arab goat keepers.

None of the goat keepers in this study reported the use of goat milk. According to keepers, does with high milk production were considered as good mothers to their kids. Coat color and reproductive traits such as kidding interval were also mentioned as important traits by both goat keepers. Shorter kidding interval will increase flock size for marketing and replacement. It would be also helpful for genetic improvement program by increasing selection intensity though the improvement of kidding interval through selection may be slow because of the low heritability of the trait [6].

Mean ± SE values for dentition and some production and reproduction traits of does from own-flock ranking experiment are presented in Table 2. Body weight, number of kidding, twinning, number of kids born and number of kids weaned significantly ($p < 0.001$) influenced the ranking decision of both goat keepers. Dentition had significant ($p < 0.001$) effect only on Oromo goat keepers' trait preference of breeding does.

Comparing the mean values of does ranked as 1st best and poor quality, there were clear and logical differences in most of the attributes considered. This indicated that the farmers' choices of does were confirmed by the objective measurements. For instance, in the Arab goat population, the magnitude difference between the 1st best and inferior does in live weight, number of kids born and number of kids weaned were 2.22 kg, 1.83 and 1.70, respectively. Similarly, in the Oromo goat keepers, the difference between the two groups for the same traits were 2.66 kg of body weight, 1.62 numbers of kids born and 1.79 numbers of kids weaned. The longer ages of the best does indicate that keepers are willing to keep them for long service years to achieve their objectives. In the study areas, where performance and pedigree recordings are completely absent, proper recognition and application of the goat keepers’ indigenous knowledge for selecting the best breeding does is possible option to start appropriate breeding programs. The picture of the two goat populations is depicted in figure 1.

Table 2: Mean ± SE values of traits in different rank groups of does from own-flock ranking experiment

Goat population	**Traits**	***p***	**Overall mean**	**Ranks**			
				1	**2**	**3**	**Inferior**
Arab	Dentition	NS	3.24 ± 0.13	3.41 ± 0.14	3.37 ± 0.11	3.20 ± 0.14	2.98 ± 0.13
	BW, kg	***	30.98 ± 0.37	31.94 ± 0.37^{a}	31.53 ± 0.28^{ab}	30.74 ± 0.40^{c}	29.72 ± 0.44^{d}
	NK	***	2.99 ± 0.11	3.30 ± 0.13^{a}	3.07 ± 0.10^{b}	2.85 ± 0.11^{c}	2.72 ± 0.10^{cd}
	Twinning	***	1.46 ± 0.07	1.72 ± 0.07^{a}	1.54 ± 0.07^{b}	1.24 ± 0.06^{cd}	1.33 ± 0.07^{c}
	NKB	***	3.86 ± 0.18	5.00 ± 0.22^{a}	4.02 ± 0.20^{b}	3.26 ± 0.15^{c}	3.17 ± 0.16^{cd}
	NKW	***	3.40 ± 0.16	4.48 ± 0.18^{a}	3.54 ± 0.16^{b}	2.78 ± 0.12^{c}	2.78 ± 0.16^{c}
Oromo	Dentition	***	3.13 ± 0.15	3.53 ± 0.09^{a}	2.78 ± 0.07^{d}	3.07 ± 0.08^{c}	3.12 ± 0.09^{b}
	BW, kg	***	32.15 ± 0.67	34.13 ± 0.31^{a}	31.21 ± 0.30^{b}	31.92 ± 0.37^{b}	31.47 ± 0.36^{b}
	NK	***	3.22 ± 0.20	3.80 ± 0.11^{a}	2.88 ± 0.08^{d}	3.15 ± 0.11^{b}	3.03 ± 0.09^{c}
	Twinning	***	1.29 ± 0.06	1.42 ± 0.05^{a}	1.36 ± 0.05^{b}	1.24 ± 0.04^{c}	1.15 ± 0.04^{d}
	NKB	***	3.76 ± 0.37	4.84 ± 0.18^{a}	3.46 ± 0.12^{b}	3.52 ± 0.13^{b}	3.22 ± 0.11^{c}
	NKW	***	3.32 ± 0.40	4.50 ± 0.15^{a}	3.00 ± 0.09^{c}	3.08 ± 0.10^{b}	2.71 ± 0.09^{d}

Row means within each goat population with different superscript letter are statistically different; ***$p \leq 0.001$; NS, non-significant; BW, body weight; NK, number of kidding; NKB, number of kids born/doe/kidding; and NKW, number of kids weaned/doe.

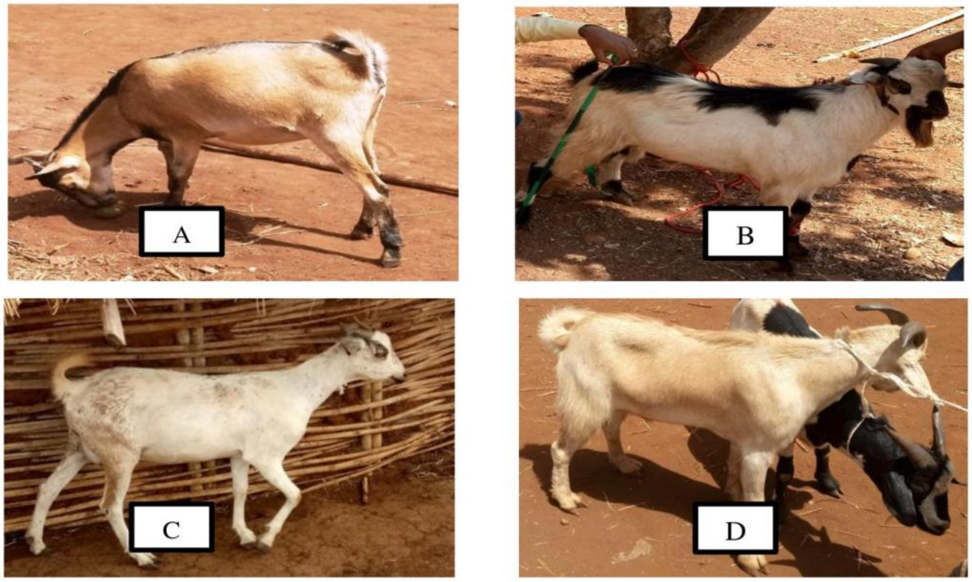

Fig 1. Representative pictures of adult Arab doe (A), young Arab buck (B), adult Oromo doe (C) and adult Oromo buck (D) included in the study

Doe traits in group-animal ranking experiments

Table 3 presents the lists of preferred doe traits in the group-animal ranking experiments. Coat color, body size, body conformation, body width and mothering ability, in that order, were found to be the most important traits in Arab goats, the sum of which accounted for 53.72% of the traits mentioned in Arab doe-ranking experiment. In Oromo doe-ranking experiment, about half (52.83%) of the mentioned traits were contributed by body size, twinning rate, body conformation, coat color and mothering ability.

Table 3: List of doe traits in group-animal ranking experiments

Traits		Arab		Oromo	
		Freq	%	Freq	%
1.	Body size	24	12.77	23	14.47
2.	Body conformation	18	9.57	16	10.06
3.	Coat color	28	14.89	15	9.43
4.	Color pattern	10	5.32	11	6.92
5.	Body width	16	8.51	5	3.14
6.	Body condition	13	6.91	7	4.40
7.	Age	13	6.91	9	5.66
8.	Horn length	4	2.13	-	-
9.	Body length	12	6.38	11	6.92
10.	Beauty/appearance	7	3.72	12	7.55
11.	Ear size	4	2.13	-	-
12.	Height	6	3.19	10	6.29
13.	Mothering ability	15	7.98	13	8.18
14.	Twinning rate	13	6.91	17	10.69
15.	Kidding interval	5	2.66	10	6.29
	Sum	188		159	

Buck traits in group-animal ranking experiments

Table 4 describes the lists of buck traits in group-animal ranking experiments. Coat color, body size, body conformation and body length were the four most important phenotypic traits which accounted for 54.12% and 52.38% of the traits mentioned by Arab and Oromo goat keepers, respectively, but with varying order. Coat color assumed the first priority with a magnitude of 18.04% followed by body size (17.53%), body conformation (9.79%) and body length (8.76%) in Arab goat keepers while the order of recurrence of traits in Oromo goat keepers was body size, coat color, body conformation and body length with magnitude of 20.63%, 17.99%, 7.41% and 6.35%, respectively.

Table 4: List of buck traits in group-animal ranking experiments

		Arab		Oromo	
	Traits	Freq	%	Freq	%
1.	Coat color	35	18.04	34	17.99
2	Color pattern	10	5.15	10	5.29
3.	Body size	34	17.53	39	20.63
4.	Body width	15	7.73	9	4.76
5.	Age	9	4.64	10	5.29
6.	Fast growth	6	3.09	8	4.23
7.	Body condition	12	6.19	9	4.76
8.	Horn shape	5	2.58	11	5.82
9.	Appearance	6	3.09	9	4.76
10.	Body conformation	19	9.79	14	7.41
11.	Temperament	-	-	6	3.17
12.	Body length	17	8.76	12	6.35
13.	Height	8	4.12	-	-
14.	Heat tolerance	5	2.58	-	-
15.	Libido	7	3.61	-	-
16.	Horn orientation	-	-	8	4.23
17.	Horn size	6	3.09	10	5.29
	Sum	194		189	

Comparisons of rankings with and without additional information of life history

Table 5 summarizes rank proportions before and following provision of information about life history of does and bucks. In Arab goat populations, of does that ranked as first, second, and third prior to provision of life history, 70.8%, 68.8% and 72.9% of them retained their position, respectively, after provision of life history. The corresponding values for Oromo goats were 52.1%, 47.9% and 50%. Unlike in does, the attached life history information only minimally altered respondents' decision in buck-group ranking. For example, in Arab goats, only 6.2% and 2.1% of the respondents changed their ranks from 1st to 2nd and 1st to 3rd, respectively. The corresponding values in Oromo goats were 4.2% and 0%. The likely reason for this is that keepers tended to judge and select female animals based on their reproductive performance and mothering ability apart from physical appearance (body size, coat color and body conformation) and dental examination. Similar research findings were reported in phenotypic group-animal ranking experiments for sheep [10] and goat breeds in Ethiopia [6] and for Ankole cattle in Uganda [28].

Table 5: Rank proportions before and after provision of information in group-ranking

Population	**RBLH**	**RALH Does**			**RBLH Buck**		
		1	**2**	**3**	**1**	**2**	**3**
Arab	1	**34 (70.8%)**	10 (20.8%)	4 (8.3%)	**44 (91.7%)**	3 (6.2%)	1 (2.1%)
	2	6 (12.5%)	**33 (68.8%)**	9 (18.8%)	2 (4.2%)	**44 (91.7%)**	2 (4.2%)
	3	6 (12.5%)	7 (14.6%)	**35 (72.9%)**	2 (4.2%)	1 (2.1%)	**45 (93.8)**
Oromo	1	**25 (52.1%)**	13 (27.1%)	10 (20.8%)	**46 (95.8%)**	2 (4.2%)	0 (0%)
	2	11 (22.9%)	**23 (47.9%)**	14 (29.2%)	2 (4.2%)	**45 (93.8%)**	1 (2.1%)
	3	11 (22.9%)	13 (27.1%)	**24 (50%)**	0 (0%)	1 (2.1%)	**47 (97.9%)**

RBLH=Rank before provision of life history; RALH=Rank after provision of life history; unchanged ranks are given along the diagonal.

Conclusions

Breeding objective traits were identified for Arab and Oromo goat populations through phenotypic ranking approaches (own-flock and group-animal ranking experiments) to design breeding programs. Given large number of traits identified in the present study, it would be useful to include only few priority traits in order to keep the breeding programs as simple as possible and for easy implementation under smallholders' circumstances. In the own-flock ranking experiments, keepers focus on productive, reproductive and behavioral traits whereas in the group-animal ranking experiments there was a generally tendency to focus on observable physical traits like coat color, body size and body conformation for both does and bucks. Thus, simultaneous use of both methods for identification of breeding objective traits in similar production systems is advisable.

Supporting information

S1 File. Raw data for breeding buck and doe phenotypic ranking.

(XLSX)

S2 File. R script for breeding buck and doe phenotypic ranking data analysis.

(DOCX)

S3 File. Formats used in the phenotypic ranking.

(DOCX)

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Author Contributions

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Formal analysis: Oumer Sheriff.

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Investigation: Oumer Sheriff.

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Paper 5: Genetic and economic evaluation of alternative breeding schemes for two indigenous goat populations of Ethiopia

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Abstract

In this study, breeding objective traits were identified and alternative breeding schemes were simulated and evaluated for two goat populations. The traits were: body size, twinning ability and kidding interval for Arab goats and body size, twinning ability and mothering ability for Oromo goats. The selection criteria were six month weight (6mw, kg), litter size at birth (LSB), litter size at weaning (LSW) and kidding interval (KI, days). The schemes were: 1) Scheme 1: 2 years of buck use and 10% selection proportion, 2) Scheme 2: 2 years of buck use and 15% selection proportion, 3) Scheme 3: 3 years of buck use and 10% selection proportion, and 4) Scheme 4: 3 years of buck use and 15% selection proportion. The predicted annual genetic gain (PAGG) for 6mw ranged from 0.29 kg to 0.32 kg for Arab goats while it varied from 0.34 kg to 0.38 kg for Oromo goats. On the contrary, the PAGGs for LSB and LSW for both populations were considerably small regardless of the different schemes. The economic return (Euro/doe) ranged from 0.99 to 1.15 for Arab goats and from 0.60 to 0.70 for Oromo goats. SCM2 is recommended over other schemes.

Keywords: Breeding scheme, Deterministic approach, Ethiopia, Genetic gain, Simulation

Introduction

The goat population of Ethiopia is estimated to be 52.46 million heads (CSA, 2021), and the number of goats used to be considerably smaller than the number of sheep. However, very recently, the goat to sheep ratio showed an increasing trend; 0.93 (CSA, 2012), 0.99 (CSA, 2015), 0.98 (CSA, 2017), 1.12 (CSA, 2020) and 1.22 (CSA, 2021) which might indicate that goats are becoming more important than sheep in Ethiopia. Almost all goats are managed by smallholder farmers and pastoralists under traditional production systems. They provide multiple functions for their owners such as source of income, food, and raw materials (skins). They also serve as means of risk mitigation during crop failures, savings and investments in addition to other socioeconomic and cultural functions (Legese et al., 2014).

Though a large number of goats are found in Ethiopia, the productivity per animal and flock off-take however are low. For instance, recent estimates of the average annual off-take rate for the years 2008 to 2010 indicate values between 30% and 38% (Legese and Fadiga, 2014). Similarly, during the year 2013, goats contributed only 11.0 and 1.4% of the annual national meat and milk production, respectively (FAOSTAT, 2016). Many interrelated factors including lack of suitable breeding programs contribute for the low productivity of indigenous goats.

Genetic improvement strategies, aimed at improving the production and reproduction potential of indigenous goats, have been executed in Ethiopia since the beginning of goat research in the mid-1970s. The most common strategy was centralized breeding scheme, usually nucleus breeding units, established at on-station and entirely managed and controlled by government organizations with minimal, if any, participation by the farmers (Haile et al., 2018). Although well intended, the schemes failed to provide sufficient number and quality of improved males and also failed to engage the participation of the end users in the process (Haile et al., 2020). Another widely followed strategy was crossbreeding of indigenous goat breeds with imported exotic breeds in the form of semen, embryos or live animals. In most cases, this is done with very little consideration of the needs, views and indigenous practices of the farmers and their limited or no participation from planning to execution of the programs (Ayalew et al., 2003). Insufficient pretesting of the suitability and adaptability of the exotic breeds and their resulting crosses to local production systems, poor management and low input production systems were also some of the limitations of the programs (Haile et al., 2020). As a result, genetic erosion of the local breeds has occurred where indiscriminate crossbreeding with local populations was practiced (Haile et al., 2018).

A recent alternative approach is community based breeding program (CBBP). Such programs consider the needs, views, decisions and active participation of farmers from inception through to implementation (Haile et al., 2020). A promising option for designing CBBP, where communal grazing and watering points are customary, is to consider the village population as one large flock or a breeding unit. In this case, breeding animals are being selected based on phenotypes recorded within the village population. The primary aim of a breeding program for smallholder conditions should be to minimize the risk by developing cost and resource saving production methods, while achieving acceptable genetic gain in important breeding traits (Sölkner et al., 1998). In Ethiopia, CBBPs have been established since 2009; for sheep (Gizaw et al., 2009; Duguma et al., 2011; Mirkena et al., 2012) and goats (Abegaz et al., 2014; Alubel, 2015; Zergaw et al., 2016; Jembere et al., 2019).

The present study simulated the most appropriate breeding schemes for two indigenous goat populations in two agro-ecologies in northwestern Ethiopia. The simulations were based on comprehensive studies of production systems and phenotypic ranking experiments (Oumer et al., 2019; Oumer et al, 2021).

