

The indigenous farm genetic resources of Somalia: Preliminary phenotypic and genotypic characterization of cattle, sheep and goats



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The indigenous farm genetic resources of Somalia: Preliminary phenotypic and genotypic characterization of cattle, sheep and goats

Anne Muigai¹, George Matete¹, Hussein Haji Aden¹, Miika Tapio², Okeyo Mwai³ and Karen Marshall³

1. Jomo Kenyatta University of Agriculture

2. Natural Resources Institute, Finland

3. International Livestock Research Institute

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Box 30709, Nairobi 00100, Kenya
Phone: + 254 20 422 3000
Fax: +254 20 422 3001
Email: ILRI-Kenya@cgiar.org

Box 5689, Addis Ababa, Ethiopia
Phone: +251 11 617 2000
Fax: +251 11 617 2001
Email: ILRI-Ethiopia@cgiar.org

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Abbreviations

ADB	African Development Bank
AU	African Union
DAGRIS	Domestic Animal Genetic Information System
EDTA	Ethylenediaminetetraacetic acid
EU	European Union
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization Statistics platform
IGAD	Intergovernmental Authority on Development
ILRI	International Livestock Research Institute
ISAG	International Society for Animal Genetics
PCR	Polymerase chain reaction
WB	World Bank

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Executive summary

This study was conducted in 2008 as a collaborative project between the International Livestock Research Institute and Terra Nuova with the main objective of evaluating the Somali breeds of livestock both phenotypically and genetically. The Somali people are mainly pastoralists and livestock of Somalia play an important role in the economy of the country contributing over 40% and 80% of the it's foreign exchange earnings (Knips 2004; FAO 2012; FAO-Somalia 2015).

The study focuses on all major livestock breeds found in Somalia namely the Somali Boran, Dauara, Gasara, Surqo and the North Somali Zebu cattle breeds, the Somali Blackhead sheep and the Somali Long-eared and Somali Short-eared goat breeds. Livestock keeping households (numbering 277, and from six administrative districts located in northern, central and southern Somalia) keeping the different breeds were interviewed on a number of issues related to livestock keeping, representatives of selected breeds (26 to 52 animals per breed) were characterized morphometrically through measurement of five traits (heart girth, body length, height at withers, rump height and pin bone width), and the breeds were genetically characterized by analysis of autosomal, Y-chromosomal and mitochondrial markers (40 animals per breed, but excluding the North Somali Zebu cattle where DNA sampling was not allowed).

All the livestock producers involved in the study practised a pastoral livestock production system. The primary reasons for keeping livestock were as a source of food and cash, whilst a secondary reason was cultural. It was also noted that while the numbers of cattle kept were relatively small with 75% of the producers owning less than 30 head, the sheep and goat flock sizes were much larger with 50% of the producers owning more than 100 head. The largest herd/flock sizes were mainly observed in the nomadic pastoral areas. The main feed source for the livestock was natural pasture. However about 30% of the producers indicated they purchased supplementary fodder. The producers had various options available to obtain breeding stock including obtaining animals from their relatives, neighbours, friends and a few purchased the animals from traders and markets.

In terms of basic morphometric characterization of the cattle breeds, the Boran breed had significantly larger heart girth and height at wither measurements compared to the Dauara and North Somali Zebu breeds while the pin bone width measurements of the Boran and North Somali Zebu were larger than the Dauara breed. However, there were no significant differences between the body length measurements of the Boran, Dauara and North Somali Zebu breeds. For the goats, the Long-eared goats were found to be longer, higher at withers and rump and with a wider pin bone than the Short-eared goats. The two breeds however had similar heart girth measurements.

The genetic diversity for the Somali livestock was determined through calculation of observed heterozygosities using 15 microsatellite markers for each of the cattle, sheep and goat breeds. The average heterozygosities for the cattle, goat and sheep were high with averages of 0.75, 0.63, and 0.74 respectively. The genetic differentiation among the sampled populations was also examined, via calculation of fixation indices (F_{ST}). The mean genetic differentiation of the Somali cattle was moderate with F_{ST} value of 0.07, while that for goat was low with F_{ST} of 0.01. Low F_{ST} values of 0.025 were observed between the Somali Boran and the Kenyan Boran suggesting common recent ancestry. Principal component analysis of the microsatellite allele frequencies indicate close clustering of the two Somali goat breeds which may therefore also share a common recent ancestry. Overall, the genetic characterization of the breeds showed that the breeds contain a wide genetic base with no inbreeding issues.

I. Introduction

Somalia, located in the horn of Africa, is one of the poorest countries of the world and is experiencing an adverse climate and chronic food shortages (FAO-Somalia 2015). Despite the conflict and instability that has been witnessed in Somalia over the past two decades, the livestock sector has continued to be the main economic activity, accounting for over 40% of the GDP and over 80% of the foreign exchange earnings (FAO 2012). The sector directly engages approximately 65% of the population with livestock sales directly contributing to household incomes (FAO-Somalia 2015).

The main livestock of Somalia comprise cattle, camels, sheep and goats (Rege and Tawah 1999). These livestock have multipurpose uses and are well adapted to the environmental conditions experienced in the region. The indigenous breeds can withstand long periods of drought and are able to survive on low quality feeds.

Given the importance of livestock to the livelihood of Somali pastoralists and the current lack of information on Somali livestock this work is aimed to provide a basic characterization of Somali livestock from both phenotypic and genotypic viewpoints.

2. Background

2.1 Country background

Somalia is located in the horn of Africa and covers approximately 637,660 square kilometres (FAOSTAT 2012). In 2010, it had a human population of 6.9 million with approximately 63% of the people located in rural areas (FAOSTAT 2012). The people of Somalia are mainly livestock keepers and up to 65% of the population are engaged in the livestock sector (FAO-Somalia 2015). The importance of livestock to the people of Somalia can be explained by the terrain of which 99.9% is arid and 0.1% as semi-arid (Figure 1). In 2011, 68.5% of the land was under permanent pasture, while forests occupied 10.6% of the land (Figure 2) (FAOSTAT 2012). Pastures are mainly found in the highland plateaus located in northwest Somalia and grasslands are located in southern Somalia (ADB 2010). Although 1.1 million km² (1.8%) of the land is arable, very little of this land is under permanent crops (FAOSTAT 2012).

Most of the country records between 100 and 200 mm of rain annually, although the highland areas reports between 500-600 mm of rainfall annually (FAO/WB/EU 2004). Like most of the greater eastern Africa which experiences the convergence of the northern and southern Inter-Tropical Convergence Zone (ITCZ), Somalia experiences two main rainy seasons, with the longer rains experienced between April and June and a shorter period between October and November. Northern Somalia is generally cooler and with mean monthly temperatures between 15–25°C compared to 25–35°C in the south (FAO/WB/EU 2004).

Figure 1: Agro ecological zones in the Horn of Africa, including Somalia (Knips 2004).

