

The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation

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As the global population and global wealth both continue to increase, so will the demand for livestock products, especially those that are highly nutritious. However, competition with other uses for land and water resources will also intensify, necessitating more efficient livestock production. In addition, as climate change escalates, reduced methane emissions from cattle and sheep will be a critical goal. Application of new technologies, including genomic selection and advanced reproductive technologies, will play an important role in meeting these challenges. Genomic selection, which enables prediction of the genetic merit of animals from genome-wide SNP markers, has already been adopted by dairy industries worldwide and is expected to double genetic gains for milk production and other traits. Here, we review these gains. We also discuss how the use of whole-genome sequence data should both accelerate the rate of gain and enable rapid discovery and elimination of genetic defects from livestock populations.

Domestication and selective breeding of livestock

Livestock and poultry species were first domesticated approximately 10 000 years ago because they had the capacity to turn forage not suitable for human consumption (e.g., grass) into meat, milk, and eggs, all sources of high-quality protein, lipids and micronutrients that enabled humans to survive in wide-ranging environments. Selection of livestock for desirable traits occurred continuously over this period of time. Yet, as Darwin observed ‘our oldest domestic animals are still capable of rapid improvement or modification’ [1]. In fact, genetic variation in modern livestock exists for almost every trait that has ever been studied.

The effect of selective breeding is clear. For example, a study comparing the time to market weight for chicken strains from the 1950s versus those from the 2000s found a massive increase in efficiency, with the modern strains

achieving market weight in one-third of the time but consuming less feed [2,3]. In both Australian and US Holstein-Friesian dairy cattle, an increase in milk production of approximately 1% (40–80 kg/cow/year) between 1980 and 2010 has been achieved (<http://adhis.com.au>; <http://aipl.arsusda.gov/eval/summary/trend.cfm>), although it is important to note that trends in some countries have not been as dramatic. The effect of these gains has been to reduce the cost of milk, meat, and eggs to consumers, and enable more of the population of the world to access high-quality protein [4]. Emphasis has lately shifted in many breeding programs from only production to include health and fitness traits, such as fertility [5]. For example, poultry breeders have successfully selected for reduced incidence of ascites, a metabolic disease in rapidly growing chickens characterized by heart defects [6]. More recently, mutations underlying a variety of single-gene disorders have been identified in cattle and sheep, resulting in their rapid elimination from breeding stock [7].

New challenges

Although selective breeding has improved livestock dramatically, we are facing several new challenges that will require changes in both the pace and direction of approaches. First, little genetic improvement has been achieved in some important traits either because they are expensive to measure (e.g., feed conversion efficiency in cattle and sheep) or because genetic variation in them has been largely ignored (e.g., fertility). In fact, in some traits, such as fertility of dairy cattle, genetic change has been negative [8]. Fertility is also a good example of a trait that has a large impact on system efficiency in livestock production: more fertile females, particularly those with good longevity, have more offspring, and so dilute their own feed requirements over this increased number of offspring [9,10].

Second, there are new traits that have not been part of the breeding objective in the past but will be in the future. Ruminants produce methane, a potent greenhouse gas, as part of the rumen fermentation process. This means that

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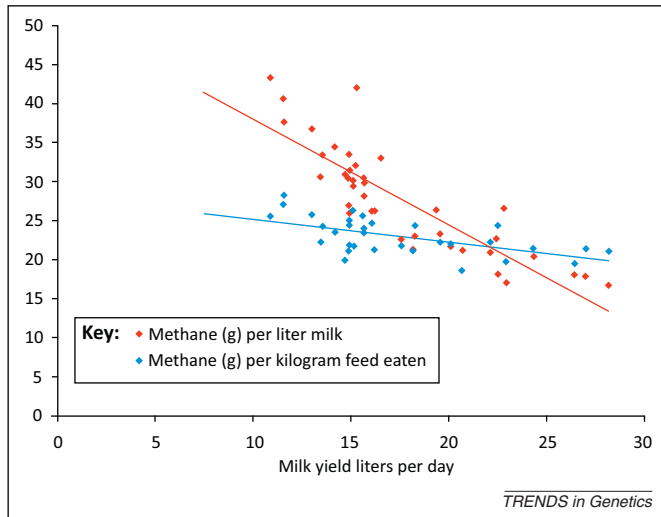


Figure 1. Selection for increased efficiency of production in ruminant livestock species tends to lower methane emissions per unit product. Because methane emissions are closely linked to feed intake, more efficient animals dilute their feed intake for maintenance requirements over more units of product. The graph shows methane emission levels in grams per liter of milk against production level (milk liters per day) for 32 Holstein-Friesian cows (Pryce et al. unpublished, and the authors are grateful to Peter Moate and Leah Marett, DPI Ellinbank, Victoria, Australia for data).

methane emission intensity (emissions per liter of milk or kilogram of meat) is likely to become part of the breeding goals for cattle and sheep. Although breeding for increased production has already reduced emissions intensity (Figure 1), faster reductions in emission levels may be achieved by selecting for traits that are more highly correlated with methane emission levels than with production. For example, there is a strong correlation between dry matter intake and emission levels; therefore, reductions in emissions could be achieved by selecting for either reduced dry matter intake while maintaining production (e.g., feed conversion efficiency [11–13]) or, in the future, reduced methane emission levels directly.

