

GENETICS AND BREEDING: Review

REVIEW: Differences between traditional and modern populations within cattle breeds: What do we not know?

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ABSTRACT

Purpose: We reviewed the genetic differences between modern and traditional cattle breeds, emphasizing the evolution of modern cattle herds, particularly the Hereford breed. With this work, we sought to enhance our comprehension of bovine genomics by analyzing the interaction between traditional and modern cattle genetics, thereby informing future breeding and conservation strategies.

Sources: We reviewed the existing literature on genomic studies of cattle breeds and highlighted a dearth of information (except in a few cases) regarding the differences between traditional and modern populations within breeds.

Synthesis: According to the limited studies available, traditional populations serve as significant stores of genetic variety, which can later be introgressed into modern breeds to improve production, resilience, and adaptation to changing environments. However, information about this diversity is severely lacking in many breeds for which traditional populations exist.

Conclusions and Applications: We made the case for more extensive surveys of genomic differences within cattle breeds where ancestral and traditionally managed populations exist. These surveys could have substantial implications for sustainable livestock management and the enhancement of cattle breeds in response to ever-changing environmental and agricultural requirements. In particular, understanding the genetic changes involved in the development of modern breeds can assist in identifying adaptive loci present in traditional populations that are at risk of being lost through selective breeding.

Key words: *Bos taurus*, breed conservation, genetic diversity, Hereford cattle, traditional breeds

INTRODUCTION

Throughout history, humans have domesticated wild animals upon realizing that they could use them to help meet their requirements in daily life. The domestication of modern livestock animals is justified by their ability to offer a wide range of benefits, such as a source of foodstuffs in the form of dairy products and meat, hides for clothing and other applications, transportation, and assistance with labor in various regions across the globe (Scheu et al., 2015). Domestic cattle originated from the aurochs (*Bos primigenius*), which used to inhabit regions throughout Europe, Asia, and North Africa (Guliński, 2021). Over time, domestication of various breeds has resulted in a change in the genetic composition of these populations, resulting in the loss of some ancestral allelic combinations. As such, conservation of traditional populations provides both historical and cultural benefit and a valuable source of genetic variation, which modern populations may take to help adjust to modern challenges through crossbreeding and introgression into the purebred lines.

HUMAN DEVELOPMENT OF CATTLE BREEDS

Throughout the history of agriculture, whether in extensive or intensive farming, the same questions have persisted: (1) Which breed is the best? and (2) What is the upper limit of production that can be attained with the existing herd? Animal breeding studies have demonstrated that the designation of a breed as the “best” cannot be ascribed solely based on its characteristics but rather hinges on its ability to adapt to the specific environmental conditions in which it is intended to be reared (Olesen et al., 2000; Burrow, 2012). Darwin described the contributions of farmers to animal breeding as follows:

“We cannot suppose that all the breeds were suddenly produced as perfect and as useful as we see

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now them; indeed, in several cases, we know that this has not been their history.”

In the text *On the Origin of Species*, Darwin goes on to state the following:

“is man’s power of accumulative selection: nature gives successive variations; man adds them up in certain directions useful to him.”

Initially, cattle breeders focused solely on observable phenotypic traits, selecting animals based on their appearance, health resilience, and high production levels. This allows for slow but steady improvement of cattle breeds, as desired by the producers, but is not necessarily the most accurate, as environmental and management practices can have large effects on the overall presentation and performance of an animal. The genetic composition of domesticated animals encodes a history of how these species were domesticated, distributed, and selectively bred by ancient farmers (Decker et al., 2014).

CATTLE BREED RELATIONSHIPS AND GENETIC DIFFERENCES

This review highlights a trend in genetic research that focuses mainly on differences between domesticated cattle breeds, often overlooking variations within the breeds themselves, except when related to key agricultural traits. Studies that reveal differences within breeds are as important as those between separate breeds, because they can illustrate the domestication process and the genetic alterations that breeds have experienced throughout history. They highlight the importance of protecting traditional breeds as pure breeds, because of their contributions to breeding programs. This is especially true when breeders aim to enhance or improve economically important traits such as milk production, meat quality, or animal welfare. It is critical to research and maintain the genetics of purebred individuals to allow crossbreeding to benefit from the superior quality of the pure breed. As such, it is important that these studies are undertaken for as wide a range of traditional populations and breeds as possible. It is also vital that they are preserved in their traditional state so that they can continue to have effects on crossbreeding programs or where they are widely used in novel environments and selected for different management schemes. For example, systematic breeding of ‘cosmopolitan’ breeds has resulted in allopatric development, wherein populations are relocated to a different region, such as the New World, and adapted to their new habitat (Felix et al., 2011). Here, to reveal the phenotypic changes observed within the same breed, genetic studies should be conducted on modern and traditional varieties of that breed, apart from the differences resulting from adaptation (environmental deviation). One of the ways to reveal what other reasons other than adaptation could have caused

