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SMALL RUMINANT HEALTH, TRAIT SELECTION AND GENETIC IMPROVEMENT IN ETHIOPIA, ACHIEVEMENTS, CHALLENGES AND LESSON LEARNT: A COMPREHENSIVE REVIEW

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ABSTRACT

Genetic improvement activities involved in small ruminants need to be coordinated across institutions in the national system (development, research and education institutions) as well as across international development partner institutions involved in similar activities. In Ethiopia, stand-alone genetic improvement initiatives as short-term projects should not be allowed. Such initiatives need to be registered and be part of a breeding program of National Animal Genetic Improvement Institute (NAGII), which is a newly established institute of the county. The current estimates indicated that the Ethiopian indigenous population of sheep and goats are 58.6 million with vast diversity. The genetic diversity exists between and within breeds which can provide the raw materials for trait selection and breed improvements as well as for the adaptation of the changing environments and changing demands. Production and reproductive performances of the small ruminants in the country remains low. To improve performances, exotic sheep breeds were introduced to the country in different times. However, the absence of national database and poor recording systems are the critical reason which hinders the trends of the genetic improvement made and many others. Recent trends show that unless focused on candidate genes for trait selection like milk and meat traits, the expected genetic improvement may not be achieved. For instance, the candidate genes and traits for milk production in goats can help for selection. In goat milk ,the four caseins; αs1, αs2, β and κ-casein coded by four closely linked autosomal genes, namely CSN1S1, CSN1S2, CSN2 and CSN3 genes, respectively were identified and mapped to chromosome 6. These genes that encode the major milk proteins are thought as candidate genes for the observed variation in protein composition. Therefore, small ruminant trait selection and genetic improvement in Ethiopia can be achieved through focusing on trait specific candidate genes and this will enhance the production and productivity.

KEYWORDS: Candidate genes, improvement, selection, small ruminant, traits.

INTRODUCTION

Small ruminants (Sheep and goats) are important component of the mixed agriculture, pastoral and agro-pastoral production systems of Ethiopia. Current estimates put the indigenous population of sheep and goats at 58.6 million (CSA, 2016). The sheep and goat production system in Ethiopia can be divided into three major and two minor production systems (Solomon *et al*., 2010). The major production systems are highland sheep barley production system, mixed crop-livestock production system and pastoral and agro-pastoral production systems. The minor production systems include ranching, urban and peri-urban areas/landless/sheep and goat production systems. The sheep and goat genetic resources in Ethiopia possess important adaptive traits which make them to cope with harsh environmental conditions such as lack of feed and water, heat and disease. The genetic diversity exists between and within breeds which can provide the raw materials for breed improvements and for the adaptation of the populations to changing environments and changing demands (FAO, 2015).

Small ruminant genetic improvement started in Ethiopia in the early 1960s with low and fragmented implementation (Markos, 2006). This is because almost all genetic improvement activities had focused on crossbreeding and was unsuccessful. The main reasons for such unsuccessful genetic improvements were indiscriminate crossbreeding with no plan on how to maintain a suitable blood level, lack of clear breeding and distribution strategy, lack of farmers' participation and trait preferences as well as incompatibility of introduced genotype with management practices (Kosgey, 2004). Most of the genetic improvement activities are not documented in Ethiopia except the works of FARM-Africa and ESGPIP, which have been implemented currently. FARM-Africa is initiated, in 1988; a dairy goat development program with the objectives of characterizing indigenous goat breed and crossbreeding them with exotic dairy goat breeds (Stern, 2007). Next to this, ESGPIP designed a crossbreeding program of sheep and goat with Dorper and Boer breed in some potential areas with the objective of enhancing meat production (Kassahun and Gipson, 2008). According to Solomon *et al.* (2013), all the previous works of genetic improvements (crossbreeding) referred hierarchical structured, characterized as unplanned, unsuccessful and unsustainable. The failure of these programs lead to a new approach of small ruminant named community-based breeding programs, which has been implemented in the country with the involvement of farmers' knowledge, needs and perceptions (Gemeda Duguma, 2010). Based on these community-based breeding programs, sheep and goats' production, productivity and production systems were characterized in north-western Ethiopia but selection towards traits for improving production and productivity were given less attention in the country. Therefore, the objective of this review was to quantify the significance of small ruminant trait selection and genetic improvement to enhance the production and productivity of small ruminant in Ethiopia.

Characterization and trait selection

Characterization and trait selection in sheep

Phenotypic characterization is a method of identifying distinct breed populations and describing their external features including productivity potentials in a given environment under the existing management practices, considering the socio-cultural and economic issues affecting them (FAO, 2012). Such information is essential for resource inventories, to design development strategy and planning the management of sheep genetic resources at local, regional and national levels. To ensure collection of adequate information and facilitate nation-wide or global comparisons of breeds, FAO (2012), developed a guideline for phenotypic characterization of various farm animal species. Accordingly, the parameters needed for phenotypic characterization of sheep include: qualitative and quantitative variables, flock level data, data related with origin and development of the animal and data on repeatedly measurable traits. So far, the Ethiopian indigenous sheep have been fairly studied in terms of qualitative description, production and management system characterizations (Gizaw, 2008; Fikirte, 2008; Tesfaye, 2008;Bimerw *et al.*, 2011; Abera *et al.*, 2013; Bireda, 2013; Gebretsadik and Anal, 2014;Asefa *et al.*, 2017) ((Table1). Fundamentally, identifying the prevailing sheep production systems, understanding the existing sheep breeding practices and examining performance variability for economically important traits have paramount significances to design sustainable breeding programs (Kosgey, 2004; Gizaw et al., 2011). It is from these perspectives that the phenotype based studies conducted on Ethiopian indigenous sheep.

Table 1: Phenotypic characterization of indigenous sheep breeds/populations.

Breeds/ populations	Phenotypic characterization parameters	References
Washera and Farta	Flock structure, growth and reproductive performance, survival, linear body measurements	Mengistie, 2008; Shigdaf, 2011; Bimerw et al., 2011; Taye *et al.*, 2011; Mekuriaw *et al.*, 2013
Bonga, Horro, Black head Somali, Menz, Afar, Arsie-Bale,	flock compositions, socio-economic importance, husbandry practices, reproduction and breeding management, qualitative and quantitative characters, production constraints	Zewdu, 2008; Fikirte, 2008; Tesfaye, 2008; Gizaw *et al.*, 2010
Indigenous sheep in Norther Ethiopia	Qualitative traits, linear measurements, flock compositions, reproductive and productive performance, management and husbandry practices	Gebrestadik and Anal, 2014; Tesfaye *et al*., 2017
Indigenous sheep in southern Ethiopia	Qualitative characters, quantitative morpho-metric traits, Hierarchical cluster analysis based on morpho-metric variables	Abera *et al*., 2013
Indigenous sheep in Bale zone	Qualitative traits, linear measurements	Assefa *et al*., 2017
Indigenous sheep in east Gojam zone	flock compositions, socio-economic importance, husbandry practices, reproduction and breeding management, qualitative and quantitative characters, production constraints	Michael, 2013
Indigenous sheep in north Wollo zone	Qualitative traits, linear measurements, flock compositions	Mohammed *et al*., 2015
Indigenous sheep in Selale areas	Qualitative traits, linear measurements, flock compositions	Abera *et al*., 2014

Clear understanding of the production system where a given sheep breed have been exist is important to breed best performing sheep in the best environment. For instance, when designing crossbreeding program in the lowland area with mixed crop-livestock production system, one should make sure that the crossbreeds obtained through crossbreeding must perform well under the existing production environments. Sheep found in the higher altitudes often have wool that could play significant role for adapting the cold environment while those in the lowland have hairy fiber type (Gizaw *et al.*, 2007).