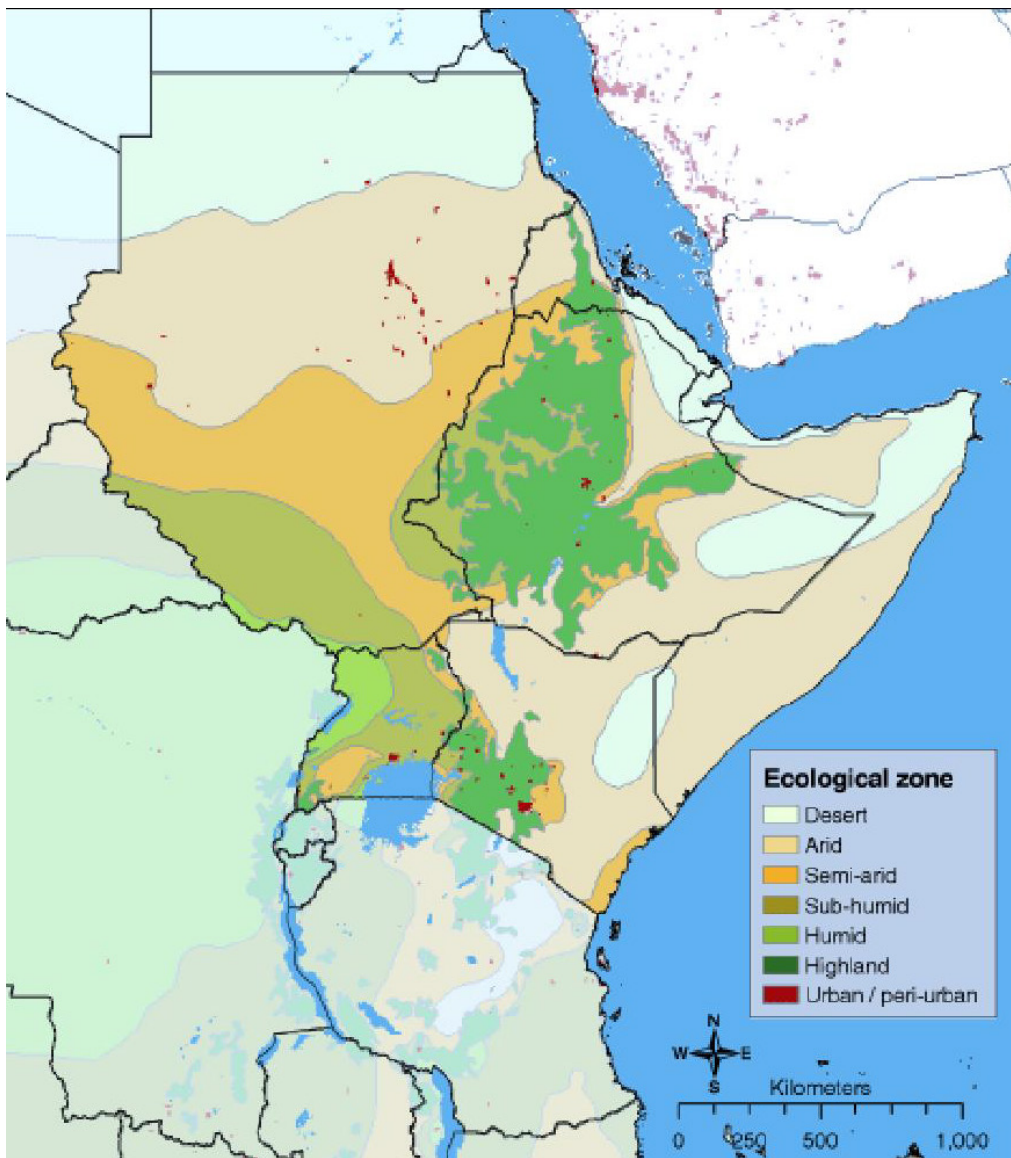
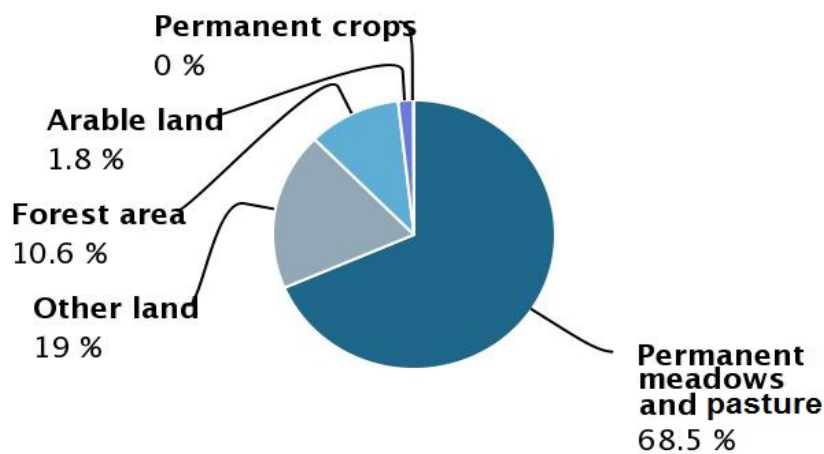


Figure 2: Land use in Somalia (FAOSTAT 2012).



2.2 Livestock production systems

There are two main types of production systems found in Somalia namely pastoral and agro-pastoral (Knips 2004; ADB 2010). The main livestock comprise camel, cattle, sheep and goats, with numbers of livestock estimated at 7.1 million for camel, 4.9 million for cattle, 12.3 million for sheep, and 11.6 million for goat (FAOSTAT 2012). The pastoral and agro-pastoral production systems are found throughout the country, but with a higher concentration of pastoralists in the north and central areas, and a mix of pastoralists and agro-pastoralists in the southern areas. Seasonal migration of pastoralists and their animals in search of pasture and water is common. Generally the productivity of livestock in Somalia is low but it can be improved with improved management practices (Knips 2004, ADB 2010).

2.3 Livestock marketing

Livestock are Somalia's main export earner (FAO-Somalia 2015). Despite challenges such as political instability and bans in past years imposed by the Gulf States to prevent the spread of the Rift Valley Fever, the number of live animals and meat exports have continued to grow steadily thereby directly impacting the economy and the livelihoods of farmers in rural areas (FAO-Somalia 2015). Estimates made in 2011 valued the trade in Somaliland alone, which mainly consists of exports of sheep and goats, at more than USD 200 million per annum (SLCCIA 2013). The sheep and goats are mainly exported through the port of Berbera to the Middle East with the Kingdom of Saudi Arabia taking up 70% of the exports (FAO/WB/EU 2004; Nisar 2010). In addition to exports, trading of small ruminants within domestic markets plays an important role of providing employment of the local population especially women who are directly involved in selling of meat and milk (Marshall et al. 2014; Wanyoike et al. 2014).

2.4 Indigenous animal genetic resources of Somalia

The indigenous genetic resources of Somalia comprise a wide range of livestock species including cattle, camels, sheep and goats, each with a few recognized breeds. The Somali livestock keepers graze their animal within geographical Somalia and in Djibouti, Ethiopia and Kenya.

Cattle breeds

The cattle of Somalia are mainly the East African Zebu type of which the following types are recognized, the Somali Boran (Figure 3a), Gasara (Figure 3b), Dauara (Figure 3c) and Surqo (Figure 3d) (Rege and Tawah 1999; Nur 2005).

The Somali Boran are believed to be a descendant of the first introduction of zebu into Africa from West Asia and are thought to have evolved following the migration of Ethiopian cattle into Somalia and Jubaland along the Somalia-Ethiopia border (Rege and Tawah 1999). The Surqo breed is a zenga breed (Rege and Tawah 1999; Nur 2005). The zenga breeds are breeds that resulted from zebu-sanga crosses that came about following the introduction of zebu cattle into Africa from Asia. The Surqo breed is a crossbred of the Boran of Somalia or Ethiopia with an unknown sanga population (Rege and Tawah 1999). Details on the breed characteristics and distribution of each breed are indicated in Table 1.

Sheep breeds

The Somali Blackhead (Figure 3f), is the predominant type of sheep in Somalia. It is of note that this breed was the founder for the Blackhead Persian breed (an improved type found in South Africa; Wilson 1991), and further that the Dorper breed (found in southern and eastern Africa) resulted from a cross of the Blackhead Persian breed with the Dorset Horn breed.

Goat breeds

The main types of goats found in Somalia, are the Long-eared Somali goat (Figure 3g), the Short-eared Somali goat (Figure 3h), and, to a lesser extent, the Somali Arab goat. The Somali Long-eared goat is thought to be a descendent of the Somali Arab goats, which were introduced from Arabia (FARM-Africa 1996). The Somali Arab goat, as the name implies, was introduced into Africa by Arabian traders (Epstein 1971).

