

## Genetic Distance and Differentiation among Cattle Breeds in Ethiopia: A Review

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### ABSTRACT

*Studies conducted on genetic diversity and population differentiation of Ethiopian cattle breeds have been reviewed. Out of 22-28 phenotypically and geographically recognized cattle breeds in Ethiopia about 17 breeds were characterized at molecular level. The population differentiation indicated that Ethiopian breeds significantly differ from taurine referenced Hanwoo and Friesian breeds. They exhibit lower observed heterozygosity than Hanwoo and Friesian breeds. Most studies in Ethiopia witnessed low between breeds and high within breed variations. The genetic distance among Ethiopian breeds did not necessarily depend on geographic distance. Zero genetic distance was estimated between Boran and Horro and between Abigar and Sheko populations based on mitochondrial cytochrome b gene analysis. From Ethiopian breeds, better genetic diversity was recorded in Abergelle (0.795) than Bagait (0.590), Afar (0.559), Raya (0.582), Arado (0.636), Fogera (0.541) and Irob (0.527) breeds. Similarly higher heterozygosity was found in Horro breed (0.387) followed by Ambo (0.386), Arsi (0.376), Boran (0.374) and Danakil (0.363). The low genetic diversity and heterozygosis observed in some populations could reflect inbreeding due to uncontrolled mating. Generally the high within breed variation observed in Ethiopia cattle population could create favorable condition for further improvement through selection. In addition, the previous studies might indicate higher admixture among Ethiopian cattle populations and absence of artificial selection pressure. The study conducted at molecular level so far were fragmented and not exhaustively included all breeds that were classified by phenotype or geography. Thus it is essential to carry out further studies which encompass all breeds in order to have full picture of breed diversity and differentiation among Ethiopian breeds. Furthermore, it will have an immense impact if the studies started on molecular characterization advanced to the level of utilizing genomic information for genetic improvement, resource conservation and disease resistance.*

**Keywords:** Cattle, Heterozygosity, Genetic diversity

### INTRODUCTION

Ethiopia has huge cattle population with an estimated 60.39 million heads (CSA, 2017). Of these the indigenous cattle population accounted for 98.5% of the national cattle population. The cattle production has been noticeably contributed for family nutrition, income generation, social values and overall livelihood improvement for several million farmers and pastoralists. According to Land O'lakes (2010), 83% of milk produced in Ethiopia comes from cattle. In pastoral area milk consumed by pastoral children accounted for 67% of the mean daily energy they require and 100% of their protein requirements during the wet season (Sadler and Catley, 2009). Furthermore, it was noted that adopter of crossbred cows technology generated 44% more income than non-adopters in some milk shed area of Ethiopia (Agajie Tesfaye *et al.*, 2016).

The country is believed to have diverse cattle genetic resources distributed in different part of the country (Rege, 1999; EBI, 2016; Abreham Assefa and Abebe Hailu, 2018). It is indispensable to understand and document the diversity, genetic relationship and admixture of the available breeds for future genetic improvement, conservation and utilization of genetic resources. Most of breed classification and characterization in Ethiopia were conducted based on morphological features, historical evidence and geographical habitation. However, the animal movement, environmental factors and

admixture (exchange of genetic material) could limit the accuracy of phenotypic characteristics (Hanotte and Jianlin, 2005).

Application of genomic information is more advanced method and being practiced for evolutionary study, disease identification, genetic diversity, genetic conservation, genetic improvement and forensic studies (Kotze et al., 2000; Carlos et al., 2002; Shi et al., 2010; Gubta et al., 2015). The genomic evaluation methods have created favorable condition to study the genetic relationship between breeds and classification as compared to conventional method. Furthermore, the genetic improvement through progeny testing and application of best linear unbiased prediction (BLUP) has been significantly supported by molecular technique as it improves the accuracy of estimation of breeding value and genetic progress. Different studies were conducted on Ethiopian cattle population using molecular techniques. Having information on past research works in this regard will help to exploit the available potential and identify the gap for further studies. Hence, the aim of this paper was to review the genetic diversity and relationship among Ethiopian cattle breeds characterized at molecular level and suggest future research points for genetic improvement programs of cattle.

## **METHODOLOGY**

All available published papers on genetic distance and differentiation among cattle populations in Ethiopia were used for this review. A total of 35 papers published from 1999 to 2018 were considered. Rege (1999) and EBI (2016) were used as references for population (breed) classification and then to identify population that was not studied at molecular level so far in Ethiopia. Parameters included in the reviewed papers are proportion of taurine alleles, expected and observed heterozygosity, genetic distance and population differentiation. Genetic markers used, locations studied, breeds considered and results of different studies were compared and discussed.

