A LOOK AT GENOMIC SELECTION TECHNIQUES FOR CLIMATE CHANGE ADAPTATION AND PRODUCTION IN LIVESTOCK

Abstract

Livestock production profoundly intersects with global climate dynamics, contributing to greenhouse gas emissions and confronting vulnerability to climate impacts. In addressing these challenges, imperative adjustments are requisite to fortify the climate robustness of livestock systems. Notably, the prevalent reliance on commercial breeds with limited genetic diversity exposes production strategies to disruption, especially if these breeds are confined to environments that may lose economic viability under future climate scenarios. Consequently, understanding the adaptability of animal populations to forthcoming environmental conditions is paramount for sustaining livestock production.Assessing the genetic underpinnings of climate adaptation necessitates the exploration of tailored genomic selection techniques encompassing both production traits, presumed to have moderate heritability, and adaptation traits, presumed to have low heritability. Through a nuanced examination of genomic selection dynamics, insights into the genetic mechanisms fostering resilience in livestock populations amidst shifting environmental contexts are garnered. Employ genomic analysis to pinpoint genetic markers associated with traits like heat tolerance, disease resistance, and feed efficiency in livestock. Collaborate across disciplines to develop tailored breeding programs integrating these markers, and validate their effectiveness through rigorous field trials and ongoing monitoring to enhance livestock resilience and productivity in varied climatic conditions.Elucidating these mechanisms and their application in breeding programs offers a comprehensive understanding of how genetic advancements can enhance both production efficiency and climate resilience in livestock.This discourse aims to bridge the chasm between scientific inquiry and pragmatic implementation, thereby facilitating informed decision-making in livestock breeding strategies tailored to mitigate the ramifications of climate change.

Keywords: Livestock, climate, genomic selection, breeding strategies,ramifications,livestock

INTRODUCTION

The adaptation of livestock to environmental challenges is increasingly critical for optimizing cost-effective animal production, particularly as climatic conditions shift towards warmer temperatures, rendering disease propagation more favorable and escalating production costs (FAO, 2015; Phocas *et al.,* 2016). Among these challenges, heat stress emerges as a predominant factor significantly impacting livestock production dynamics (Niyas *et al.,* 2015). Empirical evidence suggests that heat stress induces a notable decrease in milk production by 5–15% and adversely affects conception rates in cattle (Berman, 2011). Furthermore, chronic exposure to stress triggers metabolic perturbations, precipitating stress-related pathologies and compromising innate immune responses (Das *et al.,* 2016).

However, there exist compensatory mechanisms within selection processes to mitigate the impacts of thermal stress. Notably, traits such as the slick hair coat phenotype play pivotal roles in thermoregulatory mechanisms observed in tropically adapted cattle breeds (Pitt *et al.,* 2019). Climate change poses significant challenges to existing livestock systems on a global scale, exerting profound influences on feed availability, water resources, animal health, and overall production dynamics (Bernatchez et al., 2024; Sinha et al., 2023). The resultant implications extend across the entire livestock product supply chain, encompassing processing, storage, transport, retail, and consumption (Godde *et al.,* 2021). In light of these unprecedented challenges, livestock farming confronts the dual imperatives of sustaining productivity levels while effectively adapting to shifting environmental conditions.

In this context, genomic selection techniques emerge as promising strategies to address these multifaceted challenges by facilitating the breeding of livestock populations endowed with traits conducive to resilience and productivity amidst evolving climatic conditions (Wray-Cahen *et al.,* 2022).

Genomic selection is a methodology that employs genomic data to estimate the breeding value of animals. While traditional breeding methods rely on observable traits and genetic relatedness, genomic selection delves deeper by leveraging comprehensive genomic information (Banos and Coffey, 2017). By scrutinizing specific genetic markers associated with desirable traits like disease resistance, heat tolerance, and feed efficiency, genomic selection empowers breeders to make more precise predictions regarding an animal's genetic potential (Strandén *et al.,* 2019). In practical terms, adaptation encompasses a spectrum of traits, including those affecting fitness such as longevity and disease resistance. Typically, these traits exhibit low heritability and have experienced decline concurrent with the increase in milk production (Mirkena *et al.,* 2010). Genetic correlations between milk yield and functional longevity have been estimated to range from −0.11 to −0.84 (Sasaki 2013; Pritchard *et al.,* 2013a, 2013b). Given the generally low heritability of adaptation to local environments and the potential for antagonistic genetic correlations with milk production, implementing long-term and efficient breeding strategies becomes imperative.