the differences observed in phenotypes is through genetic studies. Although numerous studies have compared different breeds within the same species, there is a notable scarcity of research exploring genetic variances within individual breeds, particularly contrasting modern and traditional variants. The lack of these studies could lead to lapses in genetic maintenance of these traditional breeds, which would result in multiple detrimental outcomes. The first of these would be the disappearance of culturally and historically important populations representing different ethnic groups and cultures, leading to a loss of history. The second, and more economical detriment, would be the loss of their unique genetic markers. Traditional breeds often are maintained in such a way that there is little introgression into their population, meaning that their markers and traits have been maintained with little external influence. These unique genetics have great potential to be used in crossbred populations or to quickly shift modern day breeds (often very homogeneous compared with modern populations) in a direction to better adapt to environmental changes or market demands. Davis et al. (2020) showed this in a study of low-input dairy farming, and they showed how the value of traditional Ayrshire can greatly increase the value of the crossbred cattle because of their superior milk traits. Genetic studies have been designed to demonstrate differences or similarities between breeds using various methodologies. These investigations have often used breed distinctions to classify groups and, in some cases, have even used genetic analyses to determine the geographic origins of modern cattle breeds.

A particularly in-depth study was done by Decker et al. (2014), in which the researchers used 43,000 single-nucleotide polymorphism (SNP) markers across ~1,500 animals from 134 domestic cattle breeds to evaluate different methodologies of genomic analysis and population structure. Using principal component analysis (PCA), as well as the Admixture program (Alexander et al., 2009), this study provided a first look at the relationships among the different breeds. Primary differences were seen between the *Bos taurus* and *Bos indicus* breeds, as expected based on current understandings of cattle breeds and the historical migration of cattle out of the fertile crescent region (Decker et al., 2009). Creating a phylogram of the representative populations resulted in a clear clustering of breeds by their geographic origin, further supporting the already understood separation of breeds based on historical records. The clusters also showed evidence of migration patterns, such as *Bos taurus* from southeast Europe to the northwest. The researchers even compared specific regional breeds to those of the broader European continent to look for evidence of supposed introgression of African indicine breeds and found that Spanish breeds were no more introgressed than the rest of European breeds and that, when it did occur, it was primarily of taurine influence and not indicine. This observation was contrary to existing literature, which suggested that many of these southern European breeds had a much greater influence

on external breeds to make them what they are today (McTavish et al., 2013).

Another study by Solodneva et al. (2023), took a similar, but more focused, approach by looking at 155 native and transboundary cattle populations, along with yak and zebu populations from Russia, Mongolia, and Kyrgyzstan. Similar to Decker et al. (2014), this study used PCA and clustering methods to compare the genomic relationships between various populations. The goal was to better understand the number of unique breeds in the region and provide a foundation for protecting native breeds. Although the authors acknowledge potential sources of errors in their populations and the low number of individuals or samples, the study still indicates a common process of comparing expected unique populations and breeds in cattle. Sometimes the use of various breeds, both purebred and crossbred, arises from the desire to better understand the ability to predict the breed of an unknown individual or population and improve the accuracy of selection within genomic evaluations. Studies by Signer-Hasler et al. (2017), Huson et al. (2020), and Schmidtman et al. (2021) all examined the genetic makeup of a small number of breeds either in the same region or for the same purpose of better distinguishing the various breeds and providing a better understanding of what genomic variants exist with them.

Several other studies have made use of methods such as PCA and programs such as Admixture, PLINK (Purcell et al., 2007), and TreeMix (Pickrell and Pritchard, 2012), highlighting the value of these methods for analyzing differences between populations (Signer-Hasler et al., 2017; Huson et al., 2020; Schmidtman et al., 2021; Ryan et al., 2023). Ryan et al. (2023) went on to use machine learning methods such as Random Forest to separately verify results from clustering analyses. Again, these studies found genomic differences between their populations of interest and were able to better characterize how these genomic differences could be used to assign breeds to an unknown individual or to better inform genomic evaluations and selections within these populations.

Another reason that many studies look at different cattle breeds instead of examining within-population or breed differences is to examine the genetic basis of economically important or welfare traits for production purposes. Research by Vanvanhossou et al. (2020) examined the genomic differences among cattle breeds in Benin, Africa, identifying those that show disease resistance and increased productivity in challenging conditions. Another study, by Doyle et al. (2020), looked at 5 beef breeds within the Irish national beef breeding program for commonalities and differences in their genetic architecture. Both studies wanted to compare the genetic differences for specific traits between breeds for the purpose of better selection and use of these genomic regions in future breeding decisions.

