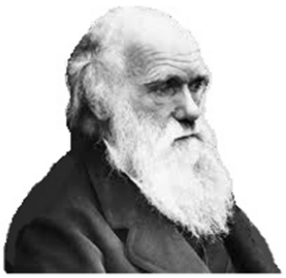
Available online at www.worldnewsnaturalsciences.com



World News of Natural Sciences

An International Scientific Journal

WNOFNS 49 (2023) 88-110 EISSN 2543-5426

Origin of cattle breeds in East Africa and introduction to general breeding science: A – review

Dejenie Mengistie

National Agricultural Biotechnology Research Center, P.O. Box: 31, Holeta, Ethiopia

*E-mail address: dejeniebiot2006@gmail.com

ABSTRACT

Since the domestication of cattle more than 10,000 years ago, cattle have been critical in the shift of human society from nomadic hunter-gatherers to sedentary farming communities across most of Europe, Asia, and Africa. Although our understanding of ancestral population relationships is limited, cattle domestication is thought to have occurred on two or three occasions, giving rise to the taurine (*B. taurus*) and indicine (*B. indicus*) species, which share a common ancestor with the aurochs (*B. primigenius*) 250,000 years ago. Indicine and taurine cattle were domesticated in the Indus Valley and the Fertile Crescent, respectively; however, a third domestication event for taurine has been hypothesized in Egypt's Western Desert. Because of their recent split, African indicine cattle share a lot of genetic variation with Asian indicine cattle, as well as with African taurine cattle through gene flow. Although further research is needed to detangle the complicated human-mediated dispersion patterns of domestic cattle, scenarios involving unidirectional or bidirectional migratory events between European taurine and Asian indicine cattle are also feasible. As a result, our research contributes to a better understanding of the impact of previous demographic history on present cow genetic variation, laying the groundwork for future research into alternate migration pathways for early domestic populations.

***Keywords*:** Adaptation, Domestication, Genetic divergent, Selection, *B. indicus, B. primigenius, B. taurus*

1. INTRODUCTIONS

Animal species, breeds, and strains are the source of economic, scientific, and cultural interest to humankind in terms of food and agricultural production, both now and in the future.

(Received 29 April 2023; Accepted 25 May 2023; Date of Publication 27 May 2023)

These animals are the result of domestication processes that have been ongoing for almost 200,000 years ago, cattle, also known as *B. taurus* (humpless) or *B. indicus* (humped), were split into two distinct lineages (Daetwyler *et al*., 2014). Since the domestication, cattle have been essential in the transformation of human society from nomadic hunter-gatherers to sedentary farming societies across much of Europe, Asia, and Africa. Although our knowledge of ancestral population relationships is poor, cattle domestication is thought to have occurred on two or three occasions, giving rise to the taurine (*B. taurus*) and indicine (*B. indicus*) species, which share a common ancestor with the aurochs (*B. primigenius*) 250,000 years ago (Pitt *et al*., 2019).

The last known herd of this formerly common wild species was discovered in Poland in 1627AD (Pitt *et al.,* 2019). Around 10,000 years ago, according to archaeological and genomic data the ancestors of taurine cattle (*B. taurus*) were domesticated from B. primigenius in the Fertile Crescent during the Neolithic period, (MacHugh *et al*., 2017). However, 1,500 years later, in the Indus Valley, a second domestication event occurred from B. primigenius nomadicus, which was isolated from the taurine branch between 250 and 330,000 years ago, eventually giving rise to the extant indicine cattle (*B. indicus*), also known as zebu cattle (Pitt *et al.,* 2019). Around 8500 years BC, taurine cattle were domesticated and the shape with long horns phenotype is still popular in many British, French, Mediterranean, and African breeds, and is the first domestic cattle. The first cattle with short horns appeared in Mesopotamia around 3000 years before Christ. This phenotype was more appropriate for those habitats and substituted for most long-horn forms in Asia and neighboring continents by the second wave of migrations, reaching Britain around 1000-2000 years BC. From around 1000 years BC, this short-horn bovine was the most common type in Europe (Pitt *et al*., 2019).

1. 1. African cattle domestication

In Sub-Saharan Africa, approximately 180 cattle breeds have been recognized, including 150 indigenous cattle breeds and newly introduced exotic and commercial composites (Mwai *et al*., 2015). However, since the genetic differentiation between these cattle breeds is often unclear, it may be more fitting to refer to African cattle populations or ecotypes. The indigenous cattle of Africa include different crosses between longhorn cattle (*B. taurus*), zebu cattle (*B. indicus*). New cattle breeds (zebu and sanga-types) were established as the result of migration of human activity progressed across Africa (Angress and Reed, 2014).

Cattle have been migrated to Africa from around 4000-5000 years BC (Mwai *et al*., 2015). Other large-scale cattle migrations were related to the migration of Germans during the fall of the Western Roman Empire (Rivollat *et al.*, 2015). For example, from its ancestor the Bos primigenius namadicus in the Indus Valley, the widespread modern zebu was domesticated around 6000 years BC and acquired its characteristic hump only after domestication (Angress and Reed, 2014). Crossbreeding in East Africa led to the creation of cervico-thoracically humped sanga cattle taurindicin, which spread southward and reached 250-500 AD in most areas of the south-east part of Africa (Koolmees and Lenstra, 2014). During the migration of the San and Sudanese Bantu tribes to southern Africa and the arrival of Europeans during the 15th century, Sanga cattle were introduced to Ethiopia (Gifford-Gonzalez and Hanotte, 2011).

B. taurus is humpless and includes two classes of shorthorns and longhorns that are found primarily in Central and West Africa. *B. indicus* are humped and in Africa, they are essential types of cattle (Gifford-Gonzalez and Hanotte, 2011). *B. indicus* cattle come primarily from western and eastern parts of Africa, and the commercial taurine breeds are found all over the

world, with their crossbreds. These breeds have been made more attractive to local farmers by their substantial body mass and higher productivity in tsetse-free areas, which somewhat explains the proliferation of these breeds and wide distribution across Africa. On the African continent, there is no pure *B. indicus*, as all cattle bear taurine mitochondrial DNA (Mwai *et al.*,2015). The distribution of cattle in various regions of the world has resulted in the creation of many ecotypes adapted to their local environments (Theunissen and Lenstra, 2015).

In addition, several different "agrotypes" were developed by human selection, which preceded the creation of breeds that differ in coat color, horn development, and docility. In the last 200 years, through a systematic selection of isolated populations that became the new breeds, cattle diversity has been increased. Many cattle acquired, for example, large udders when dairy and beef production began and this type of domestication process resulted in a decrease in the size of the breed (Theunissen and Lenstra, 2015, Pitt *et al*., 2019). A taurine Y-chromosome was maintained by most sangas, suggesting that male zebu introgression in these cattle was only partial (Li *et al.*, 2013, Koolmees and Lenstra, 2014). By about 1500 AD, in East and Central Africa, sanga cattle were the dominant type of cattle. After 700 ADS (Li *et al.* 2013, Koolmees and Lenstra, 2014) or even earlier, Zebus eventually emigrated to the west (Koolmees and Lenstra, 2014).

According to mtDNA sequences from Europe, Africa, and India, both African and European cattle are in one large taurine cluster, while all Indian breeds are in the other. Surprisingly, only taurine mitochondrial genomes were discovered in African breeds, with no evidence of female zebu imports. We reasoned that the absence of zebu mtDNA genomes seen in previous studies may have been due to the sampling procedures used. The researchers excluded samples from Ethiopia, which had the most extensive hybridization (Tarekegn *et al.*, 2018).

1. 2. Ethiopian cattle domestication

Ethiopia is home to over 28 cattle breeds or populations, which can be grouped into four categories: zebu (B. indicus), sanga (*zebu* × *B. taurus*), zenga (*sanga* × *zebu*), and the humpless *B. taurus* (Edea *et al*., 2013). East Africa including Ethiopia considered the cradle of the Near-East *B.taurus* as well as the Arabian and Indian *B. indicus* cattle migration corridors, and are often referred to as the secondary hybridization zone. *B. indicus* cattle descended from the Indus Valley, a presumed cattle domestication hub in the northern Indian subcontinent, and arrived in East Africa between 2,000 and 3,000 BC. Both the *B. taurus* and *B. indicus* cattle groups hybridize in the East African region, which includes Ethiopia in particular and the continent as a whole. Three key lines of reasoning were used to justify this hybridization zone: To begin with, Ethiopia has one of the most diverse populations of indigenous cattle in the world. Second, it is strategically located near the Horn and the East Coast, which serve as cattle entry points into Africa. Finally, microsatellite data analysis showed Ethiopian cattle to be hybrid populations (Dadi *et al.* 2008). All Ethiopian cattle mtDNA sequences converged on one maternal lineage (T1), which corresponds to African Bos taurus cattle; no zebu mtDNA haplotypes have been discovered in the Ethiopia population (Tarekegn *et al.*, 2018).