In the face of a rapidly changing environment, one viable approach involves introgressing locally adaptive genes identified in indigenous breeds into major production breeds or vice versa (Nardone *et al.*, 2006; Hoffmann, 2010; Berman, 2011; Hoffmann, 2013). Consequently, an efficient strategy may necessitate the swift introduction of adaptive traits into commercial breeds, or alternatively, the replacement of these breeds with populations better suited to prevailing environmental conditions (Åby and Meuwissen, 2014).

Adaptation and production are considered polygenic traits, meaning they are influenced by multiple genes. Ødegard*et al.* (2009b) conducted simulations of a fish breeding scheme where both production traits and disease resistance were polygenic and varied in heritability. They found that genomic selection yielded greater genetic improvements compared to classical selection methods, particularly in introgression backcrossing schemes. Notably, the largest gains were observed for traits with low heritability and those not directly recorded in selection candidates. Similarly, Åby and Meuwissen (2014) simulated two divergent populations of livestock based on their production and fitness profiles, employing both pure and crossbreeding strategies across discrete generations. Both production and fitness were considered polygenic traits with moderate heritability and no genetic correlation between them. Their findings demonstrated that selection based on breeding values estimated through genomic best linear unbiased prediction (GBLUP) outperformed conventional breeding value estimation methods (BLUP) in terms of genetic enhancements in both production and fitness.

In conclusion, genomic selection demonstrates efficacy in facilitating the integration of traits with low heritability into populations exhibiting high production levels, especially when the traits in question, including both the introgressed trait and production performance, are polygenic and exhibit no genetic correlation.

Adaptation of livestock to climate change

According to the United Nations Framework Convention on Climate Change (UNFCCC), climate change refers to modifications that are either directly or indirectly caused by human activity and that cause the composition of the Earth's atmosphere to change, leading to noticeable variations in the natural variability of the climate over similar time periods. The main cause of climate change is the increased emissions of greenhouse gases, such as carbon dioxide, which create a "greenhouse effect" that traps energy in the Earth's atmosphere and causes global warming. This phenomenon manifests in extreme weather patterns, compromised food security, and heightened incidence of vector-related and climate-related diseases and fatalities (IPCC, 2014). Evidence suggests that diverse human-induced activities have led to substantial releases of carbon dioxide and other greenhouse gases into the atmosphere, thus exacerbating climate change and global warming. The majority of these emissions arise from burning fossil fuels for energy production, alongside deforestation, industrial processes, and agricultural practices, all of which serve as significant contributors (Hickmann *et al.,* 2021).

The ramifications of climate change span various sectors of society and are intricately interconnected. Drought conditions can detrimentally impact food production and human health while flooding events can facilitate disease transmission and inflict damage on ecosystems and infrastructure. Human health concerns stemming from climate change can escalate mortality rates, disrupt food availability, and curtail workforce productivity (IPCC, 2014). Climate change impacts pervade all facets of the world; however, their distribution is uneven across regions and even within individual communities, exhibiting disparities between neighborhoods or individuals. In response to the changing environmental landscape intensified by climate change, the importance of adaptation in livestock breeding is heightened to mitigate greenhouse gas emissions (Thornton *et al.,* 2017). Although increased production has already contributed to reductions in greenhouse gas emissions within many global livestock populations, achieving sustainable and resilient production in such intensified contexts may necessitate prioritizing traits such as adaptation, feed efficiency, fertility, and health over simply focusing on production increases (Thornton *et al.,* 2017).

The adaptation of livestock to environmental challenges is increasingly crucial for maintaining cost-effective animal production, particularly in light of escalating temperatures, heightened disease susceptibility, and anticipated rises in production expenses (FAO, 2015). Among these challenges, heat stress emerges as a significant factor significantly impacting livestock productivity (Shaji *et al.,* 2015). Empirical evidence indicates that heat stress induces a notable decrease in milk production by 5–15% and adversely affects conception rates in cattle (Berman, 2011). Furthermore, chronic exposure to stress triggers metabolic perturbations, resulting in stress-related diseases and suppression of innate immunity (Das *et al.,* 2016). Nevertheless, selective breeding can mitigate the impacts of thermal stress, with the slick hair coat phenotype aiding in thermoregulation among tropically adapted cattle breeds (Pitt *et al.,* 2019).

The genetic basis of adaptability

Adaptation encompasses various traits, including those related to fitness such as longevity and disease resistance, which typically exhibit low heritability and have declined with the increase in milk production (Mirkena *et al.,* 2010). Genetic correlations between milk yield and functional longevity have been estimated to range from -0.11 to -0.84 (Sasaki, 2013). Given the generally low heritability of adaptation to local environments and potential antagonistic genetic correlations with milk production, long-term and efficient breeding strategies are imperative.