## **FINDINGS**

### **Molecular markers used for genetic analysis**

The most widely used markers for breed characterization in Ethiopia are single-nucleotide polymorphism (SNP), microsatellites, and dam and sire line markers (mtDNA and Y-chromosome). A single-nucleotide polymorphism (SNP) is a variation in a single nucleotide that occurs at a specific position of DNA sequence. Currently, analyses of SNP markers are used for diversity analysis and genome-wide studies. This is attributed to abundance in the genome, dispersed equally throughout the genome, genetically stable, and suitable to automated analysis to measure genetic variations found within and between populations (McKay et al., 2008; Lin et al., 2010; Zewdu Edea et al., 2012). Several authors used SNP markers to characterize different species and breeds in East African countries. For instance genetic diversity of 6 cattle populations in Ethiopia (Zewdu Edea et al., 2012), 3 local strain of Tanzanian Zebu, Boran and Friesian (Msalya et al., 2017) and 6 Ethiopian sheep population (Zewdu Edea et al., 2017) were conducted using SNP markers.

Microsatellites have been commonly used as a marker for DNA profiling in cancer diagnosis, kinship analysis and forensic identification over the past years. Similarly, it has been widely used to study the genetic diversity and other characterization of livestock species. They are highly informative, co-

dominant, multi-allele genetic markers that are experimentally reproducible and transferable among related species (Mason, 2015). According to Vieira et al (2016) and Mburu and Hanotte (2005), it is a short sequence of 1 to 5 bp or more nucleotides which are randomly repeated. Microsatellites occur at thousands of locations within an organism's genome (Moniruzzaman et al., 2015; Ambreen et al, 2015, Anand et al, 2017).

Microsatellites markers were used for genetic analysis of cattle breeds in Ethiopia (Hailu Dadi et al., 2008), cattle breeds in East Africa (Adhiambo, 2002), Sheep breeds in China (Chen et al., 2016), Cattle breeds in Asia (Shi et al., 2010) and domestic cattle in African, Europe and Asia (Freeman et al., 2005). On the other hand Hanotte et al. (2000) studied the geographical distribution and the frequency of an indicine and a taurine y specific allele amongst African cattle breeds using Y chromosomes as it is transmitted paternally. In addition Li et al. (2007) explore the paternal gene pool and the mechanisms behind the genetic structure of 6 North Ethiopia breeds.

Mitochondrial DNA (mtDNA) is essential tool to study evolution and population genetics. The mode of maternal transmission of mtDNA makes uniform population of mtDNA transmitted through the female germ line from one generation to the next (Srirattana and John, 2017). As a result, mtDNA has been used as a marker for phylogenetic studies since control region of mtDNA has potential for high mutation rate, lack of recombination and maternal inheritance. Different studies were undertaken using mtDNA for phylogenetic analysis. For instance, Getinet Mekuriaw et al. (2018) and Hailu Dadi et al. (2009) studied the maternal ancestry and diversity of Ethiopian cattle population and Kim et al (2013) has also estimated genetic diversity and phylogenetic status for the Korean Chikso breed.

### **Proportion of taurine alleles in Ethiopian breeds**

According to Rege (1999), there were 22 phenotypically characterized cattle breeds/populations in Ethiopia. However, this figure was escalated to 28 in the report of EBI (2016). Of these, about 17 cattle breeds were characterized at molecular level (Table 1). The group of breeds characterized and compared at molecular level at a time consist of ten breeds by Hanotte et al. (2000), three by Adhiambo, (2002), five by Fedlu Hassen et al. (2007), seven by Li et al. (2007), ten by Hailu Dadi et al. (2008), five by Zewdu Edea et al. (2013) and five by Getinet Mekuriaw et al. (2018).