The third reason for changes in breeding objectives is that the environment under which production occurs will change in the future. Global warming is likely to lead to hotter climates than in the recent past [14]. In the case of dairy cattle, increased temperature and humidity levels above a certain threshold decrease the production of milk and milk proteins, and this loss can be substantial (Figure 2) [15]. The adverse effect of increased heat stress on fertility is even more dramatic [16]. Fortunately, genetic variation in heat stress response has been observed in livestock species where this has been measured, including dairy cattle and pigs [15–21]. That is, the production and fertility of some individuals is less affected by heat stress than of others, and this response is heritable. In addition to selective breeding for heat resistance, more rapid gains may be possible using adapted breeds and crossbreeding. For example, *Bos indicus* cattle show some remarkable physical and physiological adaptations to heat stress (Figure 3) [22]. In the future, it may be possible to introgress desirable genes from one breed or subspecies into another more quickly than in the past by using genomic selection combined with advanced reproductive technologies (discussed below).

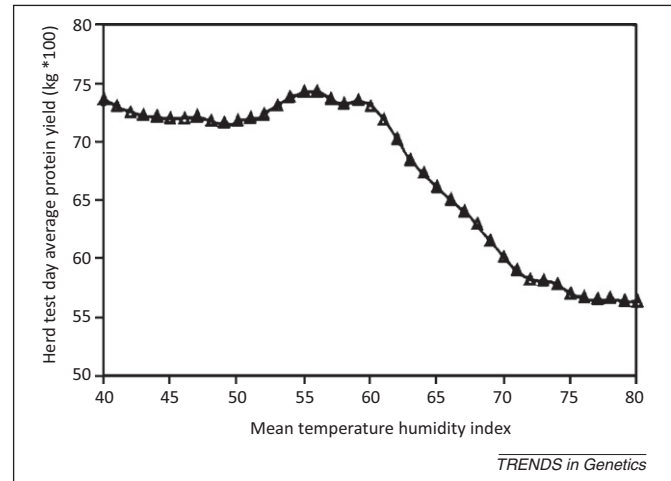


Figure 2. Adaptation to global warming is a key desirable trait in livestock. Heat stress has an effect on yield from dairy cattle, shown here as the effect of the temperature humidity index (THI) on average daily protein yield from Australian dairy cattle [15]. A temperature of 18 °C and moderate humidity equates to a THI of approximately 60. Extrapolating the loss per day per cow across the entire Australian dairy herd (approximately 1.8 million cows) means that, for every 1 °C increase in temperature above 18 °C, approximately 21 000 kg of protein are lost daily.

Future breeding objectives may also emphasize performance under lower levels of nutrition. Before the 20th century, livestock used resources with little or no alternative value, such as pastureland unsuitable for cropping. However, modern livestock production uses expensive inputs, such as grain. Both the competition for grain (for human consumption and biofuels) and the impact of climate change on grain production are likely to continue to drive grain prices higher [23]. These economic factors may change livestock production systems and, consequently, the desired genetic attributes. A reversion to lower quality feed inputs if grain becomes too expensive to use for livestock feed would require selection for performance at lower levels of feeding or, better yet, for animals that perform well across a range of nutrition levels [15,24,25]. Because it is difficult to predict the future, genetic improvement systems that can respond rapidly to changes in breeding objective are desirable.

Finally, for meat and milk production from livestock to remain competitive, their appeal to consumers must be retained or even increased. This could mean improving the healthiness of fatty acid profiles in milk, for example, or increasing the level of omega-3 in meat [26].

Based on the extent of natural variation that exists, the opportunity is available to further improve livestock and to breed for these new traits to meet the challenges in the coming decades. Three new technologies will make it possible to accelerate genetic gains in livestock and help address these issues: genomic selection, whole-genome sequencing, and advanced reproductive technologies, including *in vitro* fertilization (IVF).