Materials and Methods

Description of the study areas

Genetic and economic evaluation of the alternative breeding schemes targeted Arab and Oromo goat populations in Benishangul Gumuz region, northwestern Ethiopia. The locations, Homosha and Bambasi, are believed to be the breeding tracts for Arab and Oromo goat populations, respectively. Homosha has semi-arid agro-ecology with average annual temperature that varies from 20–30 °C. The rainfall pattern of the area is erratic and uneven with a mean annual range of 700–1,200 mm. It covers around 645.78 km^2, positioned at 6° 44` to 6° 84` north latitude and from 37° 92’ to 38° 6’ east longitude at an average latitude of 1,373 masl (elevationmap.net 2018). The area is characterized by limited crop production due to poor soil fertility (Homosha BoARD, 2018).

Bambasi has sub-humid agro-ecology with geographical coordinates of 9° 45′ north latitude and 34° 44′ east longitude with an elevation of 1,668 masl (Latitude.to, maps, geolocated articles, latitude longitude coordinate conversion 2018). The mean annual rainfall ranges from 900–1,500 mm and the average annual temperature is 28 °C. The total area coverage is 2,210.16 km^2. The production system is mixed crop-livestock system with high priority of Oromo goat production (Bambasi BoARD 2018). Description of the two goat populations is given in Table 1.

Table 1: Description of the goat populations

Parameters		Name of the goat populations	
		Arab	Oromo
Production system		Semi agro-pastoral	Crop-livestock
Agro-ecology		Semi-arid	Sub-humid
Use		Income, meat, saving, wealth status, manure and skin	Income, meat, saving, wealth status, manure and skin
Mating system		Predominantly uncontrolled	Predominantly uncontrolled
Dominant coat color		Plain white	Plain brown (deep and light)
Coat color pattern		Plain and patchy	plain, patchy and spotted
Facial profile		Slightly concave	Straight
Horn		Most horned	Most horned
Ear		Droopy	Lateral
Measurements*	Body weight	31.7 kg	37.0 kg
	Chest girth	71.1 cm	77.0 cm
	Body	61.6 cm	69.5 cm

	length		
	Wither height	66.7 cm	72.2 cm
	Rump height	69.3 cm	74.0 cm

* = measurements were taken from adult female goats

Selection of villages

Multistage stratified purposive sampling was employed to select villages/peasant associations (PAs)—the lowest administrative units in Ethiopia. Four villages were selected from each district based on goat population size (≥ 300 breeding does per village) (using previous flock inventory results taken from each village and secondary data from the respective districts' agricultural offices), presence of communal grazing areas, relative significance of goats to the livelihood of the communities, access to market and road. The villages were Gumu-Abush, Sherkole, Tumet and Tsore-almetema from Homosha and Bambasi 02, Mutsa 01, Shebora and Womba-selama from Bambasi.

Determination of breeding objective traits and selection criteria

Two approaches, production system study (Oumer et al., 2019) and phenotypic ranking experiments (Oumer et al., 2021), were used to determine breeding objective traits for the two indigenous goat populations. Based on results from the two approaches, three measurable breeding objective traits were selected for each population. The traits were: i) body size, twinning ability and kidding interval in Arab; and ii) body size, twinning and mothering abilities in Oromo goat population. Some of the traits such as coat color and beauty which had higher preference by goat keepers were intentionally excluded to avoid the complexity during implementation. Since animals may be selected independently for desired coat color and beauty, it is not worthwhile to include them in simulations. The selection criteria were six month weight (6mw), litter size at birth (LSB), litter size at weaning (LSW) and kidding interval (KI) for body size, twinning ability, mothering ability and reproduction performance, respectively.

Selection groups

Three selection groups; breeding bucks (BB), breeding does (BD) and production does (PD), consisting of six selection paths were defined for both populations. Generation and dissemination of genetic gain occur in the breeding unit (BU) and production unit (PU), respectively. The defined selection paths are: 1) bucks to produce breeding bucks (BB > BB) where buck selection occurs to improve bucks used in the BU, 2) bucks to produce breeding does (BB > BD) where buck selection occurs to improve does used in the BU, 3) does to produce breeding bucks (BD > BB) where doe selection occurs to improve bucks used in the BU, 4) does to produce breeding does (BD > BD) where doe selection occurs to improve does used in the BU, 5) bucks to produce breeding does (BB > PD) where buck selection occurs to improve does used in the PU, and 6) does to produce breeding does (PD > PD) where does selection occurs to improve does used in the PU. Transmission of genetic gain to the PU is only through the selection group (BB > PD). The selection groups and the gene flow pathways are summarized below in Table 2. Genetic gain is generally expected from selection groups originating from the breeding unit where selection decisions are made and breeding costs are incurred (Nitter et al., 1994). The contribution from the other selection groups in terms of genetic gain is very minimal only through the 5% replacement young does.

Table 2: Selection groups and the gene flow pathways

		Genes from		
		Bucks in BU[a] (BB)	Does in BU (BD)	Does in PU[b] (PD)
Genes to	Bucks in BU (BB)	BB > BB	BD > BB	-

	Does in BU (BD)	BB > BD	BD > BD	-
	Does in PU (PD)	BB > PD	-	PD > PD

[a] BU = breeding unit; [b] PU = production unit

Simulation methods

The computer program ZPLAN (Willam et al., 2008) was used to simulate the alternative breeding programs. This computer program is based on comprehensive evaluation of both genetic and economic efficiencies of breeding strategies considering one cycle of selection. Important outcomes of ZPLAN include annual monetary genetic gain for the aggregate genotype, annual genetic gain for individual trait, discounted return and discounted profit for a given investment period. The gene flow method (Hill, 1974; McClintock and Cunningham, 1974) and selection index procedure constitute the core of the program. For the selection index part, information available for the evaluation of an individual candidate have to be defined by the number and type of relatives contributing to the index of an animal as well as records on individual's own performance (Willam et al., 2002). For further information on ZPLAN, see Nitter et al. (1994).

During the simulation, we first defined and evaluated a breeding scheme considering ten percent selection proportion and two time unit of buck use for breeding. Then alternative breeding schemes with regard to variation of these two factors (either 2 or 3 years of buck use for breeding and either 10 or 15% selection proportion) were run and evaluated. Thus, the following four alternative schemes were simulated: 1) Scheme 1 (SCM1): 2 years of buck use and 10% selection proportion, 2) Scheme 2 (SCM2): 2 years of buck use and 15% selection proportion, 3) Scheme 3 (SCM3): 3 years of buck use and 10% selection proportion, and 4) Scheme 4 (SCM4): 3 years of buck use and 15% selection proportion.

Input parameters

Essential input parameters for the simulations are given in Table 3. In calculating the numbers of initial does, the flocks from 60 households with an average of 7 breeding does per household were considered as one breeding unit for Arab goats, while the flocks from 60 households with an average of 6 breeding does per household were considered as one breeding unit for Oromo goats. Numbers of candidate males were calculated as the product of initial does, conception rate, twinning rate, number of parturition per year, survival rate to six month, kidding rate and sex ratio.

The period for which breeding does and bucks remain in the flock were adopted from previous study on indigenous sheep breeds in Ethiopia (Mirkena et al., 2012) whereas conception rate, kidding rate and kid survival to six month of age were based on published literature. The KI and LSB were obtained from monitoring data generated on the two goat populations. The rest biological parameters were derived from production system study and phenotypic ranking experiments done on the two goat populations in their respective study areas (Oumer et al., 2019; Oumer et al., 2021).

Regarding the cost parameters, only costs of additional activities to the normal management practices were considered (Nitter et al., 1994). In the current study, these were enumerator salary, cost of items for animal identification, cost of stationary materials and cost of drugs. The costs were computed as of late March 2019 (1 EURO = 1.1374 USD, 1 USD = 28.8439 Ethiopian birr and 1 EURO = 32.8070 Ethiopian birr) when all the information were gathered and compiled from the study areas. Analogous to Jembere et al. (2019) but contrary to Mirkena et al. (2012) and Abegaz et al. (2014), we assumed higher interest rate of discounted returns than costs as such assumptions lead to more conservative discounted profit (Ehret et al., 2012).

Table 3: Input parameters by goat populations

Parameters	Arab	Oromo

Population parameters		
Initial does (IND)	420	360
Number of candidate males/year	217	164
Proportion of bucks selected	0.10; 0.15	0.10; 0.15
Biological parameters		
Breeding doe in use (year)	5	5
Breeding buck in use (year)	2; 3	2; 3
Mean age of does at birth of 1st offspring (year)	1.20	1.30
Mean age of bucks at birth of 1st offspring (year)	1.10	1.20
Conception rate	0.90	0.90
Kidding rate	0.85	0.85
Litter size at birth	1.22	1.11
Kidding interval (KI) (year)	0.81	0.84
Kid survival to six month of age	0.90	0.90
Cost parameters		
Enumerator cost for recording/doe/year(€)	0.94	0.91
Animal identification/doe/year(€)	1.64	1.55
Stationary materials for recording/doe/year(€)	0.13	0.15
Drug/doe/year(€)	1.64	1.55
Interest rate of discounted return (%)	8	8
Interest rate of discounted cost (%)	5	5
Investment period/year	15	15

The phenotypic standard deviations and economic weights of breeding objective traits used in the simulations are given in Table 4. The phenotypic standard deviations were obtained from the respective data generated on the two goat populations. Economic weight for each trait was computed using indices from goat keepers' trait preference (i.e., from production system studies). Indices of the selected breeding objective traits were scaled to unity and inversely weighted by additive genetic standard deviation (σ_a) of each trait. Similar approach has been recommended by FAO (2010, page 73) when only few socio-economic data are available as in the present case. Genetic and phenotypic correlations among the breeding objective traits and their heritability values are presented in Table 5. Genetic parameters are lacking for Arab and Oromo goat populations. Hence, published reports on goats (Abegaz et al., 2014; Jembere et al., 2017) and sheep (Mirkena et al., 2012) were consulted to estimate these parameters. Investigation of genetic and phenotypic correlation between traits could allow for optimal sound selection criteria to match the targeted breeding objectives and yield higher selection accuracies (Wasike et al., 2007).

Table 4: Phenotypic standard deviations (σ_p) and economic weights (EW) for selection criteria by goat populations

Goat populations	Traits	Unit	σ_p	EW	σ_a
Arab	6mw	Kg	2.01	0.57	1.06
	LSB	№	0.41	4.0	0.09
	KI	Day	35.06	0.004	10.52
Oromo	6mw	Kg	2.41	0.27	1.28
	LSB	№	0.32	3.00	0.11
	LSW	№	0.36	3.67	0.09

6mw = six month weight; LSB = litter size at birth; KI = kidding interval and LSW = litter size at weaning.

Table 5: Genetic correlation (above diagonal), heritability (along diagonal) and phenotypic correlation (below diagonal) for selection criteria in two goat populations

Selection criteria	Arab				Oromo		
	6mw	LSB	KI		6mw	LSB	LSW
6mw	0.28	0.00	0.10	6mw	0.28	0.00	0.30
LSB	0.00	0.15	0.61	LSB	0.00	0.15	-0.20
KI	0.50	-0.06	0.09	LSW	0.10	0.15	0.05

6mw = six month weight; LSB = litter size at birth; KI = kidding interval and LSW = litter size at weaning.

Results

Predicted annual genetic gains (PAGG) in breeding objective traits

Table 6 presents the PAGG for 6mw (kg) and LSB for the two populations, PAGG for KI (days) for Arab goats and PAGG for LSW for Oromo goats. When the four alternative breeding schemes in both populations were considered, 6mw (kg), the major selection criterion in this study, had the highest PAGG that is quite substantial for an on-farm situation. The PAGG for 6mw, if realized, will result in 288 to 322 g and 342 to 382 g per year in Arab and Oromo flocks, respectively. In other words, there would be around 34.4 g difference in 6mw for Arab goat population between the alternative with highest gain and the alternative with the lowest gain. The difference was, however, around 39.5 g for Oromo goat population. The PAGG for KI ranged from 0.63 days (SCM3) to 0.70 days (SCM2) for Arab goat. SCM3 improved KI of Arab goat better than any other scheme. The PAGG for LSB in both goats and LSW in Oromo goats were considerably small regardless of the different breeding schemes. In general, for most selection criteria and both populations considered, the PAGG was highest at SCM2 (2 years of buck use and 15% selection proportion) and lowest at SCM3 (3 years of buck use and 10% selection proportion). This was expected as SCM2 benefited from the higher selection intensity and shorter generation interval (Table 7) contributed from strong selection pressure and use of breeding bucks for short durations.

Table 6: Predicted annual genetic gains (PAGG) for the breeding objective traits in different schemes of selection

Goat population	Trait	Scheme			
		SCM1	SCM2	SCM3	SCM4
Arab	6mw	0.3077	0.3222	0.2878	0.2990
	LSB	0.0067	0.0070	0.0062	0.0065
	KI	0.6731	0.7048	0.6296	0.6542
Oromo	6mw	0.3627	0.3816	0.3421	0.3577
	LSB	0.0023	0.0025	0.0022	0. 0023
	LSW	0.0069	0.0073	0.0066	0.0068

6mw = PAGG in six month weight (kg); LSB = PAGG in litter size at birth; KI = PAGG in kidding interval (days); LSW = PAGG in litter size at weaning.

Monetary genetic gain and predicted discounted returns

The annual monetary genetic gains (AMGG), discounted returns, discounted profits, generation intervals and selection intensities from the four alternative breeding schemes for the two populations are presented in Table 7. The AMGG (Euro/doe) ranged from 0.19 (SCM3) to 0.21 (SCM2) for Arab goat and from 0.12 (SCM3) to 0.14 (SCM2) for Oromo goat; where the AMGG from SCM1 was similar to that of SCM4. The discounted profit, calculated as the difference between the discounted return and discounted cost per doe, obtained in all the alternatives and in both populations was substantial. However, the discounted profit obtained in this study must be seen with caution as economic weight attached to each trait is not in the real monitoring term and only additional costs to the normal management practice were considered as the cost parameters. Hence, it may not be appropriate to compare the alternative breeding schemes in this study based on the discounted profit. As mentioned above, economic weight for each trait was computed using indices from goat keepers' trait preference (i.e., production system studies). For the two populations, the accuracies of selection (r_{TI}) were moderate and the generation intervals and selection intensities obtained from the alternative breeding schemes were within the ranges of 2.58 to 2.98 years and 1.20 to 1.36, respectively.

Table 7: Annual monetary genetic gain (AMGG), discounted costs (Cost), discounted returns (Return), and discounted profit (Profit) in Euro from the four schemes (SCM) for Arab and Oromo goat populations

Goat population	Parameter*	Scheme			
		SCM1	SCM2	SCM3	SCM4
Arab ($r_{TI = 0.435}$)	AMGG	0.20	0.21	0.19	0.20
	Return	1.09	1.15	0.99	1.04
	Profit	0.85	0.91	0.75	0.80
	Generation interval	2.58	2.58	2.89	2.89
	Selection intensity	1.23	1.30	1.30	1.36
Oromo ($r_{TI = 0.434}$)	AMGG	0.13	0.14	0.12	0.13
	Return	0.65	0.70	0.60	0.63
	Profit	0.42	0.46	0.37	0.40

	Generation interval	2.67	2.67	2.98	2.98
	Selection intensity	1.20	1.27	1.27	1.34

* = breeding costs were per doe and in EURO

Discussion

Genetic responses of indigenous Ethiopian goat breeds under selective breeding programs have not been well studied. Indeed, Abegaz et al. (2014) optimized alternative breeding schemes for two Ethiopian goat breeds. The authors reported PAGG for 6mw (kg) that ranged from 0.36–0.37 for Abergelle goat and this was comparable with the magnitude of the present result. On the contrary, the authors presented higher PAGG for 6mw, which varied from 0.870–0.872 kg, for Western Lowland goat. Jembere et al. (2019) also evaluated genetic and economic responses of alternative breeding schemes for three indigenous goat breeds of Ethiopia and found relatively lower PAGG for 6mw (kg) that ranged between 0.09–0.25, 0.13–0.47 and 0.10–0.27 for Abergelle, Central Highland and Woyto-Guji goat breeds, respectively.

Except Abegaz et al. (2014) and Jembere et al. (2019), literature reports on similar breeding schemes are generally lacking on indigenous goat breeds of Ethiopia. Nevertheless, there are reports available on sheep breeds in Ethiopia and elsewhere. For instance, Dagnew et al. (2018) reported PAGG of 0.15–0.34 kg for yearling weights of Gumuz sheep which concurs well with the current study though the species are different. Similarly, Mirkena et al. (2012) simulated breeding programs for indigenous sheep breeds of Ethiopia and found much higher PAGG for yearling weights in kg of 0.81–0.89 for Bonga, 0.85–0.94 for Horro and 0.62–0.70 for Menz. The results from Mirkena et al. (2012) were indeed challenged by the recent findings of Haile et al. (2020) who analyzed ten-year (2009 to 2018) performance data from the same sheep breeds: Bonga, Horro and Menz. They found an annual average genetic gain for 6mw (kg) of 0.21, 0.18 and 0.11 in the same order of the three breeds. This implies that the values reported by Mirkena et al. (2012) are too high and hence it is less realistic to achieve these much gains under on-farm condition. On the other hand, PAGG of 0.12 to 0.29 kg for 6mw of Menz sheep was reported by Gizaw et al. (2014).