1. 2. 1. Types of indigenous cattle and their geographic distribution in Ethiopia

Large East African Zebu, Sanga, Small East African Zebu, and Zenga (defined as Sanga Zebu backcross) are the four main groups of Ethiopian indigenous cattle. Other Ethiopian cattle

breeds have recently been derived from modern crossbreeding with exotics, in addition to these four types. North Sudan zebu (Begait cattle), Boran (Ethiopian Boran cattle), and Abyssinian short-horned zebu are all large east African zebu (Arisi cattle). They mainly live in Ethiopia's northwest, south, and central highlands, respectively. Both of these species have evolved special adaptations to harsh climates and endemic diseases (Hagos, 2017).

The Abyssinian shorthorn zebu is a small east African zebu that can be found in a variety of agro-ecologies and is known by a variety of breed names, including (Bale and Jem-Jem cattle) in the Sidamo and Bale mountains, (Harar cattle) in the Hararghe highlands, (Ogaden cattle) in Eastern Ethiopia, and (Sheko/Smad cattle) in the highlands of southern Gondar, (Adwa cattle) in northern Ethiopia's Tigray area, (JigJiga cattle) in Somalia's south-eastern region, (Goffa cattle) in Ethiopia's wet and warm south-western highlands, Guraghe cattle) in the tsetse-infested valleys of the Ghibe tributaries, (Hammer cattle) in southern Ethiopia's South Omo district, (Ambo cattle) in western Shoa. The majority of cattle in Ethiopia are zebu cattle (*Bos indicus*). They have a big dewlap and a fatty thoracic hump on their shoulders. Trypanosomosis is a disease that affects zebu cattle. However, the Sheko, a large East African zebu breed, has shown tolerance to the disease. They are more resistant to tick infestation than Bos taurus cattle because they are adapted to dry environments and high temperatures (Hagos, 2017). Their small body size and high (Sheko/Smad cattle) in the southern Gondar highlands, (Adwa cattle) in northern Ethiopia's Tigray region, (JigJiga cattle) in Ethiopia's Somali region, (Goffa cattle) in Ethiopia's wet and warm south-western highlands (Guraghe cattle) in the tsetse-infested valleys of the Ghibe tributaries, (Hammer cattle) in southern Ethiopia's South Omo region, and (Ambo cattle) in central Ethiopia's western Shoa (Hagos, 2017).

The Sanga is cattle breed that is a hybrid between the *Bos taurus* and the *Bos indicus*. They're humped, so it's a cervicothoracic hump rather than a thoracic hump. The term 'Sanga' refers to the origin and dispersal center of this group of cattle breeds. It is an Ethiopian word that means 'bull'. This breed group includes the (Anuak cattle) of Gambela in south-western Ethiopia, the (Raya Azebo cattle) of Tigray, and the (Wello cattle) of Ethiopia's northeastern highlands. These animals are slightly larger, owing to selection for draught power in the settled agricultural activity (Mwai *et al.*, 2015). The Sanga has a combination of zebu (humps and dewlap) and humpless cattle characteristics (long horns and no humps). Recent molecular genetic evidence indicates, however, that genetic introgression of the Bos indicus (zebu) spread from the Horn of Africa to the west of the continent, and that the zebu genes dispersed quickly among indigenous African populations (Mwai *et al.*, 2015). The current distribution of Sanga cattle spans Eritrea, Ethiopia, and eastern Africa's southern Sudan. They are found in the southwest and north-eastern Ethiopia and are considered to be well suited to harsh seasonal conditions. Production levels in tsetse-free areas have made them more attractive to local farmers, which explains their abundance and broad distribution (Mwai et al., 2015).

Crossbreeding between Sanga cattle and newly introduced zebu resulted in the development of a new cattle breed known as "Zenga." The Ethiopian Zenga breed community includes (Fogera cattle) in the western Amhara region, as well as (Arado cattle) in Eritrea's highlands (Akale-Guzay and Seraye in the north) and northern Ethiopia (northern Shire, Adwa, and parts of Agame). As a result, the country is regarded as the home of the most significant cattle breeds for eastern and southern Africa, as well as 28 indigenous cattle breeds (Hagos, 2017). The country's diverse agroecology, cultural and ethnic diversity, and long-standing agricultural practices and farming systems have all contributed to the country's status as a secondary livestock diversification hub.

Despite the benefits of having a diverse genetic resource, the massive loss of livestock genetic diversity would severely jeopardize attempts to achieve food security and poverty reduction, as well as have a long-term impact on global biodiversity (Hagos, 2019).

In combination with isolation and genetic drift, natural and artificial selection, new mutations, and backcrossing of domesticated animals with their wild ancestral species have created taurine cattle (*B. taurus*) breeds that exhibit wide phenotypic and genetic variation (Bradley, 2020). Systematic breeding began at the same time as the first breeding organizations and herd books were founded in the 19th century (Weigel, 2015). The aim of breeding was initially to harmonize the appearance of animals, but performance characteristics were also considered shortly afterward. To choose the best potential candidates for future use, modern breeding systems systematically use genetic information. Intensive artificial selection has resulted in highly efficient global cattle breeds replacing local breeds, leading to a situation in which cattle have the largest number of mammalian livestock breeds at risk (FAO, 2019). A situation where breeds are mainly used either for milk or meat production has also been produced by artificial selection. The accomplishment of breeding is indisputable. However, the increase in productivity of cattle achieved by breeding and improved management was followed by adverse effects on animal robustness that posed ethical questions regarding animal welfare (Rauw and Gomez-Raya 2015, Strucken *et al.*, 2015).

1. 3. Breed diversity and its importance

Isolation-by-distance, historical and geological influences, physical barriers, and ecological factors by morphological adaptation to local adaptation are some of those factors that interrupt gene flow (Denney *et al*., 2020). In most cases, especially in domestic animals, the disruption of gene flow is supervised more by human interference than by physical barriers. Local management and cultural separation can also cause genetic isolation of populations that lead to reduced effective population size and further divergence. Genetic variation is the foundation for the existing diversified living species, which are still contributing factors. It is important to properly use, enhance and preserve this diversity. Strategies for conservation and improvement should be focused on adequate genetic characterization following phenotypic assessment.

Genetic characterization involves knowledge of genetic variation that can be efficiently assessed within and between populations and is seen as an initial step in considering the sustainable management or protection of a specific population. Important causative factors explaining genetic variations between current populations are differences in ancestral backgrounds and migration events.

Phenotypic characters and biochemical and molecular markers are the most commonly used approaches to measure genetic diversity (Orr and Garland, 2018). However, while phenotypic characters are cheap and easy to apply, because of the existence of the qualitative and quantitative characteristics to be considered, they are subject to environmental influences (http://www.fao.org/biotech/logs/c13logs.htm). Moreover, the adequacy of phenotypic characteristics to research genetic variation between populations is very limited (Ploi *et al.*, 2020). Similarly, biochemical markers are low like polymorphism, such as isoenzymes. As a result, the danger of loss of remaining genetic diversity is very strong in the absence of adequate genetic recognition (Hoda *et al*., 2012).

A decade ago, it was proposed that morphological characterization findings should be complemented by genetic characterization, which includes the classification of breeds using a

range of neutral and non-neutral reference molecular markers in terms of relative allele frequencies, genetic distances, degree of polymorphism using a set of neutral and non-neutral reference molecular markers (Habimana *et al.*, 2020).

Molecular markers have played a leading role in characterizing diversity since the early 1990s and offered relatively simple and inexpensive assays in the absence of quality phenotypic measures. The use of DNA has thus become an option for the study of various genetic, breeding, and physiological questions in animal sciences since the advent of polymerase chain reaction techniques. This facilitates the best use of farm animal genetic resources and enables effective genetic enhancement to meet the needs of production and conservation. In addition, such studies help to plan and incorporate enhancement programs in the sense of a population's specific efficiency (Hu *et al*., 2018).

2. ADAPTABILITY

2. 1. Why Variation in Adaptability Exists?

Adaptation is usually a nongenetic (short-term or phenotypic) and genetic (long-term or generational) reaction to an obstacle (stressor). Resource rivalry takes place between and within organisms, resulting in natural selection (Decker *et al*., 2014). The idea of adaptability revolves around 'fitness' that defines an individual's relative ability to survive and replicate the next generation to ensure the population's continued survival. While certain individuals in the population can reproduce at typical rates, others are not due to various limiting factors, such as nutrition and the climate.

For centuries, these tiny isolated communities continue to produce and replicate in their new local climate, leading to loss of genetic diversity due to chance, otherwise called genetic drift (Sejian *et al*., 2013). Environmental adaptation by correcting desirable gene and gene combinations by selection may produce more population-wide genetic variation and can also increase inbreeding. There are numerous examples to demonstrate the case of difference in adaptabilities, such as zebu cattle that are uniquely adapted to hot and humid climates due to their smooth coat, primary hair follicles, enhanced sweat and sebaceous glands, and greater ability to lose moisture by evaporation than Bos taurus cattle (Bernatchez, 2016). Zebu may be due to their origin in different climates in which *B. Indicus* may have received thermotolerant genes (Bernatchez, 2016).

