GENOMICS AS A TOOL FOR IMPROVING DAIRY CATTLE POPULATIONS

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Abstract

The dairy industry plays a pivotal role in meeting the global demand for high-quality milk and dairy products. To address the ever-increasing need for efficient and productive dairy cattle populations, the integration of genomics has emerged as a transformative tool. Genomic selection, a revolutionary advancement in cattle breeding, has allowed for the identification of superior individuals at an early age based on their genetic potential. Genomic selection has not only accelerated genetic progress but has also minimized generation intervals, leading to more efficient breeding programs. Furthermore, the incorporation of genomic data in selection decisions has increased the accuracy of breeding values, ultimately resulting in the production of dairy cattle with improved milk yield, fertility, and disease resistance. Beyond traditional breeding goals, genomics has also enabled the identification of genetic variants associated with traits that are difficult to measure, such as feed efficiency, heat tolerance, and environmental adaptability. By deciphering the genetic basis of these traits, it is now possible to develop breeding strategies that enhance the resilience of dairy cattle populations in the face of changing environmental conditions. This paper also explores the role of genomics in addressing health and welfare concerns within the dairy industry. Genetic markers associated with susceptibility to diseases and stress-related conditions have been identified, providing opportunities to select for healthier and more resilient animals. Furthermore, genomics has opened avenues for tailoring nutritional strategies to individual cattle based on their genetic predispositions, optimizing feed efficiency and reducing environmental impacts. The utilization of genomic data is not limited to breeding and production. Genomics has facilitated the development of innovative tools for managing dairy cattle populations. Precision management, including genomic-based early disease detection and personalized healthcare, is becoming increasingly viable, enhancing animal welfare and reducing production losses. In conclusion, genomics has revolutionized dairy cattle breeding and management by providing accurate and efficient tools for selecting animals with superior genetic potential, improving production, health, and welfare, and enhancing the overall sustainability of dairy cattle populations. As genomics continues to evolve, the dairy industry stands to benefit from a more precise and sustainable approach to cattle production, ensuring a resilient and productive future for the dairy sector.

Key words: molecular markers, genomic selection, dairy production, cattle improvement

TRADITIONAL SELECTION IN DAIRY CATTLE POPULATIONS

Genetic improvement has been the focus of breeders since the domestication of animals, and with the industrial revolution and increased demand for livestock products, breeders intensified efforts to create more productive animals through selection, along with improving the conditions in which animals were raised. One of the oldest methods for improving the genetic foundation of cwows was the mating of the "best" animals. In the nineteenth century, cattle breeding relied on the pedigree and phenotype of cows

and bulls. In the seventies of the twentieth century, breeding work was based on progeny testing, where the breeding values of a bull are assessed based on monitoring the productivity of its offspringz.

The application of artificial insemination in dairy cattle populations allows groups of relatives to be sufficiently numerous so that there is a connection in different production conditions due to the common gene pool. Progeny testing is a crucial tool in the genetic improvement of dairy cattle populations. Through the systematic evaluation of the performance of offspring, this method enables dairy farmers and breeders to make informed decisions about the selection and breeding of superior animals. In dairy cattle populations, progeny testing is primarily conducted for milk production traits. Since milk production traits are sex-limited, they can only be measured in the female sex, and the production results of daughters are used for the precise assessment of the breeding value of bulls. Dairy cattle breeding programs aim to enhance desirable traits such as milk yield, reproductive performance, and disease resistance. Progeny testing plays a pivotal role in these programs by providing accurate and reliable information on the genetic potential of breeding animals. The method involves the systematic evaluation of the performance of offspring, allowing breeders to make informed decisions about the selection of superior sires and dams. Progeny testing involves the careful monitoring and assessment of a sire's or dam's progeny for specific traits of interest. These traits may include milk yield, fat and protein content, reproductive performance, and disease resistance. The process typically spans several years, as it requires the observation of multiple generations to account for genetic variations and environmental influences (Cole at al., 2011).

Progeny testing stands out as a powerful and indispensable tool in the genetic improvement of dairy cattle populations, offering several advantages that contribute to the sustained development of the dairy industry. Progeny testing allows for a more accurate evaluation of the genetic potential of breeding animals by assessing the performance of their offspring over time. This comprehensive evaluation provides valuable insights into heritability and genetic correlations for specific traits, enabling breeders to make informed decisions in selecting superior sires and dams for future generations.

Progeny testing enables simultaneous selection for multiple economically important traits, such as milk yield, reproductive performance, and disease resistance. This multi-trait selection approach allows for the development of well-rounded and high-performing animals that contribute to overall herd productivity and sustainability.