Genomic selection

Genomic selection refers to the use of genome-wide genetic markers to predict the breeding value of selection candidates [27]. This method relies on linkage disequilibrium between the markers and the polymorphisms that cause variation in important traits. Consequently, a linear

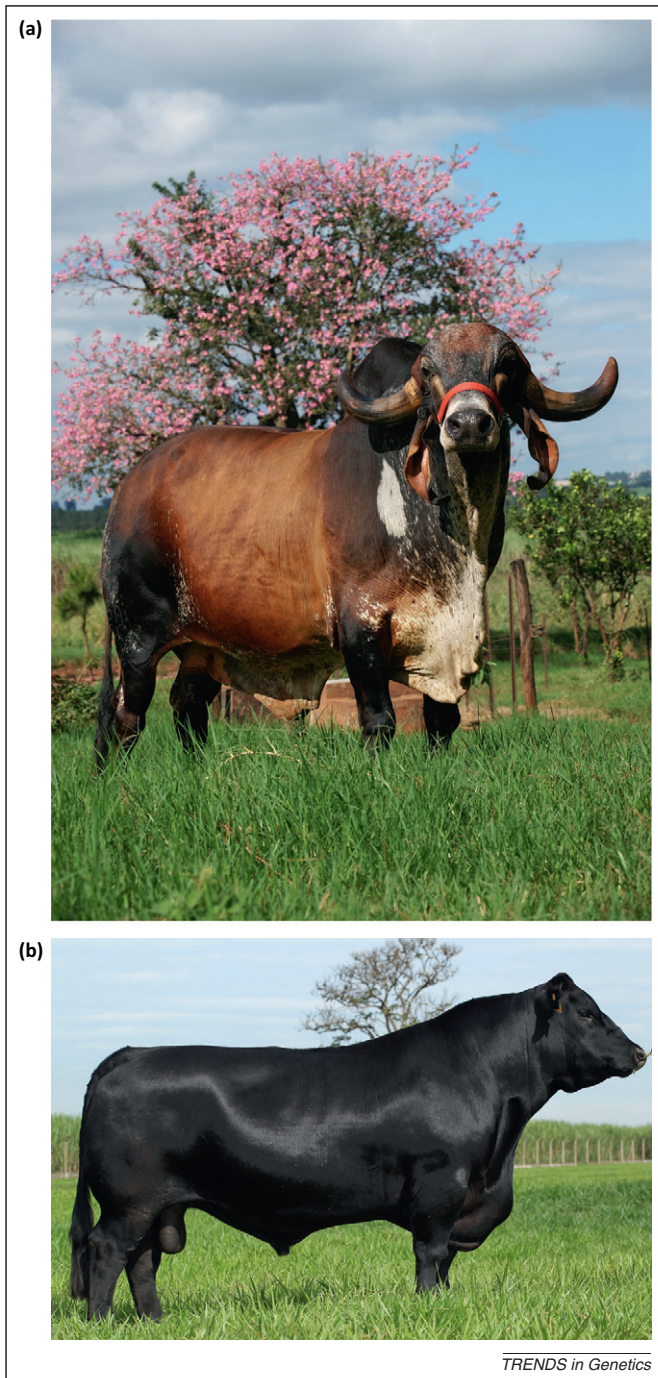


Figure 3. *Bos indicus* (a) and *Bos taurus* (b) bulls. The elongated ears and large dewlap of the *B. indicus* bull are potential adaptations for heat dissipation. *Bos indicus* cattle and their crosses dominate in the tropical areas of the world, including Asia, Central America and the northern countries of South America, particularly Brazil, northern Australia, and parts of Africa. Images reproduced, with permission, from CRV Lagoa, Brazil.

prediction equation, based on the marker genotypes, can predict the cumulative effect of many causal variants on the additive genetic value or breeding value of the animal. The markers used in genomic selection are most commonly SNPs, because it is possible to genotype individuals for 100 000s of SNPs at a reasonable cost. Earlier methods of marker-assisted selection, which relied on identifying a small number of causal variants, were not successful for complex traits because most of these are affected by

hundreds or thousands of polymorphisms, each with small effects [28,29]. However, genome-wide DNA markers in linkage disequilibrium with the causative mutations can be used to capture the effect of all these loci [27]. The equation that predicts breeding value from SNP genotypes must be estimated from a sample of animals, known as the reference population, that have been measured for the traits and genotyped for the SNPs (Figure 4). This prediction equation can then be used to predict breeding values for selection candidates based on their genotypes alone. The candidates are ranked on these estimated breeding values, and the best ones are selected to breed the next generation. More details of genomic selection are given in Box 1.

The advantage of genomic selection over traditional selection (based on pedigree and phenotype alone) is that animals can be selected accurately early in life, based on their genomic predictions, and for traits that are difficult or expensive to measure: fertility, disease resistance, methane emissions, and feed conversion are prime examples. In dairy cattle, for example, dairy bulls are traditionally selected following progeny testing, because genetic merit for milk production of a bull can only be accurately evaluated through the milk production of his daughters. Progeny testing results in accurate selection, but with a generation interval of 5 years or longer. With genomic selection, the generation interval can be reduced to 2 years, potentially resulting in a 60–120% increase in the rate of genetic gain [30,31]. Needless to say, genomic selection has been adopted rapidly by dairy industries around the world [31]. There are some encouraging results from the Irish dairy cattle population, suggesting that the rate of genetic change for milk production and fertility has already increased as a result of the adoption of genomic selection, although this evidence must be treated as preliminary [32].