Although some studies do exist to look at a single breed and better characterize a specific trait or set of traits, it is rare for a study to look at the history of a single breed and

showcase the differences between older maintained populations relative to their newer relatives and, subsequently, the change in their SNP frequencies and homozygosity over time. For that reason, it is of great importance to promote this type of research because it can provide a long-term view of a single breed and show how it has changed with regional demands and how it has been maintained in its more native original form. These studies, if performed well and on well maintained and recorded populations, will increase the amount of well characterized genetic differences between modern and traditional breed populations, leading to more opportunities for using traditional population genetics in modern herds.

CHANGES IN BREEDING PRACTICE CAUSE DIVERGENCE BETWEEN TRADITIONAL AND MODERN POPULATIONS

Customer demands are the driving force behind animal agriculture, and cattle varieties transform their focus over time in response to these changes. Some changes are purely economical, such as the increase in milk yield over time from dairy cattle (VanRaden et al., 2009; Davis et al., 2017; Lee et al., 2020). Others may be due to more societal reasons such as grass-fed beef and welfare traits (Wall et al., 2005; Carlson et al., 2016). These adjustments, from the standpoint of breeding programs, result in a divergence of the population from the native population's phenotypes. Emphasis on production is the primary driver of changes in breeds, as it often alters the physiology of animals to meet new demands. An extreme example of this can be seen in the broiler industry, where the growth of the pectoralis major has increased by more than 80% over 50 years of selective breeding. (Zuidhof et al., 2014).

Returning to cattle breeds, a study by Zhang et al. (2018) looked at the difference between the modern Danish Red Dairy cattle and its traditional populations. The Danish Red Dairy breeding practices have been focused on increased milk yield, protein and fat content, fertility, and body conformation traits, among others. One way in which the Danish Red Dairy was improved over its original form was through the introgression of both Holstein and Brown Swiss, introduced because of their favorable milk production and content traits. This admixed population was put under a more standard breeding program, resulting in higher performing cattle populations (Kantanen et al., 2000). The use of analyses such as Admixture and PCA further showed the distribution of the Brown Swiss and Holstein versus the traditional and modern Danish Red Dairy populations, indicating a significant shift in the modern populations away from their traditional counterparts.

A recent publication by Zhou et al. (2022) used cattle genome sequences from 57 different breeds to create a comprehensive pangenome. The purpose of this study was to provide a framework within which the changes in diversity of different breeds could be examined and the

evolutionary history and divergence of these breeds could be better understood. One major point of this study is that the individuals being used to represent the breed can have drastic effects on the genomic variants being represented, highlighting that the original cattle reference genome was derived from a single Hereford cow. This can greatly influence how different breeds are viewed from a genomic perspective and shows how breeding practices can result in a breed that has differed quite significantly from its original population. In Korea, Hanwoo cattle have undergone extensive selection for beef production over the last few decades. Park et al. (2013) and others have shown that the modern Hanwoo contains multiple signatures of selection that are absent in the traditional population (Seo et al., 2022).

Because of the nature of the industry, cattle breeds will continue to undergo selection as time progresses and new breeding practices are introduced. For this reason, it remains important to maintain traditional populations for the conservation of their unique allelic combinations and frequencies to ensure that the genetic diversity of the breed does not diminish unduly (Biscarini et al., 2015; Upadhyay et al., 2019; Schmidtmann et al., 2021). Conservation of original populations needs to be carefully undertaken to avoid harmful levels of inbreeding and population bottlenecks. Additionally, this maintenance will allow for the use of unique allelic combinations found in traditional breeds to be deployed in modern populations when the need arises.

CONSERVATION OF TRADITIONAL BREED POPULATIONS

It is important when discussing the differences between modern and traditional cattle populations to note that many breeds still have original ancestral populations that have been maintained for decades. These populations serve as a focus for preservation and can be used as a source of genetic variation that can be introgressed into modern populations to improve productivity, resilience, and adaptability (Hoffmann, 2013). Therefore, part of the focus is on cultural preservation, specifically the protection of local breeds that are significant to the culture or region they originate from. The other focus is more practical; it involves preserving unique genetic lines that can contribute to our understanding of cattle breed development and offer new possibilities for modern breeds.

Identification of traditional cattle can be achieved via genetic testing, though the number of markers required may vary. A report by Ogden (2012), for meat provenance testing, showed that Traditional Hereford and Welsh Black breeds could be separated from other breeds on the basis of their genotype across a small number of SNP markers that were largely monomorphic within those breeds or showed highly different allele frequencies. Commercial (modern) Hereford and Red Poll, however, were found to

be less genetically distinct from other breeds (which Ogden attributes to recent derivation from—or crossbreeding with—other breeds) and thus required more markers to distinguish them.