Table 1: The livestock breeds of Somalia: classification, distribution and breed characteristics*

Species	Breed name (Local names where available are indicated in brackets)	Classification	Distribution within Somalia	Main characteristics
Cattle	Somali Boran	Large East African Zebu	Gedo, Lower Jubba, Middle Juba, North-western Somalia, eastern Somalia Districts	<p>It is a large animal with a typical mature height at withers of 117–147 cm and 114–127 cm for adult males and females respectively and mature weights of 500–850 kg and 380–450 kg for adult male and females respectively.</p> <p>The coat colour is predominantly white with black points and can also be pigmented. Small horns may be present but a portion of the population is naturally polled. The hump is present and well developed. The neck is short, hump is musculo-fatty and is thoracic in position, the topline rises to the hind quarters and is wide and well-muscled, the upper thigh can be thick and rounded, the tail is long and set on low, dewlap and sheath are well developed.</p>
Cattle	Gasara (Mudugh, Nogal, Mjiertein Abgal, Aria)	Small East African Zebu, Sub-group Somali Short-horned Zebu	Central and northern Somalia	<p>It is a small animal, maximum weight of between 250 and 300 kg, the coat colour is lead-grey, dark grey, dark red, pied or fawn with a white face, horns are short and thin but polled animals have also been reported, the hump is very pronounced and the dewlap and sheath are less developed.</p>
Cattle	Dauara (Dawara, Garre)	Small East African Zebu, sub-group Somali short-horned Zebu	The breed is kept by the Garre or Ghera tribe who inhabit the middle and upper Webi Shabelle area of southern Somalia.	<p>The animals are small with a maximum weight of between 280–320 kg, the coat colour is red or sandy red sometimes with patches of black, the hump is small, the horns are short and thin and they can be loose or absent, the back slopes sharply upwards raising the rump higher than the withers.</p>
Cattle	North Somali Zebu	Small East African Zebu, sub-group Somali Short-horned Zebu. The breed is further divided into two strains the western and eastern North Somali Zebu	<p>The western North Somali Zebu is found in north Somalia from the Borama Hargesia area of the north-west province of Somalia bordering Jijiga on the Ethiopian border.</p> <p>The eastern strain is found in the Burao area on the eastern side of north-east province of Somalia.</p>	<p>The western strain is variable in size and colour with majority of the animals being roan and spotted. They have a small hump and lyre-shaped horns. The eastern strains are less variable morphologically, are smaller and are spread in small and isolated pockets.</p>

Table 1: The livestock breeds of Somalia: classification, distribution and breed characteristics*

Species	Breed name (Local names where available are indicated in brackets)	Classification	Distribution within Somalia	Main characteristics
Cattle	Surqo (Tuni, Surco, Macien, Serenele, Serenli)	Zenga breed	This breed is only found in central Somalia, lower Shabelle Bay and Lower Jubba The Surqo breed that was located in North-eastern Kenya has disappeared	The breed has is the same size as the Somali Boran with a large body and short legs, the coat is white coat, light brown and dark mahogany, it has a moderate thoracic to cervico-thoracic hump. The breed is mainly used for meat and milk.
Sheep	Somali Blackhead (Blackhead Somali)	fat-rumped	Throughout Somalia	The breed is characterized by a fat-rump tail, a black head and the rest of the animal is white, though the hooves may be black, it has a strong head with poll and nose pads of fat giving a convex appearance to the head profile, the horns are absent and the ears are moderately long, the mature body weight of the males in Somalia is between 35–45 kg.
Goat	Somali Long-eared goat (Large-White Somali, Digodi, Melebo, Boran Somali, Benadir Gigwain)	NA	Widely distributed in the arid and semi-arid lands in southern Somalia but is also found in northern Kenya and in Ethiopia.	The body is relatively large between 70 and 75 cm and weighs up to 42 kg in adult mature males the facial profile is straight, the coat colour is white and relatively shiny, the coat hair is short and fine and 19% of the males 8% of the females have been reported to be polled, the ears can be horizontal or semi-pendulous.
Goat	Somali Short-eared goat (Ogaden, Galla, Modugh, Mudugh Galla (in Kenya))	NA	Northern and eastern parts of Ogaden in Jijiga, Degeh Bur and Werder in predominantly arid and semi-arid regions	It is a small goat with a height of 61–65 cm and a body weight of 28–33 kg in mature males, the coat colour is predominantly white and the hair is short, the facial profile is straight and up-to 19% males and 8% females have been reported as polled, the ears are horizontal or semi-pendulous.
Goat	Somali Arab goat (Benadir, Deguen)	NA	Mainly found in the northern parts of Somalia as well as in the south along the coast, though some long eared milk goats are kept in villages and towns in Somalia.	This goat is the smallest goat found in Somalia, with females averaging 65cm in height and 26 kg weight in mature males. It is dark or light brown in colour with long hair. The goat is prolific with many twin and triplet births. Some long eared ('deguen') milk goats are kept in villages and towns.

*Rege and Tawah 1999

NA- Not Available:

Information on the performance of the breeds was also not available

Figure 3: Livestock breeds in Somalia.

(a) Somali Boran bull



(b) Gasara bull



(c) Dauara Bull



(d) North Somali Zebu bull



(e) Surqo bull



(f) Somali Blackhead ram sheep



(g) Somali Long-eared goat



(h) Somali Short-eared goat



3. Research methodology

3.1 Study sites and time period

The study aimed at performing preliminary characterization of the major livestock breeds found in Somalia, namely the Somali Boran, Dauara, Gasara, Surqo and the North Somali Zebu cattle breeds, the Somali Blackhead sheep and the Somali Long-eared and Somali Short-eared goat breeds. Livestock-keeping households and the animals themselves were sampled from six administrative districts in Somalia (Figure 4 and Table 2), with one breed sampled per district. The choice of districts was dictated by the availability of the breed of interest, and accessibility of the district by road. Boran cattle were also sampled from two districts in Kenya, to act as reference populations during the analyses.

3.2 Rapid assessment tool and sampling of households

A rapid assessment tool in the form of a questionnaire was developed, tested and translated into local dialects with the assistance of local partners, for use at the individual household level. The questionnaire was administered to 38 to 50 households from one village in each of the six targeted districts, for a total of 277 households. The household head was interviewed. Information collected included the purpose for keeping livestock, type of livestock production system, livestock ownership, the source of breeding stock, and breeding preferences, in relation to cattle, sheep and goat. While the importance of camels to the Somali is recognized, they were not a focus of this study. Due to the lack of prior information on the households keeping particular breeds, the snowball sampling technique was used to identify households keeping targeted breeds. In this case producers keeping the targeted livestock breeds were asked to recommend other producers keeping the same breeds from their networks.

Figure 4: Map highlighting sampling areas in Somalia and Kenya.

