



Role of Marker-assisted Selection for Genetic Improvement in Livestock: A Review

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ABSTRACT

Marker Assisted Selection (MAS) is a valuable tool in livestock breeding that helps improve desirable traits by using genetic markers linked to specific genes. Unlike traditional methods that rely on visible traits, MAS allows selection based on genetic makeup, making it more accurate and efficient. Introduced in the late 20th century, MAS has evolved significantly with the integration of genomic technologies, advanced statistical modelling and gene-editing techniques. The key advantage of MAS is that it enables early selection, even before an animal's phenotype is fully expressed, thus speeding up the breeding process and improving genetic gain. MAS has been successfully applied in various livestock species, including cattle, pigs and poultry, to enhance production traits like growth rate, feed efficiency, milk yield and disease resistance. The future of MAS lies in its integration with advanced genomic technologies, enabling precise selection for complex traits across diverse species. Continued advancements in gene editing and data analytics will enhance breeding efficiency, sustainability and genetic improvement in animal populations. Therefore, this comprehensive review explores the journey of MAS, highlighting its historical significance, the technological tools used in marker development, key properties, advantages and limitations, practical applications and future prospects.

Key words: Livestock, MAS, QTL, Selection, Traits.

Selection is the process of preferring certain individuals in a population for reproduction while denying others, resulting in non-random differential mating (Lerner, 1958). Genetic improvement in livestock focuses on choosing elite males and females to breed offspring that outperform the parental average. Selection in breeding programs can be categorized based on criteria and methods used. Natural selection occurs without human intervention, favouring individuals with traits that enhance survival and reproduction, such as disease resistance. Artificial selection is guided by humans to promote desirable traits. This includes mass selection, based on observable traits like body weight or milk yield and family selection, where average family performance is evaluated especially useful for traits influenced by the environment. Progeny testing, commonly used for sex-limited traits like milk production, involves evaluating an individual's offspring for selection. Most economically important traits in livestock and poultry are quantitative, making phenotype-based selection alone less effective. The development of molecular markers revolutionized animal breeding by leveraging quantitative trait locus (QTL) maps, which identify marker proximity to gene regions affecting traits. These maps guide molecular techniques to accelerate the attainment of desired traits. Marker-Assisted Selection (MAS) involves selecting individuals based on markers linked to traits like feed efficiency or disease resistance. Genomic selection goes further by using genome-wide data to predict genetic potential for multiple traits, enabling more precise and efficient breeding. MAS is an indirect selection method where a trait is selected based on a linked marker (Ribaut *et al.*, 2007). It plays a pivotal role in genetic improvement

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by allowing early, accurate and efficient selection, unlike traditional methods that rely on observable traits influenced by the environment. MAS uses genetic markers such as DNA sequences or genes to identify chromosomal regions affecting single-gene traits. Common marker types include restriction fragment length polymorphisms (RFLPs), microsatellites and single nucleotide polymorphisms (SNPs) (Sharma *et al.*, 2024).

Therefore, the review paper will cover several key topics related to Marker-Assisted Selection (MAS) in livestock.

Historical overview

The concept of marker-assisted selection (MAS), also known as marker-assisted breeding (MAB), was introduced

about 25 years ago by Smith and Simpson (1986) and Soller and Beckmann (1983). Marker-assisted breeding is expected to become more versatile, practical, efficient and cost-effective in the future (Pheirim *et al.*, 2022). The idea was that while most polymorphisms identified through advanced techniques are not themselves quantitative trait loci (QTL), many are closely linked to them, enabling indirect selection. With the discovery of restriction fragment length polymorphism (RFLP; Botstein *et al.*, 1980) and other DNA markers, it was anticipated that traditional plant and animal breeding would shift from phenotype-based selection to marker-based approaches targeting specific genes. Conventional breeding, including programs like progeny testing, selects for desirable traits based on phenotype without identifying the actual genes involved (Moniruzzaman *et al.*, 2014). Assisted reproductive technologies such as artificial insemination and embryo transfer have improved productivity (Lindhe *et al.*, 1998; Sartori *et al.*, 2006), but conventional methods are time-consuming and less effective for sex-limited, low heritability, or late-expressing traits. Molecular markers help overcome these limitations by enabling early selection of genetically superior animals (Singh *et al.*, 2014). The application of molecular markers not only enables the selection of genetically superior animals for enhanced productivity but also helps overcome the limitations associated with conventional selection methods (Karuthadurai *et al.*, 2019). MAS is particularly valuable for traits that are difficult to evaluate directly. It allows early selection, reducing the number of animals needing full evaluation and lowering breeding costs. MAS is also effective for gene pyramiding combining multiple beneficial genes. However, while it increases selection efficiency, it does not always reduce total breeding time, as selected animals must still undergo field evaluation and timelines depend on the species' juvenile phase.