Hanotte et al. (2000) had detected small proportion of the taurine alleles in Y chromosome of Sheko (10%), Abigar (7%) and Arsi breed (6%) of Ethiopia (Table 1). Several literatures classify Sheko breed into taurine type based on phenotypic characterization. The lower proportion of Y chromosome (10%) detected in Sheko breed may be justified in two ways. The first is, originally this breed could be a crossbred of taurine with zebu or sanga, and the other is, the indigenous taurine Y chromosome has been nearly eliminated from Sheko breed due to long term crossbreeding with zebu or sanga. Even though the cause of detection of taurine alleles in Y chromosome of Abigar and Arsi need further investigation, it could be related with sampling of individuals from the area where crossbreeding conducted or these breeds may have remnant of taurine alleles. Furthermore, studies on mtDNA revealed that there was no haplotype observed in Ethiopian cattle to cluster with the reference *Bos indicus* group (Hailu Dadi et al., 2008; Getinet Mekuriaw et al., 2018). The authors suggested that the zebu mtDNA of zebu cattle could be lost due to recurrent disease and rinderpest epidemics as mtDNA is more sensitive than nuclear genes to demographic processes such as bottleneck and fragmentation of population.

Table 1. List of genetically characterized cattle breed of Ethiopia

No	Breed name	Breed group	Location	Proportion of Y allele % *		References (studied by)
				indicine	taurine	
1	Boran	Zebu	South Ethiopia	100	0	Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Zewdu Edea et al. (2012); Zewdu Edea et al. (2013); Hanotte et al. (2000); Getinet Mekuriaw et al. (2018)
2	Arsi	Zebu	Central highlands of Ethiopia	94	6	Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Zewdu Edea et al. (2012); Zewdu Edea et al. (2013); Hanotte et al. (2000); Fedlu Hassen et al. (2007)
3	Ambo	Zebu	Central highlands of Ethiopia			Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Zewdu Edea et al. (2012); Zewdu Edea et al. (2013)
4	Danakil	Sanga	East Ethiopia	100	0	Zewdu Edea et al. (2012); Zewdu Edea et al. (2013); Hanotte et al. (2000); Adhiambo (2002); Li et al. (2007); Hailu Dadi et al. (2008); Hailu Dadi et al. (2009)
5	Horro	Zenga	West Ethiopia	100	0	Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Zewdu Edea et al. (2012); Zewdu Edea et al. (2013); Hanotte et al. (2000); Fedlu Hassen et al. (2007); Getinet Mekuriaw et al. (2018)
6	Bale	Zebu	South East Ethiopia	100	0	Hanotte et al. (2000)
7	Fogera	Zenga	North Ethiopia	100	0	Hanotte et al. (2000); Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Li et al. (2007)
8	Abigar	Sanga	West Ethiopia	93	7	Hanotte et al. (2000); Adhiambo (2002); Fedlu Hassen et al. (2007); Getinet Mekuriaw et al. (2018)
9	Raya-Azebo	Sanga	North Ethiopia	100	0	Hanotte et al. (2000); Li et al. (2007); Hailu Dadi et al. (2008); Hailu Dadi et al. (2009)
10	Sheko	Taurine	West Ethiopia	90	10	Hanotte et al. (2000); Adhiambo (2002); Fedlu Hassen et al. (2007); Hailu Dadi et al. (2008); Hailu Dadi et al. (2009); Getinet Mekuriaw et al. (2018)
11	Ogaden	Zebu	East Ethiopia	100	0	Hanotte et al. (2000); Hailu Dadi et al. (2008)
12	Begait	Zebu	North Ethiopia			Li et al. (2007)
13	Arado	Zenga	North Ethiopia			Li et al. (2007)
14	Abergelle	Zenga	North Ethiopia			Li et al. (2007)
15	Irob	Zenga	North Ethiopia			Li et al. (2007)
16	Guraghe	Zebu	Central highlands			Fedlu Hassen et al. (2007); Getinet Mekuriaw et al. (2018)
17	Adwa	Zebu	North Ethiopia			Hailu Dadi et al. (2008); Hailu Dadi et al. (2009)

\*(Proportion of Y allele %, Hanote et al., 2000)

## Genetic diversity and differentiation of Ethiopian cattle populations

Genetic diversity is usually described by level of allelic polymorphism, expected and observed heterozygosity. Zewdu Edea et al. (2013) found that the Ethiopian cattle breeds (Horro, Danakil, Boran, Arsi and Ambo) were less polymorphic (mean  $MAF \geq 0.05 = 83.96\%$ ) than Hanwoo breed (95.21%) which was considered as a reference of taurine breeds. Similarly the Hanwoo breed exhibit higher observed heterozygosity (0.410) as compared to Danakil (0.363), Horro (0.387), Borana (0.374), Arsi (0.376) and Ambo (0.385). However, the values estimated for observed heterozygosity by Zewdu Edea et al. (2013) are lower than that of Hailu Dadi et al. (2008) who found 7.03, 7.30, 7.47, 7.07, 7.17 and 7.30 for the same breeds, respectively. The difference could be attributed to molecular markers used, type of laboratory procedures followed, sample size and area coverage of each sample collected. On the other hand, about 10-20 percent of the loci from 10 studied cattle populations (Hailu Dadi et al., 2008) and 6 percent SNPs markers from 5 cattle breeds (Zewdu Edea et al., 2013) were significantly deviated from HWE.