In beef cattle, however, adoption has been slower. The potential for genomic selection to improve genetic gain in beef cattle is substantial, mainly because reproduction, carcass traits, meat quality, and feed efficiency are key traits that contribute to profitability [33,34]. However, the accuracies of genomic breeding value for beef cattle that have been reported for these traits are only low to moderate [35–37]. This is for two reasons: (i) the reference populations that have been assembled for beef cattle are still generally smaller than those for dairy cattle, and there are fewer sires with highly accurate progeny tests than in dairy cattle; and (ii) unlike dairy cattle, where populations around the world are dominated by just a couple of breeds, there are a large number of beef breeds of importance, and even two subspecies (*Bos taurus* and *B. indicus*). This makes assembling large enough reference populations to reach desired levels of accuracy of genomic breeding value for individual beef breeds challenging. One potential solution is to pool reference populations across countries through international collaborations. Another seemingly attractive strategy would be to pool reference populations across breeds. However, genomic prediction across breeds (be they dairy, beef, or sheep breeds) has been largely unsuccessful to date, with prediction equations derived in one breed giving low accuracies in other breeds [38,39]. This is likely due to differences in linkage disequilibrium phases between SNPs and causative mutations

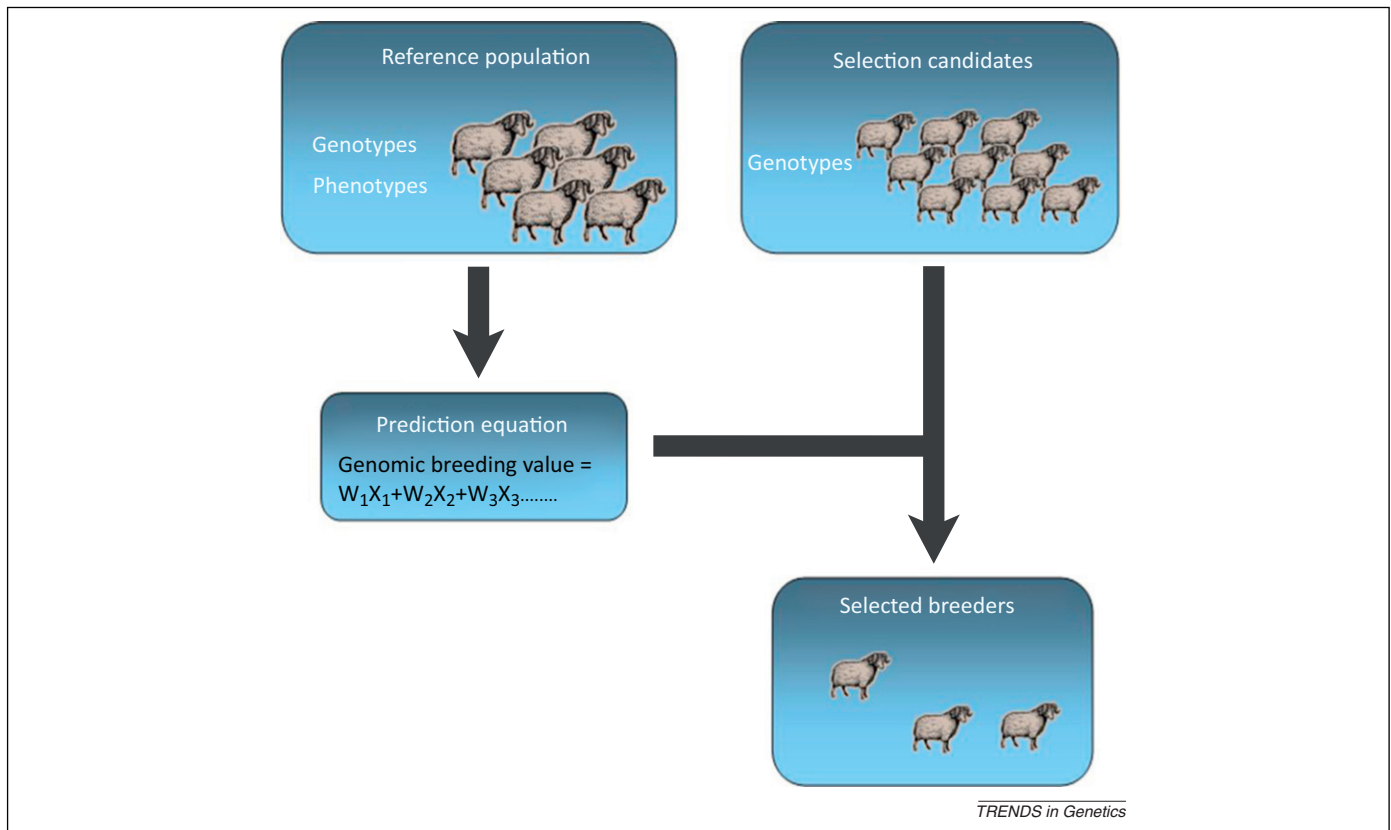


Figure 4. Genomic selection. A large number of individuals are measured for the trait and genotyped for the genome-wide markers (reference population). The genotypes can be represented by variables (x), which take the values 0, 1, or 2 corresponding to one homozygote, heterozygote, and other homozygote, respectively. Statistical analysis of the reference population estimates the effects for each marker (w), which form a prediction equation combining all the marker genotypes with their effects. This prediction equation can be applied to a group of animals that have genotypes but not phenotypes (selection candidates). The estimated breeding values calculated in this way can be used to select the best animals for breeding.

across breeds. Whole-genome sequence data may improve accuracy across breed prediction (discussed below).

In addition to their use in cattle, genomic selection methods are also being used in meat, wool, and dairy sheep [40,41]. In meat sheep, genomic predictions have been made for health attributes in lambs; specifically, genomic

predictions for the level of omega-3 fatty acids were of moderate accuracy [42].

There are already some promising estimates of the accuracy of genomic predictions for feed conversion efficiency in chickens, dairy cattle, and pigs [43–45]. In dairy cattle, female fertility is a key component of lifetime

Box 1. Statistical methods for genomic prediction

The major challenge in genomic prediction is estimating the prediction equation (the effect of each SNP on the trait) when the number of SNPs is typically much larger than the number of phenotypes. Many of the statistical methodologies that have been developed to deal with this problem make use of prior information about the distribution of the SNP effects. For example SNP-best linear unbiased prediction (BLUP) assumes that the SNP effects are normally distributed, with small effects [27]. An equivalent model to SNP-BLUP is to fit a genomic relation matrix