While progeny testing offers valuable insights into the genetic potential of dairy cattle, it is important to acknowledge and address certain disadvantages associated with this method. Understanding these limitations is crucial for the effective implementation of breeding programs and the interpretation of results. Progeny testing is a time-consuming and resource-intensive process that requires several years to observe and evaluate multiple generations. The extended timeframe, coupled with the costs associated with maintaining and monitoring large populations of animals, can be a significant drawback for dairy farmers and breeding programs with limited resources (Dekkers, 2007). The requirement for observing multiple generations introduces a longer generation interval compared to other breeding methods. This delayed genetic progress can be a significant drawback, especially when rapid advancements in

certain traits are essential for meeting industry demands. Progeny testing may have limitations in accurately assessing traits with low heritability. Traits influenced more by environmental factors than genetics may show limited response to selection, leading to challenges in achieving significant improvements through progeny testing alone.

Before genomics, bulls at the age of approximately one year entered progeny testing programs as a method for determining their breeding value. Bulls were at least five years old when their semen could be introduced to the market. The combination of a large number of phenotypic data, breeding organizations capable of investing in technology, infrastructure for data processing and evaluation, and a long generation interval made dairy cattle an ideal candidate for genomic.

GENOMIC SELECTION-NEW ERA OF ANIMAL BREEDING

During the last two decades, advances in molecular-genetic methods, primarily polymerase chain reaction (PCR) and sequencing, coupled with their increasing affordability, have enabled the application of these modern achievements in selection. Genomics is a specialized branch of science that studies entire genomes, including their mapping, sequencing, as well as the identification and functional analysis of genes. Unlike molecular biotechnology, which allows the study of individual genes, genomics enables the study of the entire genome, or at least a large number of genes simultaneously, which is particularly important in tracking quantitative traits (minor genes).

The heritable information of an animal is stored in its DNA. The DNA is divided into chromosomes, and all the chromosomes together form the genome. A cow has 30 chromosomes and 30,000 genes. Each of these genes is in a pair, with one coming from the cow and the other from the bull. Genomic selection represents a marker-assisted form of selection, where single nucleotide polymorphism (SNP) is used as a genetic marker. SNPs are distributed throughout the entire genome of cattle. Genomic selection gains significance for traits where there is low reliability in estimating breeding values (traits with low heritability) or for traits measured later in the productive life (longevity), as well as for traits measured after the slaughter of the animal.

Genomic selection has revolutionized dairy cattle breeding. Since 2000, assays have been developed to genotype large numbers of single-nucleotide polymorphisms (SNPs) at relatively low cost (Wiggans et al., 2017). In the mid- to late-2000s, assays emerged for the cost-effective genotyping of substantial quantities of single-nucleotide polymorphisms (SNPs). While SNPs typically exhibit only two alleles, the extensive availability of these markers across the entire genome enables the tracing of the inheritance of concise chromosomal segments. The application of genomic selection will allow for the decoding of the bovine genome. Genomic selection was implemented in the United States in 2007, with the first year witnessing the genotyping of 56,947 samples, as reported by Gassaway (2009). The number of samples and markers continues to grow daily, in parallel with ongoing research and technological advancements.

Silicon chips, such as those from Illumina, are utilized in genomic selection, capable of reading millions of pieces of information. An example is the BovineSNP50V chip, which can read 54,001 SNP markers (Gassaway, 2009). The rapid development of this technology is evident today with the

utilization of the Bovine HD BeadChip, reading 777,962 markers.

Until recently, the number of known DNA markers in livestock breeding was very limited, and the costs of genotyping were high. If only a limited number of markers per chromosome are available, the linkage between markers and quantitative trait loci (QTL) will exist only for a limited number of generations, influenced by DNA recombination. Due to these limitations, research soon began with the aim of using linkage mapping to detect QTL. The challenge of using QTL mapping for establishing linkage is that it requires a large number of offspring per family to reduce the confidence interval for mapping QTL along the chromosome. This problem can be overcome with a dense network of markers. In this case, linkage disequilibrium (LD) could be exploited for QTL mapping (Hayes et al., 2006). This became possible with the availability of tens of thousands of Single Nucleotide Polymorphism (SNP) markers for some of the most important animal species (Habier et al., 2010; Aguilar et al., 2010), leading to a decrease in the cost of genotyping. SNP markers are suitable primarily due to their low mutation rates and ease of application (Kolbehdari et al., 2008).