Three primary strategies can be considered for genetically altering livestock for heat tolerance, including the selection of breeds or crossbreds known for their heat tolerance, the introgression of genes associated with thermotolerance, and genomic selection based on criteria linked to heat tolerance (Burrow *et al.,* 2019; Davis *et al.,* 2017). In tropical climates, Bos indicus breeds are often crossed with temperate dairy breeds to combine the heat and parasite resistance of Bos indicus with the production qualities of temperate breeds (Burrow *et al.,* 2019; Davis *et al.,* 2017). Additionally, temperate breeds also exhibit variability in heat tolerance. For example, New Zealand Holsteins experience greater reductions in milk yield in hotter climates compared to Jerseys or crossbreds (Bryant *et al.,* 2007). In New Zealand, reductions in yield were observed when temperatures exceeded 21°C and 25°C, respectively, at 75% humidity for Holsteins and Jerseys (Bryant *et al.,* 2007). Bos indicus breeds in tropical climates are frequently crossbred with temperate dairy breeds to amalgamate the heat and parasite resistance characteristic of Bos indicus with the production attributes of temperate breeds (Burrow *et al.,* 2019; Davis *et al.,* 2017). Moreover, temperate breeds exhibit varying degrees of heat tolerance, as evidenced by New Zealand Holsteins displaying greater reductions in milk yield under hotter conditions compared to Jerseys or crossbreds (Bryant *et al.,* 2007). In New Zealand, reductions in yield occurred when temperatures exceeded 21°C and 25°C, respectively, at 75% humidity for Holsteins and Jerseys (Bryant *et al.,* 2007).

Introgression involves the incorporation of favorable alleles from a distinctly different breed, such as the slick hair gene from Senepol cattle. Traditionally, introgression entails crossing back to the original breed to reintroduce favorable dairy traits from the base breed, a process that necessitates multiple generations of crossing and is consequently time-consuming and inefficient. The mutation responsible for the slick coat phenotype involves a deletion in an exon of the prolactin receptor in Senepol cattle, predominantly associated with the coat type and exhibiting some alterations to sweating ability (Davis *et al.,* 2017).

Breeding programs have initiated the incorporation of the slick mutation into Holstein cattle (Carabaño *et al.*, 2019).

Adaptation and production are presumed to be polygenic traits. Ødegård *et al.* (2009a) simulated a fish breeding scheme wherein both production and disease resistance were polygenic with varying heritability levels. They concluded that, contrary to classical selection methods, genomic selection enhanced genetic gains in introgression backcrossing schemes, particularly for traits with low heritability and those not recorded in selection candidates. Criteria for selecting heat tolerance may encompass body temperature, respiration rate, heart rate, sweating rate, reduction in intake, or milk yield. However, for practical purposes, the impact of Temperature-Humidity Index (THI) on production traits is often prioritized (Carabaño *et al.*, 2019).

Genomic selection

The application of genomic tools within the framework of genetic enhancement in cattle constitutes a significant component of animal selection programs, as highlighted by studies (Mouresan*et al.*, 2019; Gutierrez-Reinoso *et al.*, 2021).Advancements in DNA sequencing and high-throughput genotyping techniques have facilitated the identification of a large number of single nucleotide polymorphisms (SNPs) in livestock (Van Tassell *et al.*, 2008). Commercially available automated methods for SNP genotyping have further streamlined the process. The utilization of dense SNP arrays covering the entire bovine genome has been instrumental in elucidating the majority of genetic variations associated with key livestock traits (Meuwissen *et al.*, 2001), underscoring the significance of genomic selection (GS).

Genomic selection involves making breeding decisions based on genomic estimated breeding values (GEBVs), which are calculated by integrating SNP/genotypic data with phenotypic and pedigree data to enhance the accuracy of breeding value predictions. The cost of marker technology has been steadily decreasing with the proliferation of available markers. By accelerating selection cycles, GS offers the potential to augment selection gains per unit of time (Boichard *et al.*, 2012; Meuwissen *et al.*, 2001), thereby shortening the generational interval and expediting genetic improvements (Georges & Massey, 1991; Peippo *et al.*, 2007). The wealth of genomic information can predict the genetic merit of young animals with up to twice the accuracy of traditional parent averages, suggesting that GS may supplant traditional breeding systems in the near future.