Li et al (2007) noted that Y-chromosome haplotype diversity was generally low in north Ethiopian cattle (0.527–0.636) than that of European Holstein-Friesian (0.645) except Abergelle breeds (0.795) which show higher diversity than the other 6 breeds. This is in line with the finding of Hailu Dadi et al (2009) and Getinet Mekuriaw et al. (2018) who noted 100 and 95.45% genetic variance accounted by within population variation respectively based on mtDNA analysis. Most studies in Ethiopia witnessed low between breeds and high within breed variations (Fedlu Hassen et al., 2007; Li et al., 2007; Hailu Dadi et al., 2008; Zewdu Edea et al., 2013). This might also show that most cattle populations in Ethiopia have common source of origin. The lower heterozygosity (diversity) in Ethiopian breeds than taurine counterparts could be attributed to higher inbreeding (due to uncontrolled mating) and recurrent drought which causes loss in genetic diversity.

Among Ethiopian cattle populations' better genetic diversity was recorded in Abergelle breed (0.795) than Bagait (0.590), Afar (0.559), Raya (0.582), Arado (0.636), Fogera (0.541) and Irob (0.527) (Li et al., 2007). Similarly Zewdu Edea et al. (2013) estimated higher heterozygosity for Horro breed (0.387) followed by Ambo (0.386), Arsi (0.376), Boran (0.374) and Danakil (0.363). Hailu Dadi et al (2008) estimated greater observed heterozygosity in Ambo (0.700), Horro (0.692) and Fogera (0.691) than other seven breeds (Boran, Arsi, Adwa, Ogaden, Raya, Danakil, and Sheko).

The analysis of population differentiation between Ethiopian and Hanwoo and with Friesian breeds revealed significant variation at molecular level (Adhiambo, 2002; Li et al., 2007; Hailu Dadi et al., 2008; Zewdu Edea et al., 2013). Fedlu Hassen et al. (2007) clustered Sheko differently from other 4 breeds (Horro, Sheko, Arsi, Abigar and Guraghe highland) and found the smallest genetic divergence between Guraghe highland and Abigar followed by between Guraghe highland and Arsi. Based on this, the authors pointed out that the genetic distance did not necessarily depend on geographic distance as Guraghe highland is more close to Arsi than Abigar breed geographically. Furthermore, zero genetic distance was estimated between Boran and Horro and between Abigar and Sheko populations based on mitochondrial cytochrome b gene analysis (Getinet Mekuriaw et al., 2018).

The pair-wise population differentiation ( $F_{ST}$ ) and Reynolds' genetic distance analysis conducted by Zewdu Edea et al. (2013) also indicated lower genetic distance among Horro, Ambo and Arsi breeds than with Danakil and Boran populations (Figure1).