The observed variations between the current results and the findings reported elsewhere are probably related to the difference in phenotypic standard deviations and selection intensity used during the simulations. For example, in this study, phenotypic standard deviations used for 6mw were 2.01 and 2.41 kg for Arab and Oromo goat populations, respectively. However, Abegaz et al. (2014) reported relatively higher phenotypic standard deviations, 2.74 kg for Abergelle and 3.76 kg for Western Lowland goat. Similarly, Mirkena et al. (2012) reported higher phenotypic standard deviations of 6.36 kg for Bonga and Horro breeds and 3.49 kg for Menz. Conversely, Jembere et al. (2019) used lower phenotypic standard deviations of 2.09, 2.22–3.90 and 2.29 kg for Abergelle, Central Highland and Woyto-Guji goats, respectively. The PAGG for a trait is directly proportional to the phenotypic standard deviation.

LSB, defined as the number of kids born/doe/kidding, is strongly influenced by management decisions and are of paramount economic importance. Given the low heritability of the trait, the PAGG in LSB for Gumuz sheep were within the range of 0.0017 to 0.0036 (Dagnew et al., 2018) and for Menz sheep it fluctuated from 0.0013 to 0.0031 (Gizaw et al., 2014), and hence, were equivalent to the values presented in the present work. Similarly, comparable results were also reported by Mirkena et al. (2012), Abegaz et al. (2014) and Jembere et al. (2019).

Regarding LSW, the number of kids weaned per doe per year, our PAGG for this selection criterion were very low and concurred well with the findings of various scholars elsewhere in Ethiopia (Mirkena et al., 2012, Abegaz et al., 2014; Jembere et al., 2019). Overall, the PAGG in both LSB and LSW may appear very insignificant; yet, the slightest improvements in these cumulative traits would lead to sizable gain in terms of overall change.

KI, calculated as the difference in days between two successive kiddings, had positive gain in the four alternative breeding schemes. However, the positive gain for KI is undesirable as an increase in KI implies an addition in the number of days between consecutive kidding. An Arab doe with long kidding interval will have lower chances of giving more number of kids during her lifetime. Jembere et al. (2019) also reported positive PAGG for KI that ranged from 0.18 to 0.27 days.

Conclusion

Different breeding schemes were simulated for two indigenous goat populations of Ethiopia, considering limited number of breeding objective traits. The PAGGs obtained from all schemes were reasonable, especially for 6mw in both populations and KI in Arab goat. The PAGGs in LSB and LSW were small implying that improvements of these traits are best achieved through improved management issues such as health and feeds as part of the overall genetic improvement program. Based on the results of the present study, design and implementation of the CBBP for Arab and Oromo goat populations using SCM2 had an advantage over other schemes.

Competing Interest

We all authors declare that there is no any competing interest.

Acknowledgments

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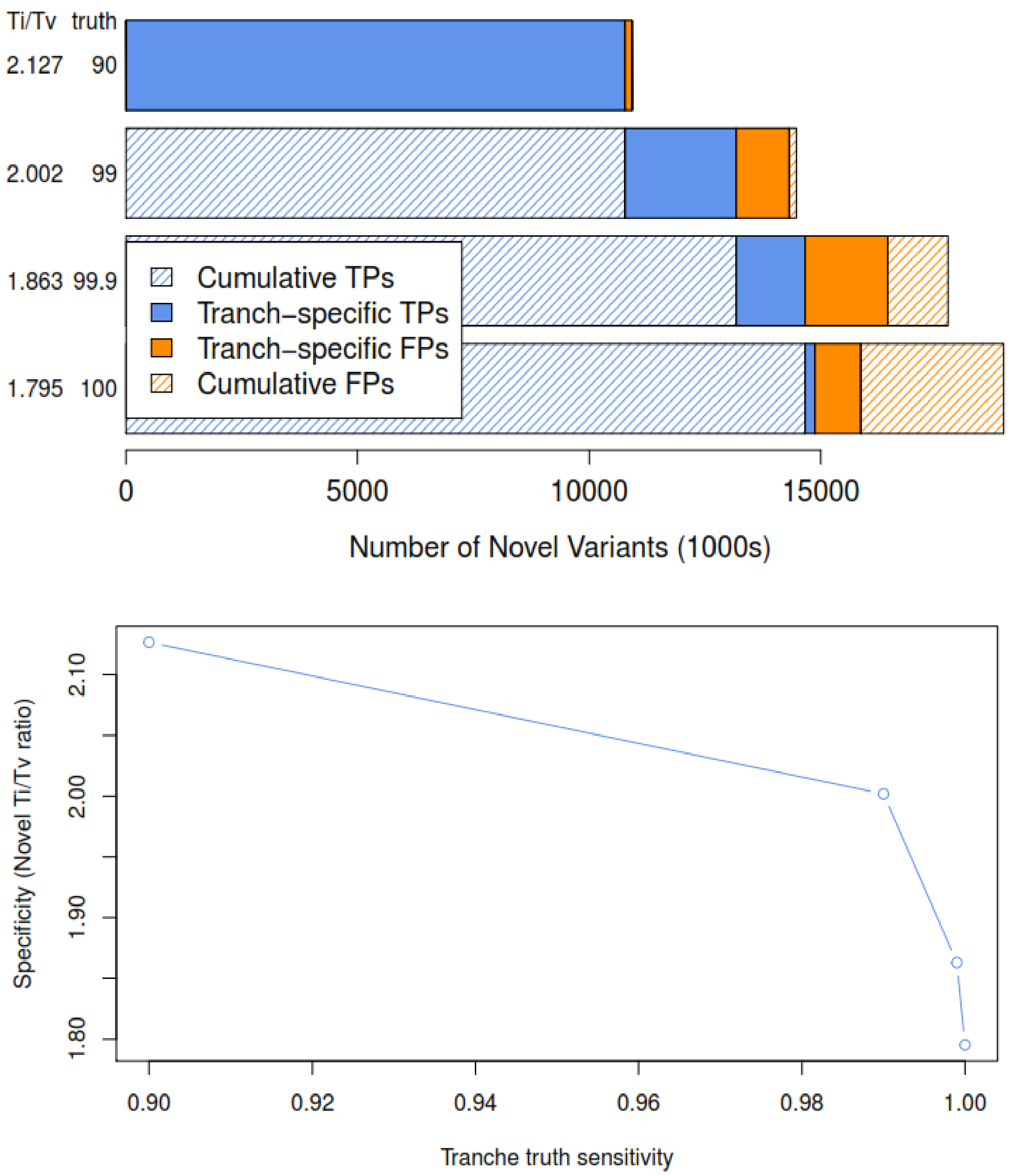
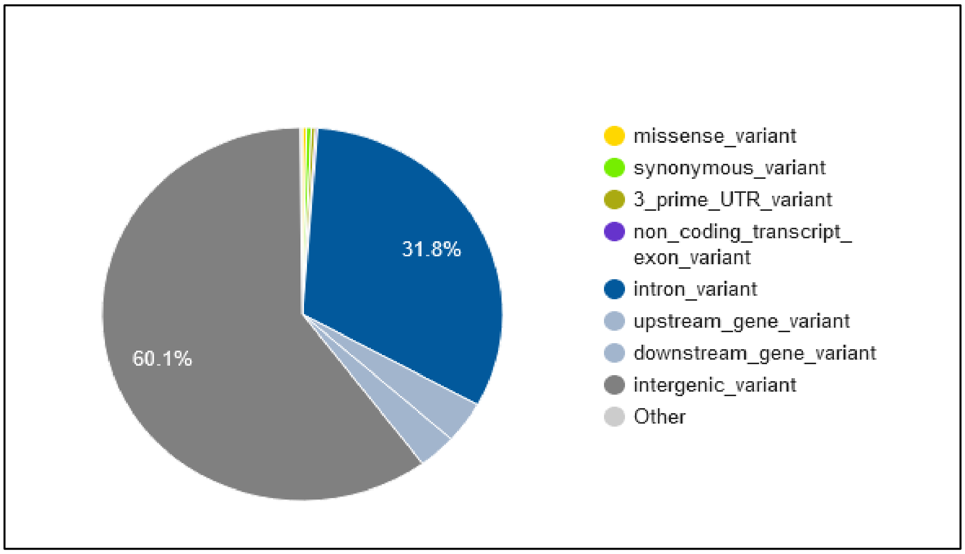
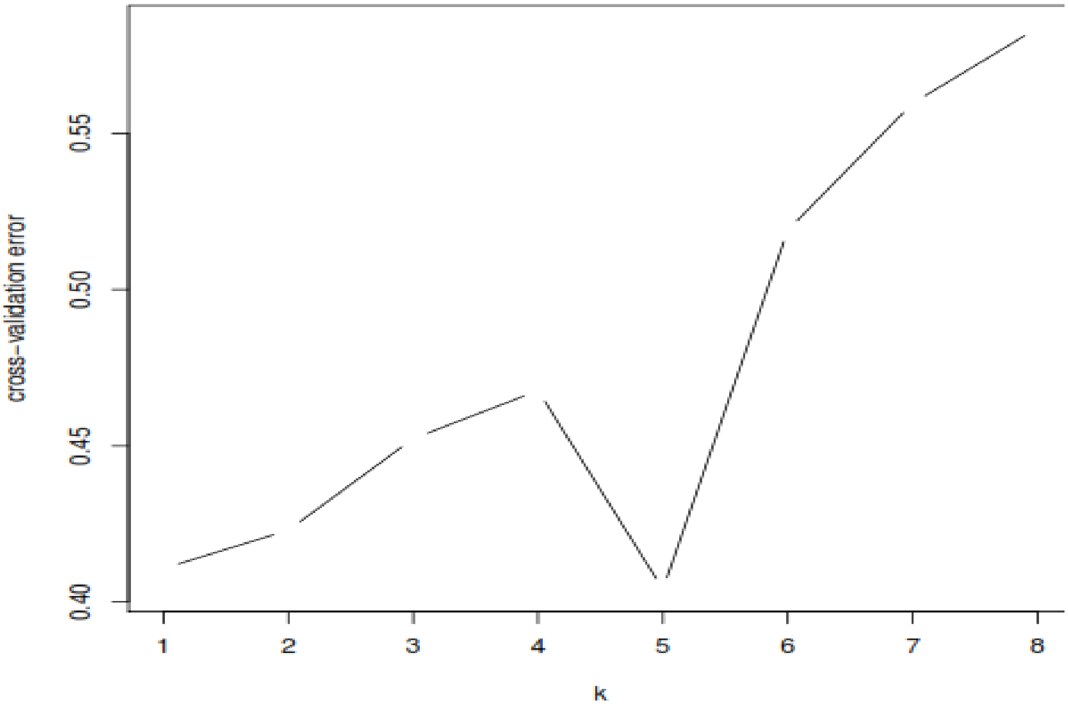
CHAPTER 10: SUPPLEMENTARY TABLES AND FIGURES



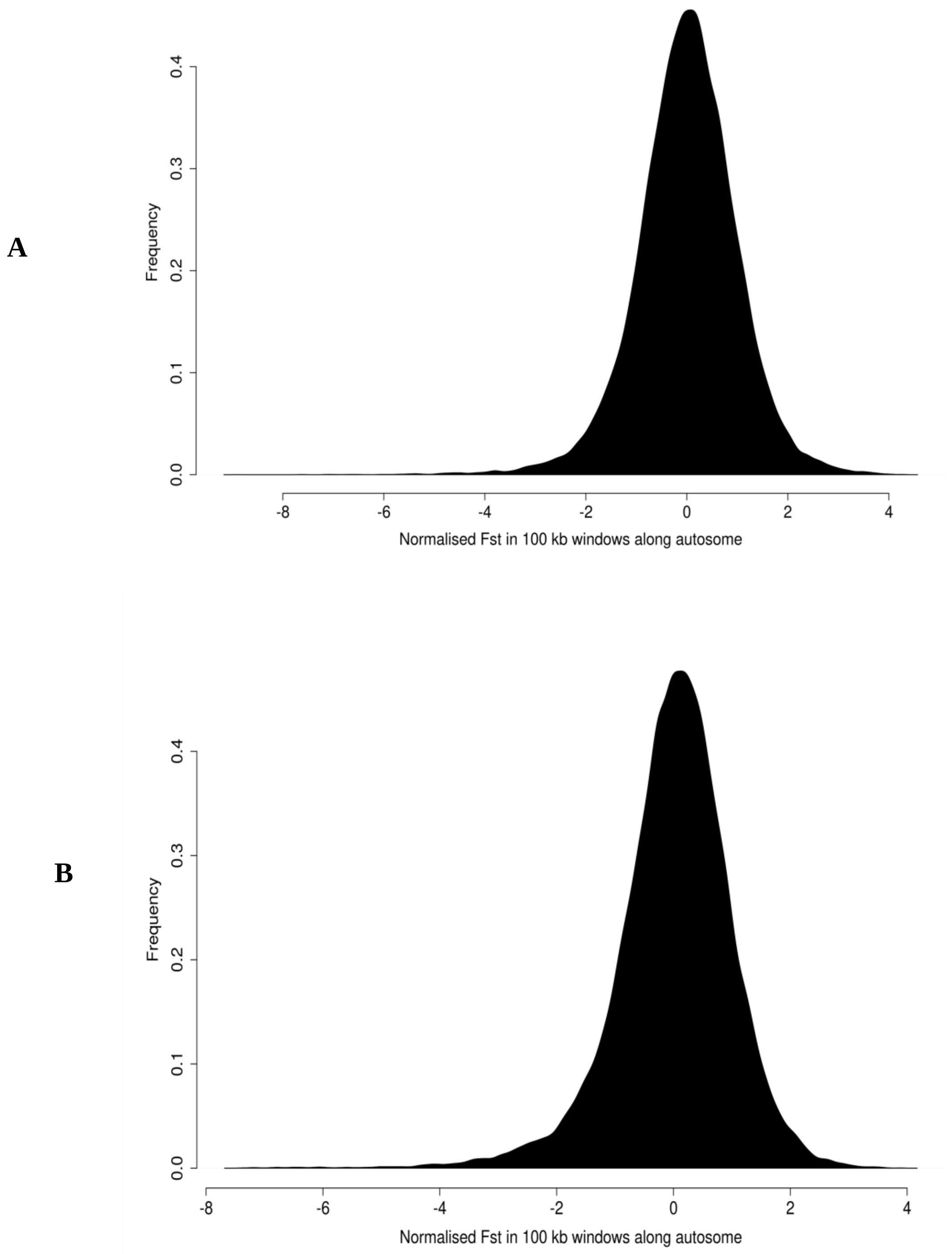
Supplementary Figure 1: Tranche plot produced by VariantRecalibrator for SNPs. Description: Partition of the call sets into quality tranches. The tranches correspond to certain levels of sensitivity relative to the truth sets (the highest tranche corresponds to a high accuracy call set but with the lowest value of sensitivity).



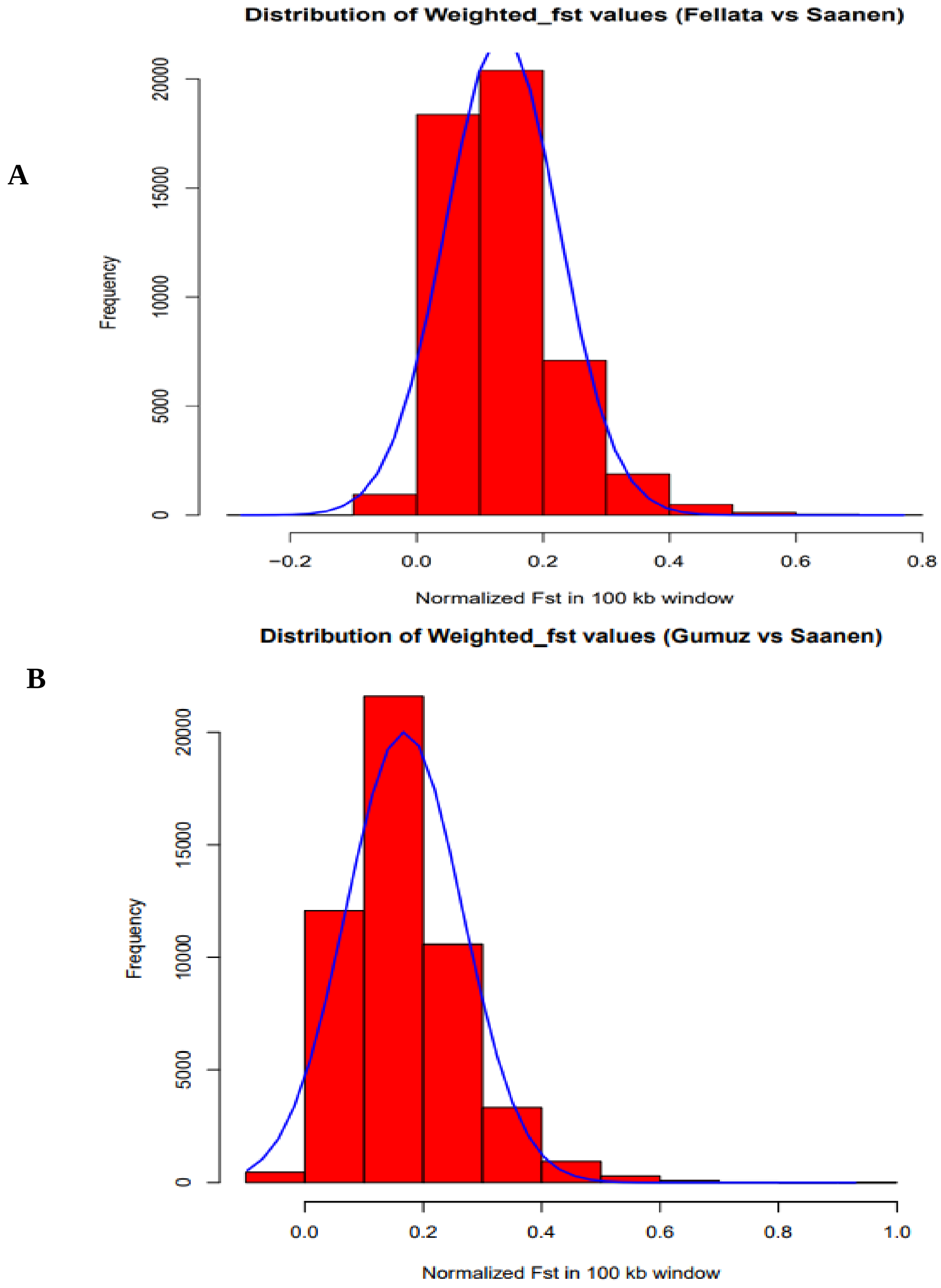
Supplementary Figure 2: Distribution of SNPs following annotation categories (78 goat samples).



