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Evolution of climate-resilient cattle using genomic information

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Abstract

The global productivity and welfare of cattle are at risk due to the current trend of climate change. In order to identify dairy cows that are climate-resilient, this review aims to combine data on the applications of several genetic technologies and statistical models. The various functional and economic characteristics that control milk production have a considerable impact on the price of milk production. Therefore, the discovery of these features may completely alter breeding strategies for dairy calves intended to be climate-resilient. The performance of dairy cattle is also influenced by the genotype-environment interaction, particularly in difficult circumstances. A few biotechnological tools and statistical models, such as next-generation sequencing (NGS), microarray technology, whole transcriptome analysis, and genome-wide association studies (GWAS), have been developed as a result of recent advances in molecular biology and can be used to measure the molecular mechanisms that control the dairy cows' capacity for climate resilience. Additionally, selection signatures can aid in defining functionally significant regions of the genome that can be utilised to identify prospective loci and candidate genes that have experienced positive selection in complicated dairy bovine milk production variables. To breed dairy calves that are climate robust, these found biomarkers can be included into the current breeding practises via genomic selection.

Keywords: Cattle, heat stress, molecular markers, genome-wide association study

Introduction

Human population raises upto 33% from 7.2B to 9.6B by 2050, which increases the demand for agricultural products upto 70%, but the total area of cultivated land is decreasing day by day (FAO, 2009; UN, 2013). Livestock products provide 17% of total kilocalories and 33% of total protein consumption which is an essential agricultural commodity for worldwide food security (Rosegrant *et al.*, 2009) [24]. The livestock sector provides livelihoods to billions of necessitous populations in the world (Thornton, 2010; Silpa *et al.*, 2021) [36, 31]. Fatten demand for livestock products has been counted to "livestock revolution" (Wright *et al.*, 2012) [41]. Milk production is predicted to rise from 664 million tonnes to 1077 million tonnes (from 2006 to 2050) (Hurst *et al.*, 2005; Steinfeld *et al.*, 2006; Thornton, 2010) [13, 32, 36]. Livestock production is adversely affected by many factors like climatic change, competition for water and land, and food availability, livestock diseases, and biodiversity loss heat stress. Worldwide climatic change is predominantly caused by GHG (greenhouse gas) emissions in which the livestock sector contributes 14.5% of GHG, which leads increase in environmental temperature (IPCC, 2014; Gerber *et al.*, 2013) [14, 11]. According to the IPCC (2014) [14], the mean worldwide temperature may be elevated up to 2.6–4.8 °C by 2100 contrast to the situation that prevailed in 2010. These circumstances will lead to heat stress, which negatively influences livestock production and performance (Rashamol *et al.*, 2019) [23]. Dairy cattle are the most vulnerable to heat stress of all livestock species (Liu *et al.*, 2017) [17]. Apart from the environmental factors, genetic factors also influence milk production. Milk production is one of the crucial economic traits in cattle which is affected by numerous genes (polygenic). Evolution in the area of molecular genetics assisted in identifying various quantitative trait loci (QTL) and candidate genes which are associated with milk yield, fat%, protein %, and other milk production related traits. Knowledge of genomic sequence variation has been utilized widely in livestock sector improvement schemes (Boichard *et al.*, 2012; Wiggans *et al.*, 2017) [5, 40].

Cattle's ability to perform regular biological activities in a variety of challenging environments demonstrates its adaptability (Madhusoodan *et al.*, 2020) [19]. Although various nutritional and

management strategies are present to improve the heat stress impact on cattle, still these approaches may not be contributing a permanent solution to the problem. Therefore, a better interpretation of the molecular mechanisms and genetic differences involved in innate resilience and heat stress tolerance is necessary.

