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Review article

Single nucleotide polymorphism markers and their applications for cattle production in selective breeding: A review for meat production traits

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Abstract

The United Nations projects the global population to reach 8.7 billion by 2030 and 10.2 billion by 2050, intensifying the demand for sustainable food security. Cattle, a cornerstone of meat production, critical to meeting this challenge. Advances in livestock genomics have revolutionized selective breeding by integrating single nucleotide polymorphisms (SNPs) into marker-assisted selection (MAS) and genomic selection. This review synthesizes the role of SNP markers in enhancing economically important growth trait related to meat production across *Bos taurus*, *Bos indicus*, and other indigenous cattle breeds. We examine SNP discovery methods, such as genome-wide association studies (GWAS) and high-throughput genotyping, and their application in identifying key genes associated with the trait. Emerging technologies, such as CRISPR-based editing guided by SNP data, are also explored. By addressing research gaps, particularly in indigenous breeds, this review highlights SNPs' potential to optimize cattle production and advance global food security.

Keywords: Cattle breeding, Genomic selection, Marker-assisted selection, Single nucleotide polymorphisms (SNP).

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INTRODUCTION

Cattle production has always played a significant role as a primary source of protein and dairy products for population consumption. Global meat consumption has recorded a steady increase, with a rise going as high as 500% since the 1960s (Katare et al., 2020), with cattle meat remaining one of the world's most consumed red meat to this day (Farchi et al., 2017). Incidentally, cow milk has also maintained its popularity among consumers albeit the rise of animal milk alternatives. Ensuring a sustainable supply of cattle meat and milk to meet consumers' demands is the primary goal of ruminant production sectors worldwide. Improving cattle productivity is the key to maintaining a sustainable supply for consumers. Breeding management is a crucial aspect of cattle productivity. Meat and milk production are essential economic traits governed by multiple genes. Thus, certain measures have to be considered to incorporate the improvement of such traits into cattle breeding efforts. Livestock selective breeding has reached new heights with newly improved tools for identifying suitable breeding candidates. Recent advancements in livestock genetics and animal breeding can improve productivity through genotypic selection in tandem with conventional selection and assisted reproduction. Traditionally, selective breeding is carried out based on phenotype and estimated breeding value (EBV), but this method is time-consuming, costly, and limited to superficial features. Recent developments in molecular genetics have introduced the use of molecular markers for improving desirable production traits. Dexyribonucleic acid (DNA) markers aid animal breeding through selection optimization by identifying genetic composition and estimating performance, enabling the use of genetic diversity. This approach enhances desirable traits, supporting better health and productivity, and accelerates growth among cattle population (Singh et al., 2014; Beuzen et al., 2000). Single nucleotide polymorphisms (SNP), a fairly novel, convenient and widespread molecular marker may hold the key to further progress in the cattle breeding industry.

MOLECULAR MARKER

Molecular Marker Identification Techniques

Molecular marker techniques have significantly evolved since the first reported technique of using restriction fragment length polymorphism (RFLP) in the early efforts of genetic mapping of the human genome (Botsteinet al., 1980). Molecular marker techniques have progressed from restriction-based markers of the first generation, which includes RFLP, followed by amplification-based markers of the second generation, such as random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP), and succeeded by third-generation sequence-based markers, like SNPs. First-generation markers use hybridization techniques to visualize DNA fragments, but such techniques are laborious. The second-generation technique unlocked a new frontier in molecular genetics as DNA amplification by polymerase chain reaction (PCR) alleviated the burdens of tedious procedures. Amplification-based or PCR-based markers can be classified into sequence-arbitrary markers and sequence-dependant markers (Singh et al., 2014) The development of genome sequencing technology established the third-generation sequence-based markers, e.g., expressed sequence tags (ESTs), SNPs and sequence-related amplified polymorphism (SRAP). The need for more cost-efficient, time-saving, and straightforward techniques has allowed molecular marker techniques to evolve further to better fit their diverse applications. Nonetheless, every technique has its benefits and its flaws. In molecular marker identification, properties typically sought include the absence of unfavorable effects on phenotype, co-dominance in expression, highly polymorphic, possess economic significance, conveniently assayable, highly reproducible and non-exhaustible (Dhutmal et al., 2018).