Identification of genes

Identifying genes that influence economically important traits in livestock and poultry is vital for improving productivity and efficiency. Advances in genomic technologies have enabled the discovery of key genes and markers linked to

traits such as growth, meat quality, reproduction and disease resistance. In cattle, SNPs within the DLK1-DIO3 imprinted domain, polymorphisms in the GNAS gene and variations at the IGF2 locus have been associated with production and dairy performance (Magee *et al.*, 2011; Sikora *et al.*, 2011; Berkowicz *et al.*, 2011). In sheep, the "callipyge" (CLPG) gene produces a large, lean rump muscle, which is valuable for meat production (Lewis and Redrup, 2005). For chickens, QTLs and candidate genes like PIT1 and FTO have been linked to growth, body weight and fatness traits (Cahyadi *et al.*, 2014). Understanding these genetic factors supports the use of marker-assisted and genomic selection in breeding programs, enhancing animal performance. Important traits and associated markers are summarized in Table 1.

Technological tools used in MAS

MAS uses advanced technologies to identify and utilize genetic markers for improving economically important traits in animals. Polymerase chain reaction (PCR) amplifies specific DNA sequences, enabling genotyping of markers like SNPs and microsatellites (Mullis and Faloona, 1987). QTL mapping locates genomic regions linked to traits such as growth and milk yield (Andersson, 2001). High-throughput SNP genotyping platforms, like Illumina and Affymetrix arrays, support large-scale SNP analysis for genomic selection (Rincen *et al.*, 2012). Next-generation sequencing (NGS) offers comprehensive genome-wide data to discover novel markers and mutations (Mardis, 2008). RNA-Seq analyzes gene expression patterns associated with traits (Mortazavi *et al.*, 2008). High-density genotyping arrays enable simultaneous analysis of thousands of SNPs to predict breeding values (Meuwissen *et al.*, 2001). Bioinformatics tools such as PLINK, GCTA and Ensembl facilitate genetic data analysis and marker discovery (Purcell *et al.*, 2007). Emerging gene-editing tools like CRISPR-Cas9 validate marker-trait links and enhance traits directly (Hsu *et al.*, 2014). Genomic prediction models, including BLUP and GBLUP, estimate breeding values to accelerate selection (VanRaden, 2008). These tools have revolutionized MAS, making genetic improvement more precise and efficient.

Table 1: Comparative analysis of various DNA markers used in genetic mapping.

Features	DNA markers			
	RFLP	RAPD	AFLP	STS
Efforts to generate marker	Moderate	Simple	Simple	Difficult
Ease in use	Difficult	Easy	Moderate	Moderate
Reproducibility	High	Moderate	High	High
Use of radioactivity	Yes	No	Yes/No	No
Use of restriction enzymes	Yes	No	Yes	Yes
Use of PCR	No	Yes	Yes	Yes
Dominance	Codominant	Dominant	Codominant	Codominant
Information required	Moderate to high	High	Very high	Very high
Time required for detection	Relatively longer	Short	Very high to short	Very high to short

Source: Fundamentals of Genetics (Singh, 2007).