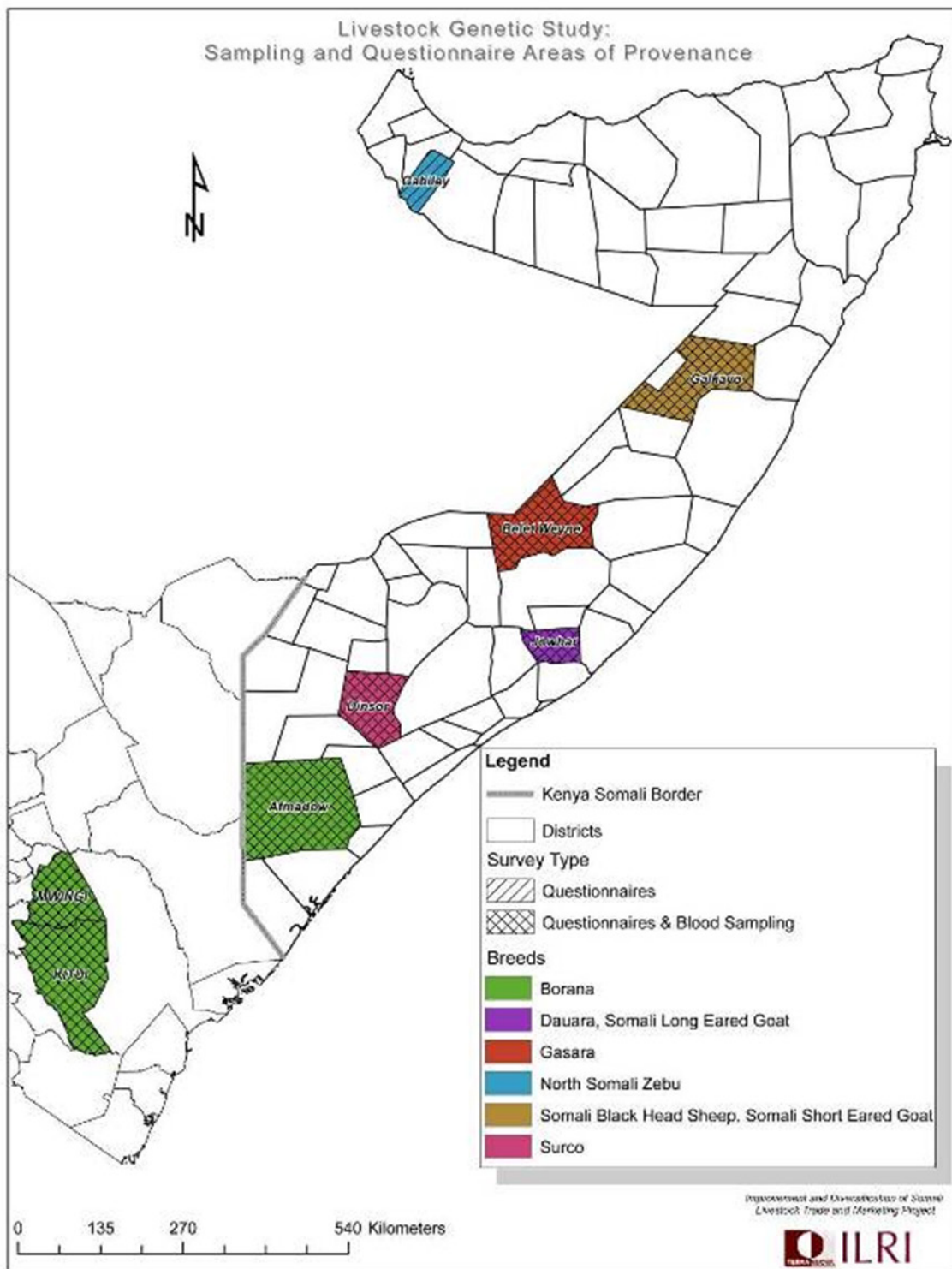


Table 2: Overview of breeds sampled

Species	Breed	Region	District sampled from	Country
Cattle	Boran	Lower Juba	Afmadow	Somalia
		Kitui	Kitui	Kenya
		Mwingi	Mwingi	Kenya
	Gasara	Hiran	Beledweyne	Somalia
	Dauara	Middle Shebelle	Jowhar	Somalia
	Surqo	Bay	Dinsoor	Somalia
	North Somali Zebu	Woqooyi	Gabiley	Somalia
Sheep	Somali Blackhead	Mudug	Galkayo	Somalia
Goats	Long-eared Somali	Middle Shebelle	Jowhar	Somalia
	Short-eared Somali	Mudug	Galkayo	Somalia

Phenotypic characterization

Basic phenotypic characterization was performed on all targeted breeds, with the exception of the Gasara and Surqo cattle breeds. Between 26 to 52 animals per breed were measured for a set of morphometric measures. Both female and male animals were measured; whilst the number of males animals measured was small, results are still presented due to the scarcity of data of this type. Animals were sampled from the same households to which the household questionnaire was administered.

The morphometric measurements collected were heart girth, body length, height at withers, rump height and pin bone width. These were taken of each animal using a chest band, measuring stick, measuring tape and an inclinometer, in centimetres, according to the procedure described by Wanderstock and Salisbury (1946). Heart girth measurements were taken by standing the animal with the head facing forward, in a 'normal' position and with the four legs set squarely under the body. A tape was passed tightly around the body just at the back of the shoulders at the smallest circumference. The body length was taken by measuring the length of the animal from the point of shoulder to the point of the buttocks. The height at withers was measured by measuring the vertical distance between the ground and the point of withers while the rump height was the vertical distance between the ground and the rump. The pin bone width was taken as the distance between the pin bones at the widest point. The measurements were repeated three times for each animal, and the average of these three measurements used. The sex, breed and coat colour of the measured animals was also noted, and the GPS point of the sampling location recorded. Measurements were only taken from mature animals, with age of the animal estimated by examining the animal's teeth as suggested by Pace and Wakeman (2003).

Genetic characterization

The development of polymerase chain reaction (PCR) and sequencing technologies has enabled the rapid measurement of genetic diversity available in a population (Hanotte and Jianlin 2005). Genetic diversity has been defined as the variety of alleles and genotypes present in a population (Frankham et al. 2002). This can be determined through the use of molecular markers that measure genetic polymorphisms, with different markers providing different types of information. The markers used in this study included autosomal microsatellite, Y chromosome, mitochondrial DNA and sequenced genomic regions. Autosomal microsatellite loci are commonly used to determine estimates of population diversity within and across breeds, population differentiation, genetic relationships and inbreeding (Hanotte and Jianlin 2005; FAO 2011). Mitochondrial DNA analyses are often used in domestication studies and in determining the origin of a population (Bruford et al. 2003; Ajmone-Marsan et al. 2010; Groeneveld et al. 2010), while Y chromosome markers are a powerful tool used to trace gene flow by male introgression (Petit et al. 2002). Sequencing of specific genomic regions can be used to identify signatures of selection and genes associated with particular traits (FAO 2011).

In this study, the genetic characterization performed was as follows: a) representatives of Boran, Gasara, Duara and Surqo cattle breeds, the Somali blackhead sheep breed, and the Somali Long-eared and Somali Short-eared goat breeds were characterized using 15 autosomal microsatellite markers per breed, selected from the International Society for Animal

Genetics (ISAG)/FAO recommended list of microsatellite markers (FAO 2011); b) Y chromosome analyses were conducted for representatives of the Boran, Gasara, Duara and Surqo cattle breeds using the Y chromosome marker INRA124, and the Somali blackhead sheep breed using the Y chromosome marker SRYM18; c) mitochondrial analysis, D-loop sequencing, were conducted on representatives of the Boran, Gasara, Duara and Surqo cattle breeds, and the Somali blackhead sheep breed, and d) four candidate genes for environmental stress (GOT1 and Dopa decarboxylase), growth (GRPI0), and meat quality (SORBS1) were sequenced on representatives of Boran, Gasara, Duara and Surqo cattle breeds. As permission was not granted for blood/DNA sampling of the North Somali Zebu cattle, this breed was excluded from the genetic analysis. In addition to the marker information generated from this study, publically available information on a number of additional reference populations was included in the analysis. The number of animals analysed per breed and marker type is given in Table 3.

Table 3: Breeds and number of animals analysed

Species/country	Breed	Sample numbers			
		Microsatellite analysis, 15 markers	Y-chromosomal analysis, 1 marker	Mitochondrial analysis, control region	Candidate genes
Cattle**					
Somalia	Dauara*	40	11	20	20
	Gasara*	40	10	20	20
	Surqo *	40	4	20	20
	Somali Boran*	40	7	20	20
Kenya	Kenyan Boran*	40	9	17	17
	Orma Boran –Kenya	-	-	15	15
Ethiopia	Jijiga	36	10	20	20
	Ethiopian Boran	-	-	-	19
	Ogaden Zebu	-	-	-	20
	Sheko	-	-	-	19
Eritrea	Baherie	-	-	-	19
Mali	N'dama	-	-	-	15
Senegal	N'dama	-	-	15	15
Non-African	Gobi-altai	-	-	15	15
	Brown Atlas	-	-	15	15
	Texas Longhorn	-	-	15	15
Total for cattle		236		192	284
Goat					
Somalia	Somali Short-eared*	40	-	-	-
	Somali Long-eared*	40	-	-	-
Italy	Sarda	40			
	Orobica	40			
	Argentata	40			
	Girgentana	40			
Total for goat		240	-	-	-
Sheep					
Somalia	Somali Blackhead*	40	10	36	-
Kenya	Red Masai	40	-	15	-
Ethiopia	Tekur	40			
Ethiopia	Wello	40			
Namibia	Damara	40	-	15	-
Nigeria	Djallonke	40	-	15	-
South Africa	South African	40			
	Blackhead Persian				
USA	Rambouillet	-	-	15	-
Total for sheep		280	10	96	0

* Sampled in the current project.