Furthermore, nearly all indigenous sheep have fat accumulated in the hindquarter such as in the tail and rump region, which could be hydrolyzed for energy source as maintenance requirement considering the fact that feed shortage is the common problem in different production system in Ethiopia. Noteworthy to mention, sheep production system in Ethiopia is very diverse and any genetic improvement program should fit with a specific production system.

Performance characterization of indigenous sheep

Characterization of average growth of indigenous sheep in Ethiopia generally shows lower performance as compared to other exotic sheep breeds. For example, Dorper sheep in South Africa weighs four times than that of Menz sheep in about one year age (Table 2). Dorper is a composite breed developed through crossbreeding followed by selection while the Menz sheep is the result of natural selection that favors mostly traits related with survival than growth. As a result all indigenous sheep have yearling weight below commercial market requirements, which is about 30kg. This implies indigenous sheep requires significant genetic improvement works. Although average growth is low, variation exists within breeds which are a merit for genetic improvement through selection. More importantly, reproductive performance of indigenous sheep was examined in terms of some economically important fertility and survival traits (Table 2). Litter size varies from 1 for Afar to 1.4 for Horro sheep. However the age at first lambing of indigenous sheep is often longer as compared to South African Dorper. On the other hand, lambing interval is relatively shorter in Gumz sheep and is comparable with the scientifically acceptable lambing interval, which is about six to seven months with one to two month of uterine involution period followed by about five months of gestation period. Pre-weaning mortality (birth to about 90 days) is about 10% in most indigenous sheep except for Horro where it was reported about 75%. This may be associated relatively to its high twining rate compared to other indigenous sheep.

Table 2: Growth performance of some indigenous sheep breeds compared with Dorper sheep.

Breeds/ populations	Management type	Birth weight	Weaning weight	Yearling weight (kg)	Daily growth rate from birth to yearling (gram)	Source
Menz	On-station	2.08 ±0.04	7.22 ±0.37	16.2 ±0.41	47.31±1.17	Kassahun, 2000; Tibbo *et al.*, 2004
Afar	On-station	2.7±0.02	11.5±0.08	26.6±0.14	-	Yibrah, 2008
Farta	On-farm	2.50±0.02	9.94±0.74	20.08±0.73	53.69±4.82	Mekuriaw *et al.*, 2013
Gumz	On-farm	2.79 ±0.03	12.64 ± .24	23.05 ±0.645	-	Solomon, 2007
Horro	On-station	2.43 ±0.03	8.21±0.13	19.7 ±0.63	50.25±1.68	Kassahun, 2000
Washera	On-farm	2.61±0.0	12.78±0.45	24.70±1.13	64.09±3.13	Shigdaf, 2012
Bonga	On-farm	-	-	28.69 ± 0.48	-	Zewdu, 2008
Blackhead Somali	On-station	2.5±0.03	11.3±0.12	23.1±0.22	-	Yibrah, 2008
Dorper (South Africa)	On-farm	-	18.4	64.4± 1.1kg	180	Cloete *et al.*, 2000; Snyman and Olivier, 2002; Notter *et al.*, 2004

Table 3: Reproductive performance of some indigenous sheep breeds compared with Dorper.

Breeds/ populations	Liter size	Age at first lambing (days)	Lambing interval (days)	Pre-weaning Lamb survival (percent)	Reproductive life span of ewes (years)	Source
Menz	1.13	470.10 ±106.6	255.10± 54.8	89.4±0.02		Kassahun, 2000; Mukasa-Mugerwa, 2002; Tibbo *et al.*, 2004
Afar	1.0	405.60 ±91.6	270.50±72.3	-	-	Tesfaye, 2008
Farta	1.01	410.19±6.7	283.97±13.72	96±0.03	-	Shigdaf, 2012

Gumz	1.17	410	200		8.57±1.14	Solomon, 2007
Horro	1.4	399	234	75.7±0.03	7.9 ± 3.1	Kassahun, 2000; Edea *et al*., 2012
Washera	1.11± 0.02	399.48±5.2	293.43±17.05	91±0.02	-	Shigdaf, 2012
Bonga	1.36	447	267	-	7.4 ± 2.7	Edea *et al*., 2012
Blackhead Somali	-	503	-	-	8.77±0.09	Bireda *et al*., 2016
Dorper (South Africa)	1.4 - 1.6	346	144 - 153	96	NA	Cloete *et al*., 2000; Notter *et al*., 2004

Molecular characterization

Molecular characterization involves examining the genetic make-up of an organism at DNA, Protein and other small molecules level. It is important to estimate the level of within and between breed genetic diversity, population structure/admixture, genetic differentiation and selective sweep targeting genetic improvement and resource conservation (Toro *et al*., 2011). According to Frankham *et al*. (2002), genetic diversity refers to the presence of different gene variants and genotypes in a population and consequently reflected by differences in morphological, physiological and behavioral characteristics between individuals within a population. Genetic diversity is a vital indicator of the evolutionary potential of a given population that requires survivability and reproducibility at the right time within the right place (Toro and Caballero, 2005). Thus, assessment and management of genetic diversity are important to setup conservation priorities and design genetic improvement programs (Toro *et al*., 2011). Currently, molecular markers such as microsatellites, single nucleotide polymorphism (SNP), mitochondrial DNA copy number variations, Y-chromosome are widely used for genetic diversity studies (Gizaw, 2008; Groeneveld *et al*., 2010; Burno *et al*,. 2012).