Single Nucleotide Polymorphisms (SNP) and their Genotyping Techniques

SNPs are DNA sequence polymorphisms caused by single-nucleotide variations within the genome, including insertions, deletions, transversions, and single-base transitions, with an allelic variation frequency greater than 1%. These polymorphisms are widely distributed, in which approximately one SNP can be found for every 700 base pairs (bp) in *B. taurus* and 300 bp in *B. indicus* (Seidel, 2010), on both the coding and non-coding regions of the genome (Cortes et al., 2022). They are typically biallelic as a single base pair has extremely low mutation rates and the possibility of two-point mutations occurring at the same position over time is highly implausible. Moreover, there is an apparent bias for transition as compared to transversion (Vignal et al., 2002; Børsting and Morling, 2013). Presently, SNPs have emerged as one of the most common genetic markers genotyped by researchers as they are widespread, typically biallelic and conveniently assayable by automated techniques (Zalewska et al., 2021). Since its initial discovery in the early 2000s, these markers have benefitted the cattle industry in numerous aspects.

SNP analysis can be divided into two categories, which are the discovery of unknown SNPs and the identification of known SNPs in a population. The first category can be carried out through methods based on gene sequencing, PCR, nuclease-assisted probe system, allele specific hybridization and mass spectrometry. The purpose is to find genetic markers of specific attributes and raise the marker density of genetic maps (Xu et al., 2009). Gene sequencing is considered the gold standard for SNP discovery despite its low sensitivity, labor-intensiveness and time-consuming nature (Kwok and Duan, 2003, Huang et al., 2015). The second category involves genotyping SNPs at known positions in the genome. The general basis of SNP genotyping involves a two-step procedure, in which allele-specific products for targeted SNPs are amplified and subsequently detected for genotype determination. Genotyping can be carried out traditionally, utilizing standard molecular means, such as RFLP, amplification refractory mutation system (ARMS), single-strand conformation polymorphism (SSCP) and denaturing gradient gel electrophoresis (DGGE). High throughput genotyping allows for simultaneous genotyping of thousands to several hundred-thousands of SNP markers in targeted groups of hundreds of thousands of individuals (Singh and Singh, 2015). Methods for high throughput genotyping involve allele discrimination methods (e.g. allele-specific PCR or TaqMan assay, high-resolution melt (HRM) analysis), whole genome sequencing, mass spectrometry, SNP arrays, pyrosequencing and denaturing high performance liquid chromatography (DHPLC) (Kirsanova et al., 2019). In recent years, high-throughput sequencing technologies have lowered the cost of whole genome sequencing, and substantial volumes of population genotyping data from diverse species have been released (Goodwin et al., 2016; Gao et al., 2022).

Applications in Selective Cattle Breeding

Applications of SNP in selective cattle breeding can be observed in many ways. MAS, GWAS, and genomic selection (GS) are some of the most common methods of applications carried out in the cattle industry. Cattle breeders apply these methods based on respective goals, capital and availability of knowledge and expertise.

Marker-Assisted Selection

The livestock industry has long since integrated the use of genetic markers into their breeding programs in tandem with traditional breeding methods and assisted reproductive technologies. Development of cattle linkage maps in the early 1990s triggered the shift in dairy cattle breeding from phenotypic to molecular genetics, focusing on identifying genetic markers to improve genetic gain and