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The introduction of genomic selection in cattle breeding, as compared by Gassaway (2009), is likened to the significance of introducing artificial insemination. Given that in the future both bulls and dairy cows will be selected based on DNA markers, Goddard (2008) raises the question of the need for a national assessment of genomic value. An alternative could be for companies selling bulls or bull semen to also sell DNA tests and perform genetic evaluations. This scientist believes that a national genetic assessment is better because it utilizes all national data to calculate the most accurate Genomic Estimated Breeding Values (GEBV), thereby facilitating the work for farmers themselves.

IMPLEMENTATION OF GENOMIC SELECTION IN MODERN DAIRY CATTLE BREEDING PROGRAMS

Since officially confirmed and accepted as a selection method in the USA in 2009, genomic selection has continuously evolved and improved, now considered the dominant approach in dairy cattle populations. The number of genotyped animals is increasing daily, especially in countries with developed dairy farming. According to the Council Dairy Cattle Breeding (2016), nearly 359,000 animals, of which 91% were female, were genotyped in the USA in just one year. As of April 2016, eight AI organizations, four breed associations, three genotyping laboratories, and the National Association of Animal Breeders had successfully met quality certification requirements and were officially designated by the CDCB as nominators of animals eligible to undergo genomic evaluations (Council Dairy Cattle Breeding, 2014).

The genomic testing procedure in the USA involves bulls, or rather their semen, reaching breeders through selection organizations. The genotyping process begins with dairy farmers sending samples from heifers to DNA laboratories, and samples from the sire or dam are sent to selection companies, which in turn forward them to DNA laboratories. Genotyped samples then go to the U.S. Department of Agriculture (USDA), where the results are collected. The results are subsequently returned to selection companies for further use. This system will be in use until 2013, after which each breeder can send samples directly to the USDA through a laboratory to receive results

Genomic selection has become the de facto standard in advanced breeding programs, presenting challenges in small national breeding programs and developing countries. While larger breeding programs may extend services to some smaller national initiatives, developing countries require tailored breeding goals to meet the rising demand for sustainable dairy production in local environments (Marshall et al., 2019; Mrode et al., 2019).

The application of genomic selection in dairy cattle populations brings about the same genetic progress in a shorter time and with less cost compared to conventional selection, increasing the intensity and accuracy of selection for young animals (Obšteter et al., 2019). Although it does not achieve the high accuracy of estimated breeding values as traditional selection, genomic selection doubles the rate of genetic gain per year in dairy cattle (Wiggans et al., 2017).

Introducing genomic selection into the genetic evaluation of dairy cattle has not only reduced the generation interval and increased genetic progress but also allowed more effective control of animal pedigrees (secure confirmation of parentage) and inbreeding in dairy cattle populations. In addition to these benefits, the contribution of genomic selection in controlling genetic defects, which can have a negative impact on the production and health of dairy cows, should be emphasized. Also, the proportion of young bulls are used in artificial insemination programs, has increased to over 50% due to the implementation of genomic selection (Ducrocq and Wiggans, 2014).

International organizations for the control of domestic animal productivity, such as INTERBULL, have already recognized the use of genomic selection in assessing the Estimated Breeding Values (EBV) of bulls, and semen tested in this manner is available in the market (Goddard, 2009; Boichard et al., 2010). Therefore, when applying genomic selection, data on animal performance, as well as pedigree data, should still be used, and it is also necessary to periodically adjust the SNP equation (Đedović et al., 2012).

Based on the above, it can be concluded that the advantages of implementing genomic selection in dairy cattle are manifold: a) no additional funds need to be used for the identification and verification of individual genes influencing traits of interest; b) the reliability of GEBV for young bulls is relatively high; c) the generation interval is shortened, thereby increasing the annual effect and selection progress.

CONCLUSION

Genomic selection represents a revolutionary method in the selection of dairy cattle populations. Its integration into breeding programs for the genetic improvement of dairy cattle has led to a shortened generation interval and faster genetic progress. Additionally, the application of genomic selection allows for more precise control of pedigree data and inbreeding. Genomic selection is becoming a technology that will yield the highest increase in the rate of genetic gain in livestock production in the last 20 years. In the near future, Genomic Estimated Breeding Values (GEBV) based on DNA markers will become the primary tool for the selection of domestic animals. Technological advancements and the introduction of microchips into genomics have reduced costs and increased available information during genotyping. The entire process is now automated and relatively inexpensive compared to the price of a breeding animal. Genomic selection makes its greatest contribution in selecting traits with low heritability (health and reproductive traits) and in traits measured later in the productive life of cows (longevity). The control of genetic

defects is also an area where this method has made significant contributions. Defining and incorporating new traits into breeding programs for the genetic improvement of dairy cattle, such as resistance to heat stress or feed efficiency, will be greatly facilitated by the application of genomic selection.

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