among the individuals constructed from the SNP information, in place of the expected relation matrix derived from pedigree in the standard equations for breeding value estimation [51]. Other methods assume prior distributions with a small probability of large to moderate effects, for example a Student's t distribution (this method has been called BayesA [27]), or an exponential distribution (Bayesian LASSO, reviewed in [74]). When the number of SNPs is very large, perhaps an even better assumption is that a proportion of the SNPs will have zero effect, whereas the remainder will be normally distributed (called BayesCpi [75]) or Student's t distributed (a method called BayesB, as for BayesA but some SNPs are assumed to have zero effect [29]). For computational efficiency this can be modeled as a

series of normal distributions, one with mean and variance of zero (BayesR [38]).

In real data, for most traits, the accuracy of genomic predictions from the methods is surprisingly similar [76]. Only for those traits with mutations of moderate to large effect are differences between the methods observed, with BayesA, BayesB, and BayesR outperforming SNP-BLUP [38,75,76]. The methods that allow for a large proportion of SNPs with zero effect also outperform SNP-BLUP when there is a very large number of SNPs [38], which is important when genomic predictions are based on sequence data. For a detailed review of genomic selection methodologies, see [74].

The genomic prediction methods used in animal breeding have largely focused on predicting breeding values, that is the additive genetic component that is passed on to the next generation. However if the goal is to predict future phenotypes (i.e., how an animal will perform over its lifetime, rather than breeding values) then capturing all the genetic variation, including imprinting, dominance, epistasis, and perhaps even epigenetic variation may become important. There are some methods that have been described in the literature to improve potentially the accuracy of predicting future phenotypes by capturing contributions from these sources of variation [73,77,78].

efficiency, and high accuracy genomic predictions of this trait are already available [46]. To date, there are no reports of genomic predictions for methane emission levels. Genomic predictions of feed intake have been suggested as a proxy for this trait [47].

Genomic selection for resistance to heat stress is also possible. Researchers have described a reference set of genotyped sires with phenotypes for the response of the milk production of their daughters to heat stress, predicted by temperature and humidity measurements from weather stations in close proximity to the farms where the cows were milked [48]. The accuracy of genomic prediction for tolerance to heat stress was moderate at 0.37. However, this was much higher than the accuracy of pedigree-only predictions, which was 0.16.

There have not yet been any reports of genomic predictions for robustness to nutrition level (that is, the ability to produce under low or high levels of nutrition). However, there is evidence that individual loci may interact with the level of nutrition to alter phenotypes [25,49]. One group investigated the effect of a mutation in the gene encoding myostatin on muscling in sheep at high and low levels of nutrition [49]. They reported that a heterozygous myostatin mutation increased growth of muscle on a high plane of nutrition, whereas the same genotype in lambs with a poor nutritional background resulted in reduced muscling.