Phenotypic plasticity (Schmid and Guillaume, 2017), which is a genetic phenomenon discovered phenotypically by local and global expression of genotypes, is the property of organisms to systematically evolve different phenotypes in different environments. When the difference in phenotypic value between animals between different environments is not constant, there is a variation in plasticity among different genotypes. This difference between genotypes in phenotypic plasticity results in the GxE (Schmid and Guillaume, 2017). Biologically, we understand that the environment regulates the expression of genes in the living system, which, depending on the need for genotype expression, can be up-regulated or down-regulated (Cuypers *et al.*, 2017). The trait is partially affected by various genes in different environments in GxE interactions, suggesting the genes' skewed expression patterns in different environments. Weak GxE interactions lead to non-identical discrepancies between the breeding values of animals, while strong GxE interactions lead to a substantial re-ranking of the breeding values of animals in different environments (Cuypers *et al*., 2017).

2. 2. Variation in Beef Cattle Adaptability

It is very necessary to adapt to the environment in which every animal is being reared for production (Carvalheiro *et al.,* 2019). The adaptability of beef cattle has become an issue of concern with the awareness of changing climate and its possible effects on the animal production system, where the balanced genetic potential for adaptation, production, and product quality is anticipated within unique environments (Carvalheiro *et al.,* 2019). With the emergence of scientific awareness and increasing demand for product quantity and quality, the degree of stress has increased with more pressure on animals to adapt to evolving conditions (Carvalheiro *et al*., 2019).

In the beef cattle production system, genotype and environmental interaction have several roles to play. (Rauw and Gomez-Raya, 2015) have argued that in commercial beef cattle production, genetic adaptation to local environments is significant. Their classical experiment to investigate GxE presented evidence supporting these guidelines, which makes it clear why adaptation is a crucial problem in the production system of beef cattle (Rauw and Gomez-Raya., 2015).

2. 3. Selection

Continuous selective sweep signals indicate the existence of genetic variants that are likely to influence phenotypes but may also occur because of genetic drift or demographic processes, particularly in artificially selected organisms (Jacobs *et al.,* 2016).

2. 3. 1. Positive Selection

Darwin and Wallace came up with the notion of natural selection in the 1850s. Darwin's theory of natural selection claimed that "If variations useful to any organic being ever occur, people thus characterized will surely have the best chance of being preserved in the struggle for life; and these will tend to produce offspring similar to the strong principle of inheritance" these will appear to generate similarly characterized descendants. This principle of preservation, or the survival of the fittest, is called natural selection (Emlen *et al.,* 2005). If the phenotype increases the fitness of an organism, it becomes more prevalent in a population over time. This phenomenon is called Positive Selection. The allele(s) behind the beneficial phenotype would finally become more common at the population level. At the sequence stage, genomic signals of positive selection are characterized by reduced local variability, a deviated spectrum of allele frequencies, and unique patterns of linkage disequilibrium.

2. 3. 2. Negative selection

Negative selection is defined as the selection of the context. Deleterious mutations are normally eliminated from the gene pool before any measurable frequency is reached within a population so that Genome regions are under intense negative selection pressure where no differences are accepted and are thus typically highly conserved across organisms (Vitti *et al*., 2013).

2. 3. 3. Balancing selection

When multiple alleles are retained in a population at an intermediate frequency, such a phenomenon is called the selection of balancing. Balancing selection will occur due to

heterozygote gain (i.e., the individual heterozygote has greater fitness compared to any of the homozygotes) or frequency-dependent selection (i.e., when it is uncommon, an allele has greater fitness and several alleles will be retained in population) (Vitti *et al.*, 2013). Balancing selection is the most difficult type of selection to detect and current methods suffer from low power and high false-positive frequency (Fijarczyk and Babik., 2015).

2. 3. 4. Methods to detect selection

Most methods for detecting selection have been established (Utsunomiya *et al*., 2015) because it creates visible footprints on the genome. Owing to the very subtle effects on the genome, identification of balancing selection is more difficult, and negative selection is usually observed for conserved regions. In the age of genomic data, adaptive processes can now be inferred in the absence of phenotypic data. Therefore, methods of selection signature are sometimes described as "genome to phenotype" approaches involving the statistical evaluation of population genomic data irrespective of phenotype to identify probable prior selection targets (Qanbari and Simianer, 2014). Depending on the test statistics, selection signatures can be found either from intergenic regions, coding regions, or from both (Vitti *et al*., 2013).

2. 3. 5. Development of genomic tools

Initially, to identify cattle, scientists relied on chromosome karyotypes. Some African zebu cattle were either classified as having zebu male ancestry, e.g., Malawi zebu, or taurine male ancestry, e.g., Tuli cattle, because of the different Y chromosome karyotypes in the two cattle subspecies, acrocentric on zebu and sub-metacentric in taurine cattle (Mwai *et al.*, 2015). Other markers, such as protein electrophoresis and restriction fragment length polymorphism, have been used to study the population structures of different cattle populations. Both of these genetic marker groups display low variance to perform population genetic analysis effectively. In cattle population studies, microsatellites, tandem repeats of very brief (one to six base pair) nucleotide motifs, are commonly used genomic markers.

They have been used to define the evolutionary relationships between cattle subspecies, population levels of genomic admixture, migration history, as well as to map genomic quantitative trait loci (QTL) within species, due to the high level of polymorphisms usually observed at microsatellite loci (Hanotte *et al*., 2003). Although microsatellite markers have shown great success in enhancing our understanding of cattle population structure and history, their relatively restricted bovine genome coverage is a downside. It has opened new avenues for scientists to further study the genetic history of cattle populations by incorporating recent developments in genomic tools into bovine full genome characterization. Genotyping of the bovine genome with SNPs is one of these developments. In customized arrays that are generally referred to as DNA SNP chips, these variants are arranged. The low SNP density array (BovineSNP50 Genotyping Bead Chip, versions 1 and 2), which genotypes more than 54,000 SNPs (Bejarano *et al.*, 2018), and the higher density array (BovineHD Genotyping Bead Chip), which genotypes more than 777,000 SNPs, are two examples of these arrays for cattle built by Illumina (Rincón *et al.*, 2011).

Centered on the dual-color, single-base extension Infinium HD assay, both of these arrays are genotype SNPs (Bejarano *et al.*, 2018). For genome-wide association research purposes, SNPs genotyped by these two arrays is validated principally in commercial taurine cattle breeds. This bias of European taurine breeds, which is more important in the lower density array, will

make this method less successful in analyzing the genome of zebu cattle and indigenous taurine cattle populations outside of Europe (Bejarano *et al.*, 2018).

2. 4. Influence of Genetics on meat production

The genetic makeup of animals is one of the most important factors that determine meat production. Some selected breeds like Angus and Hereford are well known for their meat quality nature (Zhao *et al.*, 2015). Genetic traits determine the degree of how much the level of meat quality differs. A good plan of nutrition contributes to marbling scores and tenderness, certainly, in animals genetically able to marble. Animals that have several cells rather than bigger cells in the early stages of life are almost the key effect on the potential to deposit fat later (Lee *et al.*, 2014).

2. 5. Influence of candidate genes on meat production

Agronomical important genes have been selected through breeding for particular phenotypic characteristics as growth; meat quality and milk yield (Makina *et al.*, 2016). When it is identified that genes are linked to phenotypic characteristics, they are called candidate genes (Chen *et al*., 2020). Candidate genes hypothetically regulate morphological differences of interest and are kindly determined based on some prior knowledge about the gene function and/or observed association between the phenotypic variation and DNA variation (polymorphism) or differential gene expression. Candidate genes for the genetic regulation of phenotypic difference of interest such as beef quality can have the causative mutations in protein-coding sequences or in noncoding sequences that may affect gene expression, mRNA splicing or post-translational modifications of the encoded protein. Polymorphisms in the DNA can affect the translation to amino acids building up all the proteins the body needs. Mutations that alter the protein composition by an amino acid change may alter the 3D folding of protein, and thereby affect its function. If it is one nucleotide variation it is called a single nucleotide polymorphism (SNP). The SNP genotypes of individual animals can be determined and hypothetical associations between different SNPs and phenotypic observations can be tested. The use and interest of DNA tests as replacements or complements to phenotypic evaluation has increased since the late 1900s and the benefits are many. For example, beef animals with desired genotypes can be selected for further breeding. Also, interesting studies on genetic historical relationships between cattle populations can be done with SNP analysis (Ghoreishifar *et al.*, 2020).