Supplementary Figure 3: Cross-validation error plot for ADMIXTURE analysis of the studied populations in the global context.



Supplementary Figure 4: Distribution plot of *ZHp* values of **(A)** Fellata and **(B)** Gumuz



Supplementary Figure 5: Distribution plot of *ZFst* values of **(A)** Fellata vs Saanen and **(B)** Gumuz vs Saanen

Supplementary Table 1: Description of the environmental characteristics the distribution area of the study goat populations

Breed name	Country	Area of the breed in the country	Climatic characteristics of the distribution area	Sample location (latitude/ longitude)
Arab	Ethiopia	Semi-arid: Oumer et al., 2019	Mean altitude: 1,373 m Annual mean temperature: 20–30 °C	6.44/37.92
Fellata	Ethiopia	Hot arid: Getinet et al., 2005	Mean altitude: 725 m Annual mean temperature: 19–38.7 °C	10.34/34.22
Oromo	Ethiopia	Sub-humid: Oumer et al., 2019	Mean altitude: 1,668 m Annual mean temperature: 28 °C	9.45/34.44
Abergelle	Ethiopia	Warm sub-moist lowland: Birhanie et al., 2018	Mean altitude: <1,500 m Annual mean temperature: 21–41 °C	13.09/38.95*
Keffa	Ethiopia	Humid and forest area: Getinet, 2016	Mean altitude: 1,814 m Annual mean temperature: 10–27.5 °C	5.87/36.47*
Gumuz	Ethiopia	Hot arid: Getinet et al., 2005	Mean altitude: 630 m Annual mean temperature: 23.5–30 °C	9.15/40.49*
Woyto-Guji	Ethiopia	Semi-arid to sub-humid: Zergaw et al., 2016	Mean altitude: 600–1,200 m Annual mean temperature: 12–33 °C	6.86/37.81*
Boran: BOR	Kenya	Northern arid and semi-arid: Porter et al., 2016	Mean altitude: 590.6 m Annual mean temperature: 26.7 °C	-0.02/37.91*
Unknown	Morocco	http://boujenane.com/phocadownload/Small%20ruminant%20breed%20in%20Morocco.pdf	Mean altitude: 1,500 m Annual mean temperature: 14–22 °C	31.79/-7.09*
Thyolo	Malawi	Semi-arid: Banda et al., 2009	Mean altitude: 820 m Annual mean temperature: 29 °C	-13.25/34.30*
Guera	Mali	Semi-arid: Traoré et al., 2021	Mean altitude: 850 m Annual mean temperature: 16–22 °C	16.56/-1.62*
Saanen	France	Cool: https://en.wikipedia.org/wiki/French_Alps	Mean altitude: 1,125–4,810 m Annual mean temperature: -8°C	45.92/7.04*
Tibetan	China	Cool: https://www.britannica.com/place/Tibet/Climate	Mean altitude: 4,800–6,100 m Annual mean temperature: -19–30°C	30.15/88.79*

Supplementary Table 2: SNP statistics for each goat population

Population	Total no. of SNPs	Average per sample	Reported SNPs (rs)	Novel SNPs	het/hom	dbSNP (%)	
						rs	novel
ARB	15,878,802	8,078,778	10,891,308	4,987,494	1.27	68.59	31.41
FEL	16,903,989	7,983,054	11,648,111	5,255,878	1.32	68.91	31.09
ORO	15,889,419	7,989,569	10,900,991	4,988,428	1.27	68.61	31.39
ABR	16,408,691	7,701,195	10,851,974	5,556,717	1.34	66.14	33.86
KEF	14,936,598	6,591,579	10,173,862	5,826,286	1.03	68.11	31.89
GUM	16,682,139	8,751,774	11,294,508	5,387,631	1.44	67.70	32.30
WGU	17,262,645	8,866,137	11,677,476	5,585,169	1.55	67.65	32.35
GAL	17,400,421	8,781,270	11,783,862	5,616,559	1.57	67.72	32.28
UNK	18,266,925	8,589,128	12,986,129	5,280,796	1.62	71.09	28.91
THY	14,750,501	8,281,573	9,945,667	4,804,834	1.14	67.43	32.57
GUE	15,853,996	8,075,373	10,885,132	4,968,864	1.39	68.66	31.34
SAN	14,389,837	7,225,373	9,841,654	4,548,183	1.15	68.39	31.61
TIB	17,459,764	8,346,515	11,412,217	6,047,547	1.31	65.36	34.64

Supplementary Table 3: InDel statistics for each goat population

Population	Total no. of InDels	Average per sample	No. of Insertions	No. of deletions	Reported InDels (rs)	Novel InDels	dbSNP (%)		*ts/tv* ratio*
							rs	novel	
ARB	1,823,938	862,959	828,360	995,578	353,604	1,470,334	19.39	80.61	2.30
FEL	1,911,951	835,348	857,076	1,054,875	383,715	1,528,236	20.07	79.93	2.30
ORO	1,824,730	847,620	825,643	999,087	351,739	1,472,991	19.28	80.72	2.30
ABR	1,929,864	976,619	896,970	1,032,894	351,515	1,578,349	18.21	81.79	2.27
KEF	1,910,158	660,074	872,679	1,037,479	372,662	1,537,496	19.51	80.49	2.25
GUM	1,739,360	962,116	797,045	942,315	319,335	1,420,025	18.36	81.64	2.29
WGU	1,953,928	965,809	887,880	1,066,048	388,506	1,565,422	19.88	80.11	2.31
GAL	1,973,805	953,,145	896,188	1,077,617	391,179	1,582,626	19.82	80.18	2.29
UNK	2,033,758	904,149	900,464	1,133,294	447,785	1,585,973	22.02	77.98	2.29
THY	1,757,884	938,703	816,560	941,324	318,880	1,439,004	18.14	81.86	2.27
GUE	1,851,019	884,809	854,534	996,485	355,442	1,495,577	19.20	80.80	2.29
SAN	1,768,578	797,437	846,837	921,741	310,913	1,457,665	17.58	82.42	2.26
TIB	1,895,948	825,717	837,036	1,058,912	343,528	1,552,420	18.12	81.88	2.30

***_ts/tv_ ratio**: transition-to-transversion ratio

Supplementary Table 4: Number of SNPs in each category after annotation with VEP (78 goat samples)

Category		Number and percentage of SNPs	
		Number	**Percentage**
Total		35,161,094	100%
Upstream		1,267,587	3.61
Exonic	Missense	121,695	0.35
	Stop-gained	2,043	0.006
	Stop-lost	186	5.29e-4
	Start-lost	354	0.001
	Stop retained	109	0.001
	Synonymous	133,878	0.38
Intronic		11,195,100	31.8
Coding sequence		63	1.79e-4
5_prime UTR		29,441	0.08
3_prime UTR		120,360	0.34
Non coding transcript exon		56,712	0.16
Mature miRNA		15	4.27e-5
Splicing		23,331	0.07
Splice donor		1,028	0.003
Splice acceptor		628	0.002
Downstream		1,086,842	3.1
Intergenic		21,121,722	60.1

Supplementary Table 5: Results of f3 statistics for the study populations as generated with TreeMix

Breeds (A; B, C)	f3-statistics	Standard Error	Z
Abergelle;Boran,Saanen	0.0030465	4.55E-05	66.9278
Boran;Abergelle,Saanen	0.00234849	4.48E-05	52.3955
Saanen;Boran,Abergelle	0.0268598	9.17E-05	292.889
Abergelle;Boran,Gumuz	0.0038312	3.79E-05	101.115
Boran;Abergelle,Gumuz	0.00156379	3.73E-05	41.9264
Gumuz;Boran,Abergelle	0.00339484	4.10E-05	82.812
Abergelle;Boran,Keffa	0.00217472	3.35E-05	64.9655
Boran;Abergelle,Keffa	0.00322027	3.82E-05	84.2633
Keffa;Boran,Abergelle	0.00357851	3.32E-05	107.89
Abergelle;Boran,Thyolo	0.00435251	4.51E-05	96.4205
Boran;Abergelle,Thyolo	0.00104248	4.25E-05	24.5233
Thyolo;Boran,Abergelle	0.0135241	7.08E-05	191.047
Abergelle;Boran,Fellata	0.00339792	3.78E-05	89.9906
Fellata;Boran,Abergelle	0.00348461	3.74E-05	93.2082
Boran;Abergelle,Fellata	0.00199707	3.46E-05	57.7932
Abergelle;Boran,Arab	0.00288004	3.70E-05	77.7646
Arab;Boran,Abergelle	0.00467454	4.27E-05	109.425
Boran;Abergelle,Arab	0.00251496	3.78E-05	66.5967
Abergelle;Boran,Guera	0.00355551	4.30E-05	82.6163
Boran;Abergelle,Guera	0.00183948	3.94E-05	46.6583
Guera;Boran,Abergelle	0.0116452	5.92E-05	196.819
Abergelle;Boran,UknMorocco	0.0033781	3.95E-05	85.5861
Boran;Abergelle,UknMorocco	0.00201689	3.74E-05	53.9778
UknMorocco;Boran,Abergelle	0.00714501	4.70E-05	152.062
Abergelle;Boran,Woyto-Guji	0.00485972	3.93E-05	123.749
Boran;Abergelle,Woyto-Guji	0.000535268	3.12E-05	17.1604
Woyto-Guji;Boran,Abergelle	0.000845518	3.24E-05	26.0571
Abergelle;Boran,Oromo	0.00264815	3.51E-05	75.4888
Boran;Abergelle,Oromo	0.00274684	3.78E-05	72.5728
Oromo;Boran,Abergelle	0.00398283	3.76E-05	105.981
Abergelle;Boran,Tibetan	0.00309189	4.37E-05	70.6979
Boran;Abergelle,Tibetan	0.0023031	4.32E-05	53.3556
Tibetan;Boran,Abergelle	0.0209418	7.34E-05	285.121
Boran;Saanen,Gumuz	0.00121444	4.72E-05	25.755
Gumuz;Boran,Saanen	0.00374419	4.87E-05	76.9585
Saanen;Boran,Gumuz	0.0279938	9.42E-05	297.182

Boran;Saanen,Keffa	0.00336026	4.74E-05	70.9184
Keffa;Boran,Saanen	0.00343852	4.40E-05	78.163
Saanen;Boran,Keffa	0.025848	8.98E-05	287.944
Boran;Saanen,Thyolo	0.00216507	5.56E-05	38.9107
Saanen;Boran,Thyolo	0.0270432	9.78E-05	276.491
Thyolo;Boran,Saanen	0.0124015	7.43E-05	166.906

Supplementary Table 6: Results of f4 statistics for the study populations as generated with TreeMix

Breeds (A,B; C,D)	**f4-statistics**	**Standard Error**	**Z**
Boran,Abergelle;Saanen,Gumuz	-0.0007847	4.44E-05	-17.687
Boran,Gumuz;Abergelle,Saanen	-0.000349352	4.40E-05	-7.93399
Boran,Saanen;Abergelle,Gumuz	-0.00113405	4.43E-05	-25.5839
Boran,Abergelle;Saanen,Keffa	0.000871779	4.14E-05	21.0446
Boran,Keffa;Abergelle,Saanen	0.000139987	4.34E-05	3.22692
Boran,Saanen;Abergelle,Keffa	0.00101177	3.93E-05	25.7639
Boran,Abergelle;Saanen,Thyolo	-0.00130601	4.87E-05	-26.8401
Boran,Saanen;Abergelle,Thyolo	-0.000183427	5.52E-05	-3.32195
Boran,Thyolo;Abergelle,Saanen	0.00112258	5.39E-05	20.8445
Boran,Abergelle;Saanen,Fellata	-0.000351422	3.90E-05	-9.01638
Boran,Fellata;Abergelle,Saanen	0.00198217	4.21E-05	47.1173
Boran,Saanen;Abergelle,Fellata	0.00163075	4.32E-05	37.7196
Boran,Abergelle;Saanen,Arab	0.000166463	4.25E-05	3.91882
Boran,Arab;Abergelle,Saanen	0.000171487	4.45E-05	3.85494
Boran,Saanen;Abergelle,Arab	0.000337951	4.46E-05	7.57294
Boran,Abergelle;Saanen,Guera	-0.000509008	4.08E-05	-12.4822
Boran,Guera;Abergelle,Saanen	0.00457978	5.25E-05	87.181
Boran,Saanen;Abergelle,Guera	0.00407077	5.45E-05	74.6337
Boran,Abergelle;Saanen,UknMorocco	-0.000331598	3.52E-05	-9.43018
Boran,Saanen;Abergelle,UknMorocco	0.00717045	5.18E-05	138.432
Boran,UknMorocco;Abergelle,Saanen	0.00750205	5.13E-05	146.232
Boran,Abergelle;Saanen,Woyto-Guji	-0.00181323	4.27E-05	-42.4521
Boran,Saanen;Abergelle,Woyto-Guji	-0.00209513	4.25E-05	-49.315
Boran,Woyto-Guji;Abergelle,Saanen	-0.000281907	3.71E-05	-7.60638
Boran,Abergelle;Saanen,Oromo	0.000398348	4.20E-05	9.48859
Boran,Oromo;Abergelle,Saanen	-0.00010104	4.33E-05	-2.33407
Boran,Saanen;Abergelle,Oromo	0.000297309	4.10E-05	7.25567
Boran,Abergelle;Saanen,Tibetan	-4.54E-05	3.78E-05	-1.201
Boran,Saanen;Abergelle,Tibetan	0.0085436	6.06E-05	141.097
Boran,Tibetan;Abergelle,Saanen	0.00858899	6.08E-05	141.322
Boran,Abergelle;Gumuz,Keffa	0.00165648	3.17E-05	52.234
Boran,Gumuz;Abergelle,Keffa	0.000361452	2.97E-05	12.1811
Boran,Keffa;Abergelle,Gumuz	-0.00129503	3.34E-05	-38.7495
Boran,Abergelle;Gumuz,Thyolo	-0.000521311	3.91E-05	-13.3381
Boran,Gumuz;Abergelle,Thyolo	3.13E-05	4.09E-05	0.766482
Boran,Thyolo;Abergelle,Gumuz	0.000552647	4.06E-05	13.6005
Boran,Abergelle;Gumuz,Fellata	0.000433278	3.37E-05	12.8637
Boran,Fellata;Abergelle,Gumuz	-0.00048681	3.20E-05	-15.208
Boran,Gumuz;Abergelle,Fellata	-5.35E-05	3.26E-05	-1.63961

Boran,Abergelle;Gumuz,Arab	0.000951163	3.29E-05	28.8679
Boran,Arab;Abergelle,Gumuz	-0.000220737	3.48E-05	-6.3382
Boran,Gumuz;Abergelle,Arab	0.000730427	3.35E-05	21.8029
Boran,Abergelle;Gumuz,Guera	0.000275692	3.99E-05	6.90366
Boran,Guera;Abergelle,Gumuz	-0.000476888	3.79E-05	-12.5916
Boran,Gumuz;Abergelle,Guera	-0.000201197	3.96E-05	-5.07771
Boran,Abergelle;Gumuz,UknMorocco	0.000453102	3.77E-05	12.0203
Boran,Gumuz;Abergelle,UknMorocco	-0.000327468	3.54E-05	-9.2565
Boran,UknMorocco;Abergelle,Gumuz	-0.000780569	3.49E-05	-22.3717
Boran,Abergelle;Gumuz,Woyto-Guji	-0.00102853	3.22E-05	-31.9014
Boran,Gumuz;Abergelle,Woyto-Guji	-0.000416378	3.38E-05	-12.3062
Boran,Woyto-Guji;Abergelle,Gumuz	0.000612147	2.94E-05	20.8166
FBoran,Abergelle;Gumuz,Oromo	0.00118305	3.22E-05	36.791
Boran,Gumuz;Abergelle,Oromo	0.000811348	3.18E-05	25.5374
Boran,Oromo;Abergelle,Gumuz	-0.000371701	3.44E-05	-10.8058