selection accuracy (Dekkers and Werf, 2007). MAS is one of the earliest application methods adapted into cattle breeding strategies. Quantitative trait loci (QTL) are specific loci in the genome correlated with certain phenotypic traits. Correlation is based on linkage disequilibrium (LD), which is defined as non-random association of alleles at various loci in a population brought on by selection, genetic drift, and other causes (Sabir et al., 2014). A strong LD suggests markers in the genomic region are located proximal to the gene encoding the desired trait. Breeders utilize MAS by selecting animals using DNA markers linked to desirable QTLs to screen animals with genetically superior traits. In the past, breeders had depended on pedigree and phenotypic traits to select distinguished individuals for breeding to produce offspring with better traits to boost production. MAS allows breeders to reach a similar outcome with shorter generation intervals and the ability to tackle traits that are sex-limited, low heritability, difficult to assess or expressed later into the animal's growth (ul-Hassan and Ceyhan, 2021). There are three types of causative relationships distinguishing MAS markers: (i) direct markers, which directly code for the underlying causative mutation, (ii) LD markers, which are in population-wide linkage disequilibrium with the causative mutation, (iii) linkage equilibrium (LE), which are in population-wide equilibrium with the causative mutation (Dekkers, 2004). RAPD, AFLP, single sequence repeat (SSR) and SNP are markers typically utilized for MAS. However, SNP remains the genetic marker of choice due to its various advantages and functionalities. For application in animal breeding, SNP markers are first selected from SNP databases or SNP marker pools via computer simulation. Selected SNPs are then validated to establish polymorphism of SNP markers between two different gene pools within the target population. A secondary selection is carried out by genotyping the polymorphic SNPs in the target population to conduct association analysis. SNP markers highly associated with QTL can be applied as a potential genetic marker in MAS (Huang et al., 2015). However, MAS application is not without its limitations. As MAS was initially pursued using the candidate gene approach, the technique required strict significance testing. Moreover, the scarcity of reliable techniques for accurate QTL identification and the insufficient number of markers, along with the rise of genomic selection in the early 2000s, contributed to the diminishing interest of researchers and breeders in MAS. Despite that, in a review on MAS on bull fertility, Huang et al. (2022) highlighted the possibility of re-igniting MAS through the advancements of genomic tools such as GWAS and genomic selection.

Genome-wide Association Study

GWAS is an application method that aims to identify the best candidate genetic variant for selection by assessing the effects of each variation to determine significant associations between the variants and the phenotypes for the targeted gene (Sahana et al., 2023). Variation or SNP effect is dependent on whether SNP is in LD with causative genes and the degree of association between the SNP and the gene (Schmid and Bennewitz, 2017). In GWAS, DNA profiles of 1000 or more individuals with altered traits are compared to a control group of a similar number of individuals. The genome-wide distributed markers are obtained by subjecting the DNA profiles to microarray analysis or next-generation sequencing (NGS), followed by in-silico analysis. The large sample size is a requirement of the methodology to ensure statistical analysis robustness and enhance test power (Mukhopadhyay et al., 2020). Nowadays, commercial SNP arrays are available for all major livestock species, allowing the identification of specific nucleotides present at millions of different positions across their respective genomes. Breeding companies routinely use SNP arrays to genotype individuals and gather phenotypic data (Long, 2020). The key to GWAS analysis is the interpretation of the final results. The analysis of the final results is critical for a conclusive GWAS interpretation. After obtaining an association value for genome-wide SNPs, it is important to eliminate any false positives (Pal and Chakravarty, 2020). This study utilizes PLINK (genome association analysis software) as quality control by setting stringent conditions to

rule out non-reliable SNPs. Schmid and Bennewitz (2017) suggest two statistical models that can be applied to GWAS analysis. The first model is a single-marker model, in which a model fits a single SNP at a given time, resulting in repeated tests. The rate of type 1 error from multiple tests can be minimized through various techniques. The second model is the Bayes multi-marker model, which simultaneously fits all SNPs as random effects. Unlike single-marker GWAS, applying multi-marker models requires careful parameter selection. The represented study utilizes a single-step marker model and Bonferroni correction. Quantitative features are often linked to many SNPs distributed throughout the genome. Therefore, selecting genes around SNPs requires functional annotation and network analysis. The study references ARS-UCD 1.2 (cattle genome reference) to screen for candidate genes and employs an enrichment analysis to identify pathways for candidate genes. GWAS is beneficial in terms of robustness, reproducibility, and its ability to genotype large numbers of SNPs (Marigorta et al., 2018; Raza et al., 2020). However, concerns have been raised in regards to the high incidence of false positives and the lack of regard for SNP interactions of the same gene (Santana et al., 2014; Li and Kim, 2015; Alqudah et al., 2020). All things considered, SNP-based GWAS remains favourable among researchers and breeders while others consider GWAS a vital piece in ushering in the age of genomic selection.