**The genetic characterization of the North Somali Zebu was not performed

Blood samples for DNA extraction and genetic characterization were collected from one to three adult animals per study household, for a total of 40 animals (30 female and 10 male) per breed and district (Table 3). An attempt was made to select the least related animals from each household, based on the household's recall of pedigree. Blood was collected by puncturing the jugular vein or from under the tail using a sterile needle and transferring the blood into tubes containing the anticoagulant, ethylenediaminetetra-acetic acid (EDTA) and subsequently FTA filter paper. DNA was isolated from the FTA filter papers using the protocol described by Tack et al. (2007).

Details of the amplification and allele calling of the autosomal microsatellite and Y chromosome markers are given in Appendix 1, details of the amplification and haplotype calling of the mitochondrial *D*-loop are given in Appendix 2, and details of the amplification, sequencing and polymorphism detection of the candidate genes are given in Appendix 3.

The genetic diversity of the Somali populations was assessed by calculating the mean observed heterozygosity for each population across all the autosomal and Y chromosome markers used. Measurements of heterozygosity (Nei 1987), which is the proportion of individuals in a population that are heterozygous at a particular locus, are commonly used to measure genetic diversity (Hanotte and Jianlin 2005). Assuming that loci are in Hardy-Weinberg equilibrium, heterozygosity values range from zero (all individuals homozygote at a locus) to 1 (all individuals heterozygote at a locus). The genetic differentiation among the sampled populations was also examined, via calculation of fixation indices (F_{ST}). F_{ST} range from 0 to 1, where 0 indicates that a pair of populations has identical alleles (i.e. they do not genetically differ) and 1 indicates fixation of a specific allele in a particular population that is different from the allele fixed in the other population (i.e. they completely genetically differ) (Balloux and Lugon-Moulin 2002). Variation among the microsatellite allele frequencies was analysed via principal component analyses.

4. Results and discussion

4.1 Purpose for keeping livestock

Most of the livestock keepers (87%) indicated that the main reason they kept livestock is as a source of food. This was expected since livestock and livestock products such as milk and ghee are very important dietary component for the Somali people. The contribution of livestock to the quality of food consumed by the pastoralists cannot be underestimated because livestock contribute high quality protein and vitamins that are especially important in the nutrition of children. It was therefore not surprising that 88% of the cattle keepers and 83% of the sheep and goat keepers indicated that the most important attribute for livestock was its ability to produce milk. Similar findings have been reported in the Intergovernmental Authority on Development (IGAD) countries (Djibouti, Eritrea, Ethiopia, Somalia, Uganda and Kenya) where pastoralists keep livestock to provide food (Sanford and Ashley 2008).

Another important reason for keeping livestock was as a source of income, with 83% of the respondents indicating that they kept livestock for this purpose. In the past milk was a main dietary component, however in recent years pastoralists have diversified their food, and now cereals make up a significant part of their diet. To finance these purchases pastoralists sell or exchange livestock or their products (Sanford and Ashley 2008). Income from livestock has been found to contribute up to 75% of the incomes of pastoralists in IGAD countries (Sanford and Ashley 2008). These results are in agreement with the findings of Rege et al. (1996) and Kosgey et al. (2008) who have documented the importance of livestock and their products as a source of household cash for pastoralists.

A further important reason for keeping livestock is for cultural purposes, as indicated by 80% of respondents. Livestock has been reported to form a large part of the livestock keeper's cultural identity and they contribute immensely to their ability to form and maintain cultural networks (Rege et al. 1996; Sanford and Ashley 2008).

An additionally named reason for keeping livestock (15% of respondents) was for economic reasons for income generation. In this case the livestock keepers bought animals, kept them for a short period, and then sold them for profit after their condition had improved.

4.2 Livestock production system

All the respondents practised pastoral livestock production systems where they grazed their livestock on natural pasture comprising grass, shrubs and trees. However 30% of the respondents indicated that they had to supplement their livestock feed using purchased fodder. This was mainly due to the harsh environmental conditions that places limits on the carrying capacity of the land.

4.3 Livestock ownership

Most of the respondents owned all the targeted livestock species namely cattle, sheep and goats. In relation to cattle herd size, 75% owned less than 30 head of cattle, and 17% owned between 30 and 100 head of cattle, while a few (8%) owned more than 100 head of cattle. Sheep flock size was larger with 50% owning more than 100 head, 30% owning between 30 and 100 head, and few (13%) owning less than 30 head. The numbers of goats was more than cattle but less than the sheep with 42% of the respondents owning between 30 and 100 head. Twenty-four percent of the respondents kept large goat herds of more than 100 head, while the rest (34%) owned less than 30 head. This trend has also been observed in the IGAD countries where the 71% of the regions livestock are sheep, compared to 65% and 53% for goats and cattle respectively (FAO/WB/EU 2004). The practice of keeping large herd sizes has also been observed in the IGAD countries where the pastoralists keep large herd sizes for savings and insurance purposes (particularly against drought) and to enable them to meet their dietary and cash needs (Roba and Witsenburg 2004; Sanford and Ashley 2008).

4.4 Source of breeding stock

The livestock keepers in this study indicated that they had various options that they are using to obtain animals for breeding. In addition to their own animals they obtained animals from their neighbours, clansmen, relatives or from open markets and livestock traders. Thirty percent of the respondents indicated that they used their own animals for breeding while 27% used animals from their relatives or clansmen. Further, 30% indicated that they obtained their breeding animals from their friends and neighbours, while 13% obtained them from open markets and livestock traders. A clear breeding strategy was evident with 70% of the breeding animals procured from external sources specifically for herd/flock upgrading.

The exclusive use of animals born in their own herd/flock can, over-time, result in high levels of inbreeding and loss of genetic diversity which leads to loss of viability, fertility, disease resistance and the frequent occurrence of recessive genetic diseases (Keller and Waller 2002; FAO 2007; Taberlet et al. 2008). That breeding animals are available, and being used, from outside sources is thus encouraging in relation to keeping the level of inbreeding at acceptable levels.

4.5 Breed preferences

The geographic distribution of cattle, sheep and goats in Somalia is limited to specific areas. This was probably due to the fact that particular breeds of livestock are associated with certain local tribes. Thus not all the respondents kept more than one breed of cattle and were therefore not able to give their breed preferences. In a few districts where respondents kept more than one breed of cattle it was possible to determine their breed preferences. The livestock keepers in the Dinsoor district keep both Surqo and Dauara cattle breeds but have a preference for the Surqo breed over the Dauara breed. The Dauara breed however was the preferred breed in Afmadow district over the Somali Boran, while the Beledweyne district where the Dauara and Gasara breeds are both found, the Gasara was the most preferred. It appeared that the Dauara breed was the preferred breed in the relatively high potential agropastoral areas in the middle Shebelle region, while the Somali Boran was favoured in the drier parts of the Juba district.

The livestock keepers mainly reared either the Somali Long-eared or Somali Short-eared goat with the exception of the keepers in middle Shebelle region who reared both breeds. Among the respondents keeping both breeds (which numbered 40) 93% indicated that they preferred the Long-eared breed because it had higher production of milk and meat. This is supported by FARM-Africa (1996) who reported that the Long-eared goats attain a maximum adult weight of 42 kg compared to the Short-eared that attain a maximum adult weight of 32 kg.