Impact of heat stress on milk yield and composition

Heat stress has both direct and indirect effects on dairy cattle, affecting both milk production and milk quality as well as the reproductive performance of the animal. Increasing environmental temperature and/or relative humidity causes a decrease in feed intake of animals, resulting in a reduction in reproduction and production activities (Sheikh *et al.*, 2017; Wiggans *et al.*, 2017; Pragna *et al.*, 2017) [30, 40, 22]. Tao *et al.* (2013) [34] states that during dry period, thermal stress also influences mammary gland development and proliferation, eventually leading to a reduction in milk yield, especially in high yielders. The drop in milk output owing to thermal stress might be as much as 10–15 percent on farms that use cooling management, and up to 40–50 percent on farms that do not exercise cooling management. Garner *et al.* (2017) [9] reported that during heat stress, 53% decline in milk production in lactating animals. Heat stress affects both milk protein fraction and lipid profile, represents a significant decrease in milk yield and casein percentage, and changes in the polar and triacylglycerol lipid profiles (Bernabucci *et al.*, 2002; Liu *et al.*, 2017) [4, 17]. Therefore, the protection of the productive performance of cattle from the unfavourable effect of climate change is an emerging concern, and appropriate measures are taken in developing heat-resilient cattle breeds.

Genomic applications for detection of superior dairy cattle

Conventional breeding approaches have played a crucial role toward superior animal production; These procedures, however, were time-consuming and did not always account for all sources of genetic variation (Teneva and Petrović, 2010; Silpa *et al.*, 2021) [31]. The progressive molecular technologies mainly concentrate on the recognition of molecular markers located in the genome (DNA fragments), which can appraise the phenotypic variability (Teneva and Petrović, 2010; Yang *et al.*, 2013). Various DNA markers were investigated by geneticists to assess the genetic diversity of livestock animals, with a vision to increase the livestock breeding programs (Hiendleder *et al.*, 2005; Rashamol *et al.*, 2019) [23]. Progression in molecular biotechnology has led to the discovery of many methodologies such as microarray technology, genome-wide association studies, next-generation sequencing, and whole transcriptome analysis aiding in systematic selection and incorporation of these genetic information ameliorate the accuracy of selection and accelerated the genetic achievements in the population (Rashamol *et al.*, 2019; Boichard *et al.*, 2012) [23, 5].

Functional genomics is a branch of molecular biology that investigates the relationships and activity of genes and proteins using genome-wide approaches (Boichard *et al.*, 2012; Hiendleder *et al.*, 2005) [5]. Studies on functional genomics tackle analyzing the functionality of many candidate genes located in a DNA fragment for milk production traits (Sheehy *et al.*, 2009; Silpa *et al.*, 2021) [31]. They also reported that candidate genes indicate differential expression in cattle mammary tissue during the lactation phase. Functional genomics could initiate an assured link

associated with phenotype and gene expression and is anticipated to have a significant positive impact on livestock production resilience (Sheehy *et al.*, 2009; Silpa *et al.*, 2021) [31]. Incorporating such integrated approaches in thermal stressed dairy cattle could disclose novel pathways assumed due to heat stress. Moreover, it may also unroll the hidden pathways interlinked with the adaptation that occurs during heat stress. Various precise functional genomics approaches are concentrating on the DNA, RNA, protein, and metabolite level (genomic and microarray technologies, transcriptomic studies, proteomics, and metabolomics) (Sheehy *et al.*, 2009; Rashamol *et al.*, 2019) [23]. These techniques can play an important role in screening a population to detect its genomic variants which could be helpful in genomic selection.

Application of genome-wide association studies in the dairy sector

In Cattle, GWAS (genome-wide association studies) have been utilized widely to map the QTL of essential traits like production, reproduction, and adaptive traits for heat-tolerance, methane emission traits, and so on (Seabury *et al.*, 2017; Macciotta *et al.*, 2017; Liu *et al.*, 2018; Abdoli *et al.*, 2019; Sarghale *et al.*, 2020) [28, 18, 16, 1, 26]. Iso-Touru *et al.* (2016) [15] experimented the genome-wide association studies for traits associated with milk production in cattle by attribute variants of whole-genome sequence which, is a robust procedure, cost-effective in expanding the available information, and also extending the knowledge of mutations that affect the milk production traits in cattle. Genome-wide association studies were also used to evaluate the milk production per lactation, persistency, milk yield at an initial stage, and age at 1st calving in multiple breeds of cattle in Thailand (Yodklaew *et al.*, 2017) [43].