With regard to molecular characterization of Ethiopia indigenous sheep, Gizaw (2008) has conducted compressive studies covering large number of traditionally recognized indigenous sheep breeds using microsatellite markers. The author reported high within breed genetic diversity for all indigenous sheep, with expected heterozygosity ranging from 0.658 to 0.746. Most of the indigenous sheep, particularly those in the central highlands, appeared to have short genetic distance (“Farta”,”Menz”, “Wello”, “Tikur” and “Sekota”), thus clustered close together in the phylogenetic tree (Gizaw *et al*. 2007). Similarly, based on molecular and phenotypic data analysis, the 14 indigenous sheep populations are grouped into 9 breed categories. On the other hand conservation priorities have been identified by Gizaw *et al*. (2007) based on contributions to gene pool diversity, breed merit and extinction probabilities. These suggestion, however, need to be reassessed to examine the current status of genetic diversity threats considering the growth of sheep population size at national level. A recent study by Helen (2015) also identified high within breed genetic diversity for Afar and blackhead Somali sheep breeds using microsatellite markers. However, Tesfaye (2015) reported relatively low genetic diversity for Wello and Menz sheep using 50K SNP marker. Generally, the molecular information reported so far is a good indicator of the potential of indigenous sheep for genetic improvement through selective breeding. Selective breeding is the best strategy to explore within breed genetic variability (Kosgey *et al*., 2006).

Genetic Improvement

Genetic improvement in sheep

Exotic sheep breed introduction trend

The first introduction of exotic sheep breeds into Ethiopia traced back to 1944 when Merino sheep were introduced from Italy by an American aid organization and maintained at Entoto (located near Addis Ababa) sheep breeding station (DBHBMC, 2007). Later on Romney, Corriedale, Hampshire, and Rambouillet were introduced from Kenya in 1967 and were kept at the government farm Debre Berhan Sheep Breeding and Multiplication Center (DBSBMC) which was established in 1967 near Debre- Berhan town, Ethiopia. Another state owned farm, Chilalo Agricultural Development Unit (CADU) was also established in the same year in the former province of Arsi. However, the detection of maedi-visna (respiratory viral disease) in the flock of CADU in 1988-1989 prompted closure of the farm (BoA, 2000). In 1980, Awassi sheep were introduced from Israel and kept at DBSBMC and Amede Guya Sheep Breeding and Multiplication Center (AGSBMC)) located in Ethiopia. In addition, Dorper sheep were introduced into the Jijiga area (Somali Region) in the late 1980s (Awgichew and Gipson, 2009) (Getachewet.al, 2016). There were also continuous importations of a total of 45 purebred Awassi sheep (ram and ewe lambs). The two government farms have been engaged in multiplication and distribution of crossbred rams to farmers at a subsidized price. However, ram dissemination was banned between the years 2001 and 2009 following the confirmed maedi-visna disease in crossbreds and associated sheep flocks (DBHBMC, 2007). In 2011, about 170 pure Awassi sheep were again imported from Israel to recommence crossbreeding in the farms.

Genetic improvement of indigenous sheep through selection

Within breed selection is an important option to explore within breed genetic variations of indigenous sheep breeds (Kosgey *et al*., 2006). In Ethiopia, selective breeding for some sheep breeds have been conducted for decades although significant changes not yet achieved. Through a review of Ethiopian sheep breeding research, Gizaw *et al*. (2013) reported that the central nucleus based breeding programs have been tried for Menz, Horro and Afar sheep breeds. So far, selective breeding resulted in notable genetic improvements in Menz sheep breed, which is about 7 kg body weight improvement over the base population achieved in 8 to 9 generations (Gizaw *et al*., 2011). More recently, community based pure breeding selection scheme has been tested for Menz, Bonga and Horro indigenous sheep breeds in pilot areas (Haile *et al.*, 2011; Mirkina *et al*., 2012). Although it covers limited villages when viewed from the country's sheep population size perspective, early results reported so far are promising (Gizaw *et al*., 2013; Haile *et al*., 2014) The traits included for the three breeds community based program are growth traits, lamb survival, twining rate and fleece weight. Appreciable genetic improvement has been achieved in the Menz community based sheep selection program with body weights at birth, 3 and 6 months of age increased by 0.42, 2.29 and 2.46 kg, respectively in the third generation over those in the base generation (Gizaw *et al*., 2013).

Characterization and trait selection in goats

Characterization of goat genetic resources

The goat is among the earliest small ruminant species to be domesticated and was used for meat, milk, fiber and pelt at least since 2500 B.C. (Qureshi *et al*., 2014). Goats are distributed over all types of ecology with more concentrated in the tropics and dry zones of developing countries. Of approximately 617 million goats in the world, 97.3 % are found in the developing world. Of these, 65.9 % are found in Asia, 27.4 % in Africa, 3.5 % in Europe and 3.0 % in Americas. The number of dairy goats in the world is 191 million goats, 47.7 % of them are in the 25 least developing countries as reported by FAOSTAT (2012).Information compiled on physical description and management system revealed that there are 14 goat types in Ethiopia and Eritrea (FARM-Africa, 1996). According to earlier characterization work, indigenous Ethiopian goats have been phenotypically classified into 12 types while a genetic characterization showed only eight distinctively different types (Tesfaye, 2004).

Almost all indigenous goat types in Ethiopia fall under the general group of short eared small-horned goats found throughout eastern, central and southern Africa. Abergelle, Afar, Arsi-Bale, Begait (Barka), Central Highland, Harerghe Highland, Keffa, Somali, Western Highland, Western Lowland and Woyto-Guji goats are indigenous goat breeds of Ethiopia. However, there is only one breed (the Barka) from a different breed group, and it comes mainly from Eritrea (Nigatu Alemayehu, 1994). Some of the exotic dairy goat breeds that have been introduced into Ethiopia are; Anglo Nubian, Damascus or Shami, Saanen, and Toggenburg (Adane Hirpa and Girma Abebe, 2008).They inhabit all agro-climatic zones and production systems in the areas. According to Tesfaye (2004) indigenous goats of Ethiopia can be grouped as eight distinct genetic entities: Arsi-Bale, Gumuz, Keffa, Long-Ear Somali, Woyto-Guji, Abergelle, Afar, Highland Goats (previously separated as Central and North West Highland) and the goats from the previous Hararghe province (Hararghe Highland and Short-Ear Somali). The reports of CSA (2013) showed that 99.99% of the Ethiopian goats are indigenous.

Even though Ethiopia has large size of goat population, the productivity per unit of animal especially milk production and the contribution of this sector for both the national and the regional economy is relatively low. This may be due to different factors such as poor nutrition, prevalence of diseases, lack of appropriate breed and breeding strategies and poor understanding of the production system as a whole(Tesfaye, 2009). Because of less productivity, local goat breeds were subjected to replacement and crossbreeding with imported goat breeds like Anglo-Nubian, Saanen and Toggenberg introduced by different organization in different periods. However, indiscriminate crossbreeding of indigenous goats caused genetic erosion, loss of genetic diversity and reduction of adaptive value for efficient utilization of the existing adapted goat genetic resources (Halima *et al*., 2012).This is because different indigenous goat breeds have different relative advantage in their natural habitat. Therefore, genetic progress in milk production from indigenous goats could be achieved through designing a sustainable within breed selection programs. The existing traditional breeding techniques in dairy animals take many years and do not efficiently take into account all sources of genetic variability. Correspondingly, in sex limited, a low heritable and late expressed trait, the impact of traditional breeding is limited and needs high cost. Even within breed phenotype selection program for goat in Ethiopia is still toddler except some works on Arsi-Bale goat, Abergele and Barka goat designed breeding program for Abergele and Western lowland goats. However using only phenotypic selection does not influence the economy of farmers. Hence, the use of molecular information for trait selection will help to address the problems associated with traditional selection and thus help to select genetically superior animals for better productivity and disease resistance (Singh *et al*., 2013).

