**Application of genomic selection in animal breeding**

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**Abstract**

Research findings and simulations indicate that genomic selection can accurately predict breeding values for young animals even without their own performance data. Genomic selection is a form of marker-assisted selection that employs genetic markers spanning the entire genome to ensure that all quantitative trait loci are associated with at least one marker. The ability to select animals at an early stage enables the development of novel breeding strategies aimed at enhancing genetic advancement while minimizing expenses. Genomic selection holds immense potential for livestock breeding companies as it enhances genetic gain by reducing the genetic interval and enhancing reliability. However, additional research is necessary to enhance the precision of genomic estimated value and effectively manage long-term genetic gain. The objective of this review was to present a summary of the advancements in genomic selection and its implementation in animal breeding.

**Keywords**: Genomic evaluation, Breeding value, Genomic selection

**Introduction**

The global population is steadily increasing, leading to a higher demand for food production. The Food and Agriculture Organization of the United Nations (FAO) has stated that in order to meet the needs of the growing population, food production must be doubled in the near future (FAO, 2006). The expected productivity gap could be filled by improving genetic. Animal breeding involves the deliberate selection of animals based on their performance records, with a focus on multiple traits. This selection process is primarily carried out by breeders who rely on traditional animal breeding methods to produce superior animals, even in the absence of molecular knowledge (Ventura et al., 2016; Garner et al., 2016). The traditional animal breeding method relies on the realistic physical characteristics or phenotype of an animal and its family to estimate the breeding value (EBV). However, the reliability of these methods is questionable, leading to uncertainty in animal production. Over the years, animal breeding using quantitative genetics has significantly enhanced animal production. Nevertheless, the integration of genetic markers into breeding programs has been relatively restricted due to technological constraints (Deng et al., 2016). Currently, the emergence of comprehensive sets of single nucleotide polymorphism (SNP) markers has provided fresh prospects for the identification of optimal animals for breeding purposes, commonly known as genomic selection. The fundamental principle of this approach involves utilizing the quantitative trait locus (QTL) associated with a specific phenotypic trait and leveraging them for the purpose of selection. The extensive knowledge of numerous genetic markers has facilitated the more precise estimation of breeding values for young candidates compared to previous methods. The concept of genomic selection involves utilizing both genotypic and phenotypic data from a reference population to develop prediction equations for assessing the genetic value of individuals (De Koning, 2016). The larger the reference male or female populations, the more reliable genomic selection is expected to be (Azizian et al., 2016). Conversely, progeny-tested bulls often form the training set of genomic selection due to the reliable phenotypic information obtained from a large group of daughters. The utilization of a shared reference population, which involves gathering diverse data from various populations, has been acknowledged as a proficient approach to enhance the precision of genomic selection (Zhou et al., 2013). The utilization of genomic selection has greatly enhanced the efficiency of animal breeding programs, both technically and economically (König et al., 2017). Initially, the benefits of this approach were observed in dairy cattle, where it led to a decrease in the time between generations, an improvement in the accuracy of estimated breeding values (EBV), and a reduction in costs associated with progeny testing (Shumbusho et al., 2015). The swift integration of genomic selection into dairy cattle breeding programs was driven by these theoretical discoveries. The primary aim of this analysis was to outline the progression of breeding strategies, transitioning from traditional animal breeding methods to the utilization of genomic selection.

**Classical breeding methods**

Animal breeding is the process of carefully choosing domestic animals in order to enhance specific traits, whether they are quantitative or qualitative, in the offspring. Various breeding techniques have been employed to enhance the quality of animals, but the primary objective has consistently been to enhance the production of superior animals with desired characteristics (Plieschke et al., 2016). In the past, animals were chosen for breeding based on their physical characteristics. As a result, traits that were hard to measure, such as those that only appeared later in life, were specific to one gender, or had a low likelihood of being inherited, posed greater challenges in terms of improvement (Calus et al., 2013). Consequently, the integration of individual records and those of relatives into EBV, known as best linear unbiased predictions (BLUP), enhances the accuracy of performance predictions (Henderson, 1973). By enhancing the reliability of EBV, the BLUP method amplifies the genetic response to selection (Dekkers, 2012). The reason behind this is that the method has the capability to consider all systematic effects (such as sex, environment, and age) that are frequently linked to economically important traits in farm animals. Moreover, the BLUP method enhances the accuracy of EBV by utilizing all available pedigree information through a numerator relationship matrix, which helps in addressing changes in additive genetic variance caused by inbreeding or assortative mating (Cowling et al., 2015). Despite the considerable success of animal selection based on EBV estimated from phenotype, there exist several limitations. These limitations primarily pertain to the ability to consistently collect phenotypic data of chosen candidates and/or their immediate relatives in a prompt manner. Such timely data collection plays a crucial role in expediting selection decisions at a young age, thereby reducing generation intervals. Expensive phenotype recording for traits that are challenging to measure or have low heritability also holds significance in this context. Additionally, another drawback of traditional animal breeding is the specific trait of interest, which is only recorded at a later stage in an animal's life and only for one gender. This necessitates the sacrifice of animals (for meat quality) or subjecting them to conditions that could hinder their ability to be marketed or have their germplasm exported (for disease resistance). Furthermore, the breeding procedures continue to be relatively sluggish due to the significant amount of time needed to gather sufficient daughter phenotypes for precise genetic evaluations.