4.6 Morphological characterization

Cattle

The morphometric measurements of mature cattle of Boran, Dauara and North Somali Zebu breeds are shown in Table 4. Generally the males had larger body measurements, broader girths and were longer than their female counterparts (Table 4). The heart girth has been found to be a good indicator of how heavy an animal is. Animals that have a broader heart-girth have been found to be heavier (Kashoma et al. 2011; Lesosky et al. 2012). The Boran breed had significantly larger heart girth and height at wither measurements compared to the Dauara and North Somali Zebu breeds while the pin bone width measurements of the Boran and North Somali Zebu were larger than the Dauara breed. However, there were no notable differences between the body length measurements of the Boran, Dauara and North Somali Zebu breeds (Table 4).

Table 4: Means \pm standard errors of the morphometric measurements for mature Boran, Dauara and North Somali zebu cattle breeds^{1,2}

Body part measurement (Means)	Breed					
	Boran		Dauara		North Somali Zebu	
	Male (n=4)	Female (n=48)	Male (n=2)	Female (n=25)	Male (n=4)	Female (n=22)
Body length (cm)	136.0 \pm 6.2	129.7 \pm 1.1	140 \pm 7.3	133.3 \pm 1.5	135.3 \pm 3.6	122.9 \pm 1.6
Heart girth (cm)	171.0 \pm 5.3	154.0 \pm 1.1	150.0 \pm 7.6	151.1 \pm 1.5	169.0 \pm 3.8	146.4 \pm 1.6
Wither height (cm)	140.0 \pm 4.9	121.9 \pm 1.0	121.9 \pm 1.4	119.0 \pm 7.0	125.0 \pm 3.4	118.0 \pm 1.5
Rump height (cm)	141.0 \pm 4.2	127.9 \pm 0.9	130.0 \pm 5.9	127.9 \pm 1.2	131.0 \pm 3.0	120.3 \pm 1.3
Pin-bone width (cm)	46.0 \pm 2.0	40.5 \pm 0.4	44.0 \pm 2.8	41.3 \pm 0.6	47.5 \pm 1.4	39.2 \pm 0.6

¹Morphometric measurements were not taken from the Gasara and Surqo cattle

²Although morphometric measurement were taken from few males these figures are given for record purposes, given the scarcity of data to this end

Somali Goats and the Somali Blackhead sheep

The monomorphic measurements of mature goats of the Somali Long-eared and the Somali Short-eared breeds, and sheep of the Black Head breed, are summarized in Table 4. The Long-eared goats were found to be longer, higher at withers and rump and had wider pin bone than the Short-eared goats. The two breeds however had similar heart girth measurements (Table 4). The female Short-eared goats were found to be longer and had higher rump heights than their male counterparts. They also had wider pin bones (Table 4). Similar to cattle, heart-girth of goat is a predictor of weight, with animals of broader heart-girth found to be heavier (ESGPIP 2009). For example in the Nguni goats of South Africa the heart girth accounted for 86-89% of the weight variation in bucks and does respectively (Myeni and Slippers 1997). Similar findings have also been reported by Slippers et al. (2000). In this study, however, there were no significant differences in girth measurements between the Long-eared and Short-eared goats although this could be due to the fact that the breed identification and classification was done by the farmers and thus could have varied across the different regions.

In all the traits measured for the Somali Blackhead sheep all the males were found to be taller, longer and larger than the females (Table 4). The marked differences between male and female Somali Blackhead sheep is evidence of sexual dimorphism within the Somalia indigenous sheep breeds, with the males, as is the norm, having relatively greater measurements for all traits studied.

Table 4: Mean \pm standard errors of the morphometric measurements for mature Somali goats and sheep breeds¹

Body part measurement (Means)	Species/Breed					
	Somali Long-eared goat		Somali Short-eared goat		Black Head sheep	
	Male (n=7)	Female (n=30)	Male (n=4)	Female (n=30)	Male (n=10)	Female (n=31)
Body length (cm)	69.6 \pm 1.9	67.9 \pm 0.9	61.3 \pm 2.3	65.9 \pm 1.1	69.5 \pm 1.4	65 \pm (1.2)
Heart girth (cm)	75.4 \pm 2.6	73.6 \pm 1.3	73.0 \pm 3.2	73.8 \pm 1.6	80.2 \pm 1.9	76.8 \pm 1.1
Whither height (cm)	72.5 \pm 2.0	71.3 \pm 1.0	68.6 \pm 1.2	62.6 \pm 2.5	70.1 \pm 1.3	64.9 \pm 0.8
Rump height (cm)	72.5 \pm 2.0	72.2 \pm 1.0	62.3 \pm 2.4	68.5 \pm 1.2	69.3 \pm 1.3	65.6 \pm 0.7
Pin-bone width (cm)	22.3 \pm 0.7	20.5 \pm 0.3	18.8 \pm 0.8	20.6 \pm 0.4	24.9 \pm 0.6	22.8 \pm 0.3

¹Although morphometric measurement were taken from few males these figures are given for record purposes, given the scarcity of data to this end.

4.7 Genetic characterization

Cattle

Four Somali cattle breeds (Dauara, Gasara, Surqo, Somali Boran) were characterized with 15 microsatellite markers. The results were then compared to reference populations that consisted of European (European Holstein) and African breeds (Kenyan Boran, Orma Boran and West African N'Dama).

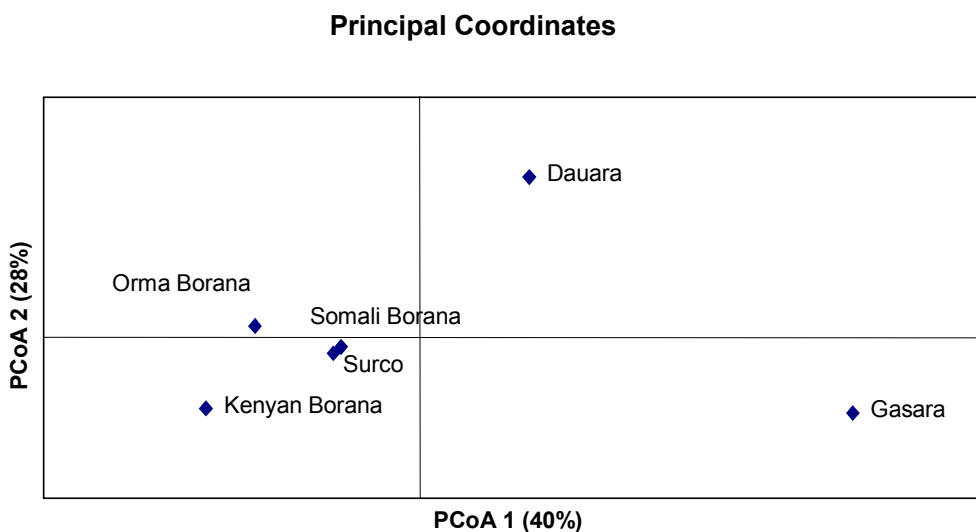
The average heterozygosity for the Somali populations was 0.75 and was higher than that observed for the Kenyan Boran (0.69) and West African N'Dama (0.58).

The mean genetic differentiation analyses among the Somali cattle breeds and with the exclusion of the reference populations was moderate with an F_{ST} value of 0.07. The average genetic differentiation between the Kenyan and Somali Boran populations was low at $F_{ST} = 0.025$ suggesting that some genetic exchanges could have occurred between the two populations. Similar results were obtained following candidate gene analysis where an average fixation index of $F_{ST} = 0.028$ was obtained.