Markers

Genetic marker can be defined as any stable and inherited variation (insertions, deletions, translocations, duplications and point mutations) that can be measured or detected by a suitable method and can be used subsequently to detect the presence of a specific genotype or phenotype other than itself, which otherwise is non-measurable or very difficult to detect. Such variations occurring at different levels, *i.e.* at the morphological, biological, chromosomal, biochemical or DNA level can serve as the genetic markers. The markers that reveal variations at the DNA level are referred to as the molecular markers. Based on the techniques used for their detection, they have been classified into two major categories: Hybridization-based markers and PCR-based markers (Mitra, 1999). Markers may also be classified based on visually evaluated traits such as morphological and productive traits, gene products as in biochemical markers and DNA analysis-based molecular markers (Teneva *et al.*, 2010). Fig 1 provides an overview of different molecular marker technologies used in livestock.

Hybridization-based markers

Hybridization-based marker technologies use probes such as cDNA, cloned DNA elements, or synthetic oligonucleotides. These probes are labelled with radioisotope or with conjugated enzymes that catalyse a coloured reaction, to hybridize DNA. Hybridization-based DNA markers are of two types:

Restriction fragment length polymorphisms (RFLPs)

This method was first developed by Botstein and co-workers in the year 1980. RFLPs utilize restriction enzymes

that cleave DNA at specific sequences. Differences in these sequences generate varying fragment patterns upon gel electrophoresis. Hybridization with a radioactively labelled gene-specific probe reveals genetic polymorphisms at particular loci (Williams, 2005). RFLP markers are Southern blot-based (Jiang, 2013) and are effective for locating genetic variations within genes.

Oligonucleotide fingerprinting

This technique uses short, synthetic oligonucleotide probes to generate unique hybridization patterns representing specific DNA or RNA molecules. It helps detect genetic similarities or differences and is notably applied in identifying and classifying RNA viruses for epidemiological studies (Oxford, 2025; Kew and Nottay, 1986).

PCR-based markers

Random amplified polymorphic DNAs (RAPDs)

RAPD markers employ PCR with single short primers (8-15 nucleotides) to amplify random DNA segments (Williams *et al.*, 1990; Welsh and McClelland 1990). High GC content (50-80%) in primers improves efficiency (Premkrishnan *et al.*, 2012; Cao *et al.*, 2015). RAPDs are useful for quickly detecting polymorphisms without prior sequence knowledge.

Simple sequence repeats (SSRs) or microsatellites

Microsatellites, also known as STRs or VNTRs, are short DNA repeats (1-6 bp) found throughout the genome, including regulatory and coding regions (Bidichandani *et al.*, 1998). SSR markers are also referred to as DNA microsatellites (Munsaka *et al.*, 2024).

Their high polymorphism and abundance make them valuable markers in livestock genetic studies (Civanova *et al.*, 2006; Sunnucks, 2000).

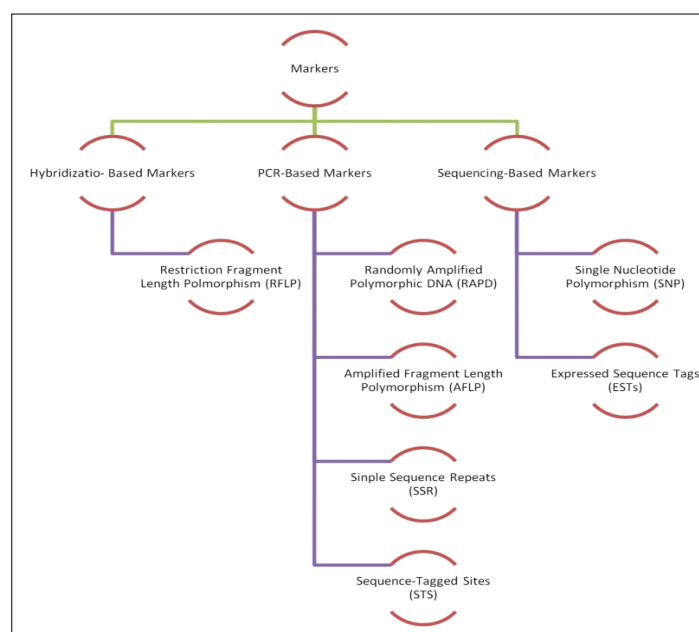


Fig 1: Overview of different molecular marker technologies.