Application of genomic breeding model in the selection of dairy cattle

The extent of decrease in milk yield due to thermal stress varies between individuals which have heritability from low to moderate levels (0.13–0.23) (Bernabucci *et al.*, 2014; Silpa *et al.*, 2021) [3, 31]. A drop in milk production due to thermal condition could be a potent indicator of heat stress. However, traditional selection strategies comprising phenotype and pedigree information, which is essential for the improvement in milk yield, but these strategies had lesser genetic gain due to the larger generation interval and inferior heritability for the resilience traits in milking cattle. This will reveal the gateway for many refinements in breeding techniques, and genomic selection and hence, making it an attractive choice to overcome this limitation of elite cattle selection based on their Genome-wide association studies for heat tolerance (Nguyen *et al.*, 2016) [10]. This technology utilises genome-wide DNA markers to facilitate capturing the results of diverse genomic variations that impact complex traits (Silpa *et al.*, 2021) [31].

Biomarkers associated with thermo-tolerant dairy cattle

Genetically designated thermal-resilient cattle would help to ameliorate dairy animals' production during the high environmental temperature (Silpa *et al.*, 2021) [31]. There are few observations which identified many biomarkers in the cattle genome having an interrelation with thermo-tolerance like HSF1 and HSPA6; HSP70; ATP1B2; TNF1/4, KIF9; IL2/6; SELENBP1; EIF2AK4 and XDH (Bernabucci *et al.*, 2014; Garner *et al.*, 2016; Wakchaure *et al.*, 2016; Yodklaew

et al., 2017; Iso-Touru *et al.*, 2016; Saowaphak *et al.*, 2017 and Cheruiyot *et al.*, 2020) [3, 10, 39, 43, 15, 25, 6].

Applications of selection signature in the dairy sector

According to the postulates in population genetics, gene alleles that are significantly selected are either strayed or enhanced in population frequency until it gets anchored. Selection signatures assist to demarcate such functionally essential regions in the DNA fragments using diverse statistical approaches (Schwarzenbacher *et al.*, 2012; Silpa *et al.*, 2021) [27, 31]. Several techniques have been developed, including haplotype homozygosity extension and relative extended haplotype homozygosity to detect recent selection, Tajima's D and Fay and Wu's H-test to detect selected mutations, FST and pairwise FST, integrated Haplotype Score (iHS) which measures differences in large-scale allele frequency among populations, Rsb test which detects the loci under selection (Macciotta *et al.*, 2017; Tajima, 1989; Fay and Wu, 2000; Akey *et al.*, 2002; Patterson *et al.*, 2006; Voight *et al.*, 2006) [18, 33, 8, 2, 21, 38]. These practices have been utilised to detect candidate genes and potential loci in livestock that have influenced complex traits and undertake positive selection (Silpa *et al.*, 2021) [31]. These genomic techniques influence different economic traits like animal reproduction, milk production, and traits related to meat and carcass production. Adopting similar models to detect the potential selection signatures in thermal-stressed dairy cattle would supplement to build of the database for expanding the climate-resilient dairy cattle population (Macciotta *et al.*, 2017; Silpa *et al.*, 2021) [18, 31].

Conclusion

In the latest climate change scenario, investigators are now concentrating to incorporate heat-tolerance and shallow methane emission traits into breeding strategies which were principally looking into productive traits. Such integrated breeding perspectives would ensure livestock production sustainability. This chapter has extrapolated the information concerning the effects of thermal stress on milk yield of dairy cattle and the numerous genomic appliance that are available to detect climate-resilient dairy cattle. The various economical and functional traits which control milk yield can be identified by using modern statistical models and biotechnological tools to ameliorate thermo-tolerance in dairy animals. Although many refinements have been taken in these areas, in which selection signatures and GWAS were mostly chosen by researchers across the world and incorporation of such strategies can be used to identify and improve resilient cattle associated with climatic change.

Conflict of interest

The authors declare that they have no conflict of interest.

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