2. 6. Effect of a major gene

To put it, if a gene has a significant influence on a large percentage of the variance of a certain trait, it is called a major gene. But how large is considered large? The difference in the phenotypic value of a certain characteristic measured on individuals carrying a gene's homozygous genotype is greater than one standard deviation of the measured value relative to those not carrying the same gene alleles, we consider the gene to be a significant gene affecting the characteristic. Major genes can be easily identified by simply using distinct phenotypic data. Until now, several major genes, including the pleomorphic adenoma gene 1 (PLAG1), Rendement Napole (RN-) gene, the MSTN gene, the DGAT gene, the CAPN1 gene, and the CAST gene, have been detected.

PLAG1

pleomorphic adenoma gene 1 (PLAG1) directly controls a wide variety of target genes, including several growth factors such as IGF21, which is involved in cell proliferation (Zhou *et al*., 2019). The PLAG family consists of PLAG1, PLAGL1/LOT1/ZAC1, and PLAGL2 and is highly conservative in form and work. Genetic studies have shown that PLAG1 influences cell apoptosis and cell cycle arrest of gap 1 (G1) and is associated with the development of several tumors, such as Adi blastoma. Examination of the genome-wide association showed that single nucleotide polymorphisms (SNPs) in the PLAG1 gene area were strongly linked to adult height (Gudbjartsson *et al.,* 2008). PLAG1 is also an important candidate gene influencing domestic animal growth and development. Some research has shown that the PLAG1 gene plays a certain regulatory role in the development of milk, reproductive success, muscle formation, and livestock body height (Hoshiba *et al.,* 2013, Fink *et al.,* 2017).

3. 6. 1. RN- Gene

The RNgene, named after the Rendement Napole (RN) test, is the key gene that causes' acid meat '(very low ultimate pH with rapid postmortem pH drop. The RNgene causes abnormal glycogen accumulation in the skeletal muscle in terms of meat quality, which increases its glycolytic capacity and contributes to a drastic decrease in postmortem pH very early. As a result, PSE meat is often formed by muscles with a low pH when it is still warm. A dominant PRKAG3 codon 200 (protein kinase AMP-activated non-catalytic subunit gamma 3) mutation, primarily found in animals Milan *et al*. (2000), which was responsible for replacing arginine with glutamine in the RNgene (Milan *et al.*, 2000) and three non-synonymous replacements (I199V, 199V-200R, 199I-200R) were found in the PRKAG3 gene.

3. 6. 2. MSTN gene

Bovine muscular hypertrophy generally referred to as 'double muscled' in animal breeding, has been prevalent among some breeds of European beef cattle since 1888. This phenomenon is caused both by an increase in the number of muscle fibers and by an increase in the accretion of myofibrillar protein (Fiems, 2012) and by the inhibition of myostatin production, resulting in an exaggerated growth of muscles. MSTN (Myostatin) is a protein-coding gene, also known as GDF8 (growth differentiation factor 8), and research has shown that variants of MSTN genes are associated with muscle hypertrophy and that the gene is strongly preserved across species of mammals (Grobet *et al*., 1997). In the coding sequence of the bioactive carboxy-terminal domain of the protein responsible for the muscular hypertrophy of Belgian Blue cattle, Grobet *et al*., (1997) identified an 11-bp deletion by using a candidate approach. In addition to the 11-nucleotide deletion in the third exon of the MSTN gene in Belgian Blue Cattle, researchers found a missense mutation in exon 3 of the MSTN gene in addition to the 11-nucleotide deletion in the third exon of the MSTN gene in Belgian Blue Cattle, which caused tyrosine to be replaced by an invariant cysteine in the protein, resulting in double-muscled Piedmontese cattle. While double-muscled cattle have extra muscle disproportionately in the costly meat cuts, within this phenotype there are some serious defects, including decreased fertility, dystocia, low viability of calf, and increased susceptibility to disease. This phenotype has persisted and was in reality selected deliberately since cattle with the MSTN gene have muscle with less insoluble intramuscular collagen and smaller cross-sectional area of muscle fiber, resulting in increased tenderness (Allais *et al.,* 2010). The muscle

also has lower intramuscular fat and a less appealing taste, but the increased tenderness of the meat outweighs these factors.

3. 6. 3. DGAT gene

DGAT is a protein-coding gene that encodes Acyl CoA: diacylglycerol acyltransferase, a microsomal enzyme that catalyzes the final stage of triacylglycerol synthesis. Two major DGAT forms, type 1 (DGAT1) and type 2 (DGAT2), are encoded by DGAT1 and DGAT2, respectively (Yen *et al*., 2008). A lysine/alanine polymorphism in the DGAT1 gene is involved in milk fat content based on previous studies (Winter *et al*., 2002) and the lysine allele of DGAT1 may have a beneficial impact on intramuscular fat content. Two SNPs were found to be correlated with back fat thickness, longissimus muscle area, marbling score, fat color, and Warner-Bratzler shear force by examining the candidate SNPs in the exon region of the DGAT1 gene in Chinese commercial cattle (Yuan *et al.*, 2013).

3. 6. 4. CAPN1 and CAST gene

μ and m calpain are two well-characterized calcium-dependent neutral proteinases in the skeletal muscle, with μ-calpain primarily responsible for myofibrillary protein post-mortem degradation and meat tenderization. CAPN1 (Micromolar Calcium Activated Neutral Protease) is the μ-calpain gene code and this gene is located on bovine chromosome 29, and SNPs that affect meat tenderness have been identified in this gene (Page *et al.*, 2002; Casas and Kehrli, 2016). Calpastatin, which is coded by the CAST gene, located on bovine chromosome 7, is the natural inhibitor of both calpains (m- and μ-calpain) (Casas and Kehrli, 2016). An SNP in the CAST gene (a G to C substitution) was associated with beef tenderness. The marker profile will explain about 44% of the variance in cooked beef tenderness by combining CAPN1 and CAST (Greenwood *et al*., 2013).

2. 6. 5. Polygenic effects

It is also possible to enhance the quality of meat using conventional selection methods, including production and reproductive characteristics. In practice, however, because of their low to moderate heritability, most meat quality characteristics are not easy to pick, ranging from 0.10 to 0.30 in beef, and because they are difficult and costly to calculate. It is widely recognized that many genes regulate meat quality characteristics because they are affected by a variety of factors. Marker-assisted or genomic selection has irreplaceable advantages over conventional selection for such traits because of its effectiveness and reduced cost. The discovery of quantitative trait loci (QTL) that correlate with variation in a phenotype is one prerequisite for marker-assisted or genomic selection and this has become possible now that the full bovine genomes have been constructed. In recent years, after the reference genome sequence was available, whole-genome scanning using dense SNP markers to identify QTLs affecting meat quality has grown to be a gold standard technique in marker-assisted selection or genomic selection. Several studies on beef production using SNP markers (Magalhães *et al.*, 2016; Santiago et al. 2017, Bhat *et al*., 2018, Kanungo *et al.*, 2018, Xing *et al.*, 2019). None of those studies, however, conducted a thorough study of objective and subjective characteristics of meat quality or considered whether samples were fresh or frozen and then thawed or examined various organisms, and only a few of those studies integrated meat science, biochemistry, genetics, and functional genomics to explain the relationships with meat quality.

2. 7. Genetic marker

Genetic markers are used to differentiate individuals and populations from each other, for parentage testing and mapping phenotype-influencing genomic regions. Restriction fragment length polymorphisms (RFLP) were among the first genetic markers used in animal genetics and nowadays RFLP is applied for candidate genes. The advent of the polymerase chain reaction (PCR) in 1983 allowed DNA fragment amplification to be used as genetic markers for sequence variations in various types of DNA. In the 1990s, laborious methods for detecting RFLPs were replaced by microsatellites. A microsatellite is a repetitive region of DNA consisting of short repeats of nucleotides with a variety of repeats between alleles. For both population genetic and linkage mapping studies in animal genetics, microsatellites have been commonly used (Groeneveld *et al*., 2010) and are still used, for example, in parentage testing and population genetics. Progress in genetic science has increased dramatically with the publication of the first draft of the human genome sequence and the advancement of next-generation sequencing (NGS) methodologies in the early 21st century (the first NGS machine was commercially available in 2004). The first version of the cattle genome sequence was published in 2009 (Bovine Genome Sequencing and Analysis Consortium in 2009) and microsatellites in cattle research were replaced by single nucleotide polymorphisms (SNPs). In 2008, the first commercial version of the whole-genome SNP array (more than 50,000 SNPs) came on the market and in 2010, a higher density version of the array (more than 700,000 SNPs) followed. With the genome-wide SNP array, approximately 2 million milk cattle have now been genotyped (Meuwissen *et al.*, 2016). Whole-genome SNP arrays enable the analysis of genetic population histories and detection of chromosomal regions under selection more accurately than was previously possible. Two alleles compose the majority of the SNPs. Compared to microsatellites, the drawback of SNPs is the small number of alleles; polymorphic information content (PIC) is high for microsatellites compared to SNPs. Microsatellites are typically mostly neutral (i.e., not causing a difference in phenotype but SNPs are potentially causative).