Goat trait selections

Goat milk, in the world, is mainly produced in four continents, namely, Europe, America, Asia and Africa. Asia is the most producing continent of goat milk, with the share of approximately 57.8%. Africa produces 25.2%, Europe produces around 13.7% and the remaining 3.2% is produced in the Americas (Agro-processing Support, 2016). Although Ethiopian indigenous goat breeds are not characterized for specific product, their milk production potential is very low (Table 3).

In the smallholder farming system, goats are mainly produced for generating cash income and providing the family with milk. Goat milk is an important dietary component of pastoralists in the Ethiopian lowlands where an estimated 75% of the country`s goats is maintained. For example, 70.7% of the Ebinat, Farta and Gonji kolela farmers prefer goat than cow milk for its nutritional and medicinal values. In general, the goat production accounts for 16.7% of milk consumed in the country (Tsedeke, 2007) and daily milk yield of indigenous Ethiopian goats range between 0.28 kg (Kassahun *et al*., 1989) to 1.13 kg (Mestawet *et al*., 2012).

Although their number is limited to 0.23% (CSA, 2012), some exotic goat breeds such as Anglo-Nubian, Toggenberg, Sannen and Boer goat were introduced with the aim of improving milk and meat production of the local goat breeds. Anglo-Nubian x Hararghe Highland and Anglo-Nubian x Somali crossbreds are being used for milk production by smallholders in central, southeastern, eastern, and southern parts of the country (Solomon *et al*., 2014) and crossbreeding showed increments in milk yield. The milk yield of crossbreds Sannen × Afar was 0.37 kg/day (Kassahun *et al*., 1989), 0.93 kg/ day for Toggenburg × ArsiBale (Mestawet *et al*., 2012). This shows thatthe milk yield of crossbred goat is not significantly higher than the indigenous goats and indigenous goats have higher major milk components than most of the exotic breeds (Mestawet *et al*., 2012). In general, small ruminants cross breeding programs in tropical countries were not successful because of the incompatibility of the genotype with the farmers breeding objectives, management methods and the prevailing environment of the tropical low input production systems (Ayalew *et al*., 2003; Kosgey *et al*., 2006).

The milk production potential of Ethiopian goat on station management ranges from 0.28 kg/day for Afar goat (Kassahun *et al*., 1989) to 1.13 kg/ day for Arsi Bale goat (Mestawit *et al*., 2012). On the other hand, under smallholder management it ranges from 0.29 kg/day for Arsi Bale goat (Tatek *et al*., 2004) to 0.55 kg/day for Begait goat (Hagos *et al*., 2017). These variations between breeds indicate higher probability of enhancing milk production through phenotypic and marker assisted selection.

Table 3: Daily milk production potential of indigenous goats in Ethiopia.

Breed	Daily milk yield (kg)	Management	References
Arsi-Bale	1.13	On station	Mestawet *et al*. (2012)
Arsi- Bale	0.29	On farm	Tatek *et al*. (2004)
Abergalle	0.46	On station	Berhane and Eirk (2006)
Afar	0.28	On station	Kassahun *et al*. (1989)
Begait	0.63	On station	Berhane and Eirk (2006)
Borena	0.45	On station	Lemma *et al*. (2003)
Begait	0.55	On farm	Hagos *et al*. (2017)
Begait	0.75	On station	Hagos *et al*. (2017)
Somali	0.84	On station	Mestawet *et al*. (2012)
Short-eared Somali	0.45	On farm	Farm-Africa (1995)
Long-eared Somali	0.33	On farm	Degen (2007)
Hararghe highland	0.40	On farm	Dereje (2011)

Goats' genetic improvement through selection of Candidate genes

A candidate gene is a gene supposed to be responsible for a considerable amount of the genetic variation of a trait. The candidate gene approach is based on the search for DNA polymorphism in genes that are expected, from knowledge of their physiological role for their position along the genome or for their level of expression, to have an influence on the target trait. Therefore, rather than searching for a relative gene randomly through the whole genome, it is desirable to focus on genes, which may already be suspected to have a role in the expression of the trait, that we want to investigate. Candidate gene approach has been proven to be extremely powerful for studying the genetic architecture of complex traits, which is far more effective and economical method for direct gene discovery.

In goat milk the four caseins; αs1, αs2, β and κ-casein coded by four closely linked autosomal genes namely *CSN1S1*, *CSN1S2*, *CSN2* and *CSN3* genes, respectively were identified and mapped to chromosome 6 in goat (Hayes *et al*., 2006). The *CSN1S1*, *CSN2* and *CSN1S2* genes encode the calcium-sensitive caseins and are evolutionarily related, whereas *CSN3* is a physically linked gene having the functional role of stabilizing the casein micelle (Rijnkels, 2002). The 4 caseins represent about 80 % of milk proteins. They are characterized by specific properties which are of low solubility at pH 4.6 and an organization in clusters of protein chains called micelles. These genes that encode the major milk proteins are thought of as candidate genes for the observed variation in protein composition (Rijnkels, 2002; Hayes *et al*., 2006).

As1-Casein: The αs_1-casein fraction is encoded by the *CSN1S1* gene. The CSN1S1 gene spreads over a quite large transcriptional unit of 16.7 kb and consists of 19 exons varying in length from 24 bp to 358 bp (Ramunno *et al*., 2004). In goats there are 17 co-dominant alleles. They are associated with different rates of protein synthesis ranging from 0 g·L−1 to 3.5 g·L−1 per allele. On the basis of the milk content of s1-casein, the variants can be classed into four groups: strong alleles (A, B1, B2, B3, B4, C, H, L, M) producing almost 3.5 g/L of s1-casein each; intermediate alleles (E and I: 1.1 g/L); weak alleles (F and G: 0.45 g/L) and null alleles (O1, O2 and N) producing no s1-casein (Rando *et al*., 2000; Ramunno *et al*., 2005). Goats carrying the strong variants produce milk with a significant higher total protein, casein, and fat content than goats carrying the weak variants.