The Traditional Hereford discussed by Ogden (2012) is also referred to as the Hereford Original Population (HOP) from the United Kingdom. The more modern Commercial Hereford is primarily North American Derived (NAD; Hegarty et al., 2020). The Hereford breed quickly became a prominent breed for the production of beef across the world and in the process became the focus of selections involving outside breeds to better adjust the cattle's productivity and robustness to their local conditions (Blott et al., 1998). For this reason, Hereford genetic diversity has greatly increased, and the NAD has changed significantly from the HOP. This led to the HOP becoming a minority breed within the greater Hereford space, being used primarily for genetic conservation as an ancestral population (Blott et al., 1998). This distinction allows the preservation of the original Hereford breed while also allowing them to be used for new crosses or introgressions using the HOP. Many current modern European breeds can in fact have their ancestry traced back to traditional ancestral populations that have been maintained to this day. For example, in a study by Weldenegodguad et al. (2019), whole genome sequencing was performed on 3 different northern European native cattle breeds (Eastern Finncattle, Western Finncattle, and Yakutian cattle) with a goal of both characterizing their genetic diversity within the population and using their sequence to identify their relationships with the broader Eurasian taurine cattle breeds. They identified unique genomic changes related to the adaptation of these breeds to the harsh environment among all 3 of the breeds in comparison with the modern breed version in the Finnish Ayrshire and Holstein breeds. This points to a lack of artificial selection among the native breeds compared with their modern contemporaries, which have been highly selected for milk production and other economic traits. Their original breeds came from the now extinct Aurochs *Bos primigenius*, but this is still a prime example of the divergence and maintenance of local traditional populations that have progressively been replaced with modern powerhouses (Kantanen et al., 2000).

A paper by Nyamushamba et al. (2017) examined efforts to maintain traditional African cattle breeds in the face of extensive crossbreeding with European cattle, which threatens to eliminate these native populations. These efforts aim to preserve the cultural significance of the native breeds to small-stakeholders and maintain their unique attributes and genetic variation.

Stronen et al. (2019) examined the maintenance and conservation of the threatened Danish Jutland cattle in the face of decreased genetic variation and increased use of more modern variations. Relative to other native and modern breeds that see more widespread use (i.e., Holstein and Jersey), Danish Jutland were found to contain unique

genetic variation (at immediate risk of loss) because of the small population sizes, making closed management of them more difficult. This led the authors to note studies that indicated potential ways to maintain the original genetic diversity when population management may no longer be viable (Charlton et al., 2018).

Globalized agricultural industry practices pose a threat to traditional breeds, risking the loss of genetic diversity and the cultural significance they provide to a region and its people. In light of the fact that the industry is currently being forced to re-evaluate its populations and management practices as a result of climate change and societal pressures, it is of even greater significance that these breeds have their original populations preserved. It is in the unique genetics of the traditional populations that the cattle industry may find the answers needed for these external pressures. With rising demands from consumers for more sustainable milk and dairy production, the management of animals will need to change, and the original hardiness and adaptive genetics of many traditional breeds may soon come to the forefront of cattle breeding and genetics.

TRADITIONAL VERSUS MODERN CATTLE

Here, we examine the history and some studies regarding 5 European cattle breeds that are in use today because of their adaptability and superior phenotypic traits. All of these breeds were chosen because traditional populations are still being maintained to preserve their genetic and trait diversity compared with modern populations. These traditional herds could be used in modern breeding programs through introgression of important phenotypic differences. Such efforts can support better management and adaptation to modern needs and environmental conditions. This could be through their direct insertion into modern purebred populations or by using crossbreeding with other breeds to take advantage of their unique allelic combinations and the resulting hybrid vigor. Only 2 of these breeds (Dexter and Hereford) have received any real genetic investigation of the differences between their traditional and modern populations, which highlights the scarcity of such studies.

Ayrshire Cattle

The Ayrshire breed of dairy cattle is native to Scotland and was first discovered in the County of Ayr. The Ayrshire breed received official recognition from the Ayrshire Agricultural Society in 1853 (Paterson, 1951).

Traditional Ayrshires are medium-sized cattle, weighing over 550 kg, with strong, rugged traits, and they are known for their exceptional ability to survive in difficult conditions and on low-quality grazing areas (Ormiston, 1942). Traditional Ayrshire cows have long been renowned for their ability to produce large quantities of milk, and although their individual yields may not be exceptional, they excel in their average milk output (Eckles, 1914).

According to reports, the first Ayrshires were imported to the United States in 1822 by H. W. Hills of Windsor, Connecticut (OSU, 2025). Ayrshire cattle were also introduced to Canada in the early 1800s.