**Marker Assisted Selection (MAS)**

Marker-Assisted Selection (MAS) is the utilization of genomic information alongside phenotypic information to enhance reliability. This approach was initially introduced in 1900 by Sax (1923) for the selection of superior animals. The genes that control specific traits are distributed throughout the genome, with only a small number having significant effects, while many more genes have progressively smaller effects (Wells et al., 1998). In MAS, marker genes are employed to indicate the presence of desirable genes (Ribaut and Ragot, 2007). The selection response is enhanced by the combination of traditional breeding methods with molecular genetic techniques. The success of this approach relies on the identification of associations between genetic markers and linked QTL, as highlighted by Meuwissen and Goddard (1996). Additionally, the strength of these associations is influenced by the distance between the marker and the target traits, as emphasized by Ron and Weller (2007). With the aid of MAS, it becomes feasible to identify the desired characteristic that will be inherited by the next generation. This approach also facilitates the detection of traits with minimal phenotypic manifestation, such as disease resistance. Recessive genes and mutants can be selected through the process of MAS selection, which is faster due to the ability to predict an individual's phenotype at an early stage. MAS is more advantageous than traditional animal breeding for traits that are limited to one sex or have a poor predictor of breeding value (Hiendleder et al., 2005), as well as traits that manifest later in life (Rothschild and Ruvinsky, 2007). In cross-breeding programs, MAS could prove particularly beneficial for incorporating desirable genotypes into local breeds with superior overall breeding values. Despite the fact that the MAS technique enhances animal production by improving reliability, it is not suitable for timely implementation in animal breeding programs due to the influence of numerous loci on most traits of interest. Consequently, the genetic gain achieved may be limited as the utilization of a restricted number of loci can only capture a fraction of the genetic variance (VanRaden et al., 2009). Additionally, the complexity of the calculations involved in estimating breeding values, along with the incorporation of information from molecular markers, poses challenges to the practical application of MAS (Baruch and Weller, 2009).

**Improvement of genomic selection**

The utilization of the MAS approach proves to be effective in traits that have a straightforward genetic determinism. However, it fails to produce satisfactory results in more intricate conditions. The primary reasons for this lack of productivity are the restricted portion of the genetic variance and the weak correlation between markers and QTL at the population level (Boichard, 2016). Additionally, MAS is further limited by the costly nature of genotyping selection candidates, as the advantages it offers in commercial breeding programs are not as significant as initially anticipated (Dekkers, 2004). The emergence of genomics in animal breeding began with a revolutionary method, allowing for the estimation of breeding value through markers that cover the entire genome (De Koning, 2016). As a result, the significance of parental relationships in determining similar performances in animals has diminished. This is due to the availability of affordable whole-genome SNP panels, which can now validate analogous performances based on the fact that animals possess identical chromosome fragments (Kemper and Goddard, 2012). Genomic selection, a form of MAS, allows for the accurate estimation of animals' breeding value using a dense marker map of chromosomes, without the need for information about their phenotype or that of their close relatives (Rabier et al., 2016). This technique has significantly improved animal production by reducing the generation interval and the cost of proving bulls (Konig et al., 2009). The analysis of 10,000 to 800,000 SNP's forms the basis of genomic selection (Sonesson et al., 2010). Numerous animals, such as chicken, horse, sheep, cattle, Turkey, and Pig, have had their whole genomes sequenced to date (Fan et al., 2010) (Table 1).