The *αs1 casein* genotype had a significant effect on milk yield, fat content and protein content. A global effect of *CSN1S1* variation on protein content might be explained by the fact that CSN1S1 plays a pivotal role in casein transportation from the endoplasmic reticulum to the Golgi complex in mammary epithelial cells (Chanat *et al*., 1999). Besides, *CSN1S1* genotype seems to influence the structure and composition of milk fat globules (Cebo *et al*., 2012). Rheological properties of milk are also influenced by the *CSN1S1* genotype; for instance, milk from AA goats is associated with a firmer curd, a slower coagulation time, and better cheese yield than that of FF in French goat as point out by Vassal *et al*. (1994).

αs2-Casein: it is encoded by CSN1S2 gene ,the CSN1S2 gene is 18.5 kb long and consists of 18 exons which vary from 21 to 266 bp. Eight alleles have been identified, associated with three synthesis levels (Sacchi *et al*., 2005). The amount of s2-casein was associated with allergenic properties of milk. Variants A, B, C, E and F displayed a higher allergenic potency, measured by REAST, than did D and 0 (Marletta *et al.*, 2004). This gene is associated with a high content of casein to produce milk characterized by a minor diameter of micelles, a considerably higher percentage of protein, fat, total calcium and better parameters for curd firming time, curd firmness and cheese yield (Othman and Ahmed, 2007).

β-Casein : The *β*-casein fraction is encoded by the *CSN2* gene.The CSN2 gene is smaller than the other two Ca-sensitive casein genes, consisting of 9 exons ranging from 492 bp and 24 bp. β-Casein, which is the major goat's casein fraction in goat's milk, has long been considered to be monomorphic. The *CSN2* gene is composed of 3 protein variants that were found to be associated with normal β- casein content: *A*, *B* and *C* (Cosenza *et al.*, 2007).

K-casein: it is encoded by CSN3. Compared with the case sensitive caseins, CSN3 exhibits distinctive properties: it is the only glycosylated and hydrophilic casein, so it is soluble in a broad range of calcium ions and presents a lower phosphorylation level. Its signal peptide consists of 21 residues; while in Ca-sensitive caseins it is 15 residues long (Moreno, 2001). The κ-Casein gene includes 5 exons, 4 of them carrying more than 90% of the information to encode for the mature protein. The *CSN3* gene has been identified with 13 polymorphic sites in domesticated goats. Genetic polymorphisms of this gene were associated with protein and casein content (Cosenza *et al*., 2007).

Growth hormone (GH): it is a single polypeptide hormone produced in the anterior pituitary gland is a promising candidate gene marker for improving milk and meat production in goats and other farm animals. Growth hormone gene is encoded by 1800 base pairs (bp), consisting of 5 exons separated by four intervening sequences. Genetic polymorphisms of GH have been reported in various domestic livestock, mainly in cattle, and several studies have related association effects between bovine GH (bGH) polymorphisms and milk yield traits (Malveiro *et al*., 2001).

Signal transducers and activators of transcription (STATs): a family of transcription factors mediates the actions of a variety of peptide hormones and cytokines. STAT5, also known as mammary gland factor (MGF) and it was discovered initially as a PRL-induced transcription factor (Wakao et al., 1994). It is a key intracellular mediator of prolactin signaling and can activate transcription of milk protein genes in response to prolactin (Wakao *et al*., 1994; Dario *et al*., 2009). STAT5 exists in two isoforms: A and B which differ by a few amino acids in the carboxylic end of the protein molecule; separate genes code both of them.

Diacylglycerol O-Acyltransferase 1 (*DGAT1*) gene: The *DGAT1* gene is known to influence milk composition. This gene codes for a microsomal enzyme that catalyzes the last and limiting step of triglyceride synthesis, i.e. the transformation from a diacylglycerol to a triacylglycerol. This enzyme, which was first known for its action in the formation of adipose tissue, has been shown to play a key role in lactation (Smize *et al*., 2000).

PITX2 gene: The Paired-like homeodomain transcription factor 2 (PITX2) genes plays a critical role in cell proliferation, differentiation, hematopoiesis and organogenesis. This gene regulates several genes' expressions in the Wnt/beta-catenin and POU1F1 pathways, thereby probably affecting milk performance. The SmaI and RsaI polymorphisms were significantly associated with the milk fat content, milk lactose content and milk density in the Guanzhong (GZ) dairy goats, respectively. At the same time, the RsaI locus was also found to significantly link to the the second lactation milk yield, milk fat content, milk lactose content, milk density and milk total solid content ($P<0.05$ or $P<0.01$) in the Xinong Saanen (XNSN) dairy goats, respectively. These results indicated that the caprine PITX2 gene had the significant effects on milk traits. Hence, the RsaI and

SmaI loci could be regarded as two DNA markers for selecting superior milk performance in dairy goats (Zhao *et al*., 2013). There are a lot of candidate genes whose polymorphism has been linked with milk composition traits (Table 4). These genes belong to different functional categories related with lipogenesis (*ACACA*, *DGAT1*, *DGAT2*, *ME1*, and *SCD*); lipolysis (*LPL* and *LIPE*); milk fat globule membrane proteins (*BTN1A1* and *MFGE*); hormone signaling (*GH* and *PRLR*); and transcription factors regulating gene expression (*PITX2*, *POUF1*, and *STAT5*).

Therefore, the polymorphisms of these genes contribute genetic variation in yield and quality of goat milk. The application of molecular technologies for genetic improvement relies on the ability to genotype individuals for specific genetic loci. Knowledge of these genes in dairy goat breeding programs has potential to substantially increasing selection differences and improves the accuracy of selection.

Economically important traits in dairy goat

DNA technology has resulted in the identification of loci and chromosomal regions that contribute to phenotypic variation in economically important traits (Dekkers, 2004). Identifying and confirming Quantitative Trait Loci (QTL) is the first step in the process that could lead to Marker Assisted Selection (MAS) or Gene Assisted Selection (GAS).The selection for chromosomal areas that directly contribute to the genetic variation of traits of economic importance will lead to increased genetic progress (Table 4) and offers the opportunity to better understand and exploit phenotypic variation (Dekkers, 2004).

Table 4: Quantitative trait loci for economically important traits in goats.