The Ayrshire breed remains important as an example of a traditional breed because of its valuable contribution to genetic diversity and sustainable dairy farming. Ayrshire breeds are frequently used in organic systems because of their convenient management, health conditions, and efficient milk conversion (Davis et al., 2020). In the Davis et al. study, Ayrshire cross cattle displayed the most desirable fatty acid profile in their milk compared with other cross-breeds and also had the best health and production scores, making them appealing for use in crossbred systems. According to Karhula et al. (2024), Ayrshires typically exhibit better fertility compared with other dairy breeds, as well as lower SCC (better udder health), stronger disease resistance, and greater feed efficiency, especially on roughage-based diets (CABI, 2025a). These traits make them well-suited for low-maintenance, pasture-based, or smaller-scale dairy systems. Another justification for the importance of keeping traditional breeds in production is that small-bodied breeds, such as the Ayrshire, can easily be adapted to older and smaller barns, which are still used in a significant share of dairy production in many countries. Maintaining an understanding of the traditional breed genetics will thus be critical in preventing loss of the adaptations underpinning these traits in the face of crossbreeding or use of the animals in novel environments.

Jersey Cattle

Jersey, one of the oldest dairy cattle breeds, is a small dairy breed that originated on the Isle of Jersey in the British Channel. England officially recognized the breed's existence as early as 1771 and selectively bred it as a pure breed for over a century. Although imports were restricted, export of the Jersey breed was allowed, resulting in its widespread use across England, the United States, Australia, France, and New Zealand throughout the late 1800s (Becker, 1973). However, the Royal Jersey Society required that only purebred offspring could be entered into the Jersey herd book. Exports of the Jersey breed to the United States began in the mid 1800s, and shortly thereafter a US Jersey Society was founded. Over time, the American Jersey populations were selected for greater milk yield, which resulted in an increase in the size of the individuals and less emphasis on their appearance. Consequently, the traditional Jersey breed from the Island of Jersey became known as the "miniature Jersey" (Miniature Jersey HerdBook, 2017).

The Jersey breed is today found across the globe, owing to its use as a dairy animal and its broad adaptability to different environments (CABI, 2025b). The differences between the traditional population and the US population are quite distinct, with a difference of over 3,000 kg of milk per cow (Council on Dairy Cattle Breeding, 2015).

A study by Huson et al. (2020) set out to identify the genetic differences in population structure and selection methods between the traditional Island Jersey populations and the United States Jersey populations, using Guernsey and Holstein as additional comparisons. As expected, when compared with the other populations (especially the United States Jersey), the traditional Jersey populations showed a greater degree of inbreeding, likely caused by the restricted import of cattle up until 2008.

In addition, multiple runs of homozygosity were found in common between the dairy breeds; however, the 2 Jersey breeds shared a greater number of runs of homozygosity due to common ancestral origins (Kim et al., 2013). Furthermore, the traditional Jersey populations showed selection signatures unique to that population that could potentially be taken advantage of if they provide economic benefits, either through introgression into modern populations or as part of a crossbred herd. This could include a large increase in milk yield when brought into modern populations while also adding a large degree of adaptability through the original hardiness that the traditional breeds maintain to this day. Makers of products needing a high fat content in milk could also benefit from including the traditional breeds when adaptability is a concern.

Dexter Cattle

Another example of the maintenance of traditional breeds versus the changing of their modern contemporaries is the Dexter cattle breed. The Dexter breed originated in Ireland and was introduced to England in 1882. There are currently numerous populations of the Dexter breed. However, there are still populations that are recognized as the “traditional Dexter” and can be used as an example of comparison with more modern groups (Weitzman, 1993). In addition to different populations of Dexter, the study by Bray et al. (2009) also looked at 2 other modern breeds with supposed association with the Dexter breed (Devon and Kerry). By performing this genetic Admixture study, the authors determined that the Dexter breed is now composed of multiple subgroups with levels of diversity, as found in other studies involving Dexter (Peelman et al., 1998; Wiener et al., 2004), as well as a strong parental connection to the Kerry breed. Bray et al. (2009) make an important point that the populations used for the various Dexter, Devon, or Kerry breeds were low in number and that only a limited number of microsatellite markers were used for their study. Despite this, their findings do indicate a likely scenario and provide a strong example of how a traditional breed can still co-exist alongside the now greater distribution and divergence of its own breed. They additionally note that if there is a low use of these traditional populations, there is a risk of unique alleles being lost forever because they are not present within the more modern variations of the same breed. The traditional populations boast hardiness and a smaller size and were ideal as a dual-purpose animal (CABI, 2025c). Although

modern populations have similar traits, the differences are substantial enough that further exploration of unique alleles could provide opportunities for the use of the traditional population in crossbred populations with other breeds.