Principal component analyses of microsatellite allele frequencies showed that differences between populations accounted for 68% of the total genetic variation for the first two principal components (Figure 5). A plot of these first two principal components shows one main cluster containing the Somali, Kenyan and Orma Boran and the Surqo breeds (Figure 5). The Dauara and the Gasara each cluster separately indicating that these two populations are the most highly differentiated populations among the Somali cattle breed. Notably the Somali Boran was very closely related to the Surqo with the two breeds clustering together (Figure 5). These findings can be supported by historical evidence that report that the Surqo breed was developed by crossing the Somali Boran and an unknown Central Somali cattle (Nur 2005). The Y chromosome analyses for the cattle showed that there were no distinct paternal lineages with all bull showing the zebu allele.

At the mitochondrial DNA level, only taurine mtDNA were present in Somali cattle. No significant differences in allele frequencies at the studied genes was observed between the Somali cattle breed ($P > 0.05$, data not shown).

Figure 5: Two dimensional plot representing the relationship between the first two principal coordinate axes (PCoA) using allele frequencies data from 15 microsatellite loci genotyped in the four Somali and two Kenyan reference cattle breeds.

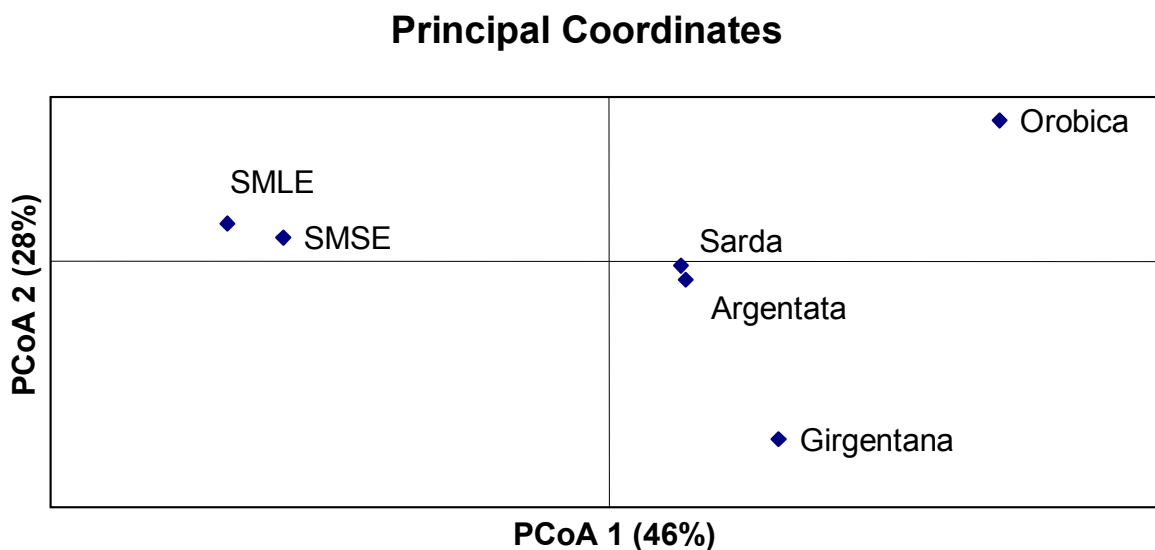


Goat

The two goat breeds, the Somali Long-eared and the Somali Short-eared, were characterized using 15 microsatellite markers. The heterozygosity values for both the Somali goat breeds were high, 0.62 and 0.64 for the Somali Long-eared goat and Somali Short-eared goat, respectively. The genetic differentiation between the two populations was low with a fixation index F_{ST} being only 0.01.

Principal component analyses (PCA) were conducted on the two Somali breeds and four well established reference populations from Italy namely, Sarda, Orobica, Argentata, and Girgentana. The variation accounted for by the first and second principal component was 74%. The principal component analysis indicate a close clustering of the Somali goats suggesting low breed differentiation and a common ancestry. There was no Y chromosome analysis nor mitochondrial analysis performed for the goats.

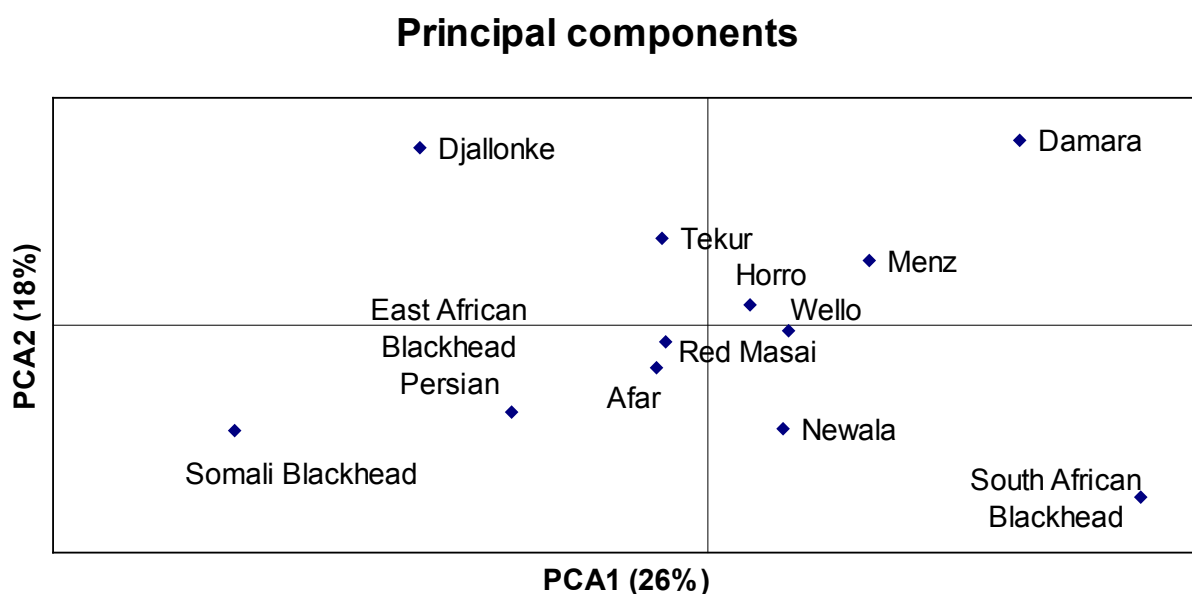
Figure 6: Two dimensional plot representing the relationship between two first principal coordinate axes (PCoA) using allele frequency data from 15 microsatellite loci genotyped in the for Somali Long-eared (SMLE), Somali Short-eared goat (SMSE) and four Italian reference breeds.



There was only one sheep population studied, the Somali Blackhead Persian hence the Red Maasai (Kenya), Tekur and Wello (Ethiopia), Damara (Namibia), Djanllonke (Nigeria), South African Blackhead Persian (South Africa) and Rambouillet (USA) (Muigai 2002) were used as reference populations. The heterozygosity of Somali Blackhead was 0.74 and was comparable to other population from the region namely Tekur and Wello from Ethiopia with a heterozygosity of 0.75. Population differentiation showed that the South African Blackhead Persian breed to be the most closely related population to the Somali Blackhead in agreement with the known history of the breed.

Principal components analysis using allele frequencies (Figure 7) show that the East African Blackhead Persian as the most closely related population to the Somali Blackhead examined. This is in agreement with previous phenotypic and genetic studies (Muigai et al. 2002; Mwacharo et al. 2002; 2003; Ole Kwallah 2007) that this population is closely related to the Kenyan Somali Blackhead sheep.

Figure 7: Two dimensional principal coordinate axes (PCoA) plot, using allele frequency data from 15 microsatellite loci, representing the relationships between Somali Blackhead Persian and East and South African sheep breeds.



Y-Chromosome analysis of the Somali Blackhead sheep showed that the Somali sheep carried the microsatellite allele 143, previously found in African sheep (Meadow et al 2006). Mitochondrial D-loop DNA analysis showed that the B haplogroup was the predominant haplogroup in the Somali sheep as well as in other African populations. The haplogroup B is found throughout the African and Arabian Peninsula sheep populations (Finlay et al 2007).