<table>
<tr><th>Type of trait</th><th>Specific traits</th><th>Chromosomes</th><th>Breed</th><th>References</th></tr>
<tr><td rowspan="9">Milk traits</td><td>Milk yield</td><td>6, 14</td><td>-</td><td rowspan="3">Roldán et al. (2008)</td></tr>
<tr><td>Fat content</td><td>14, 20</td><td></td></tr>
<tr><td>Protein content</td><td>3, 20</td><td></td></tr>
<tr><td>Milk yield</td><td>21</td><td>Saanen and Alpine</td><td>Martin et al.(2017)</td></tr>
<tr><td>Protein content</td><td>1, 6, 21</td><td>Saanen and Alpine</td><td>Martin et al.(2017)</td></tr>
<tr><td>Fat Content</td><td>8, 14, 21</td><td>Saanen and Alpine</td><td>Martin et al.(2017)</td></tr>
<tr><td>Protein content</td><td>1</td><td>Alpine</td><td>Martin et al.(2017)</td></tr>
<tr><td>Fat Content</td><td>8</td><td>Alpine</td><td>Martin et al.(2017)</td></tr>
<tr><td>Milk yield, protein yield, Fat Yield</td><td>19</td><td>Saanen</td><td>Martin et al.(2017)</td></tr>
<tr><td rowspan="3">Growth traits</td><td>Body weight, average daily gain</td><td>5,2,1</td><td>Rayini</td><td>Mohammad et al. (2009)</td></tr>
<tr><td>Weaning weight</td><td>19, 16</td><td rowspan="2">Angora</td><td rowspan="2">Visser et al. (2013)</td></tr>
<tr><td>Birth weight</td><td>8,4, 17, 27</td></tr>
<tr><td rowspan="3">Resistance to gastrointestinal nematodes</td><td>Fecal egg count</td><td>22,6</td><td>Creole</td><td rowspan="2">De La Chevrotière et al. (2012)</td></tr>
<tr><td>Packed cell volume</td><td>5,9,21</td><td></td></tr>
<tr><td>Worm egg count</td><td>23</td><td>Angora, Cashmere</td><td>Bolormaa et al. (2010)</td></tr>
</table>

In Ethiopia, Tesfaye (2004) studied 11 indigenous goat populations using 15 microsatellite markers and categorized them into 8 genetic clusters namely: Arsi-Bale, Abergelle, Afar, Keffa, Gumuz, Woyto-Guji, highland, and eastern and southeastern goats. Lately, Getinet (2016) evaluated the genome-wide genetic diversity and structure of 14 Ethiopian goat populations using SNP CHIP array and grouped them into seven goat types.

Table 4: The observed heterozygosity (*HO*) expected heterozygosity (*HE*) and fixation indices of subpopulation(*FIS*).

Population	N	HO	HE	FIS
Agew	28	0.373	0.380	0.018
Arsi-Bale	29	0.367	0.381	0.034
Abergelle	30	0.373	0.380	0.011
Afar	33	0.378	0.388	0.022
Woyto-Guji	25	0.373	0.381	0.008
Nubian	34	0.359	0.390	0.073
Barka	8	0.408	0.407	-0.013
Ambo	30	0.371	0.381	0.011
Gondar	27	0.378	0.381	0.000
Long eared Somali	27	0.378	0.381	0.002
Harergh hihgland	29	0.381	0.388	0.016
Kaffa	30	0.351	0.373	0.045
Gumuz	27	0.371	0.378	0.013
Short eared somali	20	0.379	0.389	0.017

Source: Getinet (2016).

Disease constraints

Major diseases reported were Ceonurosis (Azurit), Kurdid (external parasites), Mieta (pastorolosis), Wekei (blackleg) and Hasakut (internal parasites) as the farmers pointed out with index values 0.24, 0.22, 0.21, 0.19 and 0.13 respectively (Table 5). Prevalence of diseases and parasites were mentioned as one of the most important constraints that caused high mortality and morbidity of sheep in study PAs. More specifically, respondents emphasized that Coenurosis locally known as 'Azurit/Zarti' was the major disease which caused them to lose large number of flocks and stressed the need for urgent interventions. Other reported important health constraints were external parasites, Pasteurellosis, Internal parasites and Blacklag in their order of importance respectively.

Table 5: Disease and parasites that affect sheep production as ranked by the respondents.

Disease name								
Local name	**Common name**	**1st**	**2nd**	**3rd**	**4th**	**5th**	**Index**	**Rank**
Azurit/Zarti	Coenurosis	35	58	55	23	0	0.24	1
Kurdid/kumal	Ext.parasites	40	31	33	41	21	0.22	2
Mieta	Pasteurellosis	22	45	55	34	2	0.21	3
Hasakut	Int. Parasites	26	23	17	12	2	0.19	4
Wekie	Blacklag	34	21	14	10	9	0.13	5

Index= (5 for rank 1) + (4 for rank 2)+ (3 for rank 3) + (2 for rank 4) + (1 for rank 5) divided by the sum of all weighed mentioned by the respondent

This result is in line with the research finding of Getachew Legesse *et al.* (2014), who emphasized that next to feed shortage, diseases and parasites were the major bottle necks to sheep production .According to Markos Tibbo (2006), high prevalence of diseases and parasites cause high mortality that diminishes the benefits of reproductive performance of sheep. Other authors also pointed out that diseases and parasites were among the top challenges in sheep production in Ethiopia (Zewudu Edea *et al*., 2012; Helen Nigussie *et al*., 2013).

Veterinary service constraints

Inadequate veterinary service, shortage of veterinarian, shortage of drugs, few veterinary clinics and expensive drug price were mentioned as major bottle necks with corresponding index values 0.24, 0.22, 0.21, 0.19 and 0.13 respectively (Table6).

Table 6: Reported veterinary service related constraints by households.

Constraints	**1st**	**2nd**	**3rd**	**4th**	**5th**	**Index**	**Rank**
Inadequate veterinary service	41	58	55	23	0	0.24	1
Shortage of veterinarian	40	31	33	41	21	0.22	2
Shortage of drugs	22	45	55	34	2	0.21	3
Few veterinary clinics	26	23	17	12	2	0.19	4
Expensive drug price	34	21	14	10	9	0.13	5

Index= (5 for rank 1) + (4 for rank 2) + (3 for rank 3) + (2 for rank 4) + (1 for rank 5) divided by the sum of all weighed mentioned by the respondent

Achievements

Achievements made in sheep production

Genetic improvement requires long term investments, appropriate polices, strategies and well-designed breeding programs as evidenced in developed countries. In the absence of such requirements, sustainably genetic improvement could not be achieved as observed in developing countries where breeding programs such as crossbreeding and on-station nucleus herd selection have been collapsed without benefiting the smallholder farmers (Kosgey *et al.*, 2006; Philipsson et al., 2011). So far, Ethiopia had no sheep breeding policy designed with the state of art technology that most developed nations have been applying frequently but now the policy already approved. The Sheep breeding strategy is being reviewed and expected to be approved in 2018. Nearly, all phenotypic and molecular characterization studies have been conducted as academic fulfillments in higher education institutions. Often in practice, academic research typically has little influence on policy development due to poor linkage of the researcher and decision makers. In developing countries, it is crystal clear that decision makers are politicians and their priority is staying in power as much longer as their life than solving developmental issues. This is a clear indication in Ethiopia that a country without breeding policy and strategy for a resource that puts the country in number 9thposition in the world, only in terms of sheep population size (http://www.fao.org/faostat).