Angus Cattle

Angus originated in northeastern Scotland. This cattle breed is small in stature but incredibly well-developed and bred for beef production throughout the world. Being originally from Scotland, the Angus breed is hardy and can handle cold, harsh weather, allowing it to proliferate across a wide range of environments and regions (Rare Breeds Survival Trust, 2020). With its expansion to many different regions, the genetics of the breed have changed over time. American Angus, for example, are much larger; in America the focus has been on more mass for beef production. Additionally, dietary differences have changed some of the development of the animals as well as their feed efficiency, leading to further deviation. On top of these phenotypic changes for production and efficiency, Angus breeds outside of Scotland are often crossed with other lines to bring in changes to marbling, feed efficiency, yield, and performance in hotter environments. Despite these crosses, many of these herds are still classified as Angus, leading to a further separation genetically from the Aberdeen traditional population (Speer, 2019). In parts of Europe, such as Hungary, crossbreeding programs were also created using Angus cattle populations to increase meat yield and feed efficiency, resulting in a greater genetic distinction from the traditional population over time (Horn et al., 1959). Márton et al. (2024) looked at 16 different Angus populations and compared them using microsatellite markers, finding clusters of herds with more similar genetic backgrounds. Further investigation into the background from these herds revealed connections back to more ancestral populations out of Aberdeen, Germany, and England. These findings indicated that this more modern version of the Angus breed had become genetically distinct from the traditional Aberdeen population and should be considered for the conservation of this modern fork. Breeders who want a herd that is hardier and more resilient to harsh environments, or who practice grazing style management, may find themselves preferring some of the genetic benefits that come from the traditional Aberdeen populations (Rare Breeds Survival Trust, 2020). Although the increase in meat yield and extensive crossbreeding has made the modern populations a powerhouse in the beef industry, it has left them open to a changing environment that is more often than not characterized by extremes.

Angus has also been used in the production of offspring from dairy cattle sold for beef. As most offspring from dairy cattle represent a cost rather than a revenue, use of beef cattle on dairy breeds can turn this necessary mating for milk production into a more profitable venture. Cross-

ing a beef and dairy animal, however, results in offspring with reduced beef quality compared with standard Angus animals. As such, the use of Angus populations with double muscling genetics can be a workaround to produce viable beef offspring (Mckimmie et al., 2024). This process is used to maintain the “certified Angus beef” labeling within the required specifications of meat quality. The myostatin gene has been extensively researched because of its effects on muscle growth and fatty acid deposition (McPherron et al., 1997; Sellick et al., 2007), and its effect on calving performance has also been a focus of research (Berry et al., 2019). This all leads to Angus herds with homozygous deletions in the myostatin gene to create this double muscling. This is another example of the different selection pressures in these modern breeding programs when compared with the traditional herds. As the effect of beef production continues and new applications of Angus genetics are found among the cattle industry, it highlights the importance of understanding the traditional Aberdeen Angus genetics that eventually led to this widespread breed, and the importance of conserving these original populations and genetic architectures. Furthermore, as the modern Angus populations continue to mix with other breeds to allow for more localization for desired traits, it becomes even more important to conserve the traditional breed to allow for returning to a more baseline state if introgression proves to lead in an unfavorable direction.

Hereford Cattle

The HOP cattle breed has been present in the United Kingdom since the mid-1600s. The breed attained a reputation for having superior cattle, easily kept because of a gentler temperament (greater docility), and great diversity of coat color (Willham, 1937). These animals were bred to perform optimally under their native environmental conditions. They were able to produce high-quality and dense meat products despite lower-quality grazing conditions, often on terrain that was difficult to traverse, which showcases their hardiness. These production traits, in combination with the breed’s docility and better rearing, led to the exportation of the HOP to other countries despite suboptimal conditions. These exported populations were nevertheless able to adapt and thrive in these new and challenging environments and continued to perform well and produce high-quality products.

The HOP is the progenitor of the Hereford (NAD) breed (Hegarty et al., 2020). Following the end of the American Civil War, there was a significant expansion of transportation within the United States. This, along with foreign investments and the availability of cheap land, contributed to the beef cattle industry’s explosive growth in the western United States (Grundy, 2002).

The Hereford (NAD) are now commonplace in North American cattle breeding and said to retain some of the original traits (high-quality meat, docile temperament,

and adaptability) that are hallmarks of the HOP. As time has progressed, both the NAD and other Hereford populations from around the world have had their genetics imported back into the UK, which, although providing new genetic variants for use in cattle breeding, also has the potential to threaten the purebred status of the HOP. This has resulted in a reduction in the hardiness of the Hereford breed, along with a change in how the animals were managed by finishing in a feedlot system instead of grazing systems (Church, 1989).