Supplementary Table 7: Results of signature of selection for Fellata goat (*Hp*)

Chr	Windows		Number of SNPs	Hp	BP	ZHp
	Start	End				
1	119650001	119750000	316	0.164971656	119700000.5	-4.473425561
2	21050001	21150000	220	0.093956858	21100000.5	-6.498538402
2	21100001	21200000	188	0.150747243	21150000.5	-4.879059922
2	34850001	34950000	188	0.112988045	34900000.5	-5.95583038
3	46700001	46800000	349	0.170606431	46750000.5	-4.312739981
3	46750001	46850000	315	0.177151926	46800000.5	-4.12608359
3	107500001	107600000	828	0.168245871	107550000.5	-4.38005551
3	110850001	110950000	75	0.155220847	110900000.5	-4.751487182
3	110900001	1.11E+08	150	0.179110494	110950000.5	-4.070231545
4	7550001	7650000	1903	0.172136099	7600000.5	-4.26911878
4	7600001	7700000	1313	0.16144768	7650000.5	-4.57391799
4	40700001	40800000	235	0.155337751	40750000.5	-4.748153432
5	18500001	18600000	456	0.154031828	18550000.5	-4.785394156
5	23500001	23600000	308	0.128854152	23550000.5	-5.503380203
5	23550001	23650000	488	0.176072129	23600000.5	-4.156875901
5	100650001	100750000	576	0.166006365	100700000.5	-4.443918998
6	34300001	34400000	331	0.18024712	34350000.5	-4.037818631
6	44550001	44650000	363	0.177176375	44600000.5	-4.125386371
6	48500001	48600000	536	0.181157277	48550000.5	-4.011863887
6	48550001	48650000	369	0.071911906	48600000.5	-7.127189296
6	48600001	48700000	294	0.121385077	48650000.5	-5.716374129
6	70450001	70550000	515	0.175048226	70500000.5	-4.186074322
6	70650001	70750000	261	0.11329913	70700000.5	-5.94695924
6	70700001	70800000	220	0.157223192	70750000.5	-4.694386738
6	70750001	70850000	181	0.159287452	70800000.5	-4.635520726
6	114550001	114650000	730	0.151155625	114600000.5	-4.867414172
7	59000001	59100000	145	0.180550222	59050000.5	-4.029175144
7	66750001	66850000	93	0.178854074	66800000.5	-4.077543801

7	66800001	66900000	103	0.156124478	66850000.5	-4.725718515
8	38500001	38600000	23	0.181110147	38550000.5	-4.013207901
8	43350001	43450000	284	0.161500274	43400000.5	-4.572418166
9	83500001	83600000	220	0.118111711	83550000.5	-5.80971996
9	86050001	86150000	299	0.16802132	86100000.5	-4.386458991
9	86100001	86200000	212	0.174984503	86150000.5	-4.18789148
10	51500001	51600000	125	0.121725148	51550000.5	-5.70667641
10	51550001	51650000	125	0.110237497	51600000.5	-6.034267126
10	51600001	51700000	126	0.128576442	51650000.5	-5.511299594
10	51650001	51750000	144	0.141478746	51700000.5	-5.143367548
10	51700001	51800000	171	0.129267393	51750000.5	-5.491595911
10	71500001	71600000	114	0.156803509	71550000.5	-4.706354766
10	71550001	71650000	89	0.178516804	71600000.5	-4.087161667
10	84600001	84700000	328	0.175095857	84650000.5	-4.184716033
11	4350001	4450000	200	0.175465779	4400000.5	-4.174167062
11	37750001	37850000	278	0.165918538	37800000.5	-4.446423539
11	37800001	37900000	198	0.133690032	37850000.5	-5.365476533
11	37850001	37950000	142	0.128560091	37900000.5	-5.511765891
11	37900001	3.80E+07	144	0.123430115	37950000.5	-5.658056234
11	37950001	38050000	192	0.091118929	38000000.5	-6.579466983
11	38000001	38100000	237	0.086953306	38050000.5	-6.698257103
11	38050001	38150000	248	0.13314998	38100000.5	-5.380877074
11	38100001	38200000	262	0.151255759	38150000.5	-4.864558691
11	38300001	38400000	135	0.149013879	38350000.5	-4.92848987
11	38350001	38450000	156	0.134346352	38400000.5	-5.346760388
11	38400001	38500000	280	0.154934175	38450000.5	-4.759662136
11	38450001	38550000	419	0.162451155	38500000.5	-4.545302125
11	51400001	51500000	492	0.178130428	51450000.5	-4.098179872
11	69700001	69800000	514	0.161550115	69750000.5	-4.57099688
12	50650001	50750000	182	0.164609019	50700000.5	-4.4837668
12	50700001	50800000	212	0.156901649	50750000.5	-4.703556107

12	50750001	50850000	108	0.161639967	50800000.5	-4.568434592
12	50800001	50900000	56	0.174361342	50850000.5	-4.205662028
12	50850001	50950000	42	0.168739859	50900000.5	-4.365968568
12	50900001	5.10E+07	33	0.164924548	50950000.5	-4.474768927
12	54750001	54850000	255	0.162782345	54800000.5	-4.535857664
12	54800001	54900000	240	0.140827424	54850000.5	-5.161941128
12	54850001	54950000	293	0.166195717	54900000.5	-4.438519302
13	19300001	19400000	871	0.17674539	19350000.5	-4.137676683
13	19350001	19450000	491	0.170479675	19400000.5	-4.316354646
13	39950001	40050000	129	0.135498863	40000000.5	-5.313894505
13	40000001	40100000	168	0.146531026	40050000.5	-4.999292804
13	53300001	53400000	182	0.135329533	53350000.5	-5.318723252
13	53350001	53450000	190	0.133721706	53400000.5	-5.364573273
13	53400001	53500000	220	0.127362554	53450000.5	-5.54591578
13	78050001	78150000	312	0.158022695	78100000.5	-4.671587498
14	42750001	42850000	147	0.178909402	42800000.5	-4.075966048
14	47400001	47500000	221	0.14952562	47450000.5	-4.913896669
14	47450001	47550000	132	0.155216251	47500000.5	-4.751618236
14	60950001	61050000	337	0.165215389	61000000.5	-4.466475088
14	73600001	73700000	393	0.075054799	73650000.5	-7.037564134
14	73650001	73750000	329	0.07262371	73700000.5	-7.106890948
15	1	1.00E+05	372	0.150639676	50000.5	-4.882127373
15	50001	150000	386	0.169324699	100000.5	-4.349290834
17	36250001	36350000	143	0.05624228	36300000.5	-7.574036433
17	36300001	36400000	136	0.080331934	36350000.5	-6.887077262
17	36350001	36450000	93	0.109887542	36400000.5	-6.044246716
17	52450001	52550000	234	0.163835574	52500000.5	-4.505822961
18	15950001	16050000	157	0.148746854	16000000.5	-4.93610456
18	26850001	26950000	546	0.088305898	26900000.5	-6.659685532
18	26900001	2.70E+07	566	0.010085769	26950000.5	-8.890271177
18	26950001	27050000	647	0.123113653	27000000.5	-5.667080702

18	36650001	36750000	142	0.179245728	36700000.5	-4.066375102
18	55200001	55300000	160	0.10047973	55250000.5	-6.312527138
18	55250001	55350000	155	0.053039105	55300000.5	-7.665380658
19	13300001	13400000	737	0.153951924	13350000.5	-4.787672761
19	13350001	13450000	984	0.13550835	13400000.5	-5.31362395
19	13400001	13500000	1099	0.173864183	13450000.5	-4.219839399
20	27800001	27900000	259	0.147965708	27850000.5	-4.958380321
20	27850001	27950000	232	0.133277535	27900000.5	-5.377239596
20	27900001	2.80E+07	260	0.129490382	27950000.5	-5.485236998
20	32450001	32550000	434	0.158289154	32500000.5	-4.663988952
20	32500001	32600000	381	0.174273044	32550000.5	-4.208179993
20	33600001	33700000	317	0.164848992	33650000.5	-4.476923542
21	56450001	56550000	359	0.135730658	56500000.5	-5.307284466
22	56450001	56550000	280	0.150830781	56500000.5	-4.876677692
23	800001	9.00E+05	311	0.15709741	850000.5	-4.697973654
23	850001	950000	365	0.159795168	900000.5	-4.621042289
23	900001	1.00E+06	363	0.165149232	950000.5	-4.468361677
23	950001	1050000	352	0.162096992	1000000.5	-4.555401692
23	1000001	1100000	345	0.158300379	1050000.5	-4.663668867
23	1050001	1150000	364	0.163155812	1100000.5	-4.525207582
23	28200001	28300000	873	0.164813308	28250000.5	-4.477941146
24	23550001	23650000	209	0.14966469	23600000.5	-4.909930838
24	34250001	34350000	375	0.154682972	34300000.5	-4.76682564
24	34300001	34400000	335	0.161721489	34350000.5	-4.566109847
25	150001	250000	68	0.175265169	200000.5	-4.179887794
25	2900001	3.00E+06	246	0.174428713	2950000.5	-4.203740834
25	3650001	3750000	238	0.139964957	3700000.5	-5.186535907
25	3700001	3800000	259	0.178250666	3750000.5	-4.094751045
27	37250001	37350000	571	0.173353873	37300000.5	-4.234391787
28	15350001	15450000	569	0.172129975	15400000.5	-4.269293403

Supplementary Table 8: Results of signature of selection for Gumuz goat (*Hp*)

Chr	**Windows**		**Number of SNPs**	**Hp**	**BP**	**ZHp**
	Start	**End**				
1	12550001	12650000	1050	0.144360575	12600000.5	-4.273732815
1	66500001	66600000	163	0.143399576	66550000.5	-4.296034628
1	76150001	76250000	221	0.149013879	76200000.5	-4.165743996
1	81200001	81300000	224	0.113609072	81250000.5	-4.987380257
1	81250001	81350000	427	0.125515328	81300000.5	-4.711072825
2	16050001	16150000	223	0.147175	16100000.5	-4.208418705
2	21000001	21100000	334	0.151948095	21050000.5	-4.097649886
2	21050001	21150000	259	0.139788506	21100000.5	-4.379836417
2	21100001	21200000	255	0.142904652	21150000.5	-4.307520288
2	21150001	21250000	119	0.134012346	21200000.5	-4.513883269
2	21200001	21300000	241	0.021121954	21250000.5	-7.133720776
2	21250001	21350000	354	0.019063568	21300000.5	-7.181489568
2	21300001	21400000	398	0.015898561	21350000.5	-7.254939612
2	21350001	21450000	321	0.014043511	21400000.5	-7.297989588
2	21400001	21500000	150	0.044229907	21450000.5	-6.597456517
2	83650001	83750000	202	0.116467589	83700000.5	-4.921042901
2	101500001	101600000	355	0.150041447	101550000.5	-4.141897318
3	16800001	16900000	269	0.152087304	16850000.5	-4.094419289
3	87100001	87200000	179	0.132539569	87150000.5	-4.548061877
3	102000001	102100000	410	0.125327669	102050000.5	-4.715427807
3	103650001	103750000	137	0.128203109	103700000.5	-4.648697729
3	110800001	110900000	57	0.143133175	110850000.5	-4.302216981
3	110900001	1.11E+08	101	0.148680796	110950000.5	-4.173473822
4	14850001	14950000	1246	0.12985361	14900000.5	-4.610394682
4	14900001	1.50E+07	694	0.065464129	14950000.5	-6.104675767
4	26400001	26500000	186	0.116212058	26450000.5	-4.926973006
4	26600001	26700000	143	0.113990216	26650000.5	-4.978535097
4	60000001	60100000	572	0.146691615	60050000.5	-4.219636579
4	93800001	93900000	225	0.148863124	93850000.5	-4.169242546

4	93850001	93950000	277	0.146148586	93900000.5	-4.232238586
4	98650001	98750000	774	0.141432003	98700000.5	-4.341695936
4	115450001	115550000	465	0.124506435	115500000.5	-4.734486107
5	18050001	18150000	726	0.087138839	18100000.5	-5.60167267
5	26300001	26400000	126	0.12489925	26350000.5	-4.725370093
5	26350001	26450000	65	0.056394118	26400000.5	-6.315162733
5	26400001	26500000	61	0.152777778	26450000.5	-4.078395518
5	26450001	26550000	122	0.15051575	26500000.5	-4.130890206
5	99050001	99150000	2241	0.099719408	99100000.5	-5.309716502
5	100550001	100650000	659	0.1098948	100600000.5	-5.073577063
5	100600001	100700000	730	0.107690871	100650000.5	-5.124723452
6	21800001	21900000	517	0.046721513	21850000.5	-6.539634046
6	21850001	21950000	781	0.143855943	21900000.5	-4.285443765
6	32000001	32100000	233	0.138386661	32050000.5	-4.412368918
6	45600001	45700000	470	0.152187766	45650000.5	-4.092087879
6	58300001	58400000	272	0.122112794	58350000.5	-4.790035124
6	58350001	58450000	248	0.153892455	58400000.5	-4.052527297
6	86250001	86350000	1140	0.153501319	86300000.5	-4.061604366
6	86300001	86400000	921	0.146665577	86350000.5	-4.22024083
7	650001	750000	405	0.128418549	700000.5	-4.643698015
7	17500001	17600000	59	0.036249839	17550000.5	-6.782649273
7	17550001	17650000	137	0.11982485	17600000.5	-4.843131247
7	19150001	19250000	162	0.140746212	19200000.5	-4.357611015
7	19200001	19300000	152	0.093233372	19250000.5	-5.460237372
7	19250001	19350000	286	0.144887078	19300000.5	-4.261514309
7	21700001	21800000	420	0.153822096	21750000.5	-4.054160119
7	51400001	51500000	310	0.154266403	51450000.5	-4.043849123
7	55550001	55650000	99	0.087604271	55600000.5	-5.590871427
7	56100001	56200000	125	0.1315184	56150000.5	-4.571760061
7	56150001	56250000	115	0.152777778	56200000.5	-4.078395518
7	64000001	64100000	161	0.067645871	64050000.5	-6.054044278
7	66500001	66600000	100	0.11175375	66550000.5	-5.030436573

7	66550001	66650000	81	0.037872216	66600000.5	-6.74499891
7	66600001	66700000	78	0.063262209	66650000.5	-6.155775548
7	66650001	66750000	82	0.067811406	66700000.5	-6.050202715
7	66700001	66800000	73	0.067972624	66750000.5	-6.04646135
7	66750001	66850000	64	0.069907917	66800000.5	-6.001549173
7	66800001	66900000	91	0.037319825	66850000.5	-6.757818188
7	66850001	66950000	111	0.017750056	66900000.5	-7.211972126
7	66900001	6.70E+07	91	0.028667769	66950000.5	-6.958605712
7	67050001	67150000	111	0.122717755	67100000.5	-4.775995865
7	67100001	67200000	127	0.042260869	67150000.5	-6.64315182
7	67150001	67250000	169	0.048001659	67200000.5	-6.509925809
7	72950001	73050000	471	0.104414976	73000000.5	-5.200746844
7	73000001	73100000	483	0.086348834	73050000.5	-5.620006245
8	43350001	43450000	183	0.099552352	43400000.5	-5.313593337
8	43400001	43500000	100	0.11175375	43450000.5	-5.030436573
8	51500001	51600000	501	0.067500199	51550000.5	-6.057424867
8	51550001	51650000	604	0.034604647	51600000.5	-6.820829093
8	51600001	51700000	359	0.033716112	51650000.5	-6.841449256
10	46500001	46600000	229	0.14975189	46550000.5	-4.148617024
10	51550001	51650000	153	0.154579187	51600000.5	-4.03659037
10	57600001	57700000	288	0.146986819	57650000.5	-4.212785795
10	83700001	83800000	702	0.155184743	83750000.5	-4.022537292
10	83750001	83850000	553	0.136003691	83800000.5	-4.467670289
10	87700001	87800000	274	0.13900753	87750000.5	-4.397960465
11	37900001	3.80E+07	148	0.149039207	37950000.5	-4.165156195
11	37950001	38050000	196	0.113663139	38000000.5	-4.98612553
11	38000001	38100000	243	0.10877429	38050000.5	-5.099580641
11	51850001	51950000	668	0.125892927	51900000.5	-4.702309923
11	64900001	6.50E+07	54	0.116524334	64950000.5	-4.91972603
11	64950001	65050000	42	0.143020251	65000000.5	-4.304837589
11	65000001	65100000	94	0.072593106	65050000.5	-5.939234235
11	69450001	69550000	408	0.142224078	69500000.5	-4.32331432