Amplified fragment length polymorphisms (AFLPs)

The AFLP technique, developed by Vos *et al.* (1995) and widely used in genetic analysis, combines restriction digestion with selective PCR amplification. DNA is digested using rare- and frequent-cutting enzymes (e.g., EcoRI, MseI), ligated to adaptors and selectively amplified. Fragments are separated by PAGE or CE and visualized through fluorescence or radioactive labels. AFLP detects polymorphisms from nucleotide insertions, deletions, or substitutions, offering high reproducibility and suitability for automated genotyping (Mueller and Wolfenbarger, 1999; Bensch and Akesson, 2005; Salisu *et al.*, 2018). The comparison of various DNA markers used in genetic mapping is summarized in Table 1. Some livestock traits along with their associated markers are listed in Table 2.

Application of marker assisted selection

The first instance of MAS in livestock was reported in 1992 for chickens. Since then, markers have been identified in nearly all farm animals, including for milk yield in dairy cattle (Ansari-Mahyari *et al.*, 2008; Lipkin *et al.*, 2008), buffalo (Sarika *et al.*, 2013), growth and carcass traits in beef cattle (Carr *et al.*, 2006) and goats (Shen *et al.*, 2004). A 15% improvement in genetic response for growth rate in chickens when incorporating markers, compared to selection based solely on family history (Pongpisantham, 1994).

MAS enables large-scale screening to identify genes linked to disease resistance, allowing for accurate selection unaffected by environmental conditions (Wakchaure *et al.*, 2015). It eliminates the need for progeny testing, saving time and resources and allows selection among related animals not expressing sex-limited traits like milk or egg production. MAS is particularly effective in introgression strategies, helping incorporate beneficial traits while eliminating undesired ones (Hillel *et al.*, 1990). It is most beneficial for traits with high heritability and large effects that are already optimized in commercial populations.

MAS, especially when combined with reproductive technologies like multiple ovulation and embryo transfer (MOET), improves selection response for traits such as

milk yield by 6-15% (Ruane and Colleau, 1996). It is often integrated with traditional techniques like progeny testing to enhance breeding accuracy and economic gain in dairy cattle. MAS targets genes located at quantitative trait loci (QTLs) and knowledge of these loci enhances breeding value estimation. When QTL effects are large, MAS can significantly accelerate genetic improvement, with reported gains between 5-64% depending on trait type and marker information quality (Hayes *et al.*, 2003).

Beyond selection, molecular markers serve in genetic distance estimation, parentage identification, sex determination in embryos, disease diagnostics, gene mapping and twin zygosity assessments (Deb *et al.*, 2012). SNP markers are widely used to study genetic variation and relationships among and within livestock populations, helping identify unique genomic features in indigenous breeds (Edea *et al.*, 2012; Gorbach *et al.*, 2010; Lin *et al.*, 2010).

Markers allow for the direct identification of genes rather than gene products, aiding physical gene mapping via in situ hybridization (O'Brien, 1991). MAS is especially advantageous for traits with low heritability, limited conventional selection response, or sex-limited expression. Its success depends on factors like strong linkage disequilibrium, large population sizes, high marker density and the presence of heterozygotes at relevant loci (Salisu *et al.*, 2018).

Genetic evaluation using models like best linear unbiased prediction (BLUP) and genomic BLUP (GBLUP) combines genotypic and phenotypic data to improve breeding value accuracy (Meuwissen *et al.*, 2001). High-throughput genotyping tools such as SNP chips, SSR markers and NGS platforms enable rapid and cost-effective marker screening (Mammadov *et al.*, 2012). Advances in bioinformatics and automation have further enhanced genotyping efficiency, supporting large-scale breeding programs (Goddard and Hayes, 2009).

Limitations of marker assisted selection

A significant constraint of MAS is the variable expression of marker-trait associations among different populations,

Table 2: Some traits of livestock and their associated markers.