The major challenge in applying genomic selection to the traits discussed above that will be important in the future, will be assembling large enough reference populations to make accurate predictions, because thousands to tens of thousands of phenotyped individuals are required [50,51]. Genomic selection is especially desirable for traits that are too expensive to measure routinely in selection candidates. However, this expense also makes it difficult to assemble large enough reference populations, especially if each breed must have its own large reference population that must be updated relatively frequently. International collaboration and cheaper ways to measure these traits will help. Measuring methane emissions cheaply in particular is currently an active area of research, with laser technology and tracer gas techniques under development [52–54].

Whole-genome sequencing

Although genomic estimated breeding values are now widely used as the basis for selection of dairy cattle in particular, there are some limitations of the current technology. It has become clear that much of the accuracy of genomic breeding values, based on 50 000 DNA markers, in fact derives from prediction of the effect of large chromosome segments that segregate within fairly closely related animals [55]. In this situation, the accuracy of the prediction equation will rapidly decay over generations as large chromosome segments break up due to recombination. Across breeds, the problem is even greater. Within breeds, effective population sizes are generally <200 and, consequently, animals within a breed have recent common ancestors and so share large chromosome segments. However, between breeds, animals share only small segments of chromosomes, so the within-breed prediction equation, which predicts the value of large segments, does not work

well across breeds [38,39,56]. Using genomic predictions from whole-genome sequence data, may overcome some of these issues.

Given that the causative mutations are present in the sequence data, the issue of decay in associations between causative mutations and SNP, which results in the decline in accuracy over time, may be overcome. Although this has been demonstrated in simulated data [57], in practice, to achieve this will require a carefully designed reference population. This requires a population in which the linkage disequilibrium between causative mutations and other variants is as limited as possible: if the extent of linkage disequilibrium is too great, the genomic prediction algorithms will distribute the effect of the causative mutation over variants across large chromosome segments, leading to the problem described above. One possibility is a large multibreed reference population, which would leverage the fact that the extent of linkage disequilibrium is less between than within breeds [58]. More than two breeds are desirable, because all the causative mutations segregating within one breed are unlikely to segregate in another. If more than two breeds are used, it increases the chances that the same causative mutation that is segregating in one breed is segregating in at least one other breed. In addition, a genomic prediction method will have to be used to analyze the data that allows variants to have a zero effect, in other words be removed from the model. Otherwise, the effect of the causative mutation will be ‘smeared’ over a large number of SNPs in linkage disequilibrium with the mutation and each assigned a small effect (this has already been observed when increasing marker density from 50 000 SNP to 800 000 SNP for genomic predictions in dairy cattle [38]).

Even within a breed, the accuracy of genomic predictions from SNP arrays is bounded by the proportion of the genetic variance captured by the SNP, which is in turn determined by linkage disequilibrium between the SNP and the causative mutations affecting the trait. In dairy cattle, a 50 000-SNP panel explained between 50% and 80% of the total genetic variation, depending on the trait [59,60]. In other species, such as sheep, the same number of SNPs can capture considerably less genetic variation [39]. If full genome sequence data could be used in genomic predictions rather than SNP arrays, the potential accuracy is no longer bounded by linkage disequilibrium between SNP and causative mutations, because the causal mutations are in the data set.

Although the cost of genome resequencing has fallen dramatically, it is still too expensive to resequence the tens of thousands of individuals that would be required to estimate accurately the small effects of the large number of mutations affecting typical complex traits. An alternative strategy in livestock would be to exploit the fact that these populations are typically derived from a small group of common ancestors just a few generations in the past. For example, in Australian Holstein-Friesian dairy cattle, 50 of the elite ancestor bulls account for 51% of the genetic diversity in the current Holstein cow population. Provided these ancestors are sequenced, the descendant individuals can be genotyped for a low-density SNP array to infer their genome sequence, because the low-density SNPs will be sufficient to trace the large segments of chromosomes