Within breed selection is an important option to explore genetic variations of indigenous sheep breeds (Kosgey *et al.,* 2006). In Ethiopia, selective breeding for some sheep breeds have been conducted for decades although significant changes not yet achieved. Through a review of Ethiopian sheep breeding research, Gizaw *et al.* (2013) reported that central nucleus based breeding programs have been tried for Menz, Horro and Afar sheep breeds.

So far, selective breeding resulted in notable genetic improvement in Menz sheep breed, which is about 7 kg body weight improvement over the base population achieved in 8 to 9 generations (Gizaw *et al.*, 2011). More recently, community based pure breeding selection scheme has been tested for Menz, Bonga and Horro indigenous sheep breeds in pilot areas (Haile *et al.*, 2011; Mirkina *et al*., 2012). Early results reported so far could be considered as promising (Gizaw *et al*., 2013; Haile *et al*., 2014) although it covers limited villages when viewed from the country's sheep population size perspective. The traits included for the three breeds community based program are growth traits, lamb survival, twining rate and fleece weight. Appreciable genetic improvement has been achieved in the Menz community based sheep selection program with body weights at birth, 3 and 6 months of age increased by 0.42, 2.29 and 2.46 kg, respectively, in the third generation over those in the base generation (Gizaw *et al*., 2013). Although not formally studied, the impact of selective breeding both on the sheep industry and livelihood development of smallholder level is zero if not below.

Sheep breeding practice at smallholder level is almost entirely based on indigenous genotypes. However, crossbreeding of indigenous sheep with exotic breeds has been practiced for several decades in different part of the country. Despite long period practices, such strategy did not bring significant improvement in performance (Kosgey, *et al*., 2006; Gizaw *et al*., 2013). Because it requires not only importation of exotic breeds with high cost but also maintaining of pure breeds, multiplying and distribution of crossbreeds. In addition, deterioration in the survivability of crossbreeds in low-input production system, especially as the exotic blood level increases, is the main challenging issue.

Community based sheep and goat breeding programs in Ethiopia

Unlike the conventional hierarchical breeding approach, Community Based Breeding Programs (CBBP) basically needs a detailed understanding of the community's indigenous knowledge regarding breeding practices and objectives. It also considers the production system holistically and involve the local community at every stage, from planning to operation of the breeding programs and is a recently advocated option for tropical traditional low input livestock production systems (Sölkner-Rollefson, 2003; Baker and Gray, 2004; Wurzinger *et al*., 2011).

Gizaw *et al*. (2013) defined CBBP as village based breeding activities planned, designed, and implemented by smallholder farmers, individually or cooperatively, to effect genetic improvement in their flocks and conserve indigenous genetic resources. The authors also stated that the process should be facilitated, coordinated, and assisted by outsiders (development and research experts in governmental and non-governmental organizations). Designing and implementing a sustainable participatory breeding program, that would benefit the livestock keeping communities and the national economy at large, is not an easy task, rather it is demanding and worthwhile. In order to design an appropriate and feasible CBBP, selection of the communities and breeds, analysis of production system (including livelihood strategies), characterization (phenotypic and molecular) of the breeds, definition of the breeding objectives and evaluation of the breeding program should be done very rigorously (Sölkner *et al*., 1998; Kosgey *et al*, 2006; Haile *et al.,* 2011). Lately, a variety of community based cooperative breeding programs have been initiated, designed and implemented in Ethiopia. The most genetically efficient and operationally feasible scheme needs to be adopted (Gizaw *et al.,* 2013).

The first CBBP in Ethiopia, on sheep, was implemented by ICARDA, ILRI, the University of Natural Resources and Life Sciences (BOKU) and national research institutes through an Austrian Development Agency (ADA) funded project from 2007 to 2011 (Gutu *et al.*, 2015). The program was applied in four sites (Bonga, Horro, Menz, and Afar) across four regional states of Ethiopia (Duguma, 2011; Mirkena, 2011). The more successful breeding programs in Menz, Horro and Bonga were continued under the CGIAR research program on livestock and fish and expanded in to two new sites, Doyogana and Atsbi (for sheep) and one Abergelle (for goats) (Solomon, 2014; Gutu *et al.,* 2015). In these community based breeding programs, indigenous sheep and goats that have special adaptive, productive, reproductive and disease resistant features were selected by the community and mated with their selected counterparts (Mirkena, 2011; Solomon, 2014).

To date, the community based breeding programs in Ethiopia have realized several achievements. For example, the negative selection has been reverted as fast growing lambs and kids are being retained for breeding instead of ending up in markets (Gutu *et al.,* 2015). Increment of the market outlet through more births, bigger lambs at birth and weaning, reduction of mortality rates due to the combination of breeding with improved health care and feeding, better awareness about inbreeding and the need for breeding rams, formation of well-functioning cooperatives, improved performance of sheep and goats and commercialization of breeding rams were also the major achievements of the CBBP (Haile *et al.,* 2011;Gutu*et al.,* 2015).Community based selection for Menz, Horro and Bonga sheep started recently (Haile *et al*., 2011; Mirkina *et al*., 2012).

Despite the achievements, the CBBP had been tackled by several challenges that limit their impact to maximize genetic gains. The challenges include, but not limited to: disease prevalence, feed shortage, poor access to market, selling selected breeding males, poor cooperation with district extension system, delaying selection of breeding males and mating of females by unselected males (ibid). Hence, mechanisms should be devised to address these challenges. One such mechanism would be creating a strong link between the nearby higher education institutions and research centers to sustainably support the breeding programs and alleviate the challenges through their research and community service endeavors. The financial, social and economic feasibility of the breeding programs should also be assessed for sustainability of the programs.

Achievements made in goat production

The country designed livestock master plan that promotes genetic improvement of the indigenous breeds including small ruminants, presence of ample information on the genetic resources of the country and the presence of research for development approach by some research.

Community based breeding program of goat in Ethiopia

Community-based breeding program refers to village-based breeding activities planned, designed, and implemented by smallholder farmers, individually or cooperatively, to effect genetic improvement in their flocks and conserve indigenous genetic resources when it within breed selection (Solomon *et al.*, 2013). Goat breeding strategy in Ethiopia had focused on crossbreeding by importing exotic goat breeds for several years with the objectives of meat and milk production. However, as many attempts of livestock genetic improvement program had failed in the tropics, in Ethiopia, also goat genetic improvement through crossbreeding had not succeeded and sustained due to incompatibility of the breeding objectives and the management approaches of the existing production system of the area (Ayalew *et al.*, 2003). Generally, crossbreeding program in developing countries as well as in Ethiopia has been failed due to consultation with and involvement of farmers or pastoralists indigenous practices (Aynalem *et al.*, 2011). Failure of the conventional hierarchical breeding schemes has led to CBBP being suggested as viable options for the genetic improvement programs of small ruminants in low-input, smallholder production systems (Solomon and Tesfaye, 2009).