11	69500001	69600000	412	0.119788286	69550000.5	-4.843979796
11	69550001	69650000	354	0.112552073	69600000.5	-5.011909952
11	69600001	69700000	336	0.104645145	69650000.5	-5.195405348
11	69650001	69750000	399	0.100232986	69700000.5	-5.29779793
11	69700001	69800000	466	0.148900729	69750000.5	-4.168369849
11	69800001	69900000	417	0.156092529	69850000.5	-4.001470365
11	70650001	70750000	260	0.126213323	70700000.5	-4.69487451
11	94500001	94600000	176	0.114091576	94550000.5	-4.976182828
11	94550001	94650000	212	0.13313272	94600000.5	-4.534296659
12	10050001	10150000	196	0.085024059	10100000.5	-5.650750175
12	10100001	10200000	287	0.132298462	10150000.5	-4.553657216
12	51050001	51150000	28	0.151141869	51100000.5	-4.116359922
12	51150001	51250000	88	0.154863192	51200000.5	-4.029999496
12	54800001	54900000	265	0.143315683	54850000.5	-4.297981536
13	60750001	60850000	210	0.076770863	60800000.5	-5.842281393
14	49500001	49600000	397	0.152079493	49550000.5	-4.094600554
14	54000001	54100000	365	0.14349973	54050000.5	-4.293710359
14	60900001	6.10E+07	388	0.138349289	60950000.5	-4.4132362
14	60950001	61050000	403	0.154837421	61000000.5	-4.030597566
14	73650001	73750000	392	0.077191399	73700000.5	-5.832522043
14	88600001	88700000	405	0.136070223	88650000.5	-4.466126278
14	88650001	88750000	427	0.121692387	88700000.5	-4.799791474
14	88700001	88800000	417	0.068556038	88750000.5	-6.032922116
14	88750001	88850000	364	0.048638228	88800000.5	-6.495152988
14	88800001	88900000	287	0.126625426	88850000.5	-4.685310877
14	90250001	90350000	837	0.055005366	90300000.5	-6.347391383
14	90300001	90400000	887	0.092202496	90350000.5	-5.48416082
15	39500001	39600000	238	0.140466923	39550000.5	-4.364092454
15	81600001	81700000	265	0.139762464	81650000.5	-4.380440773
15	81650001	81750000	303	0.154602859	81700000.5	-4.036041027
16	62200001	62300000	495	0.14050787	62250000.5	-4.363142204
17	10200001	10300000	360	0.151237138	10250000.5	-4.114149022

18	15900001	1.60E+07	182	0.149344676	15950000.5	-4.158067215
18	15950001	16050000	160	0.147582505	16000000.5	-4.198961763
18	22950001	23050000	179	0.116376886	23000000.5	-4.923147846
18	23000001	23100000	159	0.149296875	23050000.5	-4.159176526
18	26150001	26250000	114	0.04668242	26200000.5	-6.540541271
18	26200001	26300000	53	0.033374295	26250000.5	-6.849381761
18	26850001	26950000	507	0.067156179	26900000.5	-6.065408521
18	26900001	2.70E+07	567	0.008797482	26950000.5	-7.41973372
18	26950001	27050000	606	0.020582377	27000000.5	-7.146242701
18	36500001	36600000	82	0.037572759	36550000.5	-6.751948362
18	36650001	36750000	72	0.053293301	36700000.5	-6.387123126
18	36700001	36800000	85	0.109518659	36750000.5	-5.082306133
18	36750001	36850000	112	0.146605059	36800000.5	-4.221645263
18	36800001	36900000	118	0.155108122	36850000.5	-4.02431543
18	36850001	36950000	104	0.148798186	36900000.5	-4.17074956
18	36900001	3.70E+07	98	0.101939711	36950000.5	-5.258190106
18	36950001	37050000	91	0.073192344	37000000.5	-5.92532776
18	37000001	37100000	161	0.153634587	37050000.5	-4.058511612
19	13300001	13400000	772	0.142040047	13350000.5	-4.327585094
19	13350001	13450000	990	0.116095746	13400000.5	-4.929672232
19	13400001	13500000	1044	0.151578278	13450000.5	-4.106232213
19	18250001	18350000	140	0.130465826	18300000.5	-4.596187039
19	18300001	18400000	84	0.089688581	18350000.5	-5.542501016
19	18350001	18450000	76	0.066865314	18400000.5	-6.072158605
19	18400001	18500000	115	0.059873126	18450000.5	-6.234425705
19	29350001	29450000	441	0.144093228	29400000.5	-4.279937099
19	29400001	29500000	476	0.050472885	29450000.5	-6.452576264
19	33750001	33850000	211	0.152668149	33800000.5	-4.080939667
19	34300001	34400000	125	0.141577778	34350000.5	-4.338312944
19	42400001	42500000	114	0.064534748	42450000.5	-6.126243844
19	42450001	42550000	232	0.138535785	42500000.5	-4.408908197
20	6750001	6850000	265	0.151641995	6800000.5	-4.104753537

21	56450001	56550000	410	0.120992374	56500000.5	-4.816036624
22	31450001	31550000	173	0.100669672	31500000.5	-5.287663791
22	31500001	31600000	151	0.055392044	31550000.5	-6.338417782
22	31550001	31650000	202	0.0519422	31600000.5	-6.41847801
23	550001	650000	162	0.129635851	600000.5	-4.615448211
23	600001	7.00E+05	203	0.097816867	650000.5	-5.353868595
23	650001	750000	158	0.084518197	700000.5	-5.662489683
23	850001	950000	348	0.148837121	900000.5	-4.169846003
23	900001	1.00E+06	323	0.142759981	950000.5	-4.310877663
23	30500001	30600000	250	0.123983923	30550000.5	-4.746612011
24	25100001	25200000	279	0.052730166	25150000.5	-6.400191746
24	25150001	25250000	201	0.025312295	25200000.5	-7.036475906
24	25200001	25300000	101	0.047970976	25250000.5	-6.510637866
24	25250001	25350000	112	0.036193342	25300000.5	-6.783960395
24	25300001	25400000	221	0.087397082	25350000.5	-5.595679647
24	25350001	25450000	225	0.109079009	25400000.5	-5.092509055
24	33900001	3.40E+07	198	0.150680819	33950000.5	-4.127059459
24	34250001	34350000	414	0.144776211	34300000.5	-4.264087174
25	200001	3.00E+05	206	0.141012199	250000.5	-4.351438293
25	3600001	3700000	169	0.139708637	3650000.5	-4.381689932
25	3650001	3750000	165	0.081778238	3700000.5	-5.726075667
26	21250001	21350000	200	0.150701715	21300000.5	-4.126574519
26	30350001	30450000	231	0.118443652	30400000.5	-4.875184596
27	25650001	25750000	456	0.0929227	25700000.5	-5.467447108
27	25700001	25800000	370	0.153962782	25750000.5	-4.050895217
27	25750001	25850000	344	0.110324385	25800000.5	-5.063607717
27	25800001	25900000	532	0.148452696	25850000.5	-4.178767315
29	46600001	46700000	199	0.059222002	46650000.5	-6.249536264

Supplementary Table 9: Results of signature of selection for Fellata vs Saanen goats (*Fst*)

Chr	Windows		Number of SNPs	Mean Fst
	Start	End		
1	126100001	126200000	340	0.63509
1	126050001	126150000	316	0.608577
1	102650001	102750000	1375	0.607726
1	44800001	44900000	617	0.606864
1	149200001	149300000	382	0.592668
1	83700001	83800000	234	0.561373
1	126000001	126100000	270	0.54567
1	129700001	129800000	521	0.536884
1	102600001	102700000	1145	0.521063
1	83750001	83850000	237	0.520512
1	83800001	83900000	269	0.505508
1	23950001	24050000	901	0.500626
1	129650001	129750000	834	0.498437
1	102700001	102800000	1118	0.492499
1	73900001	74000000	770	0.492022
1	68100001	68200000	419	0.490776
1	126150001	126250000	458	0.490545
1	46450001	46550000	817	0.483987
1	46400001	46500000	864	0.480268
1	149250001	149350000	489	0.476656
1	68050001	68150000	461	0.468621
1	107000001	107100000	594	0.463581
1	17650001	17750000	658	0.461736
1	135850001	135950000	1070	0.454362
1	99700001	99800000	676	0.451556
1	107050001	107150000	489	0.445309
1	24750001	24850000	1037	0.442621
1	149150001	149250000	719	0.44106

1	81000001	81100000	438	0.439723
1	30850001	30950000	1072	0.4337
1	80950001	81050000	475	0.433568
1	84850001	84950000	461	0.421066
1	73050001	73150000	327	0.420596
1	103950001	104050000	1106	0.420553
1	149450001	149550000	306	0.420215
1	30900001	31000000	881	0.418743
2	34850001	34950000	364	0.612936
2	47400001	47500000	216	0.56035
2	129950001	130050000	582	0.526495
2	32250001	32350000	537	0.508043
2	34800001	34900000	327	0.48699
2	128750001	128850000	1338	0.485009
2	47350001	47450000	191	0.482027
2	128700001	128800000	1225	0.480591
2	39250001	39350000	478	0.469412
2	32300001	32400000	482	0.455927
2	34900001	35000000	658	0.453829
2	94500001	94600000	570	0.447563
2	125300001	125400000	1264	0.435221
2	39200001	39300000	853	0.434821
2	32200001	32300000	733	0.433348
2	21050001	21150000	440	0.432067
2	104050001	104150000	795	0.429828
2	21200001	21300000	576	0.422464
2	21000001	21100000	579	0.422216
3	19800001	19900000	671	0.636935
3	66500001	66600000	4204	0.56743
3	19850001	19950000	685	0.558372
3	46700001	46800000	475	0.531723

3	19750001	19850000	524	0.523074
3	119600001	119700000	577	0.520581
3	46750001	46850000	453	0.516776
3	95750001	95850000	863	0.499605
3	68750001	68850000	461	0.494051
3	80600001	80700000	426	0.489057
3	80650001	80750000	374	0.488343
3	66450001	66550000	6149	0.484637
3	62900001	63000000	516	0.484474
3	87750001	87850000	422	0.482391
3	46650001	46750000	570	0.475362
3	62950001	63050000	468	0.474719
3	95850001	95950000	538	0.472336
3	46600001	46700000	849	0.471537
3	1600001	1700000	1179	0.465812
3	68700001	68800000	445	0.464342
3	95700001	95800000	890	0.460071
3	66550001	66650000	3944	0.459271
3	33750001	33850000	707	0.454799
3	31150001	31250000	416	0.452529
3	30950001	31050000	682	0.435215
3	119900001	120000000	892	0.429223
3	2850001	2950000	862	0.426839
4	48200001	48300000	469	0.580317
4	67400001	67500000	629	0.545786
4	98650001	98750000	1647	0.534976
4	6100001	6200000	472	0.534255
4	67350001	67450000	833	0.524081
4	62750001	62850000	626	0.52354
4	75300001	75400000	709	0.521822
4	13650001	13750000	1197	0.508037

4	75250001	75350000	551	0.505244
4	101550001	101650000	939	0.496984
4	13600001	13700000	1246	0.494317
4	48250001	48350000	567	0.490876
4	62700001	62800000	523	0.488329
4	64050001	64150000	535	0.482941
4	16550001	16650000	510	0.478274
4	44950001	45050000	625	0.473795
4	98600001	98700000	1212	0.473703
4	96500001	96600000	593	0.472529
4	89200001	89300000	295	0.469653
4	27150001	27250000	395	0.46195
4	27100001	27200000	408	0.459989
4	120250001	120350000	1180	0.459895
4	64100001	64200000	628	0.454451
4	7100001	7200000	1839	0.450221
4	14950001	15050000	1084	0.449974
4	7150001	7250000	1746	0.445584
4	89250001	89350000	398	0.443455
4	6050001	6150000	426	0.440327
4	120550001	120650000	845	0.439351
4	43200001	43300000	418	0.438829
4	120300001	120400000	1441	0.430546
4	90450001	90550000	947	0.42199
4	101500001	101600000	1173	0.419313
5	100750001	100850000	2599	0.623511
5	98700001	98800000	768	0.60267
5	100800001	100900000	2498	0.590422
5	1050001	1150000	336	0.589073
5	98900001	99000000	1449	0.562941
5	98950001	99050000	480	0.562566

5	108000001	108100000	533	0.513599
5	46900001	47000000	256	0.506768
5	99050001	99150000	90	0.500211
5	1100001	1200000	581	0.488254
5	93800001	93900000	580	0.487478
5	118800001	118900000	405	0.487078
5	99000001	99100000	111	0.484265
5	46950001	47050000	371	0.483568
5	98650001	98750000	1110	0.473843
5	23500001	23600000	693	0.459427
5	47400001	47500000	460	0.458313
5	65100001	65200000	532	0.457186
5	100700001	100800000	1418	0.456449
5	25500001	25600000	295	0.455971
5	18050001	18150000	1012	0.450555
5	107950001	108050000	480	0.434514
5	47350001	47450000	464	0.432037
5	100650001	100750000	904	0.43146
5	33750001	33850000	391	0.424163
6	48550001	48650000	617	0.619784
6	44500001	44600000	520	0.547865
6	48600001	48700000	520	0.534446
6	70750001	70850000	355	0.532854
6	48750001	48850000	532	0.527824
6	21900001	22000000	869	0.509981
6	70650001	70750000	330	0.507412
6	114600001	114700000	1069	0.503226
6	70450001	70550000	683	0.502707
6	48500001	48600000	848	0.501529
6	20300001	20400000	538	0.497963
6	25900001	26000000	1119	0.494141

6	25950001	26050000	1547	0.493505
6	114550001	114650000	1064	0.487075
6	70800001	70900000	412	0.484287
6	25750001	25850000	1799	0.48044
6	48700001	48800000	444	0.467911
6	98200001	98300000	456	0.459351
6	77600001	77700000	904	0.458285
6	51900001	52000000	928	0.458172
6	70600001	70700000	421	0.457258
6	34150001	34250000	951	0.452247
6	44450001	44550000	596	0.448901
6	57500001	57600000	986	0.447808
6	57550001	57650000	1052	0.446954
6	54200001	54300000	832	0.440777
6	2900001	3000000	1306	0.440322
6	25800001	25900000	1236	0.437011
6	51700001	51800000	1044	0.435648
6	20250001	20350000	615	0.435249
6	51950001	52050000	774	0.432741
6	21950001	22050000	755	0.429061
6	39050001	39150000	785	0.426883
6	70700001	70800000	364	0.424349
6	34200001	34300000	864	0.42365
7	99950001	100050000	2526	0.572143
7	66800001	66900000	133	0.570441
7	99900001	100000000	3663	0.54315
7	66750001	66850000	102	0.541996
7	59000001	59100000	215	0.5342
7	600001	700000	635	0.490643
7	66850001	66950000	175	0.478727
7	102050001	102150000	563	0.4603

7	12500001	12600000	441	0.452549
7	98950001	99050000	1771	0.448568
7	95300001	95400000	420	0.446978
7	12450001	12550000	362	0.439667
7	650001	750000	631	0.428747
7	99000001	99100000	1801	0.426296
7	58950001	59050000	241	0.421942
8	106000001	106100000	893	0.528143
8	1350001	1450000	432	0.450635
8	44700001	44800000	522	0.449467
8	105950001	106050000	1109	0.430582
8	43300001	43400000	450	0.422679
8	15150001	15250000	803	0.420513
9	24900001	25000000	846	0.611306
9	88050001	88150000	733	0.57115
9	77350001	77450000	1264	0.558172
9	88100001	88200000	710	0.556642
9	77300001	77400000	962	0.527297
9	29950001	30050000	535	0.507384
9	22600001	22700000	1071	0.475263
9	86100001	86200000	304	0.472399
9	24850001	24950000	910	0.463143
9	86200001	86300000	339	0.450513
9	6550001	6650000	1055	0.447266
9	30000001	30100000	362	0.4466
9	22550001	22650000	911	0.445377
9	86150001	86250000	322	0.436028
9	61100001	61200000	489	0.424956
9	47100001	47200000	601	0.423708
9	61050001	61150000	657	0.42184
9	25050001	25150000	913	0.418771

10	51650001	51750000	265	0.616084
10	60200001	60300000	513	0.598187
10	51600001	51700000	219	0.59646
10	51700001	51800000	227	0.587541
10	71500001	71600000	568	0.567774
10	51550001	51650000	214	0.536534
10	54850001	54950000	1020	0.53634
10	10550001	10650000	362	0.525265
10	60150001	60250000	499	0.498672
10	71550001	71650000	410	0.494556
10	51500001	51600000	211	0.484845
10	10600001	10700000	366	0.475474
10	30200001	30300000	576	0.474045
10	17000001	17100000	169	0.471109
10	17700001	17800000	182	0.445668
10	21450001	21550000	539	0.445662
10	71600001	71700000	332	0.445498
10	14400001	14500000	472	0.440792
10	51750001	51850000	226	0.438242
10	84600001	84700000	548	0.4348
10	11450001	11550000	669	0.433901
10	21500001	21600000	587	0.428556
10	30250001	30350000	409	0.426497
10	17050001	17150000	196	0.420978
10	71650001	71750000	347	0.418871
11	71400001	71500000	127	0.618213
11	71450001	71550000	149	0.594836
11	38350001	38450000	300	0.586098
11	38300001	38400000	311	0.519038
11	71350001	71450000	168	0.500396
11	74800001	74900000	210	0.487061