As Hereford breeders changed their breeding strategies toward having leaner animals, North American and Canadian Hereford bloodlines were imported to Britain. During that time, the genetic makeup of the Hereford population in Britain was beginning to change (Blott et al., 1998). The Rare Breeds Survival Trust (RBST) assigned the Roslin Institute in 1994 to investigate how the British Hereford population had genetically changed over the decades. Their study compared the genetic profiles of Hereford populations in different countries and examine the variation. Blott et al. (1998) claimed the proportion of Canadian Hereford genetics in the British hybrid population was predicted to have increased from 55% in the 1960s to 70% at the end of the 1990s. They also found that the estimated percentage of Herefords in the British population (born after 1980) that possessed at least one ancestor of Canadian origin was between 85% and 90%. The replacement of native British genetics with that from North American, particularly Canadian, animals may result in an accelerated decrease in genetic variation in the British population.

As a result of this influx of NAD genetics, the HOP was in the rare breed category 5 (minority 1,500 breeding cows) within the UK in 2017 but has been moved to category 4 (at risk 750 breeding cows) in the latest RBST watchlist (2023–2024). Both Hereford Herd Book International Ltd. and the RBST have the goal of preserving the breed, both in an economic sense (by testing the provenance of the meat), as well as a genetic one (by preventing hybridization with bloodlines from other breeds). Toward this goal, research by Hegarty et al. (2020) used high-density SNP data from HOP and NAD animals (as well as those of known combined pedigree) to confirm Ogden’s findings and further demonstrate a clear division between the groups (see Figure 1). In addition, this study identified several animals with high proportional assignment to other breeds—possibly indicating crossbreeding—using the Admixture software. These results form the basis for a breed purity test to maintain the HOP as a traditional breed, as well as identifying the genomic regions that differ between the groups. These substantial differences between the HOP and NAD populations provide the framework to bring back HOP genetics into modern populations if societal and economic pressures bring back a need for a harder animal that is not restricted to more managed systems.

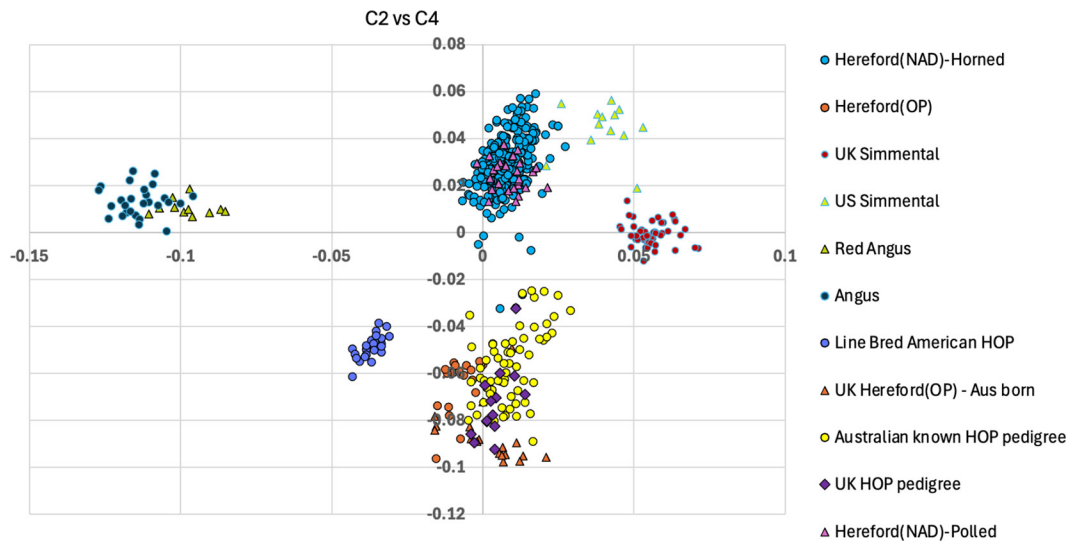


Figure 1. Multidimensional scaling plot of traditional (Hereford Original Population, HOP) versus modern (North American Derived, NAD), with reference cattle breeds. C2 (horizontal) and C4 (vertical) refer to second and fourth multidimensional scaling components. OP = Original Population; Aus = Australian. Reproduced from Hegarty et al. (2020); published under the Open Access CC BY license.