2. 7. 1. Single Nucleotide Polymorphisms

The most common type of genetic variation is SNPs, and their presence across the whole genome makes them perfect for studying genomic region inheritance (Liu et al., 2020). An SNP is a variation in the genome between the maternal haplotype and the paternal haplotype at a single nucleotide position, which occurs in at least 1% of individuals within a species (Liu et al., 2020). Relatively low mutation rates for SNPs are (10^{-8} to 10^{-9}) (Albers and McVean, 2018). There are two forms of SNP: transformation, which is a change between two bases of purine or two pyrimidines, and transversion, which is a change between the base of purine and pyrimidine. In theory, one SNP can show up to four alleles, but at each locus, an SNP is biallelic in most cases (Albers and McVean, 2018).

2. 7. 2. Dynamics of allelic diversity

Genetic diversity is an important feature of population dynamics since it is closely correlated with the population's evolutionary potential and the deleterious effects of inbreeding (Greenbaum *et al.,* 2014). However, many different forms of genetic diversity measurements exist most notably heterozygosity-based measures and allelic richness-based measures (Greenbaum *et al.,* 2014). Allelic richness (number of alleles) is a genetic diversity indicator suggesting the long-term adaptability and persistence potential of a population. It is used as a

genetic diversity metric less frequently than heterozygosity, partly because the stochastic mechanism of genetic drift for allelic richness is more difficult to take into account mathematically (Greenbaum *et al.*, 2014). According to the studies by Greenbaum *et al.* (2014) on allelic diversity (Allelic richness) using stochastic modeling by integrating gene flow and genetic drift into a source population and newly formed population, and in their studies, they stated that genetic drift and gene flow are experiencing the allelic richness of a newly founded population. For example, it is known that the number of segregating alleles in a population offers basic information on past population size fluctuations (Armando and Aurora, 2013).

In gene-frequency-diversity or allelic-diversity components, the division of diversity contributes to very different conservation strategies (Caballero *et al.*, 2010), indicating a complementarity between the two forms of measures of diversity. In general, the components of quantitative genetic variance for characteristics and gene-frequency-diversity measures are more strongly correlated with short-term selection response, whereas allelic-diversity measures are more correlated with long-term and total selection response (Armando and Aurora, 2013).

2. 7. 3. Breed-specific SNPs

Breed-specific SNPs are only polymorphic within a single breed, and in other breeds, one of the alleles is fixed. Many livestock species have evolved distinct breeds as a result of natural and artificial selection, as well as genetic drift due to limited population sizes using artificial selection, the livestock breeding industry has concentrated on producing high-yielding or high-quality breeds of broilers, layers, pigs, and dairy and beef cattle. As a result, breed names are becoming more commercialized and used as brand names and breed validation of livestock products is becoming increasingly important in determining food safety and authenticity in global and domestic markets (Pant *et al.*, 2012). This problem could be solved quickly, easily, reliably, accurately, and economically by testing an individual's genotype at unique marker loci. In recent years, there has been a lot of interest in the possible application of genetic markers to track individuals and goods back to their source breed, and various approaches to animal trace back have been investigated. The molecular markers used to assign breed to individuals, as well as the allocation process used to assign a breed to individuals based on their genotypes at unique marker loci, assess the accuracy and efficiency of breed assignment to individuals (Zwane *et al*., 2016).

2. 8. Selection Signatures

Understanding how selection affects a population will help breeders establish effective breeding plans to improve commercially valuable traits in cattle (Gurgul *et al*., 2018). Positive selection is defined as a significant difference in allele frequency between populations at a given locus (higher Fst values), while negative selection is defined as a low Fst value (Zhao *et al.*, 2015). Fst is SNP-specific, which means it can detect which genetic variants are being chosen. It is preferable to look for multiple SNPs with similar average Fst scores rather than assessing each SNP individually. Using hierarchically ordered data sets, Fst statistics can detect false positive/negative outcomes (Fariello *et al*., 2014). Selection signatures have been identified as regions of the genome that contain functionally significant sequence polymorphisms selected by natural or artificial selection, leaving behind distinct DNA patterns. Several statistical approaches are used to classify signs of selection within the genome. All statistical measures to detect positive selection are broadly focused on five signatures, a high proportion of mutation-

altering roles, reduction in genetic diversity, high-frequency derived alleles, population variations, and long haplotypes. They cannot have any functional impact on the population when mutations occur, or they may be deleterious and affect the population's fitness. Consequently, the mutation's allele frequency does not increase or become set. However, the allele frequency for those functional variants increases and can become fixed when desirable alleles are selected for a prolonged period. These trends include the hitchhiking effect (i.e., linkage imbalance) consisting of neutral position areas downstream or upstream of the functional version.

2. 8. 1. Positive selection signatures in cattle

Earlier experiments on selection signatures were made with microsatellite markers (Li *et al.*, 2010) or small numbers of SNPs (I and II). In the study of genetics, the availability of whole genome-wide genotyping arrays and whole-genome sequences has expanded research capability. In cattle, those that are correlated with domestication and adaptation are evolutionarily relevant genomic regions. Variations in coat color in cattle, for instance, are a characteristic related to domestication (Qanbari *et al.*, 2014). Minor allele frequencies were used by Ramey *et al*. (2013) to describe genomic regions exposed to selective sweeps (at least five SNPs spanning at least 200kb) With no SNPs with MAF>0.01) and identified the locus of POLL known to regulate horn production. Signatures of selection were recorded from several known candidate genes affecting development and reproduction, but novel regions were also identified. Studies merged FST with the other methods of selection and recorded selection signatures near established regions of QTL. EHH and XP-EHH is other common methodologies used in cattle research (Rothammer *et al.*, 2013).

2. 8. 2. linkage disequilibrium

In population genetics, the non-random association of alleles at different loci in a given population is linkage disequilibrium (LD). When the frequency of association of their various alleles is higher or lower than what would be predicted if the loci were separate and randomly linked, Loci is said to be in linkage disequilibrium (Hui and Burt, 2020). Despite its name, there could be a linkage imbalance between alleles at different loci without any genetic connection between them and whether or not allele frequencies are in equilibrium (not changing with time). The Hardy-Weinberg principle, also known as the Hardy-Weinberg equilibrium, model, theorem, or law, states in population genetics that allele and genotype frequencies in a population will remain constant in the absence of other evolutionary factors from generation to generation. Genetic drift, mate preference, assortative mating, natural selection, sexual selection, mutation, gene flow, meiotic drive, genetic hitchhiking, the bottleneck of the population, founder effect, and inbreeding are among these factors (Hui and Burt, 2020). At equilibrium, the Hardy-Weinberg equation tests the genetic variance of a population and it looks like:

$$p^2 + 2pq + q^2 = 1 \quad (1)$$

where p and q are allele frequencies of two alleles for a genetic locus.

It is said that genes located next to each other on the same chromosome are related. If due to random interaction, two alleles from different genes on the same chromosome appear to be

associated with different individuals at a higher frequency than predicted, there is linkage disequilibrium between these genes. Two genes are unlinked on separate chromosomes or on the same chromosome at great distances (there is Linkage-Equilibrium).

Linkage-Disequilibrium can be generated by several variables such as Genetic drift; it contributes over centuries to a lack of variability (by random disappearance of alleles or haplotype). Genetic drift is greater when the size of the population is small. Mutation; In a haplotype, mutation may occur and establish a Linkage-Disbalance between the mutated locus and this haplotype. This disequilibrium usually decreases over generations, but if genetic drift or selection occurs, it may increase. Gene flow; LD can also be produced by population mixing or by migration. Initially, LD is proportional to the variations in alleles between populations and is independent of the distance between markers.

LD decreases over generations, but the rate of decrease varies with the relationship between loci. LD tends to vanish for independent loci, and it lasts much longer for connected loci. Selection; selection leads to a decrease in the number of breeders as genetic drift and hence a decrease in the number of haplotypes in the population. Similarly, this reduction leads to a rise in consanguinity. Recombination; around the genome, the recombination rate is not constant. LD is large in medium recombination regions and high in low recombination regions.

The LD was mainly evaluated between two SNPs using r^2 and |D'|, where r is the proportion of recombinant type (Mustafa et al., 2018).