Genomic Selection

MAS selects markers associated with QTL with relatively large effects. However, most complex traits are governed by many genes with relatively small effects that may be disregarded as they are too small to be statistically significant (Xu et al., 2020). As a result, QTL was only able to explain less than 10% of genetic variance in the overall breeding objective (Meuwissen et al., 2016). Meuwissen et al. (2001) proposed genomic selection (GS) for complex traits as an alternative, where each trait-related locus is linked to at least one marker and each marker has effect over the trait. Instead of testing for marker significance, breeding values are estimated by summing the effects of evenly spaced markers across the genome, selecting superior individuals based on their genomic estimated breeding values (GEBVs) (Mateescu, 2020). GEBVs are representative of the potential possessed by animals to transmit desirable traits to their offspring. GS is executed by first genotyping and recording the phenotypic traits of a reference or training population. It is preferable if the reference population is closely related to the target population as it increases the accuracy of the GEBV upon application. GEBV is calculated based on a genomic prediction equation derived from the reference population. The equation regards SNP effects as random effects to counter the inability of traditional statistical methods to estimate the fixed effects of more than 50,000 SNP markers. By comparing their genotypes and estimated effects, the equation is then used to estimate the GEBV of the chosen or target population (Meuwissen et al., 2016). Animals with the highest GEBVs are prioritized for breeding. GS has become the breeding selection of choice for many developed countries such as the United States, New Zealand and Australia due to its many benefits (Mukhopadhyay et al., 2020). With GS, breeders are no longer impeded by QTL-linked traits or the lack of pedigree or phenotypic records for the target population. A cost-benefit analysis by Canada suggests genetic gain can be doubled with GS utilization (Obari et al., 2022). This can be attributed to the shortened generation interval and the enhanced accuracy and intensity of genomic selection. Other factors that can be taken into consideration include, the environmental effect on traits and the cost of breeding strategy implementation. Implementation of GS has been especially successful in dairy cattle as a result of the large, accessible populations of progeny-tested individuals. Moreover, several countries have banded together to generate and establish dairy cattle genotypic and phenotypic data for global referral. The homogeneity of dairy cattle breeds also plays a part in increasing the accuracy of genomic prediction and earning the favour

of dairy cattle producers. However, GS implementation in beef cattle is not as progressive as previous studies have predicted much lower accuracies as compared to dairy cattle. In contrast to dairy cattle, beef reference populations contain a smaller number of animals within breeds and some individuals have not been progeny tested, therefore lowering the overall accuracy of genomic prediction (Van Eenennaam et al., 2011). Countermeasures have been proposed to increase the accuracy of genomic predictions, particularly for beef cattle. Mukhopadhyay et al. (2020) suggest that the use of multi breed reference populations and increasing SNP density may enhance genomic predictive accuracy.

SNPS IN MEAT PRODUCTION TRAIT

Recent years have seen an increase in genotyping of cattle-meat-related traits. Growth traits typically involve body measurements or weight, while carcass traits are related to meat quality, such as fat composition and deposition on meat. SNP markers have become essential for beef cattle breeding selection, particularly for improving meat quality, as carcass traits can only be measured post-slaughter. With the available molecular markers, cattle with superior meat quality can be selected for breeding without a long waiting period or unnecessary sacrifice.

SNPs related to meat production were reported in various genes, including FASN, PLAG1, FABP4, SCD, GH, GHR, CAPN1, LEP, SREBP and CAST.