Table 1- Summary of whole-genome sequence information of important animal species

|  |  |
| --- | --- |
| Species | Genome Size (Gb\*) |
| Cattle | 2.67 |
| Sheep | 2.61 |
| Goat | 2.63 |
| Chicken | 1.04 |
| Horse | 2.47 |
| Turkey | 1.06 |
| Pig | 2.8 |

\*Giga base pair

**Genomic selection principle**

Genomic selection operates on the fundamental principle of utilizing marker information to estimate breeding value, without requiring knowledge of gene location. The initial stage of genomic selection involves gathering phenotypic and genotypic data from a reference population. In terms of genotypic information, all animals within the reference population undergo genotyping for single nucleotide polymorphisms (SNPs) across the entire genome (Boichard et al., 2016). Despite the high cost associated with genotyping a large population, enhancing the size of the animal reference population will enhance the accuracy of the outcomes (Li et al., 2011). Subsequently, the collected phenotypic and genotypic data are utilized to derive a predictive equation for calculating GEBV (Fernandes Junior et al., 2016). These effects are subsequently applied to potential candidates for selection, utilizing marker genotype information even in the absence of known phenotypes. The accuracy of GEBV is influenced by three factors: the heritability of the trait (h2), the number of animals (N) in the reference population, and the q parameter (Neves et al., 2014).

**Advantages of genomic selection**

Genomic selection enhances productivity by accelerating the rate of genetic improvement in comparison to traditional breeding techniques (Table 2).

Table 2- Impact of genomic selection on genetic gain

|  |  |
| --- | --- |
| Species | Added Genetic gain |
| Dairy cattle | 60 -120% (Pryce and Daetwyler, 2012) |
| Dairy sheep | 51.7% (Shumbusho et al., 2013) |
| Dairy goat | 26.2% (Shumbusho et al., 2013) |
| Broilers | 20% (Dekkers et al., 2009) |
| Beef cattle | 15-44% (Pimentel and Konig, 2012) |
| Meat sheep | 17.9% (Shumbusho et al., 2013) |
| Layers | 60% (Sitzenstock et al., 2013) |

The genetic gain (ΔG) observed in animal breeding initiatives is contingent upon several factors, including the level of selection intensity (i), the accuracy of predictions (r), the genetic variance (σ2g), and the generation interval (IG). The equation that represents this relationship is ΔG = i \* r \* σ2g / IG (Ibañez Escriche and Gonzalez Recio, 2011). Genomic selection enhances the speed of genetic improvement by reducing the time between generations (Meuwissen and Goddard, 2010) and increasing accuracy of prediction (Hayes et al., 2009). Genomic selection offers a significant advantage in that it allows for the evaluation of candidates without relying on progeny and phenotypic information. As a result, animals can be selected at a very young age, and this selection process can even be applied to embryos. Consequently, genomic selection has the potential to enhance productivity by reducing the generation interval. Additionally, by expanding the size of the reference population, the intensity of selection can be increased. The effectiveness of genomic selection in improving traits such as milk yield, fertility, and breeding value is significantly higher compared to traditional selection methods (Hiendleder et al., 2005). In the past, genetic improvement relied heavily on extensive phenotypic records and the use of thousands of bulls for progeny testing and artificial insemination. However, with the advent of genomics, the process has become more efficient and accurate. With the advancement of genomic selection, progeny testing is no longer required, thereby streamlining the selection process and reducing costs. This has resulted in a significant reduction in generation interval, allowing for a doubling of the yearly genetic trend. Additionally, the lower production cost of bulls enables a larger number of them to be selected and marketed, leading to improved management of genetic resources and a reduction in inbreeding trends (Henryon et al., 2014). Consequently, whole genomic selection has emerged as the most effective modern breeding method for the production and selection of superior animals.