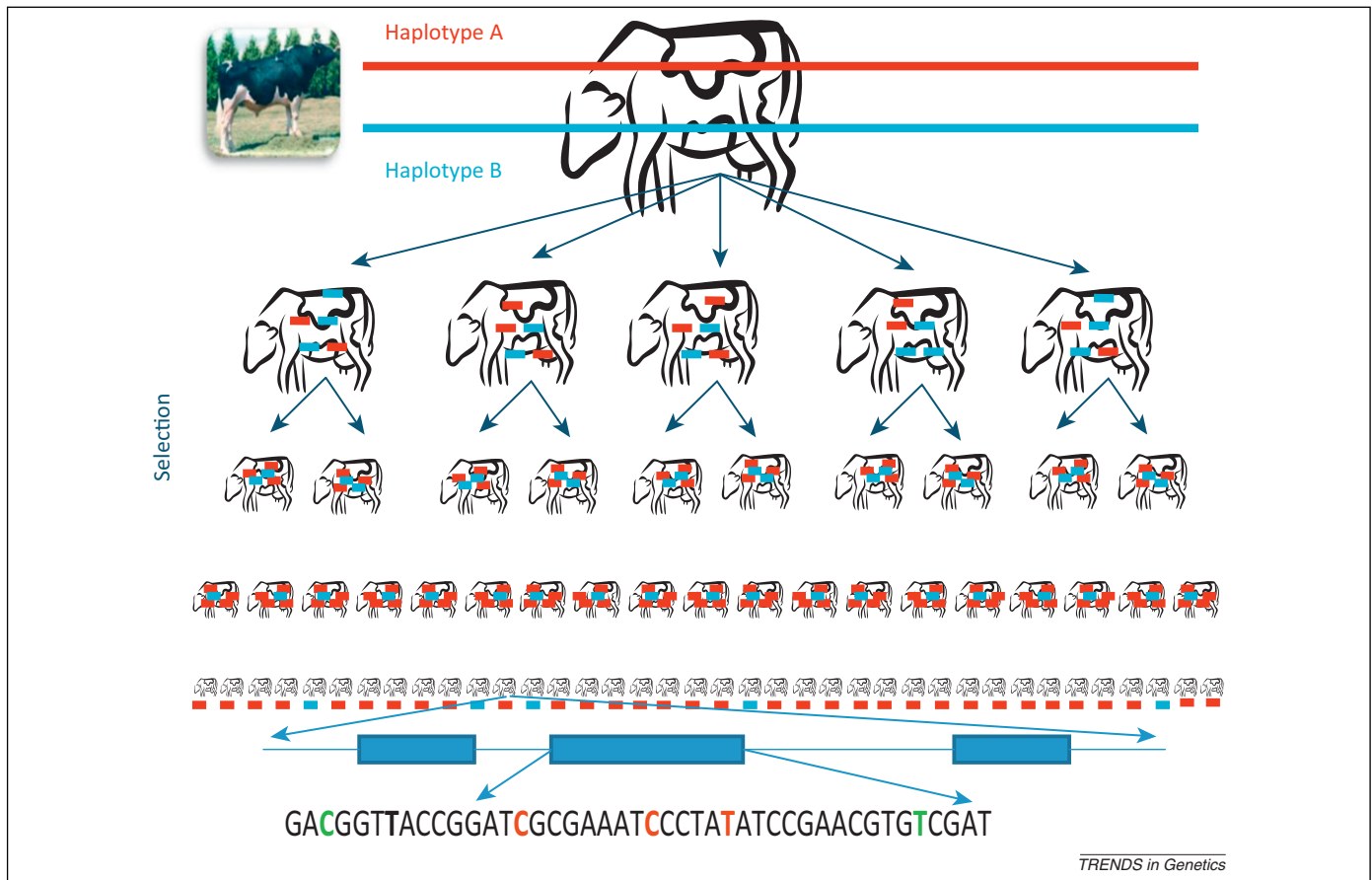


Figure 5. Identification of recent selective sweeps and causative mutations for complex traits by whole-genome sequencing and haplotracking. Bull haplotypes are reconstructed from whole-genome sequence data. After multiple generations of selection, chromosomal segments under selection can be detected by reconstruction of ancestral haplotypes from SNP genotyping of the current population, as described in [61]. This is schematized by the increase in frequency of one haplotype, coded in red, versus the alternative haplotype, coded in blue. Because the sequence and haplotypes of the ancestor are known, all identified polymorphisms (SNPs, copy number variants, etc.) in the segment can be considered as possible candidates for affecting a phenotype. This method should reveal candidate genes and regulatory polymorphisms for all selected traits, which can be distinguished from genetic drift. Imputed SNPs can be verified on selected haplotypes, and studies of historical recombination events can narrow the selection interval to a limited number of genes. Putative causative mutations can be identified for both quantitative traits and qualitative traits. The bull Chief, an important key ancestor of the Holstein breed, has been sequenced. Using haplo-tracking of the chromosome segments of Chief through seven generations, 49 Chief chromosome segments were identified that had likely changed in frequency due to selection and, using haplotype reconstruction techniques, the underlying candidate genes for economically important traits were readily identified. A recent example is identification of the source of an embryonic lethal allele that accounts for >500 000 spontaneous abortions over several decades, which was traced to Chief and some of his sons [71,72]. In this case, the SNP genotypes and phenotypic records of thousands of Chief descendants were essential to tracing the origin of this mutation. Having the DNA sequence of Chief and several of his sons, along with the mutation mapped to a narrow segment on BTA5, led to the rapid identification of a stop-gain mutation in a gene (encoding apoptotic protease activating factor 1, *APAF1*) that is known to cause severe defects in central nervous system development and embryonic lethality in homozygous knockout mice. Elimination of this allele in dairy cattle is now feasible, which will result in an increase in reproductive efficiency. In contrast to human populations, such deleterious alleles can arise rapidly in livestock populations with some frequency if they are carried by a key sire.