International Livestock research institute (ILRI) and its partners have implemented CBBP in in five zones (West Shoa, Konso, Wag Abergelle, Tanqua-Abergele and North Gondar) of Ethiopia (Tadelle Dessie *et al*., 2014). This breeding program has implemented through selection within the indigenous goat breeds. Selection is the basis for any flock improvement, can be performed based on visual appraisal, performance and the combination of these two methods for identifying traits of economic importance (the first step of selection program) such as growth rate (Weights at birth, at weaning, at age of selling…), reproductive efficiency, milk production and maternal instincts. These performances can be evaluated based on recorded information or keeping good records (Termanini *et al.*, 2012). Breeding program is evaluated by the genetic gain achieved towards the breeding objectives. The evaluation tool tells that how the predicted selection response is resembled to realize selection response, in general, describes how big is the genetic response to selection (Oldenbroek and Waaij, 2015) based on important traits (Aynalem *et al*., 2011). Thus, monitoring and evaluating breeding program in the community has an advantage of disseminating the superior genotype in to the wider animal population (FAO, 2015).

Challenges

The main challenges in small ruminant productions and genetic improvements are the lack of well established and sustainable breeding program and schemes. The absence of national database systems on small ruminant resources and poor recording systems are the main critical reasons which hinders the trends of the genetic improvement made. Underutilization of modern genetic improvement tools, unplanned crossbreeding schemes as well as inadequate, un-sustained financial support for breeding programs are also the causes to promote production and productivity. Besides, Inadequate technologies that can transform the small ruminant sub-sector and enable utilization of the wealth of genetic resources and the presence of negative selection as a result of common practice of selling superior males with uncontrolled mating are the other problems of the sector. The researches conducted in different organizations/ sectors are un-integrated and uncoordinated. The development effort made among the stake holders such as research centers/ institutes, universities, ministries and NGO's, are uncoordinated and lack complementarities. Inbreeding and its deleterious effects, interbreeding among the local breeds, inadequate support and lack of commitment to support breeding programs and impacts of climate change on feed and water availability are also impacted significantly.

Lesson Learnt

There is also sufficient information and one can learn that the nation has relatively large flock size and higher dependency on small ruminants in the highlands. The presence of diverse small ruminant genotypes with different prolificacy levels and high domestic and export demand as well as the relatively short cycle of small ruminants (8-9 months between the lambing/kidding) tell the feasible invest option in this sector. Besides, the presence of exotic small ruminant breeds fitting the low input system in some areas and preferred by smallholder producers and investors and the emerging of new stakeholders/target groups in the sector i.e agribusinesses, investors, microfinance, women and youth entrepreneurs and community based breeding programs can be a base for small remnant trait selection and genetic improvement . A research agenda that has proven to be effective in addressing some of above problems has been refined at research centers and universities through time, building on experiences in different dry regions. Within the socio-political context of a country, it is important to inventory and analyze existing policies that affect small ruminant production, markets and marketing, price regulations, product quality, and natural resource management. Careful analysis of this inventory could contribute to the design and refinement of research and development actions, and determine the investment needed to promote appropriate policies and interventions. There is a need to examine the markets with attention to threats/risks to production, and the principal factors hindering market access. Priority in planning research and development efforts should go to the experience gained by farmers' organizations and to linkages to markets.

The long time aspiration of having a breeding policy at national level was given due attention. Accordingly, breeding policy at national level was recently approved. Recent endorsement of the establishment of national animal genetic improvement institute is a way forward to better guidance and utilization of the un-tapped genetic resources in small ruminants. Germplasm acquisition and import-export of germplasm can be well handled by the recently implemented act. The high public investment in breeding infrastructure and resources in placed (breeding centers, flocks, exotic germplasm) are suitable resources to work on genetic improvement areas. The recent high research output in design of breeding programs for smallholder system could serve a lot if implemented with due consideration. Evidences from on-station selection work on Menz sheep indicated increased body weight when managed with better management and selection with appropriate feeding system. This could help the Menz sheep reach about 30 kg at yearling age. A recent study at Debre-Birhan Research Center indicated that an encouraging result on the early finishing ability of both male and female crossbred lambs at early age. Accordingly, crossbred male sheep supplemented 300, 600 and 900 gram of concentrate per day on top of grazing, reached final weight of 34.5, 39.8 and 41.2 kg, respectively at about 10 months. Crossbred male lambs born from the newly imported meat breed of Dorper also demonstrated very good growth performance under different concentrate supplementation levels. In a 90 days feeding trial of ram lambs stating feeding at about 7 months of age on average initial weight was doubled.

CONCLUSION

In Ethiopia, the current estimates indicated that the indigenous sheep and goats' population are 58.6 million with vast diversity .The genetic diversity exists between and within breeds which can provide the raw materials for breed improvements and for the adaptation of the populations to changing environments and changing demands. Many phenotypic, production system and reproductive performance works conducted by different authors about small ruminants. But these works could not help to increase production and reproductive performances and remains low. To improve performances, exotic sheep breed were introduced to the country in different times. Dorper and Awassi sheep breeds were some of the breeds introduced for sheep improvement and some of the exotic dairy goat breeds that have been introduced were Anglo Nubian, Damascus or Shami, Saanen, and Toggenburg. However, the absence of national database systems and poor recording systems are the critical reason which hinders the trends of the genetic improvement made. Recently, the livestock master plan of the country gives attention to the selection of indigenous breed so as to have sustainable breeding and increasing productivity. Recent trends show that also unless focused on trait selection like milk and meat traits, the expected genetic improvement may not be achieved. For instance, there are indicates of milk production from indigenous goat breeds in the country which ranges from 0.28 kg/day for Afar goat to 1.13 kg/ day for Arsi Bale goat. On the other hand, under smallholder management it ranges from 0.29 kg/day for Arsi Bale goat to 0.55 kg/day for Begait. These variations between breeds indicate higher probability of enhancing milk production through phenotypic and marker assisted selection.

Internationally, there are candidate genes and traits for milk production in goats which can help for selection. for instance, for goat milk enhancement , the four caseins; αs1, αs2, β and κ-casein coded by four closely linked autosomal genes namely *CSN1S1*, *CSN1S2*, *CSN2* and *CSN3* genes, respectively were identified and mapped to chromosome 6. The *CSN1S1*, *CSN2* and *CSN1S2* genes encode the calcium-sensitive caseins and are evolutionarily related, whereas *CSN3* is a physically linked gene having the functional role of stabilizing the casein micelle. The 4 caseins represent about 80 % of milk proteins. They are characterized by specific properties which are of low solubility at pH 4.6 and an organization in clusters of protein chains called micelles. These genes that encode the major milk proteins are thought of as candidate genes for the observed variation in protein composition.

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