The strength of the linkage can be characterized by the level of linkage disequilibrium (LD). There are two commonly used measures of LD: D' (the normalized) form of a linkage disequilibrium measure D and r^2 (the square of a correlation coefficient between the frequencies of loci). Consider two biallelic markers SNP-X (with alleles X and x) and SNP-Y (with alleles Y and y), the allele frequencies PX, Px, PY, and Py the frequency of the XY genotype (A1B1), r^2 and D' are calculated as shown in equations (2), respectively:

$$r^2 = \frac{freq.\ XY * freq.\ xy\ - freq.\ xy * freqxY}{freq.\ X * freq.\ x * -freq.\ y * freqY}$$

$$= \frac{D^2}{freq.\ X * freq.\ x * -freq.\ y * freqY} \qquad (2)$$

where D = freq. XY - freq. x*freq. Y

$$|D'| = \frac{D}{freq.\ X * freq.\ x * -freq.\ y * freqY} \text{ if } D>0 \quad \frac{D}{\text{freq. X}*\text{freq. x}*-\text{freq. Y}*\text{freqy}} \text{ if } D<0$$

where the frequency X, frequency x, the frequency Y, and the frequency y are frequencies of the alleles X, x, Y and y.

XY frequency, xy frequency, xY frequency, and Xy frequency are haplotypes of XY, xy, xY, and Xy frequencies, respectively. The predicted frequency of haplotype XY (freq. XY) is determined as the product between frequencies if the two loci are independent. Freq and x. Y. Oh. X freq. XY higher or lower than the predicted value will show that these two loci appear to segregate together in particular and will in LDXY's higher or lower frequency means that two loci divided between each other and in LD. The linkage disequilibrium (r^2 and |D'|) will be calculated using SnppldHD software for all marker pairs on each chromosome (Espigolan *et al.*, 2013).

2. 9. Measurements of population's genetic diversity

Traditionally, the information provided by genetic markers has been used to measure the parameters associated with the distribution of genetic variation within subdivided populations, e.g., within and among domestic breeds. For instance, the heterozygous average number of alleles or FIS statistics are measures of diversity within breeds (Carroll *et al*., 2018). In addition, the genetic relationships between races between a species, or as in our case, lineages within a group, can be determined by evaluating genetic distances. Heterozygosis, which estimates the proportion of heterozygous individuals for a single marker or, in extended terms, for an average set of markers, is one of the parameters traditionally used as a measure of genetic diversity. There are two methods in which heterozygous can be measured; one is through measuring the proportion of heterozygous individuals through counting the number of heterozygous genotypes, or by recording their genetic frequencies, defined as observed heterozygosity (Ho). The second is also known as "gene diversity," the "expected heterozygosity (He)," which is characterized as the heterozygous value that would be expected under Hardy-Weinberg equilibrium conditions. In general, a subdivided population shows lower levels of heterozygosity than expected; the reduction in heterozygosity observed can be used to measure the degree or extent of differentiation between subpopulations (Carroll *et al*., 2018).

2. 9. 1. population genetic differentiation

In any population analysis, to estimate genetic differentiation within the species as a whole, the ideal first step is to collect samples of the species over its entire range. However, most studies concentrate on selective sampling for economic or sampling constraints in particular areas with an economic or conservation interest. Genotypes or haplotypes are scored for the individuals sampled, depending on the markers used, and the data is analyzed in a variety of ways to measure genetic variation between populations (Rodríguez-Peña *et al.*, 2018). For the minimum number of individuals to sample per venue, there is no universal law. In estimating population structure, the individuals seem to be a reasonable trade-off between sampling cost and bias. Several genetic differentiation markers exist. F-statistics, which was created by Wright (1949/1950), is one of the most used measures.

2. 9. 2. Wright's F-statistics

We need to identify a key parameter in population genetics before implementing population structure measures: the fixation index also called the coefficient of inbreeding. To compare how much heterozygosity is present in the actual population compared to predicted levels of heterozygosity under random mating (and other HW equilibrium conditions), a number symbolized F, is widely used:

$$F = \frac{(He - Ho)}{He} \tag{3}$$

where HW is the predicted frequency of heterozygotes based on the frequency of the population allele, Ho is the frequency of heterozygotes observed. F is placed on a convenient scale of -1 and +1 by dividing by the predicted heterozygosity. Negative values indicate heterozygote excess and positive values indicate homozygote excess. The analysis of genetic differentiation between populations includes many new versions of the fixation index, the so-called F-

statistics, to account for the divergence of sub-populations. During the 1920s, Sewall Wright introduced the idea of F-statistics but later suggested the three parameters as we know them now. These indicators have been developed to identify the genetic composition of diploid species in the population. The basic assumptions are that all populations are of the same size and that any population has equal opportunities to exchange people with any other population. First, for each biallelic loci, heterozygosity is measured and then averaged according to the scale considered (total population, subpopulation).

So, a series of heterozygosity hierarchical measures were defined: HI: means heterozygosity observed across subpopulations, HS: mean predicted heterozygosity among randomly mating subpopulations within each subpopulation, HT: predicted heterozygosity within the total population, with random mating.

Where the total population is indicated by subscript T, S the subpopulation, and I the person level. HT and HS have maximum values of 0.5, and HI will differ between 0 (no observed heterozygotes) and 1 provided the biallelic loci (all observed individuals are heterozygous).

Now, three hierarchical F-statistics are described based on HI, HS, and HT: FIS, FST, and FIT.

FST: fixation index, $\text{FST} = \frac{(HT-HS)}{HT}$ $\quad 0 \leq \text{FST} \leq 1$ (4)

The FST coefficient reflects the discrepancy between the average predicted subpopulation heterozygosity and the expected total population heterozygosity, so it calculates the decrease in heterozygosity due to the allele frequency divergence of the subpopulation. It is possible, at a lower stage, that two alleles randomly sampled from a single subpopulation are similar by descent. An FST value close to 0 means that there is no distinction between subpopulations, and a value close to +1 means that subpopulations are fully differentiated. Although FST has a theoretical range between 0 and 1, the limit observed is typically much less than 1. The following are qualitative FST interpretation guidelines; little genetic differentiation, 0 to 0.05, Moderate genetic differentiation, 0.05 to 0.15, Great genetic differentiation, 0.15 to 0.25 and very large genetic differentiation, > 0.25.

3. CONCLUSION

Modernization of agriculture, current high levels of economic competitiveness, a subdivision of landholdings, the introduction of high-yielding breeds, and demographic pressures all contribute to the loss of valuable features and population declines in local breeds. Cattle were found to have selection signature regions, implying that selection processes in the breeds (human-driven selection during breed creation) and their founders resulted in genomic conservation in some areas.

References

[1] Armando, C., Aurora, G., Dorado, D. (2013). Allelic diversity and its implications for the rate of adaptation. *Genet*. 195: 1373–1384

[2] Albers, P. K., and McVean, G. (2018). Dating genomic variants and shared ancestry in population-scale sequencing data. *PLoS. Bio*. 8: 1–26

[3] Angress, S., and Reed, C. A. (2014). Origin and descent of domestic mammals. *Nature.* 54: 3–7

[4] Allais, S., Levéziel, H., Payet-Duprat, N., Hocquette, J.F., Lepetit, J., Rousset, S., Denoyelle, C., Bernard-Capel, C., Journaux, L. and Bonnot, A. (2010). The two mutations, Q204X and nt821, of the myostatin gene affect carcass and meat quality in young heterozygous bulls of French beef breeds. *J. Anim. Sci.* 88, 446-454

[5] Bhat, F., Morton, D., Mason, L., Bekhit, A. (2018). Role of calpain system in meat tenderness A review. *Food Sci.* 7: 196–204

[6] Bradley, D. G. (2020). Animal domestication in the era of ancient genomics. *Nat. Genet.* 21: 449–460

[7] Bejarano, D., Martínez, R., Manrique, C., Parra, L. M., Martínez Rocha, J. F., Gómez, Y., Gallego, J. (2018). Linkage disequilibrium levels and allele frequency distribution in blanco orejinegro and romosinuano creole cattle using medium density snp chip data. *Genet. and Mole. Bio*. 41: 426–433

[8] Bernatchez, L. (2016). On the maintenance of genetic variation and adaptation to environmental change: considerations from population genomics in fishes. *Journal of Fish Biology*, 89, 2519-2556

[9] Chen, J., Althagafi, A., and Hoehndorf, R. (2020). Predicting candidate genes from phenotypes, functions, and anatomical site of expression. *Bio. Rxiv*. 6: 1–7

[10] Cuypers, T. D., Rutten, J. P., Hogeweg, P. (2017). Evolution of evaluability and phenotypic plasticity in virtual cells. *Evo. Bio.* 17: 60-73

[11] Casas, E., & Kehrli Jr, M. E. (2016). A review of selected genes with known effects on performance and health of cattle. *Frontiers in Veterinary Science*, 3, 113

[12] Carvalheiro, R., Costilla, R., Neves, H. H. R., Albuquerque, L. G., Moore, S., and Hayes, B. J. (2019). Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. *Genet. Sel. Evo.* 51: 1–14

[13] Carroll, E. L., Bruford, M. W., DeWoody, J. A., Leroy, G., Strand, A., Waits, L., and Wang, J. (2018). Genetic and genomic monitoring with minimally invasive sampling methods. *Evol. Appl*. 11: 1094–1119