inherited from the ancestors, a process termed 'haplotracking' (Figure 5) [61]. *In silico* resequencing of large numbers of individuals with specific phenotypes and the assemblage of these data across breeds would then enable highly accurate genomic predictions from whole-genome resequencing data. Some progress has been made on this front. Two father and son Holstein bulls, Pawnee Farm Arlinda Chief (Chief) and Walkway Chief Mark (Mark), which have sired more than 75 000 daughters between them, have been sequenced [61]. Due to the widespread use of artificial insemination, these bulls are considered among the most influential in the history of the Holstein breed. Indeed, they account for approximately 10% of the chromosome segments in the current Australian Holstein population, even though both bulls were born in the USA (in 1962 and 1978, respectively). An exciting development is the sequencing of more dairy sires as part of the 1000 Bull Genomes Project, which is now underway [62].

Although using sequence data in genomic predictions is attractive for the reasons described above, a major challenge will be the large number of SNPs and other variant effects to be estimated, with a still-limited number of records. The numbers of variants are likely to be in the tens of millions. One strategy to deal with this will be to use biological information to filter the variants before they are used in prediction. For example, only variants in the transcribed region of the genome could be used, because these regions might be more likely to include causative mutations than might random intergenic variants.

Advanced reproductive technologies

DNA marker information can be obtained from animals at birth, allowing genomic predictions to be made early during the life of an animal. This reduces the generation interval, because selection decisions can be made potentially before the selection candidates are measured for

their own phenotypes. It may be possible to reduce the generation interval even further and so accelerate genetic gain by combining genomic selection with reproductive technologies. This has been recognized by two groups [63,64] (although in the context of marker assisted rather than genomic selection).

In sheep, for example, oocytes can be harvested from very young females (ewe lambs) and then fertilized *in vitro*, a technique called juvenile *in vitro* embryo transfer (JIVET). In one study, approximately four viable embryos were recently produced using this method per donor lamb [65]. In sheep, JIVET can reduce the generation time to approximately half of what it is now [66]. If genomic estimated breeding values were used to select donor ewe lambs, and particularly if large numbers of embryos could be produced per donor, the rate of genetic gain could be at least doubled. This would allow rapid breeding for the key traits outlined above. These breeding programs would also allow breeders to create rapidly niche lines, such as lines of lambs with high levels of omega-3 in their meat.

The meta-genotype

In addition to focusing on the genetic prediction of traits mentioned above, it is worth pointing out that livestock, similar to humans, have large numbers of symbionts, such as bacteria and protozoa, in their digestive tract. The profile of these microbiomes potentially affects key traits, such as feed conversion efficiency. In ruminants, the profile of the rumen microbiome will be particularly important for methane emissions, because this is where the methanogens reside. In the past, generating rumen microbiome profiles was difficult, because many rumen bacterial species could not be cultured. Next-generation sequencing technology has overcome this problem [67–69]. To some extent, the microbes carried by an animal depend on features of the animal and so can be regarded as part of the phenotype of the animal and subject to genetic variation. In mice, researchers were able to identify quantitative trait loci (QTL) in the hosts that affected gut microbiome composition, although there was also a substantial effect of litter and cohort [70]. Therefore selection of cattle might include selection to carry a ‘desirable’ ecosystem of rumen microbes. At the same time, microbes can alter the phenotype of the host, and so manipulation of the microbes directly (e.g., by feed additives) could lead to a more efficient host.

Concluding remarks

Demand for high-value protein, lipids, and micronutrients from livestock is likely to increase over the coming decades as global population and wealth increases. Meeting this demand will require more efficient livestock production, particularly in the face of competition from other uses for land and water resources. For ruminants, the environmental cost of methane emissions will be a further incentive for improved efficiency. Fortunately, in all livestock species, there is considerable genetic variation for the traits contributing to efficiency. Faster genetic gains for these traits can be achieved with new technologies, including genomic selection and advanced reproductive technologies. Given the expense of measuring some of the traits

that contribute to efficiency, such as feed intake, and the number of records necessary for accurate genomic predictions of these traits, large international collaborations focused on pooling phenotypes and genotypes across countries will be necessary. At the same time, use of whole-genome sequence data could increase the rate of gain and lead to rapid elimination of genetic defects from livestock populations, as has already been demonstrated in the case of an embryonic lethal recessive mutation in Holstein-Friesian cattle [71,72].

There are many challenges ahead for livestock breeding, with rapid genetic improvement necessary for both existing and new traits, including feed conversion efficiency, fertility, and adaptation to a warmer climate. These improvements must be achieved while maintaining or even improving the nutritional properties of meat and milk and emphasizing animal health and wellbeing. Although the task is large, the new technologies described here will allow animal breeders to make progress more rapidly than was possible in the past.

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