11	51500001	51600000	850	0.477303
11	15950001	16050000	398	0.475527
11	74850001	74950000	250	0.470998
11	78350001	78450000	435	0.465829
11	51550001	51650000	633	0.454606
11	40150001	40250000	646	0.45335
11	28250001	28350000	530	0.446982
11	28200001	28300000	652	0.44619
11	15900001	16000000	462	0.445968
11	71500001	71600000	271	0.431153
11	78300001	78400000	431	0.430123
11	38900001	39000000	954	0.424223
11	46150001	46250000	796	0.423192
11	63600001	63700000	605	0.421123
12	86650001	86750000	997	0.478447
12	66400001	66500000	558	0.4598
12	54750001	54850000	377	0.444909
12	54800001	54900000	313	0.425735
12	42450001	42550000	1079	0.422544
12	20550001	20650000	629	0.421023
13	40000001	40100000	336	0.708762
13	39950001	40050000	290	0.700227
13	40450001	40550000	484	0.630009
13	62950001	63050000	253	0.627431
13	53300001	53400000	232	0.62659
13	63000001	63100000	221	0.611278
13	53250001	53350000	210	0.590897
13	40400001	40500000	533	0.573429
13	39900001	40000000	331	0.571225
13	56400001	56500000	326	0.543052
13	47550001	47650000	681	0.54296

13	61850001	61950000	568	0.529442
13	40050001	40150000	367	0.525976
13	59800001	59900000	353	0.523048
13	59850001	59950000	387	0.515464
13	56450001	56550000	369	0.493522
13	53350001	53450000	224	0.474684
13	40500001	40600000	552	0.472224
13	48500001	48600000	729	0.470692
13	50300001	50400000	742	0.46629
13	48550001	48650000	735	0.46145
13	47500001	47600000	675	0.448726
13	56800001	56900000	278	0.43584
13	39850001	39950000	424	0.433029
13	49000001	49100000	652	0.431296
13	63050001	63150000	234	0.426695
13	82100001	82200000	885	0.423147
13	4200001	4300000	827	0.422684
14	16500001	16600000	422	0.586957
14	45350001	45450000	384	0.562005
14	16550001	16650000	353	0.551066
14	16600001	16700000	457	0.537989
14	51800001	51900000	455	0.519071
14	25050001	25150000	546	0.517399
14	33700001	33800000	534	0.498435
14	33750001	33850000	501	0.498121
14	25000001	25100000	612	0.497812
14	4700001	4800000	600	0.481913
14	34800001	34900000	701	0.480365
14	45300001	45400000	477	0.477992
14	45400001	45500000	269	0.462047
14	34850001	34950000	744	0.459712

14	40050001	40150000	549	0.458695
14	60100001	60200000	544	0.45207
14	47400001	47500000	494	0.436134
14	60050001	60150000	467	0.427519
14	51850001	51950000	353	0.424821
14	40100001	40200000	495	0.420783
14	16450001	16550000	486	0.4197
15	9250001	9350000	522	0.727523
15	9200001	9300000	682	0.618913
15	33950001	34050000	1223	0.61594
15	34000001	34100000	1465	0.587347
15	1	100000	485	0.530719
15	34050001	34150000	1259	0.526676
15	33900001	34000000	886	0.513541
15	50001	150000	551	0.495379
15	44350001	44450000	341	0.488256
15	44150001	44250000	750	0.479807
15	8550001	8650000	541	0.47293
15	2600001	2700000	915	0.466402
15	39650001	39750000	313	0.4561
15	2550001	2650000	875	0.425336
15	39600001	39700000	322	0.423222
16	35900001	36000000	494	0.65758
16	35850001	35950000	609	0.580046
16	30750001	30850000	936	0.479117
16	47950001	48050000	487	0.458659
16	48950001	49050000	343	0.458301
16	35950001	36050000	415	0.450735
16	45650001	45750000	413	0.450231
16	44050001	44150000	631	0.442285
16	62700001	62800000	787	0.434327

16	33400001	33500000	754	0.432531
16	48900001	49000000	393	0.428993
16	34000001	34100000	760	0.428382
16	78650001	78750000	655	0.425124
16	31800001	31900000	423	0.419863
17	38250001	38350000	965	0.57582
17	38300001	38400000	1116	0.5692
17	10650001	10750000	533	0.496746
17	57400001	57500000	458	0.458051
17	56850001	56950000	1328	0.439872
17	61700001	61800000	751	0.43744
17	61750001	61850000	881	0.435661
17	35950001	36050000	397	0.428211
17	68250001	68350000	710	0.425068
17	56900001	57000000	1015	0.420342
17	37300001	37400000	563	0.419623
18	26950001	27050000	942	0.73442
18	51700001	51800000	850	0.717362
18	55200001	55300000	260	0.706534
18	55250001	55350000	284	0.683531
18	26850001	26950000	828	0.661229
18	27000001	27100000	758	0.601939
18	15950001	16050000	227	0.573349
18	55150001	55250000	286	0.559445
18	15750001	15850000	291	0.544069
18	15700001	15800000	310	0.5389
18	55300001	55400000	380	0.507172
18	15900001	16000000	335	0.50717
18	16000001	16100000	360	0.505515
18	22400001	22500000	499	0.469674
18	51650001	51750000	1724	0.462386

18	2650001	2750000	648	0.453897
18	16050001	16150000	376	0.432965
18	9800001	9900000	1000	0.430924
18	49050001	49150000	259	0.430749
18	54250001	54350000	443	0.426869
18	53650001	53750000	538	0.426667
18	15800001	15900000	422	0.426561
18	2700001	2800000	580	0.426096
18	50950001	51050000	540	0.423204
19	13300001	13400000	682	0.568022
19	13250001	13350000	629	0.55499
19	24650001	24750000	492	0.521611
19	24600001	24700000	416	0.515022
19	24550001	24650000	385	0.485805
19	29400001	29500000	948	0.470781
19	42250001	42350000	323	0.453418
19	26800001	26900000	208	0.446865
19	26100001	26200000	301	0.4308
19	29450001	29550000	900	0.425933
20	51650001	51750000	714	0.688468
20	33650001	33750000	326	0.570153
20	51700001	51800000	978	0.552012
20	51600001	51700000	681	0.5015
20	20150001	20250000	586	0.494027
20	33600001	33700000	444	0.490903
20	3500001	3600000	628	0.465232
20	58400001	58500000	411	0.463965
20	27200001	27300000	585	0.448314
20	8700001	8800000	426	0.443468
20	39650001	39750000	1009	0.432073
20	20100001	20200000	720	0.424726

20	14100001	14200000	219	0.424389
20	6700001	6800000	492	0.421992
20	6750001	6850000	472	0.421874
20	51000001	51100000	1014	0.419276
21	56450001	56550000	500	0.755466
21	41950001	42050000	411	0.718798
21	42000001	42100000	384	0.696673
21	41900001	42000000	357	0.646026
21	42050001	42150000	337	0.553488
21	56400001	56500000	851	0.547327
21	27800001	27900000	566	0.516079
21	42100001	42200000	319	0.512963
21	27750001	27850000	670	0.505655
21	13950001	14050000	1319	0.491884
21	42150001	42250000	314	0.487984
21	56500001	56600000	467	0.469846
22	56450001	56550000	350	0.570003
22	32100001	32200000	548	0.534375
22	37450001	37550000	372	0.529939
22	56500001	56600000	506	0.489359
22	37400001	37500000	490	0.482428
22	58950001	59050000	633	0.474323
22	31500001	31600000	497	0.470174
22	32050001	32150000	467	0.459342
22	10650001	10750000	503	0.457353
22	31550001	31650000	585	0.435802
23	39850001	39950000	396	0.613665
23	1000001	1100000	585	0.554813
23	1050001	1150000	562	0.512253
23	39900001	40000000	321	0.49413
23	950001	1050000	552	0.48574

23	39800001	39900000	474	0.45468
23	28950001	29050000	868	0.424865
24	40050001	40150000	681	0.692871
24	40100001	40200000	720	0.673062
24	62300001	62400000	121	0.629278
24	62000001	62100000	1056	0.58996
24	61950001	62050000	918	0.5576
24	35050001	35150000	469	0.500566
24	62050001	62150000	1320	0.498262
24	62250001	62350000	707	0.49561
24	25150001	25250000	515	0.48601
24	25550001	25650000	632	0.478634
24	34300001	34400000	532	0.466089
24	52450001	52550000	894	0.459487
24	62100001	62200000	1627	0.455016
24	34250001	34350000	584	0.454091
24	62200001	62300000	958	0.447322
24	25100001	25200000	568	0.443371
24	25600001	25700000	824	0.438948
24	62150001	62250000	1173	0.438743
24	20900001	21000000	788	0.430643
25	3650001	3750000	303	0.741326
25	3700001	3800000	362	0.612753
25	7350001	7450000	1251	0.607608
25	7400001	7500000	853	0.605606
25	3600001	3700000	388	0.587201
25	20900001	21000000	1109	0.493057
25	3000001	3100000	259	0.484901
25	34900001	35000000	1018	0.456846
25	20850001	20950000	1000	0.451578
25	2650001	2750000	634	0.451409

25	27150001	27250000	506	0.448493
25	2950001	3050000	278	0.434972
25	34950001	35050000	1313	0.424693
26	34950001	35050000	1558	0.561911
26	48500001	48600000	1587	0.480067
26	48550001	48650000	1761	0.449832
27	30350001	30450000	513	0.584211
27	37300001	37400000	306	0.489205
27	37250001	37350000	572	0.471183
27	5300001	5400000	697	0.467371
27	30300001	30400000	542	0.462985
27	35900001	36000000	955	0.457746
27	10300001	10400000	749	0.456334
27	30200001	30300000	610	0.440377
27	35450001	35550000	799	0.43343
27	37350001	37450000	321	0.43087
27	30150001	30250000	639	0.426603
27	33350001	33450000	819	0.424566
28	24100001	24200000	884	0.450258
28	15550001	15650000	401	0.428947
29	42250001	42350000	3441	0.652658
29	18500001	18600000	1326	0.614238
29	42300001	42400000	2610	0.610435
29	18450001	18550000	1314	0.60166
29	22500001	22600000	1327	0.549723
29	23500001	23600000	1244	0.483373
29	22550001	22650000	1243	0.466908
29	22450001	22550000	1017	0.441907
29	23450001	23550000	1400	0.440652
29	41200001	41300000	251	0.438458

Supplementary Table 10: Results of signature of selection for Gumuz vs Saanen goats (*Fst*)

Chr	Windows		Number of SNPs	Mean Fst
	Start	End		
1	49550001	49650000	911	0.711785
1	49500001	49600000	635	0.656418
1	81250001	81350000	543	0.633435
1	81200001	81300000	368	0.595296
1	73050001	73150000	210	0.590967
1	64100001	64200000	667	0.587528
1	10250001	10350000	1035	0.581391
1	102650001	102750000	1428	0.574854
1	64150001	64250000	688	0.571812
1	149200001	149300000	398	0.56567
1	49600001	49700000	900	0.564371
1	102600001	102700000	1287	0.558585
1	112450001	112550000	781	0.555231
1	82500001	82600000	335	0.553643
1	44800001	44900000	628	0.533051
1	137100001	137200000	1307	0.522516
1	17650001	17750000	532	0.521711
1	83700001	83800000	254	0.520273
1	92350001	92450000	757	0.516104
1	92300001	92400000	778	0.515299
1	81300001	81400000	572	0.512413
1	30550001	30650000	1150	0.503283
1	43700001	43800000	490	0.501436
1	73900001	74000000	834	0.491537
1	129700001	129800000	567	0.489391
1	82450001	82550000	364	0.488734
1	107000001	107100000	621	0.486451
1	46450001	46550000	912	0.485964

1	44850001	44950000	365	0.485642
1	9700001	9800000	1347	0.484179
1	81150001	81250000	522	0.483311
1	17600001	17700000	689	0.482706
1	149250001	149350000	542	0.481786
1	9750001	9850000	1359	0.481554
1	23950001	24050000	863	0.480245
2	21350001	21450000	538	0.736668
2	21300001	21400000	863	0.665559
2	16100001	16200000	428	0.662284
2	21200001	21300000	569	0.638748
2	16050001	16150000	311	0.63816
2	21250001	21350000	862	0.624608
2	21400001	21500000	398	0.616741
2	129950001	130050000	484	0.573163
2	31250001	31350000	603	0.545365
2	16150001	16250000	420	0.52464
2	21000001	21100000	527	0.50956
2	32250001	32350000	634	0.503326
2	83650001	83750000	397	0.492329
2	76350001	76450000	688	0.483716
2	25200001	25300000	434	0.482102
3	68750001	68850000	376	0.651084
3	68700001	68800000	320	0.645963
3	70500001	70600000	342	0.610772
3	70550001	70650000	337	0.605552
3	33450001	33550000	594	0.602314
3	103600001	103700000	253	0.576438
3	31150001	31250000	377	0.563438
3	96200001	96300000	627	0.560789
3	96250001	96350000	585	0.553003

3	119600001	119700000	550	0.549898
3	101200001	101300000	420	0.545771
3	36550001	36650000	381	0.532825
3	119850001	119950000	736	0.531957
3	103550001	103650000	277	0.53175
3	70450001	70550000	298	0.531073
3	33400001	33500000	634	0.528543
3	30950001	31050000	648	0.525963
3	16800001	16900000	381	0.520801
3	119900001	120000000	842	0.512261
3	103650001	103750000	245	0.511614
3	40450001	40550000	429	0.509654
3	31100001	31200000	381	0.496091
3	33500001	33600000	386	0.488848
4	120550001	120650000	1185	0.683281
4	120600001	120700000	1123	0.6823
4	62750001	62850000	545	0.618764
4	87650001	87750000	1643	0.595405
4	89250001	89350000	372	0.591196
4	87600001	87700000	1123	0.580478
4	98650001	98750000	1601	0.58004
4	300001	400000	662	0.572592
4	87700001	87800000	1963	0.561127
4	14900001	15000000	953	0.555981
4	13600001	13700000	1242	0.547625
4	87550001	87650000	1389	0.536736
4	89200001	89300000	268	0.534107
4	120650001	120750000	950	0.533738
4	101550001	101650000	742	0.532993
4	75250001	75350000	525	0.52828
4	62700001	62800000	410	0.527229

4	75300001	75400000	666	0.525629
4	41800001	41900000	357	0.523144
4	26400001	26500000	266	0.509543
4	13650001	13750000	1279	0.503465
4	26000001	26100000	325	0.501793
4	40650001	40750000	647	0.498932
4	115500001	115600000	1597	0.498421
4	14850001	14950000	1471	0.498114
4	95700001	95800000	699	0.496803
4	72850001	72950000	409	0.496523
4	72800001	72900000	443	0.495805
4	26600001	26700000	371	0.493696
4	98600001	98700000	1203	0.493275
4	48200001	48300000	439	0.490932
4	72900001	73000000	434	0.490195
4	4100001	4200000	1281	0.482944
5	18050001	18150000	945	0.832155
5	18100001	18200000	1172	0.728562
5	18000001	18100000	1084	0.631864
5	7150001	7250000	950	0.621098
5	7100001	7200000	1108	0.604408
5	98900001	99000000	1767	0.603767
5	99000001	99100000	125	0.603089
5	98950001	99050000	549	0.589672
5	26300001	26400000	202	0.585352
5	31450001	31550000	714	0.58296
5	46950001	47050000	334	0.582242
5	98700001	98800000	808	0.578133
5	59800001	59900000	477	0.577457
5	48000001	48100000	497	0.576038
5	100750001	100850000	3292	0.575814

5	26350001	26450000	146	0.574412
5	26700001	26800000	429	0.574211
5	100800001	100900000	2993	0.562202
5	46900001	47000000	203	0.556675
5	1050001	1150000	406	0.554152
5	98650001	98750000	1119	0.548297
5	48050001	48150000	505	0.546237
5	26650001	26750000	486	0.538216
5	59850001	59950000	488	0.529635
5	46200001	46300000	714	0.523588
5	47000001	47100000	366	0.519177
5	46250001	46350000	935	0.507755
5	18150001	18250000	1449	0.500966
5	17750001	17850000	790	0.487187
5	31500001	31600000	628	0.484611
6	45600001	45700000	801	0.600131
6	34150001	34250000	952	0.582438
6	25750001	25850000	1757	0.551348
6	101050001	101150000	794	0.548819
6	77600001	77700000	843	0.542024
6	77650001	77750000	723	0.531405
6	55350001	55450000	880	0.526085
6	25700001	25800000	2086	0.525527
6	116300001	116400000	470	0.515934
6	21850001	21950000	898	0.511501
6	37950001	38050000	339	0.510619
6	69500001	69600000	259	0.507124
6	71150001	71250000	489	0.506525
6	21900001	22000000	993	0.504037
6	20300001	20400000	502	0.502653
6	49350001	49450000	1012	0.50234