[14] Daetwyler, H. D., A. Capitan, H. Pausch, P. Stothard, R. van Binsbergen, R. F. Brondum, X. Liao, A. Djari, S. C. Rodriguez, C. Grohs, D. Esquerre, O. Bouchez, M. Rossignol, C. Klopp, D. Rocha, S. Fritz, A. Egging, P.J. Bowman, D. Coote, A.J. Chamberlain, C. Anderson, C.P. Van Tassell, I. Hulsegge, M.E. Goddard, B. Guldbrandtsen, M.S. Lund, RF. Veerkam, D.A. Boichard, R. Fries and B.J. Hayes. 2014. Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. *Nat. Genet.* 46: 858-865

[15] Decker, J. E., McKay, S. D., Rolf, M. M., Kim, J. W., Molina Alcalá, A., Sonstegard, T. S., Taylor, J. F. (2014). Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. *PLoS. Genet.* 10: e1004254

[16] Dadi Hailu, Tibbo, M., Takahashi, Y., Nomura, K., Hanada, H., Amano, T. (2008). Microsatellite analysis reveals high genetic diversity but low genetic structure in Ethiopian indigenous cattle populations. *Anim. Genet.* 39: 425-431

[17] Denney, D. A., Jameel, M. I., Bemmels, J. B., Rochford, M. E., & Anderson, J. T. (2020). Small spaces, big impacts: contributions of micro-environmental variation to population persistence under climate change. *AoB Plants*, 12(2), plaa005

[18] Espigolan, R., Baldi, F., Boligon, A., Souza, P., Gordo, G.M., Tonussi, L., Cardoso, F., Oliveira, N., Tonhati, H., Sargolzaei, M. (2013). Study of whole genome linkage disequilibrium in Nellore cattle. *BMC. Genom*. 14: 305

[19] Edea Zewdu, Dadi Hailu, Kim, S., Dessie, T., Lee, T., Kim, H., Kim, K. (2013). Genetic diversity, population structure and relationships in indigenous cattle populations of Ethiopia and Korean Hanwoo breeds using SNP markers. *Front. Genet.* 4: 1–9

[20] Emlen, D. J., Marangelo, J., Ball, B., and Cunningham, C. W. (2005). Diversity in the weapons of sexual selection: Horn evolution in the beetle genus Onthophagus (Coleoptera: Scarabaeidae). *Evolu*. 59:1060–1084

[21] FAO. (2019). Breeding strategies for sustainable management of animal genetic resources FAO Animal Production and Health Guidelines. No. 3

[22] Fariello, M. I., Servin, B., Tosser-Klopp, G., Rupp, R., Moreno, C., San Cristobal, M., International Sheep Genomics Consortium. (2014). Selection signatures in worldwide sheep populations. *PloS One* 9: p, e103813

[23] Fiems, L.O. (2012). Double muscling in cattle: Genes, husbandry, carcasses and meat. *Anim.* 2, 472-506

[24] Fijarczyk, A., and Babik, W. (2015). Detecting balancing selection in genomes: limits and prospects. *Mol. Ecol.* 24: 3529-3545

[25] Greenbaum, G, Templeton A.R., Zarmi Y, Bar-David S. (2014). Allelic Richness following Population Founding Events—A Stochastic Modeling Framework Incorporating Gene Flow and Genetic Drift. *PLoS One* 10(3): e0119663

[26] Greenwood PL, Cafe LM, McIntyre BL, Geesink GH, Thompson JM, Polkinghorne R, Pethick DW, Robinson DL. Molecular value predictions: associations with beef quality, carcass, production, behavior, and efficiency phenotypes in Brahman cattle. *J Anim Sci.* 2013 Dec; 91(12): 5912-25. doi: 10.2527/jas.2013-6960

[27] Grobet, L., Martin, L.J., Poncelet, D., Pirottin, D., Brouwers, B., Riquet, J., Schoeberlein, A., Dunner, S., Ménissier, F., Massabanda, J., Fries, R., Hanset, R., and Georges, M. (1997) A deletion in the bovine myostatin gene causes the double-muscled phenotype in cattle. *Genet.* 17, 71-74

[28] Groeneveld, L. F., Lenstra, J. A., Eding, H., Toro, M. A., Scherf, B., Pilling, D., Weigend, S. (2010). Genetic diversity in farm animals - A review. *Anim. Genet.* 41: 6–31

[29] Ghoreishifar, S. M., Eriksson, S., Johansson, A. M., Khansefid, M., Moghaddaszadeh-Ahrabi, S., Parna, N., Javanmard, A. (2020). Signatures of selection reveal candidate

genes involved in economic traits and cold acclimation in five Swedish cattle breeds. *Genet. Sel. Evo.* 52: 1–15

[30] Gudbjartsson, D.F., Walters, G.B., Thorleifsson, G., Stefansson, H., Halldorsson, B.V., Zusmanovich, P., Sulem, P., Thorlacius, S., Gylfason, A., Steinberg, S. (2008). Many sequence variants affecting diversity of adult animal weight. *Nat. Genet*. 40: 609–615

[31] Gurgul, A., Jasielczuk, I., Ropka-Molik, K., Semik-Gurgul, E., Pawlina-Tyszko, K., Szmatoła, T., Krupiński, J. (2018). A genome-wide detection of selection signatures in conserved and commercial pig breeds maintained in Poland. *Genetics,* 19: 1-1

[32] Hui, T. Y. J., and Burt, A. (2020). Estimating linkage disequilibrium from genotypes under Hardy-Weinberg equilibrium. *Genet.* 21, 1–11

[33] Hagos Berhane, (2017). Ethiopian Cattle Genetic Resource and Unique Characteristics under a Rapidly Changing Production Environment-A Review. *IJSR.* 6: 1959–1968

[34] Hoda MR, Theil G, Mohammed N, Fischer K, Fornara P. The adipocyte-derived hormone leptin has proliferative actions on androgen-resistant prostate cancer cells linking obesity to advanced stages of prostate cancer. *J Oncol.* 2012; 2012: 280386. doi: 10.1155/2012/280386

[35] Hu., Scheben, A., Edwards, D. (2018). Advances in integrating genomics and bioinformatics in the breeding program. *Swiz. Agri.* 8, 56-69

[36] Hoshiba, H., Setoguchi, K., Watanabe, T., Kinoshita, A., and Mizoshita, K. (2013). Comparison of the effects explained by variations in the bovine PLAG1 and NCAPG genes on daily body weight gain, linear skeletal measurements and carcass traits in Japanese Black steers from a progeny testing program. *ANIM. SCI. J.* 84: 529–534

[37] Hanotte, O., Bradley, D. G., Ochieng, J. W., Verjee, Y., Hill, E. W., and Rege, J. E. O. (2002). African pastoralism: Genetic imprints of origins and migrations. *Sci.* 296: 336–339

[38] Hanotte, O., Bradley, D. G., Ochieng, J. W., Verjee, Y., Hill, E. W., and Rege, J. E. O. (2003). African pastoralism: Genetic imprints of origins and migrations. *Science,* 296: 336–339

[39] Habimana, R., Okeno, T. O., Ngeno, K., Mboumba, S., Assami, P., Gbotto, A. A., ... & Yao, N. (2020). Genetic diversity and population structure of indigenous chicken in Rwanda using microsatellite markers. *PloS One,* 15(4), e0225084

[40] Jacobs, G. S., Sluckin, T. J., and Kivisild, T. (2016). Refining the use of linkage disequilibrium as a robust signature of selective sweeps. *Genet.* 203: 1807–1825

[41] Kanungo, S., Wells, K., Tribett, T., El-Gharbawy, A. (2018). Glycogen metabolism and glycogen storage disorders. *Tran. Medi.* 6, 474–474

[42] Weigel, M. (2015). Extended phase graphs: dephasing, RF pulses, and echoes-pure and simple. *Journal of Magnetic Resonance Imaging,* 41(2), 266-295

[43] Koolmees, P. A., and Lenstra, J. A. (2014). On the history of cattle genetic resources. *Diversity,* 6(4), 705-750

[44] Li, W.F., Li, J.Y., Gao, X., Xu, S.Z., and Yue, W.B. (2013). Association analysis of PRKAG3 gene variants with carcass and meat quality traits in beef cattle. *Afri. J. Biot.* 11: 1855-1861

[45] Li, T., Song, Y., Bao, X. and Zhang, J. (2020). Mediation of miR-34a/miR-449c for Immune Cytokines in Acute Cold/Heat-Stressed Broiler Chicken. *Anim*. 10: 2160-2168

[46] Lee, T., Shin, D.H., Cho, S., Kang, H. S., Kim, S. H., Lee, H.K., Kim, H., and Seo, K.S. (2014). Genome-wide association study of integrated meat quality-related traits of the duroc pig breed. *Asia. Aust. J. Anim. Sci.* 27: 303-312