Species	Traits	Markers	Reference
Cattle	Carcass traits	SDC V293A FASN	Kawaguchi <i>et al.</i> (2020)
	Overall milk production performance	PRL	He <i>et al.</i> (2006)
Chicken	Egg production	GRB14GALNT1	Liu <i>et al.</i> (2011)
Goat	Dairy performance	IL6, IL8PTX3	Ilie <i>et al.</i> (2018)
	Wool fibre coloration	ASIP	Wang <i>et al.</i> (2016)
	Wool productivity	FGF5	Wang <i>et al.</i> (2016)
	High altitude adaptation	EPAS1	Song <i>et al.</i> (2016)
Pig	Litter size	ESR	Rothschild <i>et al.</i> (1996)
Sheep	Leptin	LEP	Erhardt and Weimann
	Spider lamb syndrome	DQA2	(2007)
	Complex vertebral malformation	SLC35A3	

genetic backgrounds and environments. Quantitative trait loci (QTL) identified in one population might exhibit different effects in another because of recombination, genotype-environment interactions, or variations in linkage disequilibrium patterns. This diminishes the dependability of MAS when utilized among various breeding populations. Markers associated with economically significant traits might lose their predictive capacity if the connection between the marker and the causal gene is weak or interrupted. As a result, validating across various populations and settings is essential but requires significant time (Naeem *et al.*, 2026). Another challenge is the variability in QTL estimates, where QTL effects vary between years or populations, undermining confidence in selection decisions based on markers. Since MAS depends on a small set of markers linked to significant genes, it tends to be less efficient for polygenic traits affected by numerous loci with minor impacts, which are prevalent in livestock production traits (Wakchaure *et al.*, 2015).

While MAS can enhance selection efficiency, the significant expenses related to genotyping, marker development and validation continue to pose a substantial obstacle, particularly in developing nations where breeding initiatives frequently function with restricted financial and technical resources. These financial limitations hinder smallholder farmers and public breeding programs from adopting MAS, consequently diminishing its overall effect on developing livestock production systems (Verma *et al.*, 2025). The advancement of high-density SNP arrays and genome-wide prediction models, genomic selection (GS) has significantly outperformed MAS in enhancing complex quantitative traits. Marker-assisted selection (MAS) is less effective than genomic selection for improving complex quantitative traits because it relies on a limited number of markers linked to major genes, whereas genomic selection uses genome-wide marker information to capture a larger proportion of genetic variation and achieve higher prediction accuracy (Meuwissen *et al.*, 2001; Dekkers, 2004 and Naeem *et al.*, 2026).

Future perspectives of marker assisted selection

Understanding the genes responsible for trait expression enables researchers to explore novel allele combinations for enhancing desirable traits, as such combinations may not naturally exist in production populations (Williams, 2005). Selective breeding strategies using marker-assisted selection (MAS) can evaluate these interactions to improve genetic traits. Integrating advanced technologies like genomic sequencing, gene editing and data analytics enhances MAS accuracy and effectiveness, supporting optimal reproductive performance (Soller, 1994). MAS is expanding into fields like aquaculture and unconventional breeding, improving productivity, disease resistance and adaptability in lesser-studied species (Dodgson *et al.*, 1997). For MAS to fulfill its potential, ethical and regulatory frameworks must evolve alongside technological advances, ensuring biosafety, food security and public acceptance

(Gao *et al.*, 2020). Transparent policies and interdisciplinary efforts are essential to address societal concerns. The future of MAS lies in its integration with genomic tools, the selection of complex traits and broader species application. Addressing current challenges such as cost, access and ethical issues will be vital for making MAS a more sustainable and efficient tool in modern breeding programs (Hasan *et al.*, 2021).

CONCLUSION

Genetic improvement of animals is a very crucial and complex process. When incorporated with traditional selection methods, MAS has been proved to be a valuable aid in selecting animals with desirable traits. In order for MAS to be devised successfully, certain issues such as identification of traits for selection. Successfully implementing MAS requires addressing several challenges, including identifying the traits to be selected and their economic significance, the limited knowledge of the genes or markers linked to these traits and understanding how these traits are associated with other important selection criteria. In the future, for MAS to be successful in large-scale breeding programs, the development of affordable, large-scale genotyping technologies and supporting infrastructure will be essential, thereby further enhancing livestock productivity, sustainability and disease management in animal breeding programs.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

Since this is a review article so, there is no use of animal procedures for experiments.

Conflict of interest

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