THE NEED FOR IN-DEPTH GENETIC CHARACTERIZATION OF TRADITIONAL BREEDS

In cattle, Hereford and Jersey have been the only breeds with significant research on differences between traditional and modern populations. Although many breeds of cattle have been examined in terms of their ancestry and to provide detailed information on the expansion of cattle across various regions of the world, direct investigation of the genomic differences of traditional versus modern populations is lacking. When this kind of research is performed, it often focuses on a specific trait rather than a comprehensive view, for example, the study by Seo et al. (2022) on the Hanwoo cattle of Korea. Other times it focuses only on the uniqueness of traditional breeds versus other breeds instead of comparing to a modern equivalent (Mastrangelo et al., 2018). What is really important is the combination of these 2 aspects, such as the study by Fraser et al. (2014), which examines methane emission differences between traditional and modern breeds by comparing Welsh Black (traditional) with the unrelated Limousin (modern). One area in which these studies are sorely lacking is in non-European cattle breeds. Part of this is likely due to the more widespread use of European breeds within global agriculture, but it could also be due to the lack of opportunity and data availability on the more unique breeds. This includes many of the *Bos indicus* breeds, which, although prevalent in many countries, are generally seen as resilient rather than productive breeds and have therefore not had much focus until recently. Many current studies are focused primarily on the differences between the *Bos taurus* and *Bos indicus* breeds, but with time more traditional versus modern analyses will likely be undertaken.

As the cost of genomic sequencing continues to decrease, and computational ability increases, it becomes feasible to sequence large numbers of individuals from a population (Hoff, 2024). By doing this, it then becomes straightforward to perform in-depth analyses of the commonalities and differences between different populations. This is already being done with pangenome approaches (Liao et al., 2023; Rice et al., 2023; Smith et al., 2023), but these currently focus on major breeds or groups within a species. Given the resources, the same process could be done for different populations within a breed (such as the Dexter populations in Bray et al., 2009); however, the approach would need to be refined as the differences would likely not be as large as between separate breeds themselves.

As genomic data being collected on different populations increases in size and complexity (provided it is properly annotated and subject to quality control), there is a wealth of information that could allow us to parse between traditional and modern populations, likely allowing for a deeper understanding of their genomic differences. Artificial Intelligence and Machine Learning approaches (Benos et al., 2021; Pedrosa et al., 2024) may assist with breed and population classification. Current projects, such as the Agricultural Genome to Phenome Initiative (Tuggle et al., 2024) or the Functional Annotation of Animal Genomes project (EuroFAANG, 2025), are working toward increasing the amount of data available across multiple species while also standardizing data collection and researching new analytical techniques. Current barriers to using these genomic tools and technologies appear to be cost, as well as lack of individuals within a population. As such, the continued conservation and management of traditional breed populations is paramount to enabling the future use of these expanding technologies in preserving this unique store of genetic variety.

APPLICATIONS

Cattle breeds have changed over time as a result of selective breeding, crossbreeding, and different management practices. These have caused genetic changes between traditional populations within breeds and their modern counterparts. When resources are dedicated toward understanding the differences between traditional and modern cattle breeds, then the industry will discover more opportunities to introgress traditional genetics and traits into current populations to assist with ever-changing market shifts. Beef breeders are facing increasing costs, environmental challenges, and consumer nutritional perception and so could use various traditional breed genetics to make adjustments and improve the viability of their herds. Globally, there is a trend toward increased beef productivity, but sustainability goals and conservation of genetic resources need to be considered. We have largely focused on understanding traditional breed resources in Western cattle, but this is also particularly relevant in the developing world, where breeding strategies often include crossbreeding of highly productive European beef breeds (such as Simmental) with traditional populations noted for their adaptation to their native environment. If not managed carefully, this could lead to the loss of adaptive alleles and diversity in those native populations. Given that similar trends are occurring across the food agricultural industry, from poultry and pork to a wide variety of plants, well-documented studies of genetic differences will help traditional breeds remain relevant in a difficult market. Research will also ensure breeding schemes stay adaptable as the environmental challenges and consumer demands shift over the years, while also aiding in reaching sustainable breeding goals.

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NOTES

Animal and Human Care and Use Approval: Because no human or animal subjects were used, this review did not require approval by an Institutional Animal Care and Use Committee or Institutional Review Board.

Acknowledgments: The authors thank the anonymous reviewers for their valuable suggestions.

Funding Sources: This study received no external funding.

Declaration of Conflicts of Interest: The authors have not declared any conflicts of interest.

Nonstandard Abbreviations Used: AG2PI = Agricultural Genome to Phenome Initiative; Aus = Australian; EuroFAANG = European Functional Annotation of Animal Genomes; HOP = Hereford Original Population; NAD = North American Derived; NGS = next-generation sequencing; OP = Original Population; PCA = principal component analysis; PLINK = population linkage; RBST = Rare Breeds Survival Trust; SNP = single-nucleotide polymorphism.

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