[47] Liu, B. J., Li, Y. L., Zhang, B. D., and Liu, J. X. (2020). Genome-Wide Discovery of Single-Nucleotide Polymorphisms and Their Application in Population Genetic Studies in the Endangered Japanese Eel (Anguilla japonica). *Fron. Sci*. 6, 1–11

[48] Makina, S. O., Whitacre, L. K., Decker, J. E., Taylor, J. F., MacNeil, M. D., Scholtz, M. M., Maiwashe, A. (2016). Insight into the genetic composition of South African Sanga cattle using SNP data from cattle breeds worldwide. *Genet. Selec. Evo.* 48, 1–7

[49] Mwai, O., Hanotte, O., Kwon, Y., and Cho, S. (2015). - Invited Review - African Indigenous Cattle: Unique Genetic Resources in a Rapidly Changing World. *J. Anim. Sci.* 28, 911–921

[50] Matukumalli LK, Lawley CT, Schnabel RD, Taylor JF, Allan MF, Heaton MP, O'Connell J, Moore SS, Smith TP, Sonstegard TS, Van Tassell CP. Development and characterization of a high density SNP genotyping assay for cattle. *PLoS One* 2009; 4(4): e5350. doi: 10.1371/journal.pone.0005350

[51] Upadhyay, M. R., Chen, W., Lenstra, J. A., Goderie, C. R. J., MacHugh, D. E., Park, S. D. E., Groenen, M. A. M. (2017). Genetic origin, admixture and population history of aurochs (Bos primigenius) and primitive European cattle. *Heredity*, 118, 169-176

[52] Milan, D., Jeon, J.-T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., and Rask, L. (2000). A mutation in PRKAG3 is associated with excess glycogen content in pig skeletal muscle. *Sci.* 288: 1248-1251

[53] Magalhães AF, de Camargo GM, Fernandes GA Junior, Gordo DG, Tonussi RL, Costa RB, Espigolan R, Silva RM, Bresolin T, de Andrade WB, Takada L, Feitosa FL, Baldi F, Carvalheiro R, Chardulo LA, de Albuquerque LG. Genome-Wide Association Study of Meat Quality Traits in Nellore Cattle. *PLoS One* 2016 Jun 30; 11(6): e0157845. doi: 10.1371/journal.pone.0157845

[54] Meuwissen, T.H.E., Hayes, B.J., Goddard, M.E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genet.* 157: 1819–1829

[55] Meuwissen, T.H.E., Hayes, B.J., Goddard, M.E. (2016). Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, 157: 1819–1829

[56] Qanbari S. and Simianer H. (2014). Mapping signatures of positive selection in the genome of livestock. *Live. Sci.* 166: 133-143

[57] Pitt, D., Sevane, N., Nicolazzi, E. L., MacHugh, D. E., Park, S. D. E., Colli, L., Orozco-ter Wengel, P. (2019). Domestication of cattle; *Evo. Appli.* 12: 123–136

[58] Pant, S. D., Schenkel, F. S., Verschoor, C. P., and Karrow, N. A. (2012). Use of breed-specific single nucleotide polymorphisms to discriminate between Holstein and Jersey dairy cattle breeds. *Anim. Biot.* 23, 1–10

[59] Page, B.T., Casas, E., Heaton, M.P., Cullen, N.G., Hyndman, D.L., Morris, C.A., Crawford, A.M., Wheeler, T.L., Koohmaraie, M., Keele, J.W., and Smith, T.P.L. (2002). Evaluation of single-nucleotide polymorphisms in CAPN1 for association with meat tenderness in cattle. *J. Anim. Sci.* 80: 3077-3085

[60] Rivollat, M., Mendisco, F., Pemonge, M. H., Safi, A., Saint-Marc, D., Brémond, A., Deguilloux, M. F. (2015). When the waves of European neolithization met: First paleogenetic evidence from early farmers in the Southern Paris Basin. *PloS One* 10: 371-521. https://doi.org/10.1371/journal.pone.0125521

[61] Ramey, H. R., Decker, J. E., McKay, S. D., Rolf, M. M., Schnabel, R. D., & Taylor, J. F. (2013). Detection of selective sweeps in cattle using genome-wide SNP data. *BMC Genomics*, 14(1), 1-18

[62] Rincón, A. D., Prevosti, F. J., and Parra, G. E. (2011). New saber-toothed cat records (Felidae: Machairodontinae) for the Pleistocene of Venezuela, and the Great American Biotic Interchange. *J. Verte. Pale.* 31: 468–478

[63] Rodríguez-Peña, R. A., Johnson, R. L., Johnson, L. A., Anderson, C. D., Ricks, N. J., Farley, K. M., Stevens, M. R. (2018). Investigating the genetic diversity and differentiation patterns in the Penstemon scariosus species complex under different sample sizes using AFLPs and SSRs. *Genet.* 19: 1335–1348

[64] Rothammer, S., Seichter, D., Förster, M., Medugorac, I. (2013). A genome-wide scan for signatures of differential artificial selection in ten cattle breeds. *Genomics*, 14: 1-17.

[65] Rauw, W. M., and Gomez-Raya, L. (2015). Genotype by environment interaction and breeding for robustness in livestock. *Fron. Genet.* 6: 1–15

[66] Santiago, G., Siqueira, F., Cardoso, F., Regitano, L., Ventura, R., Sollero, B., Souza, M., Mokry, F., Ferreira, A., and Torres, R. (2017). Genome wide association study for production and meat quality traits in Canchim beef cattle. *J. Anim .Sci.* 95: 3381-3390

[67] Schmid, M., and Guillaume, F. (2017). The role of phenotypic plasticity on population differentiation. *Here.* 119: 214–225

[68] Sejian, V., Naqvi, S. M. K., Ezeji, T., Lakritz, J., and Lal, R. (2013). Environmental stress and amelioration in livestock production. In Environmental Stress and Amelioration in Livestock Production. *Spri.* 13: 322-325

[69] Tarekegn Getenet Mekuriaw, Ji, X., Bai, X., Liu, B., Zhang, W., Birungi, J., Tesfaye Kassahun, (2018). Variations in mitochondrial cytochrome b region among Ethiopian indigenous cattle populations assert Bos taurus maternal origin and historical dynamics. *AJAS* 31: 1393–1400

[70] Theunissen, B., and Lenstra, J. A. (2015). Conservation of cattle genetic resources: The role of breeds Conservation of cattle genetic resources: the role of breeds. *JAS.* 153: 152–162

[71] Utsunomiya Y.T., Perez O'Brien A.M., Sonstegard T.S., Solkner J. and Garcia J.F. (2015). Genomic data as the "hitchhiker's guide" to cattle adaptation: tracking the milestones of past selection in the bovine genome. *Front. Genet.* 6: 36-42

[72] Vitti J.J., Grossman S.R. and Sabeti P.C. (2013). Detecting natural selection in genomic data. *Genet.* 47: 97-120

[73] Winter, A., Krämer, W., Werner, F.A.O., Kollers, S., Kata, S., Durstewitz, G., Buitkamp, J., Womack, J.E., Thaller, G., and Fries, R. (2002). Association of a lysine-232/alanine polymorphism in a bovine gene encoding acyl CoA: diacylglycerol acyltransferase (DGAT1) with variation at a quantitative trait locus for milk fat content. *Pnsus.* 99: 9300-9305

[74] Xing, T., Gao, F., Tume, R. K., Zhou, G., Xu, X. (2019). Stress Effects on Meat Quality. *Mech. Pers.* 12: 541-4337

[75] Yen, C.L.E., Stone, S.J., Koliwad, S., Harris, C., and Farese, R.V. (2008). Thematic review series: glycerol lipids. DGAT enzymes and triacylglycerol biosynthesis. *J. Rese.* 49: 2283-2301

[76] Yuan, Z., Li, J., Li, J., Gao, X., Gao, H., and Xu, S. (2013). Effects of DGAT1 gene on meat and carcass fatness quality in Chinese commercial cattle. *Mole. Bio. Repo.* 40: 1947-1954

[77] Zwane, A. A., Maiwashe, A., Makgahlela, M. L., Choudhury, A., Taylor, J. F., and van Marle-Koster, E. (2016). Genome-wide identification of breed-informative single-nucleotide polymorphisms in three South African indigenous cattle breeds. *S. Afri. J. Anim. Sci.* 46: 302–312

[78] Zhao, F., McParland, S., Kearney, F., Du, L., and Berry, D. P. (2015). Detection of selection signatures in dairy and beef cattle using high-density genomic information. *Genet. Sele. Evo.* 47: 1–12

[79] Zhou, G., Dudgeon, C., Li, M., Cao, Y., Zhang, L., and Jin, H. (2010). Molecular cloning of the HGD gene and association of SNPs with meat quality traits in Chinese red cattle. *Mole. Bio.* 37: 603-611