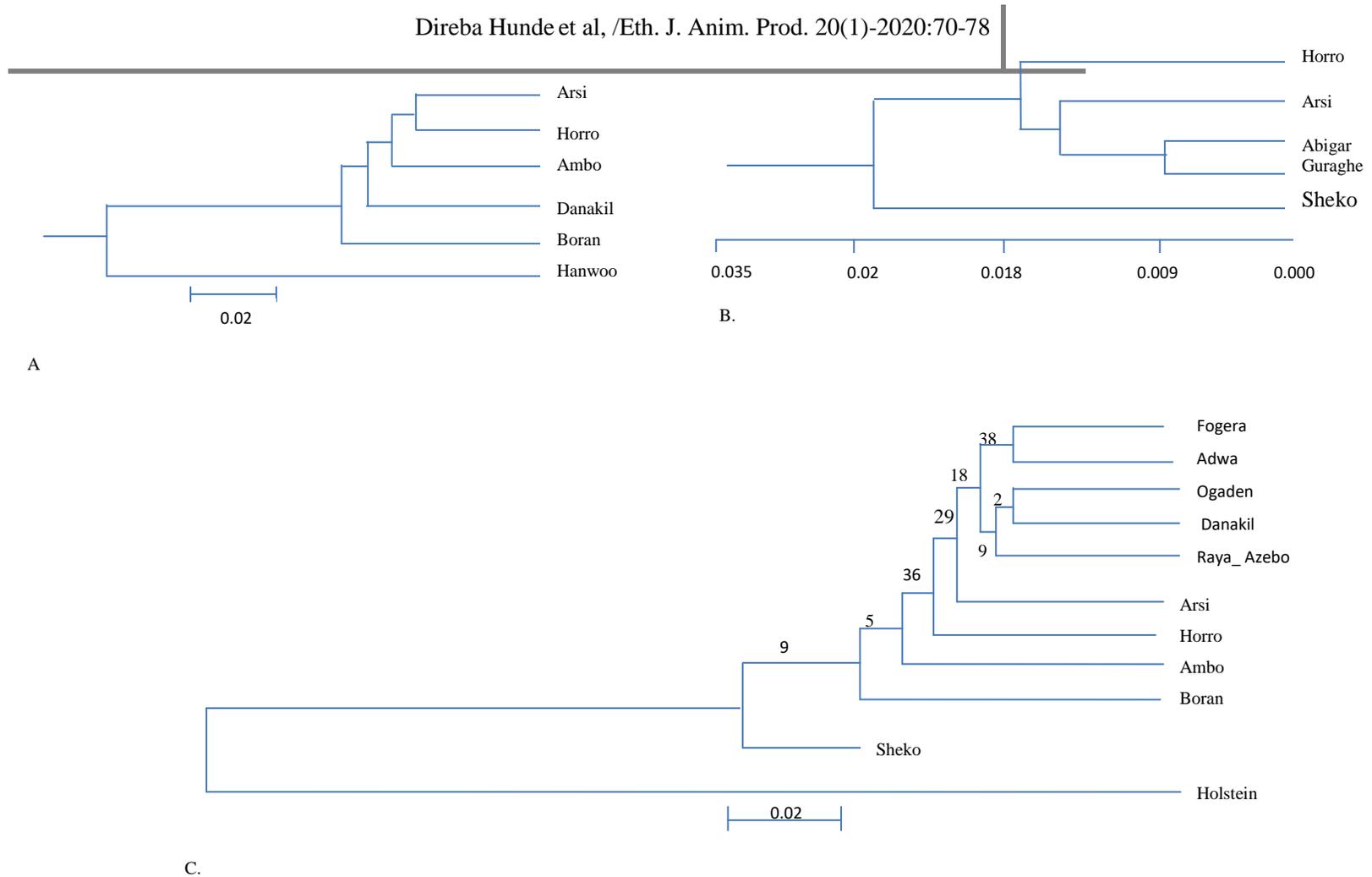


Figure 1. A. Phylogenetic tree showing the genetic relationships among the six cattle populations using Reynold setal.(1983) genetic distance. Source Edea et al. (2013); B. Dendrogram generated by the UPGMA method for Nei (1978) genetic distance using NTSYS program. Source: Hassen et al (2007); C. Neighbour-joining dendrogram summarizing genetic relationships among 11 cattle populations using DA genetic distances based on 30 microsatellite loci. The numbers on the nodes indicate the percentage bootstrap values generated from 1000 replications. Source: Dadi et al (2008)

They clustered Arsi and Horro as one sub-cluster and Borana separately while Danakil and Ambo were intermediately positioned between Arsi and Horro sub-cluster and the Boran. Even though, Horro and Ambo have more geographical linkage, the Reynolds' genetic distance estimation placed Horro more related to Arsi than Ambo. Similarly Hailu Dadi et al. (2008) found lower genetic distance between Arsi and Ambo than other 8 breeds characterized and grouped, while Sheko breed clustered differently from other Ethiopian breeds.

## CONCLUSION

The high within breed variation observed in Ethiopian cattle populations could create favorable condition for further improvement through selection. In addition, literatures might indicate the presence of higher admixture among cattle populations and absence of artificial selection pressure. However, the studies conducted so far at molecular level were fragmented and did not exhaustively include all breeds that were classified by phenotypic features and geographic location. Some of the populations like Mursi, Hammer, Gofa, Kereyu and other indigenous breeds/populations were not characterized at molecular level. Thus it is essential to carry out further studies which encompass all breeds in order to have full picture of breed diversity and differentiation among Ethiopian breeds. Furthermore, it will have an immense impact if the studies started on genetic diversity could be advanced to the level of utilizing genomic information for genetic improvement, genetic resource conservation, disease resistance and other economically important traits.

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