Meat quality is an essential production marker in breeding selection. Researchers have been looking into producing meat of satisfactory taste and beneficial dietary composition to meet consumer demands. Beef industries in Australia, America and Japan regard ≥C20 omega-3 long-chain polyunsaturated fatty acids (n-3 LC-PUFA), intermuscular fat content (IMF) and fat melting point (FMP) as vital eating quality indicators due to their association with taste, smell, texture, tenderness, flavor, and juiciness (Motoyama et al., 2016; Garmyn, 2020; Pogorzelski et al., 2021). Lipogenic genes are genes associated with fatty acid metabolism in the body. Through genetic selection, modulation of beneficial fatty acids such as n-3 LC-PUFA in muscle tissue can be accomplished for the improvement of beef quality and satisfactory consumption by selecting for lipogenic genes (Malau-Aduli et al., 2000; Zhang et al., 2008; Ward et al., 2010). A total of ten genes were studied and summarised according to biological function, SNPs and breed, that relate to meat quality and production (Table 1).

DISCUSSION

Over the past decade, numerous SNP markers have been identified for established and novel genes across the bovine genome. In this review, a large number of beef-production SNPs were observed as compared to fertility and milk production. Beef is a vital source of protein for human consumption. Cattle meat was reported the third most consumed meat and the second most consumed red meat in the world, representing 25% of the total meat consumption (United Nations Department of Economic Social Affairs, 2021). The various research into beef genetics may reflect the need for high quality meat to meet consumer demands and continually provide for the ever-expanding world population. Additionally, the findings highlighted chromosome 14 as the overall most commonly reported chromosome, housing major genes such as PLAG1, DGAT1, TG and FABP4. Several QTL association studies have identified regions on chromosome 14, particularly in the vicinity of PLAG1 and DGAT1 genes as pleiotropic QTLs affecting multiple traits such as meat tenderness, growth, fertility and milk production (Bolormaa et al., 2014; Xiang et al., 2017). These findings also coincided with Wiggans et al. (2017), that highlighted chromosome 14 and DGAT1 for their large effect on milk and fat, through the United States genomic evaluation system for dairy cattle.

Table 1 Summary of different genes and its SNPs that contribute to meat production.

Gene	Biological function	SNPs	Breed	References
FASN	Involvement in fat metabolism as a catalyst for fatty acid synthesis from acetyl coenzyme A	g. 50787138 A>G g.16024 A>G g.841 G>C g.13192 T>C g.13232 C>T	Hanwoo Angus Qinchuan	Roy et al., 2005
FABP4	Plays a part in the intake, transport and metabolism of fatty acids by binding long-chain fatty acids and executing lipid hydrolysis	g.44678794 G>A c.220A>G, 7516 G>C c.328 G>A rs41729173, rs110383592, rs110757796, 3691 G>A 2834 C>G	Angus Hereford Wagyu Holstein	Casas et al., 2003 Goszczynski et al., 2017
SCD	Convert saturated fatty acid to mono-unsaturated fatty acids through desaturation process	rs133958066	Japanese Black cattle	Sampath and Ntambi, 2006
GH	Growth hormone; regulates growth, metabolism, and carcass traits like fatness and muscle development.	GH4.1 g.2141 C>G	Korean cattle Simmental	Oh et al., 2012
GHR	Growth hormone receptor; mediates GH effects on growth and fat deposition; impacts body weight and milk production.	Nt241A/G AF140284.1 g.257A>G g.914 T>A GHR6.1	Angus Charolais Hanwoo	Di Stasio et al., 2005
CAPN1	Break down myofibrillar proteins to tenderize meat	g.232 G>T rs17871051 rs17872050 rs1121961662 AF252204 AF248054 c.580T>C c.658 T>C	Angus, Hereford, Hanwoo	Page et al., 2002
LEP	Decreases adipose tissue lipogenesis and slows insulin-stimulated glucose uptake, is an important hormone to regulate body weight, fat mass and energy metabolism	LEP g.978 g. 1180 C>T LEP 3100	Brahman cattle Kebun Ongole Grade cattle Simmental cattle	Fathoni et al., 2019 Rincón et al., 2020
SREBP	Regulator of SCD expression	rs41255691	Japanese Black cattle	Sampath and Ntambi, 2006
CAST	Inhibits CAPN1 activity to regulate post mortem proteolysis	g.98535683 A>G rs110496242 rs109221039 rs1109555059 rs41255587 g.98533962 C>G g.98545188 T>A c.1985 G>C c.182A>G	Angus, Hereford Charolais	Casas et al., 2006