6	45550001	45650000	1043	0.502194
6	69450001	69550000	303	0.501566
6	71200001	71300000	566	0.499072
6	71050001	71150000	593	0.49455
6	39050001	39150000	701	0.489641
6	28900001	29000000	735	0.482705
6	91150001	91250000	751	0.48184
6	51750001	51850000	1341	0.480645
7	66850001	66950000	156	0.768531
7	66900001	67000000	138	0.750161
7	66750001	66850000	83	0.68559
7	600001	700000	611	0.677004
7	66700001	66800000	101	0.673643
7	66800001	66900000	131	0.67098
7	66600001	66700000	156	0.660972
7	66550001	66650000	177	0.655344
7	17500001	17600000	304	0.654537
7	650001	750000	614	0.624767
7	72950001	73050000	840	0.623214
7	66650001	66750000	150	0.606913
7	73000001	73100000	999	0.593477
7	99950001	100050000	2395	0.586768
7	99900001	100000000	3444	0.574513
7	66500001	66600000	175	0.569067
7	550001	650000	576	0.543646
7	12450001	12550000	285	0.542451
7	17550001	17650000	343	0.54002
7	67100001	67200000	184	0.539964
7	22350001	22450000	336	0.539584
7	17450001	17550000	261	0.536163
7	72550001	72650000	341	0.518734

7	90950001	91050000	502	0.517792
7	60650001	60750000	159	0.517617
7	67150001	67250000	229	0.514495
7	22400001	22500000	390	0.50527
7	50250001	50350000	450	0.500989
7	98950001	99050000	1645	0.499464
7	72600001	72700000	332	0.498896
7	22300001	22400000	300	0.494248
7	51350001	51450000	973	0.492562
7	99850001	99950000	3319	0.488026
7	12500001	12600000	354	0.486902
7	56150001	56250000	167	0.481779
8	74550001	74650000	771	0.601976
8	30250001	30350000	373	0.598587
8	21800001	21900000	864	0.550764
8	106000001	106100000	1024	0.548656
8	74500001	74600000	691	0.546395
8	21850001	21950000	646	0.542333
8	43450001	43550000	394	0.53396
8	63050001	63150000	474	0.521399
8	30200001	30300000	475	0.519329
8	74600001	74700000	681	0.51842
8	43350001	43450000	516	0.507454
8	63100001	63200000	570	0.504176
8	68250001	68350000	978	0.498325
8	51550001	51650000	1158	0.494902
8	68300001	68400000	907	0.491511
8	43400001	43500000	357	0.488326
8	68950001	69050000	254	0.48265
8	2750001	2850000	1001	0.48252
9	77350001	77450000	1113	0.597333

9	77300001	77400000	909	0.558187
9	88050001	88150000	815	0.552524
9	88100001	88200000	765	0.538906
9	31500001	31600000	257	0.518655
9	27550001	27650000	626	0.513579
9	49000001	49100000	456	0.498699
9	22600001	22700000	1073	0.498587
9	31450001	31550000	365	0.489643
9	24900001	25000000	1025	0.486836
9	47000001	47100000	489	0.486148
9	47050001	47150000	603	0.486029
9	81550001	81650000	944	0.480584
10	20950001	21050000	232	0.61146
10	71650001	71750000	346	0.551106
10	78750001	78850000	1372	0.54557
10	11450001	11550000	549	0.545494
10	11500001	11600000	780	0.541327
10	44800001	44900000	468	0.53987
10	54850001	54950000	1019	0.507111
10	11550001	11650000	746	0.503419
10	78800001	78900000	927	0.501247
10	51900001	52000000	470	0.499403
10	46350001	46450000	545	0.480589
10	10600001	10700000	286	0.479982
11	70700001	70800000	461	0.599719
11	69350001	69450000	686	0.596489
11	71400001	71500000	140	0.595211
11	69500001	69600000	451	0.581806
11	69400001	69500000	759	0.570356
11	84450001	84550000	839	0.561922
11	71450001	71550000	179	0.559242

11	69450001	69550000	570	0.551085
11	69550001	69650000	427	0.544023
11	105650001	105750000	589	0.533277
11	70650001	70750000	294	0.52895
11	84400001	84500000	775	0.528153
11	70750001	70850000	499	0.526579
11	71350001	71450000	177	0.522305
11	15900001	16000000	449	0.512198
11	47150001	47250000	477	0.501503
11	65000001	65100000	420	0.500061
11	28700001	28800000	375	0.494031
11	65050001	65150000	401	0.493227
11	28750001	28850000	456	0.489118
11	72550001	72650000	497	0.481447
12	66400001	66500000	429	0.55843
12	86650001	86750000	1009	0.514218
12	15900001	16000000	5577	0.511718
13	61700001	61800000	749	0.728239
13	62550001	62650000	215	0.698717
13	40400001	40500000	465	0.697272
13	61750001	61850000	1012	0.690088
13	39950001	40050000	254	0.659181
13	40450001	40550000	384	0.656513
13	62600001	62700000	225	0.644007
13	60750001	60850000	424	0.643004
13	40000001	40100000	312	0.641517
13	53300001	53400000	189	0.615713
13	39900001	40000000	280	0.59658
13	37900001	38000000	413	0.58838
13	56400001	56500000	280	0.576859
13	53250001	53350000	214	0.571778

13	56450001	56550000	332	0.565791
13	40350001	40450000	467	0.556231
13	37950001	38050000	462	0.555686
13	39850001	39950000	356	0.554215
13	60500001	60600000	289	0.522304
13	60800001	60900000	516	0.518694
13	60550001	60650000	354	0.51311
13	47550001	47650000	632	0.511005
13	58000001	58100000	406	0.498907
13	62500001	62600000	348	0.498301
13	40050001	40150000	336	0.493132
13	62800001	62900000	495	0.492961
13	41950001	42050000	418	0.492675
13	61800001	61900000	842	0.486123
14	16500001	16600000	277	0.733251
14	90250001	90350000	1298	0.713889
14	16600001	16700000	375	0.657293
14	90300001	90400000	1527	0.64906
14	33750001	33850000	436	0.646324
14	33700001	33800000	471	0.638161
14	16550001	16650000	248	0.612798
14	51800001	51900000	444	0.549584
14	88700001	88800000	660	0.533298
14	60050001	60150000	452	0.524027
14	54000001	54100000	575	0.523211
14	25050001	25150000	471	0.52132
14	25000001	25100000	560	0.51617
14	16450001	16550000	390	0.499554
14	53950001	54050000	469	0.496555
14	88750001	88850000	575	0.496069
14	90200001	90300000	697	0.488633

14	60100001	60200000	520	0.486355
15	9250001	9350000	505	0.652484
15	34000001	34100000	1491	0.563776
15	33950001	34050000	1236	0.553867
15	8550001	8650000	464	0.551423
15	9200001	9300000	673	0.551043
15	39650001	39750000	295	0.547312
15	39600001	39700000	308	0.526019
15	2550001	2650000	766	0.511573
15	44350001	44450000	380	0.510867
15	2600001	2700000	893	0.49995
15	39700001	39800000	386	0.496196
15	34050001	34150000	1302	0.495382
15	1	100000	481	0.491019
15	44300001	44400000	498	0.485643
15	76900001	77000000	582	0.484122
15	2500001	2600000	579	0.483453
16	35900001	36000000	539	0.600865
16	48900001	49000000	333	0.575944
16	62200001	62300000	798	0.573444
16	48950001	49050000	305	0.567316
16	55500001	55600000	633	0.565086
16	17800001	17900000	858	0.562379
16	31250001	31350000	711	0.556602
16	62250001	62350000	912	0.555562
16	17850001	17950000	858	0.544018
16	47950001	48050000	399	0.51601
16	31300001	31400000	907	0.503173
16	4600001	4700000	1198	0.496687
16	35950001	36050000	385	0.493167
17	37350001	37450000	376	0.691593

17	37300001	37400000	514	0.58643
17	37400001	37500000	430	0.529312
17	68250001	68350000	703	0.527323
17	57400001	57500000	404	0.509254
17	10650001	10750000	493	0.504985
17	15800001	15900000	368	0.500581
18	26950001	27050000	918	0.803463
18	26200001	26300000	177	0.788197
18	26150001	26250000	205	0.779725
18	26900001	27000000	1012	0.771701
18	27000001	27100000	685	0.707056
18	26850001	26950000	806	0.676412
18	15900001	16000000	218	0.659397
18	16000001	16100000	320	0.65332
18	22350001	22450000	584	0.646176
18	22400001	22500000	461	0.642737
18	26250001	26350000	293	0.635691
18	36900001	37000000	140	0.63297
18	36950001	37050000	156	0.632578
18	36700001	36800000	147	0.60831
18	2000001	2100000	1261	0.603613
18	16050001	16150000	305	0.593156
18	15950001	16050000	222	0.586904
18	36750001	36850000	160	0.57508
18	7900001	8000000	474	0.571337
18	36850001	36950000	144	0.565851
18	36800001	36900000	163	0.565087
18	37000001	37100000	272	0.560381
18	37050001	37150000	368	0.558659
18	15850001	15950000	345	0.54062
18	36650001	36750000	129	0.540164

18	26300001	26400000	394	0.532888
18	26450001	26550000	298	0.5269
18	13100001	13200000	408	0.519655
18	2050001	2150000	1227	0.517757
18	8050001	8150000	732	0.508213
18	50850001	50950000	346	0.497989
18	22300001	22400000	629	0.488519
18	58650001	58750000	990	0.485914
18	14750001	14850000	398	0.482282
18	13150001	13250000	464	0.480803
19	29400001	29500000	693	0.722302
19	34300001	34400000	191	0.673939
19	29350001	29450000	597	0.664919
19	29450001	29550000	652	0.630485
19	13250001	13350000	625	0.618677
19	13300001	13400000	660	0.614754
19	40050001	40150000	314	0.566758
19	22950001	23050000	289	0.527713
19	18400001	18500000	253	0.522362
19	34350001	34450000	294	0.509932
19	34250001	34350000	277	0.508189
19	26800001	26900000	200	0.493587
19	33750001	33850000	275	0.48734
19	26850001	26950000	170	0.480678
20	51650001	51750000	795	0.682583
20	51600001	51700000	550	0.613362
20	6800001	6900000	647	0.588294
20	6750001	6850000	403	0.577491
20	38500001	38600000	710	0.548903
20	20150001	20250000	616	0.53607
20	14400001	14500000	361	0.534031

20	51700001	51800000	947	0.520075
20	34400001	34500000	1210	0.51741
20	34450001	34550000	1145	0.516972
20	38550001	38650000	708	0.5101
20	6700001	6800000	470	0.498522
20	16800001	16900000	667	0.480725
21	56450001	56550000	551	0.756954
21	41950001	42050000	455	0.57766
21	56400001	56500000	845	0.566214
21	48500001	48600000	642	0.556616
21	41900001	42000000	415	0.525227
21	21050001	21150000	374	0.523638
21	42000001	42100000	412	0.520279
21	47550001	47650000	978	0.518727
21	27750001	27850000	653	0.518334
21	34850001	34950000	580	0.507563
21	27800001	27900000	593	0.50066
21	66500001	66600000	489	0.49147
21	66450001	66550000	732	0.487092
22	31550001	31650000	469	0.742939
22	31500001	31600000	457	0.668463
22	31600001	31700000	375	0.597051
22	37450001	37550000	381	0.564929
22	37500001	37600000	321	0.558396
22	32100001	32200000	487	0.546826
22	31450001	31550000	347	0.543731
22	59050001	59150000	694	0.53245
22	37400001	37500000	492	0.515775
22	36650001	36750000	327	0.507463
22	32050001	32150000	477	0.490043
22	26550001	26650000	689	0.482511

23	36800001	36900000	506	0.565396
23	36850001	36950000	404	0.550349
23	39850001	39950000	433	0.525516
23	41000001	41100000	390	0.520356
23	1000001	1100000	641	0.479953
24	25150001	25250000	435	0.723151
24	25100001	25200000	471	0.702786
24	40050001	40150000	741	0.590396
24	62300001	62400000	114	0.584033
24	40100001	40200000	784	0.572455
24	25200001	25300000	482	0.556496
24	25250001	25350000	450	0.519043
24	20900001	21000000	740	0.514635
24	25300001	25400000	403	0.513707
24	1300001	1400000	368	0.496498
24	34250001	34350000	590	0.495995
24	62000001	62100000	1137	0.490514
24	61950001	62050000	989	0.489907
24	20550001	20650000	794	0.486549
24	34300001	34400000	550	0.481433
25	3650001	3750000	242	0.82954
25	3700001	3800000	280	0.724391
25	7400001	7500000	811	0.707523
25	20900001	21000000	1005	0.704282
25	7350001	7450000	1152	0.695493
25	3600001	3700000	310	0.695291
25	20950001	21050000	686	0.631082
25	20850001	20950000	961	0.59562
25	21200001	21300000	302	0.580294
25	3750001	3850000	269	0.534868
25	30850001	30950000	402	0.533337

25	3400001	3500000	252	0.520599
25	21150001	21250000	349	0.501762
25	3550001	3650000	326	0.496204
25	17950001	18050000	534	0.489248
25	37550001	37650000	1159	0.488915
25	30800001	30900000	403	0.483561
26	34950001	35050000	1338	0.703367
26	51250001	51350000	581	0.58197
26	51200001	51300000	593	0.572073
26	30350001	30450000	343	0.566675
26	30400001	30500000	444	0.551879
26	41250001	41350000	741	0.540772
26	41200001	41300000	975	0.537324
26	34900001	35000000	1470	0.530412
26	30500001	30600000	232	0.501659
26	48550001	48650000	1678	0.499423
26	22050001	22150000	1094	0.498941
26	35000001	35100000	1542	0.491539
27	25800001	25900000	730	0.524465
27	25750001	25850000	471	0.517317
28	19100001	19200000	617	0.549681
28	19050001	19150000	410	0.509494
28	41200001	41300000	422	0.494446
29	18500001	18600000	1271	0.710421
29	18450001	18550000	1262	0.69231
29	46600001	46700000	280	0.596154
29	48100001	48200000	567	0.58338
29	48050001	48150000	544	0.577306
29	31850001	31950000	576	0.507042
29	29600001	29700000	494	0.486226

Supplementary Table 11: Enriched functional term clusters and their enrichment scores following *DAVID* analysis for genes identified in Ethiopian indigenous goats

Population	ID	Term	P value	Associated genes
Fellata	GO:0044271	cellular nitrogen compound biosynthetic process	0.00052	*ATP5F1D*, *CREBBP*, *FANCA*, *GMDS*, *KIT*, *POLR2E*, *RAF1*, *TRAP1*, *ABLIM2*, *ADK*, *ADGRG3*, *C5AR1*, *PRKAA1*, *RPL37*, *SBNO2*, *TADA2A*, *ZGPA*
	GO:0043170	macromolecule metabolic process	0.0013	*XRN2*, *ADAM10*, *BBC3*, *CREBBP*, *FANCA*, *KIT*, *QKI*, *POLR2E*, *RAF1*, *SAE1*, *TRAP1*, *ABLIM2*, *ADGRG3*, *C5AR1*, *C7*, *CDK10*, *FLT1*, *MGRN1*, *NUDT16L1*, *PAN3*, *PFDN1*, *PRKAA1*, *RTEL1*, *RPL37*, *STK11*, *SRMS*, *SBNO2*, *TADA2A*, *ZGPAT*
	GO:0019538	protein metabolic process	0.0024	*ADAM10*, *BBC3*, *CREBBP*, *KIT*, *RAF1*, *SAE1*, *TRAP1*, *C5AR1*, *C7*, *CDK10*, *FLT1*, *MGRN1*, *PFDN1*, *PRKAA1*, *RPL37*, *STK11*, *SRMS*, *TADA2A*
	GO:0044249	cellular biosynthetic process	0.0026	*ATP5F1D*, *CREBBP*, *FANCA*, *GMDS*, *KIT*, *QKI*, *POLR2E*, *RAF1*, *TRAP1*, *ABLIM2*, *ADK*, *ADGRG3*, *C5AR1*, *PRKAA1*, *RTEL1*, *RPL37*, *SBNO2*, *TADA2A*, *ZGPAT*
	GO:0010467	gene expression	0.0028	*ADAM10*, *CREBBP*, *FANCA*, *KIT*, *QKI*, *POLR2E*, *RAF1*, *TRAP1*, *ABLIM2*, *ADGRG3*, *C5AR1*, *PAN3*, *PRKAA1*, *RPL37*, *SBNO2*, *TADA2A*, *ZGPAT*
Gumuz	GO:0030316	osteoclast differentiation	0.0026	*TCIRG1*, *EFNA2*, *FSTL3*, *MITF*, *SBNO2*
	GO:0000280	nuclear division	0.0035	*DIS3L2*, *FANCA*, *AAAS*, *CHMP1A*, *DMRT1*, *FOXJ3*, *KATNB1*, *MISP*, *SMPD3*
	GO:0097186	amelogenesis	0.0051	*TCIRG1*, *WDR72*, *SLC24A4*
	GO:0042476	odontogenesis	0.0053	*TCIRG1*, *WDR72*, *DMRT3*, *SLC24A4*, *SMPD3*
	GO:0022414	reproductive process	0.0054	*DAZAP1*, *FANCA*, *KITLG*, *ADGRG1*, *AAAS*, *AMHR2*, *CREB3L4*, *DMRT1*, *DMRT3*, *FOXJ3*, *GAMT*, *NPPC*, *PCSK4*, *PRMT7*, *SPINK1*, *STK11*