Candidate gene analysis, indicate low variation in Somali Blackhead sheep at GOT1. GOT1 is a candidate gene possibly under environmental selection, with possibly different polymorphism alleles optimal for different environments (including temperature and nutritional status).

The data generated by this study, would enable planning of cost-efficient screening of the four–six polymorphism in the large population, thereby allowing more clearer disentangling and clearer detection of chance effects (genetic drift) from deterministic effects (selection) as far as the candidate genes (meat quality and adaptation to stress) are concerned in subsequent studies. This can be done either by comparing individual animals or breeds, which differentially manifest contrasting phenotypes relative to the others in so far as adaptive and meat quality traits are concerned. Such follow-up studies have the potential of contributing to practical application of gene-based breeding strategies.

5. Conclusions

The household survey showed that the indigenous livestock breeds of Somalia are important to the livestock keepers of Somalia. The livestock keepers relied on the animals for food and income. Livestock keepers familiar with more than one breed of a particular species indicated breed preferences based on cultural values, meat and milk production. Basic phenotypic and genotypic characterization of these breeds is presented here, and further characterization of Somali breeds in relation to the environment in which they perform should be considered in future studies. This study has shown that the Somali indigenous breeds of cattle, sheep and goat are unique and harbour a wide genetic diversity which has been well preserved and maintained by the livestock keepers of Somalia and from which they will continue to depend for future resources.

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Appendix I: Autosomal microsatellite and Y chromosome markers analysis

Microsatellites markers used were selected from the FAO/ISAG panel (FAO 2011). The PCR amplification was performed in a total volume of 10 μ l containing 20 ng DNA template, 40 ng each of labelled forward (PET-Red, VIC-Green, 6FAM-Blue and NED-Yellow) and unlabelled reverse primers, 5 μ l of ReddyMix™ PCR Master Mix (ABgene, UK) and 3.6 μ l of distilled water. The amplifications were performed using a GeneAMP®PCR System 9800. The PCR reactions included a five minutes denaturation step at 95°C, followed by 35 cycles of thirty seconds at 94°C, one minute at 54-64°C annealing temperature, one minute at 72°C and a final extension step at 72°C for ten minutes. Denatured PCR fragments were separated using an ABI 3730 (Applied Biosystems, Warrington, UK) automated capillary DNA sequencer. GeneMapper® software (version 3.7, Applied Biosystems), was used to perform allele calling using the third order least squares method for fragment sizing. Heterozygosities and Fst estimates were calculated using the program GENEPOP (Raymond and Rousset 1995).

Marker class	Cattle	Goat	Sheep
Autosomal microsatellites	AGLA293	BM1818	BM8125
	BM2113	BMS1494	DYMS1
	CSSM66	CSR247	HSC
	ETH152	ETH10	HUJ616
	ETH225	ILSTS005	ILSTS005
	HEL01	ILSTS011	MAF209
	HEL05	ILSTS029	McM42
	ILSTS005	INRA0132	OarFCB11
	ILSTS006	MAF035	OarFCB20
	ILSTS033	MAF70	OarFCB226
	INRA005	MCM527	OarHH47
	INRA023	OarAE54	OarJMP29
	INRA032	OarFCB20	OarVH72
	MGTG4B	SPS113	SR-CRSP-09
	TGLA122	SRCRSP3	TGLA53
	Y-chromosome microsatellite	INRA124	

Appendix 2: Mitochondrial DNA analysis

Mitochondrial analyses were performed as described in Finlay et al (2007) for sheep, while for cattle, primers 'proline tRNA' (Loftus et al 1994) and "YakB" (Qi 2004) were used for template creation in PCR as described in Qi (2004), except that PCRs were done using one FTA card (Whatman) disk washed with Whatman FTA Purification Reagent according to manufacturer's instructions. The PCR primers and two additional primers, 'AN5' (Bailey et al. 1996) and 'mtd2' (Jianlin et al. 2000), were used in cattle sequencing. Sequencing conducted under BigDye™ terminator cycling conditions, products were purified using Ethanol Precipitation, and analysed on ABI Prism 3730xl DNA Analyser (Applied Biosystems, Foster City, CA, USA).

Appendix 3: Candidate gene analysis

Primers specific to these genes were designed from the cattle genome sequence (*Btau_3.1*) and used for PCR amplification. The PCR products were then sequenced and the amplified regions were analysed for polymorphisms.

According to *Btau_3.1* assembly for cattle, all genes are located on a narrow segment of chromosome 26 (BTA26). However, in *Btau_4.0* genome assembly, which in NCBI data bases replaced *Btau_3.1* on 01-Aug-2008, the two first genes were assigned to chromosome 4 (BTA4). Primers were designed using FastPCR Professional v 5.2.71 (<http://www.biocenter.helsinki.fi/bi/Programs/fastpcr.htm>) based on cattle genome sequence (*Btau_3.1*) and tested against the GenBank database. Primers were designed to hybridize on exons segments, allowing maximum information to be obtained from those exons and the medial intron. Short introns were preferred. PCR reactions were carried out in a 10 µl volume, one FTA card (Whatman) disk washed with Whatman FTA Purification Reagent and following concentrations were used: 1x green GoTaq flexi buffer (Promega), primers 0.2 mM, dNTPs 0.25 mM, MgCl₂ 3.0 mM and flexi Taq (Promega) 1.25 units. PCR amplifications were performed on a GeneAmp PCR system 9700 (Applied Biosystems, Foster City, CA, USA). The following thermocycler program was used; initial denaturation step at 94°C for 3 min followed by 35 cycles of 30 sec at 94°C, 0.5 min at annealing temperature 59 or 63°C, and 3.5 min at 68°C and a final extension step at 68°C for 15 min. Sequencing was conducted under BigDye™ terminator cycling conditions, products were purified using Ethanol Precipitation and analysed on ABI Prism 3730xl DNA Analyser (Applied Biosystems, Foster City, CA, USA). Base calling reliability estimation and initial polymorphism detection were done using Phred using default settings. The output was processed further to detect reliable polymorphisms using Polyscan 3.0.

Gene name	Function	Targeted segments	Successful amplification
Growth factor receptor-bound protein 10 (GRP10) [GeneID: 281206]	Candidate for growth traits: Negatively regulates the IGF growth pathways via insulin and IGF I receptors.	Parts of exon 7 and 8 and of medial intron BTA4: 5,364,789... 5,365,989	Yes
		Parts of exon 9 and 10 and of medial intron BTA4: 5,360,542...5,362,423	No
		BTA4: 5,360,542... 5,362,416	No
Dopa decarboxylase [GeneID: 280762]	Candidate for the trait of coping with stress from handling/transport: Might affect aggressiveness as well as recovery from skin wounds. Conservative regulatory and physical link with the assessed candidate for growth (above).	Parts of exon 10 and 11 and of medial intron BTA4: 5,228,093... 5,230,184	No
		Parts of exon 1 and 2 and of medial intron BTA4: 5,296,247... 5,298,729	Yes
Sorbin and SH3 domain containing 1 (SORBS1) [GeneID: 504625]	Candidate for intramuscular fat deposition: An important adaptor protein in the insulin-signaling pathway.	Parts of exon 6 and 7 and of medial intron BTA26: 17,296,383... 17,296,587	No
		Parts of exon 10 and 11 and of medial intron BTA26: 17,273,773... 17,275,626	Yes
Glutamic-oxaloacetic transaminase I (GOT1) [GeneID: 281206]	Candidate for phenotype of recovering from mild tissue damage in various organs (e.g. caused by heat, cold, or starvation). Central enzyme participating in amino acid metabolism, the urea and tricarboxylic acid cycles.	Parts of exons 5 and 6 and of medial intron BTA26: 18,864,020... 18,864,948	Yes
		Parts of exon 3 to 4 and of medial intron BTA26: 18,861,631... 18,862,194	Yes

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