**Genomic selection in ruminants**

The implications of dense arrays for SNP detection vary depending on the species of interest. In the case of dairy cattle, these arrays have been utilized to identify markers that can enhance the accuracy of traits related to milk production, cow health, and cow conformation. Australia has emerged as the frontrunner in pinpointing genomic regions associated with milk production, as evidenced by the research conducted by Bolormaa et al. in 2010. The implementation of genomic estimation has brought about substantial transformations in the breeding of dairy cattle. The accuracy of genomic prediction in dairy cattle surpasses 0.8 for production traits and 0.7 for fertility and other traits, as stated by Lund et al. (2011) and Wiggans et al. (2011). Selection is primarily conducted on the sire side, as the semen of bulls is distributed through artificial insemination (AI) for breeding purposes. With the aid of genomic selection, it is now possible to identify elite bulls at an early age. When the accuracy of Genomic Estimated Breeding Values (GEBV) for a bull calf at birth matches that of conventional breeding values obtained after progeny testing, substantial cost reductions of approximately 90% can be achieved (Schaeffer, 2006). The genotyping of young bulls has not only increased genetic gain but has also significantly reduced costs compared to genotyping heifer calves. The cost-effectiveness of genomic selection, in contrast to traditional methods, has had a remarkable impact on the advancement of the dairy industry. The use of low-density genotyping followed by imputation has led to a significant increase in the number of selection candidates being genotyped, thanks to its high reliability and relatively lower cost for genomic prediction. As of 2016, approximately 2 million dairy cattle have been genotyped globally (Meuwissen et al., 2016). The beef cattle industry could potentially gain more advantages from genomic selection compared to the dairy industry due to the longer generation interval of beef cattle. However, the traditional methods for evaluating genetic traits face challenges in storing phenotype data of sufficient quality and quantity. As a result, genomic selection has the potential to greatly enhance genetic progress by improving selection accuracy at a younger age (Jonas and de Koning, 2015). Indices for selection in beef cattle breeding are typically determined based on a specific market. However, the adoption of these indices is slower due to various factors such as the desired traits of interest including growth rate, carcass quality, reproduction, and overall health, all of which contribute to profitability (Montaldo et al., 2012). On the other hand, when compared to dairy cattle, the efficiency of genomic selection in beef cattle is still relatively lower. This could be attributed to factors such as breed heterogeneity, less advanced breeding structures and programs, the prevalence of natural service, cross-breeding in commercial herds, as well as the effective population size (Johnston et al., 2012). The reliability of genomic prediction in beef cattle has been observed to be lower compared to dairy cattle, as stated by Van Eenennaam et al. in 2014. This lower reliability can be attributed to the inferior quality and quantity of the beef cattle population in comparison to dairy cattle. Furthermore, in beef cattle, the objective population and validation animals may have a lesser degree of relatedness to the reference population when compared to dairy cattle. To address the issue of small reference populations, it is possible to enhance the accuracy of prediction by combining data from different countries and/or breeds, as suggested by De Roos et al. in 2009. Additionally, the collection of genotypic data and phenotyping can be improved to enhance the efficiency of genomic selection in beef cattle. Despite the availability of whole-genome information for small ruminants (Table 1), the potential genetic improvement in sheep and goats is comparatively lower than that observed in cattle (Table 2). Limited research has been conducted on sheep, and the most notable advancements in inter-flock genetic enhancement programs and genomic research have been documented in Australia (Brown et al., 2007). Whole-genome screening has recently emerged as a potential option for goats, although it may not become a routine practice in the near future. In small ruminants, such as goats, the level of breeding organization is typically lower compared to large ruminants. The breeding goals are often heterogeneous, and there is a lack of efficient phenotype recording. As a result, conventional genetic evaluations are more likely to be conducted within the breeding organization rather than at a national level. However, if a modified approach similar to the dairy cattle organization is adopted, genomic selection could present new opportunities for small ruminants.

**Genomic selection in poultry**

In 2004, the sequencing of poultry was initially accomplished (Knol et al., 2016). Chicken breeding programs adopt a pyramid structure, and the higher number of offspring in chickens enables a genetic improvement of more than double that of cattle or pigs through traditional breeding methods (Dekkers, 2007). Several studies have demonstrated the potential to decrease the generation interval in layer breeding programs by incorporating genomic selection (Wolc et al., 2016). The commercial egg production industry is a global enterprise that is primarily controlled by a small number of companies. In 2013, Hy-Line International conducted genomic selection in their commercial layer breeding program, following three years of genomic selection in an experimental line (Wolc et al., 2015). At the conclusion of the experiment, the birds that were chosen based on genomic prediction consistently outperformed those that underwent traditional selection methods for the majority of the 16 traits that were considered in the selection process. Sitzenstock et al. (2013) highlighted that several other companies have also acknowledged genomic selection as a viable substitute for traditional breeding methods in order to enhance the genetic traits of layer chickens. The investigation into the utilization of genomic selection in broiler breeding commenced shortly after the disclosure of the chicken genome sequence. Nevertheless, the argument for genomic selection in broilers is not as straightforward as it is in layers, as the majority of traits can be measured in both males and females at an early stage. Additionally, in broiler chickens, the enhancement in the dependability of moderately heritable traits such as fertility and egg production can vary from 20-45% (Wang et al., 2013), whereas for highly heritable traits, it can exceed 50% (Wolc et al., 2014).

**Conclusion**

The increasing global population will likely lead to a higher demand for valuable protein, lipids, and micronutrients derived from livestock. Consequently, there is a need for more efficient and rapid methods to meet the growing food demand. While genomic selection is still in its early stages, it proves to be a valuable tool in enhancing animal production by improving genetic gain. Advancements in research and technology have made it easier and more affordable to access entire genome data of livestock species for breeding purposes. Although genomic selection is less developed in other species compared to dairy cattle, ongoing research progress suggests that it will become an efficient tool for producing elite animals across all livestock species. Further research on the implementation of genomic selection in breeding programs is highly beneficial, not only for the greater good but also for private breeding companies.

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