The majority of the reported SNPs for each trait are located in coding regions, particularly exons. SNPs in coding regions have the ability to change protein structure through amino acid substitution or affect proteins by post-transcriptional alterations, translation rates or other methods (Yang et al., 2022). These SNPs directly affect the phenotype and often have larger effect sizes. However, SNPs in coding regions account for only a small portion of the genome. Recent studies have elucidated that most complex traits are governed by various traits with miniscule effects (Xu et al., 2020). Therefore, it is important to explore SNPs of coding and

non-coding regions with equal interest. Overall, the studies focused on Holstein, Japanese Black and Qinchuan cattle. Holstein cattle is an established dairy breed due to their superiority in milk production. On the other hand, Japanese Black cattle are considered the gold standard for meat quality for the tenderness and juiciness of their meat. Qinchuan cattle is one of the five most well-known indigenous yellow cattle breeds in China (Gao et al., 2022). These cattle have good adaptability, but slow intermuscular fat development (Wang et al., 2011). The large representation of Qinchuan cattle and other Chinese cattle breeds in the review may be attributed to the overwhelming number of studies reported pertaining to Chinese cattle breeds. The variation in SNP-trait association between breeds suggests there is a need for breed-specific breeding strategies as different cattle breeds may carry various predispositions for certain traits.

Oftentimes, polymorphism associated with complex traits or QTLs tend to affect multiple traits (Von Berg et al., 2022). These SNPs are known as pleiotropic SNPs. Pleiotropy can be defined as the occurrence of statistically significant correlations with several trait domains since characteristics within a domain often exhibit higher phenotypic correlations than those between domains. SNPs and genes associated with various characteristic domains may have a role in broader biological activities. The most pleiotropic gene sets primarily regulate transcription, a crucial function for all cells. In an association study involving millions of SNPs and hundreds of traits, Watanabe et al. (2019) discovered about one tenth of the SNPs were associated with more than one trait. However, it is important to note that two distinct genes of close physical linkage and actual pleiotropy are difficult to differentiate (Flint and Mackay, 2009). Thus, conscientious research to properly discern pleiotropic genes or SNPs. Apart from that, it is also crucial to consider the pattern of pleiotropy as certain SNPs may have desirable effects on certain traits and undesirable effects on others. Pleiotropic SNPs with positive effect on all desirable effects would be a favourable target for multi-trait breeding selection (Bolormaa et al., 2014). In selective breeding, the concise understanding of pleiotropy allows breeders to carefully design more precise and balanced breeding strategies specifically catered to the targeted population.

Another gene interaction in play that should be considered in regards to the SNP associations is the genotype by environment interaction (GEI). It is evident from the reported SNP associations that despite utilizing similar SNPs or genes, a number of reported studies demonstrated similar responses while others showed a different outcome. GEI refers to how various genotypes respond to different environmental situations and is typically calculated based on genetic correlation to phenotypes across different environments. It also explains how the performance of two or more genotypes differs between environments (Wakchaure et al., 2016, Digesa, 2024). Therefore, the different outcomes of the various reported association studies of similar genes or SNP may be attributed to GEI, especially when major environmental factors such as climate come into play. Environmental effects are a vital factor in the incorporation of polymorphisms for selective breeding. For the purpose of optimizing livestock productivity, Paula et al. (2009) and Usman et al. (2013) highlighted the need for proper quantification of GEI as GEI extent determines the animal's ability to fully express its genetic potential.