Utilizing high-throughput SNP assays or genome sequencing for animal characterization shows potential in elucidating the physiological underpinnings of adaptation. Initiatives like the species-wide HapMap by Jiang *et al.* (2014) and multi-species studies as demonstrated by Ajmone-Marsan*et al.* (2014) signify substantial progress in understanding the genome and its contribution to adaptation.

Genomic selection has the capacity to accelerate both purebred and crossbreeding programs for adaptation, given the availability of phenotypic data (Hayes *et al.,* 2013). Furthermore, genomic selection for heat stress resistance is feasible. A study has delineated a reference set of genotyped sires possessing phenotypic information regarding their daughters' milk production response to heat stress. This response was predicted based on temperature and humidity measurements obtained from weather stations proximal to the farms where the cows were milked (Hayes *et al.,* 2009). The accuracy of genomic prediction for heat stress tolerance was moderate, with a coefficient of determination (R-squared) of 0.37. Notably, this accuracy surpassed that of pedigree-based predictions, which yielded an R-squared value of 0.16.

Genotyping with high density and throughput.

In the entire population, each single nucleotide polymorphism (SNP) marker exists in two different forms. Numerous SNP markers, numbering in the hundreds or thousands, are distributed evenly across the entire genome in various livestock species. Advancements in laboratory technology have enabled the simultaneous extraction of all chromosomes for SNP markers in a single step process, known as high-density and high-throughput genotyping or typing. This process is facilitated by specialized chips, such as those carrying 10K, 50K, or 700K markers, which allow for the simultaneous testing of multiple markers. The first commercially available high-density genotyping assay was the 10K SNP chip developed by Affymetrix (Bovine HapMap Consortium *et al.,* 2009). However, this initial panel lacked sufficient SNP coverage for many genomic studies, necessitating the development of more comprehensive high-density chips.

Consequently, the Illumina BovineSNP50 chip was introduced, featuring approximately 50,000 SNPs per animal. This chip, developed by a consortium of animal scientists utilizing SNP discovery populations in Holstein, Angus, and mixed beef cattle breeds, became the international standard for genomic selection and genome-wide association studies in cattle. Moreover, it was utilized to investigate evolutionary relationships among horned ruminant species (Decker *et al.,* 2009; MacEachern *et al.,* 2009). Subsequent advancements led to the development of even higher density SNP genotyping chips, such as the Illumina chip introduced in 2010. This chip, employing bead technology and single base extension chemistry similar to the Bovine SNP50K chip, is capable of simultaneously genotyping approximately 700,000 SNPs.

Assessing the consequences of SNPs

SNP datasets are commonly characterized by their substantial size. For example, genotyping 2,000 animals for 10,000 SNP markers yields approximately 20 million data points. Assuming bi-allelic markers, this entails estimating 20,000 effects or covariates. Researchers have proposed three fundamental strategies for SNP selection: random selection (Vazquez *et al.,* 2010), uniform distribution throughout the genome (Zhang *et al.,* 2012), and prioritization of markers with the most significant effects on the analyzed trait (Zhang *et al.,* 2012).

Statistical analysis in genomic selection experiments, as outlined by Meuwissen *et al.* (2001), aims to elucidate the effects of all alleles or markers on performance traits. However, classical statistical methodologies encounter challenges due to a scarcity of degrees of freedom, a circumstance often referred to as the "large p, small n problem." This arises because the number of phenotypes is typically substantially lower than the number of markers, leading to insufficient degrees of freedom to estimate all marker effects through ordinary least squares regression. Consequently, models may be susceptible to multicollinearity, particularly as markers in close proximity are expected to exhibit high correlation (Solberg *et al.,* 2009).

To address the challenge posed by the limited degrees of freedom in estimating SNP effects, several statistical methodologies have been proposed. Among these, three prominent approaches are commonly employed: the Least Squares Method, Best Linear Unbiased Prediction (BLUP), and Bayesian Estimation Method.In the Least Squares Method, each marker is individually tested for its statistical significance, with non-significant markers having their effects set to zero (Vazquez*et al.,* 2010; Meuwissen*et al.,* 2001). Subsequently, significant markers are collectively included in the model for simultaneous analysis.The BLUP method treats allelic effects as random rather than fixed, circumventing the need for degrees of freedom. This enables the estimation of all allelic effects simultaneously.

However, BLUP requires an estimate of the variance of the allelic effect, assuming similar variance across all markers (Vazquez *et al.*, 2010).

Analytical methodologies for genome-based prediction of genetic values vary in their assumptions regarding marker effects (Habier *et al.*, 2011; Meuwissen *et al.*, 2001). Genomic Best Linear Unbiased Prediction (GBLUP) represents a straightforward extension of the polygenic Best Linear Unbiased Prediction (BLUP) approach. In GBLUP, all markers are assigned equal weight, overlooking the true genetic architecture of the trait. The covariance between the genomic breeding values of two individuals is proportional to their genomic similarity, based on the proportion of the genome they share. GBLUP is particularly effective for highly polygenic traits. Ridge Regression–Best Linear Unbiased Prediction (RR–BLUP) assumes that all marker effects are normally distributed and possess identical variance (Meuwissen *et al.*, 2001). This method treats SNP effects as random variables "m".

Bayesian methods, such as Bayes A, assume that markers exhibit varying variances (Meuwissen *et al.*, 2001). These approaches allow for a more flexible modeling of marker effects, accommodating potential differences in the contributions of individual markers to the trait variation.

Role of genomic selection in environmental tolerance

Genomic selection stands as a pivotal technology in this domain, optimizing the investment allocated to gathering valuable phenotypic data, notably individual animal records pertaining to methane emissions(Pryce *et al.*, 2020).The documented contributions of livestock to global greenhouse gas emissions underscore the urgency of mitigating enteric methane emissions through genetic selection. This can be achieved by enhancing feed efficiency or directly targeting methane-related traits. Environmental adaptation is a crucial consideration, aiming to breed animals resilient to changes in environmental conditions, particularly the temperature-humidity index (THI) (Garner *et al.*, 2016). Genomic data can discern cows less susceptible to heat stress, with notable variations in the onset point of heat stress-induced impairments and the rate of decline in health, fertility, and performance beyond this threshold.Similar methodologies can be applied to model animal responses to various environmental or management challenges, such as pathogen exposure or dietary protein reduction. Animal breeding emerges as a viable strategy for reducing methane (CH4) emissions, offering a sustainable and cumulative reduction in population emissions. While breeding has historically increased production, subsequently decreasing emissions per unit of output, greater reductions may be achieved by utilizing Genomic Selection (GS) to prioritize traits more closely correlated with methane emissions than with production.

Three primary pathways have been proposed for CH4 reduction via genetic selection: enhancing productivity and efficiency (e.g., residual feed intake, longevity), minimizing farming system wastage, and directly selecting for emissions or related proxies (Herd *et al.,* 2014). These strategies hold promise for achieving sustainable reductions in methane emissions within livestock populations.

Current estimates indicate that correlations between methane emissions and other traits suggest minimal impacts on reproduction and health traits through breeding for reduced methane emissions. However, correlations exist between methane emission, milk production, and dry matter intake. Selective breeding against methane production has the potential to yield healthy, fertile, and long-lived cows that emit lower methane levels. Nonetheless, further analyses on larger datasets are warranted to confirm correlations with other traits. Accurate estimation of these correlation structures is crucial for appropriately weighting methane emission in breeding goals and mitigating unfavorable correlated responses in production, fertility, longevity, or health traits (Haas and Windschnurer, 2016).

Enhancements in genetic traits related to milk production and functionality play a significant role in mitigating greenhouse gas (GHG) emissions associated with milk production (Shalloo *et al.,* 2014). This effect stems from the increased allocation of feed resources toward milk production compared to maintenance, a phenomenon referred to as the dilution effect. Consequently, there is a reduction in both the quantity of feed required and GHG emissions per unit of milk produced (Thorup *et al.,* 2016). Projections suggest that the dilution effect will persist, leading to further reductions in GHG emissions in the coming years.

In genomic evaluation, the availability of ample observations from genotyped reference animals and their progeny is critical for enhancing accuracy (VanRaden*et al.,* 2009). As the population of genotyped animals expands, the precision of genetic evaluation escalates, diminishing the relative importance of individual record data. Moreover, genomic evaluation contributes to managing the rate of inbreeding within breeding programs. Through the utilization of genomic information, rather than pedigree data, for estimating breeding values, the selection of animals from diverse lineages becomes more viable, consequently mitigating the risk of inbreeding (Pryce *et al.,* 2014).

Conclusion

Genomic selection methodologies present a potent solution for mitigating the impacts of climate change and optimizing efficiency in livestock production systems. Leveraging extensive genomic data, breeders can strategically select animals possessing traits optimized for prevailing environmental conditions, thereby augmenting resilience and sustainability amidst shifting climatic dynamics. Through ongoing advancements and cooperative efforts, genomic selection stands poised to transform the landscape of livestock breeding, heralding a future characterized by enhanced adaptability and productivity within agricultural domains.

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