At present, the state of SNP research and application in selective cattle breeding worldwide varies according to the demands, funding and state of economy of each country. SNP application, regardless of the utilized application method, comes with various challenges. In a review on meat trait associations by Zalewska et al. (2021), the use of preferred genetic markers are hurdled by three challenges. Such challenges entail correct breed association DNA data collecting, quality assurance procedures for using and interpreting DNA marker data, and improved proficiencies in utilising available genetic markers. As compared to dairy cattle, beef cattle breeds are much more diverse. Therefore, research on genetic markers is to be conducted with accurate breed information, as the effects of genetic markers may differ between breeds to produce markers of the highest

specificity and efficacy. Genetic markers are still considered novel; thus, quality assurance of interpretation and usage is essential to prevent misinformation. Lack of expertise is always a significant concern in modern technology. Mishra et al. (2017) warns that the potentially insufficient use of QTL data poses a risk, as it places undue focus on basic molecular information at the expense of the population's total economic benefit from all characteristics and their polygenic impacts. Overcoming these challenges would require adequate information dissemination to entice more researchers to delve into the subject and ensure breeder understanding for satisfactory application. Another critical aspect in molecular marker application is the cost. Excessive cost of DNA testing impedes the adoption of marker application into breeding schemes, especially in the livestock industry where adept use of capital is key to a sustainable business. A reduction or decline in the cost would expand the use of DNA testing and allow for more animals to be tested, facilitating the development of larger and more recent reference populations (Meuwissen et al., 2016). Other concerns prompted by the author include the traits that are difficult, expensive and not routinely recorded. These traits deter the progress of SNP application, especially those that require samples from large populations. When utilizing commercial arrays data from reference populations in SNP applications, reduced accuracy can be expected from the results if the target breeds are not included. The dampening of prediction accuracies can be attributed to breed difference as animals of different breeds share smaller chromosome segments. Sharma et al. (2016) highlights other challenges that may impede SNP application in selective breeding such as substantial rate heterogeneity and ascertainment bias.

The concern of selecting a suitable sample size for genetic association studies is appropriate and valid as inadequacy would lead to fallible results due to its inability to properly represent the population. On the other hand, an overly large sample would be costly and difficult to manage (Politi et al., 2023). Therefore, proper sample size calculation is a critical aspect of genetic association study design through the process of power analysis. Although the process is ideally executed before the study, sample size reassessments can be carried out mid study if there is lack of decisive information during the study preparation (Jones, 2003). Sahana et al. (2023) specified that animals selected for gene studies preferably should originate from a single or similar population. This is because sampling on focused populations enhances the detection power of the study, particularly when genotyping becomes the limiting factor (Sahana et al., 2023).

CONCLUSIONS

In summary, various SNP markers of established genes and novel genes have been reported with positive association with desired traits. The technology behind the development of genetic markers continues to evolve since its initial discovery and application. SNP markers can be configured for diverse applications in cattle genetics, not limited to enhancing main production traits, but also for the improvement of other traits such as robustness and disease resistance. SNP markers can be further utilized for diversity studies and breed identification. Proper utilization of SNP markers in the livestock industry is still limited to large industries with extensive capital. Further research would be required to reduce the cost of testing, construct more time-saving applications and increase the effectiveness for molecular marker application in the cattle industry.

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AUTHOR CONTRIBUTIONS

Izzati Izamin: Conceptualization (Lead); Writing-original draft preparation (Lead). **Luqman Abu-Bakar:** Conceptualization (Equal); Writing-review and editing (Lead); Visualization. **Mohd-Farhan-Hanif Reduan**: Conceptualization of the article (Equal). **Abubakar Muhammad-Wakil**: Conceptualization of the article (Equal); Writing-review and editing (Equal). **Norhidayah Noordin:** Writing-review and editing (Equal).

CONFLICT OF INTEREST

The authors have declared that there exists no conflict among the authors of this article.

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