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Impact of Marker Assisted Selection (MAS) on economy of production trait in animals: A review

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Abstract

Genetic markers are beyond phenotypic marker because they are free from environment effect and hence aid us to evaluate breeding value of an individual. By finding genetic markers associated with disease resistance, desirable traits (like high milk yield or lean meat), and preserving genetic diversity in endangered breeds, Marker-Assisted Selection (MAS) in animals improves breeding. Only just by selecting superior animals, the production traits can be improved as there is shift in population mean and hence, selection is considered powerful tool of a breeder. Genetic markers aid us to decipher true potential of an animal which is not measured phenotypically. Moreover, when the MAS is studied, there is always a question of its applicability at farmer level. Hence, this article is discussing in detail about MAS, its applications and limitations. Genetic markers are beyond phenotypic marker because they are free from environment effect and hence aid us to evaluate breeding value of an individual. Marker-assisted selection (MAS) in animals improves precision breeding by identifying genetic markers associated with disease resistance, economically significant traits (like high milk yield or lean meat production), and the preservation of genetic diversity in endangered breeds. Breeders can choose better animals based on their genetic potential using MAS, as opposed to traditional methods that only consider observable traits. This results in an increase in the population mean and better production traits over successive generations. Selection is therefore one of the most effective weapons a breeder can use. Furthermore, genetic markers assist in determining an animal's true genetic value, which may not be fully manifested phenotypically because of interactions with the environment. Notwithstanding its benefits, there are still concerns regarding the cost, accessibility, and technical viability of MAS's actual application at the farmer level. This article explores the fundamentals of MAS, the various ways it can be used in animal breeding, and the obstacles preventing its broad use in actual farming situations.

Keywords: Genetic improvement, marker assisted selection, genotyping, gene mapping, quantitative trait loci

1. Introduction

Marker-Assisted Selection (MAS) is a biotechnology-driven breeding approach that uses molecular markers linked to desirable traits to accelerate and enhance the accuracy of genetic improvement in plants and animals [13]. By identifying and selecting individuals with specific DNA sequences associated with traits such as disease resistance, productivity, or quality, MAS enables breeders to make more informed decisions early in the selection process, reducing reliance on phenotypic evaluations alone [1]. It offers advantages such as increased efficiency, reduced breeding cycles and the ability to target complex traits controlled by multiple genes. MAS has become a valuable tool in modern breeding programs, complementing traditional methods to achieve sustainable agricultural advancements [2].

Genetic markers are heritable variations that follow Mendelian inheritance, such as coat color, which was historically used in livestock breeding (e.g., Hereford cattle, Belted Galloway cattle) [3]. Protein polymorphisms, like blood groups, later aided pedigree verification but proved limited due to rarity and detectability issues. The advent of DNA-based markers, particularly restriction fragment length polymorphisms (RFLPs), revolutionized genomic mapping by using restriction enzymes to cut DNA at specific sites, followed by gel electrophoresis and hybridization with labelled probes to detect variations [3].

RFLPs enabled targeted screening for genetic defects (e.g., BLAD in cattle) and individual identification via "genetic fingerprints" using variable number tandem repeats (VNTRs). However, early RFLP methods were slow and relied on radioactive probes, limiting their efficiency despite their utility in pedigree analysis and genetic mapping. There are major 2 approaches to study genes behind the trait.

1.1 Candidate gene approach for monogenic traits

Finding the genes governing simple monogenic traits entails speculating about potential genes by researching the physiology of the trait and the underlying biochemical pathways. Gene cloning can be facilitated by tissue-specific expression patterns and an understanding of similar genes from other species [4]. The relationship between these candidate genes' polymorphisms and the observed phenotypic variation is then examined. This method mainly depends on previous understanding of the biology of the trait or relevant research from other species. Candidate gene selection is more difficult for complex polygenic traits, though, because several genes some of which are not part of established biochemical pathways may contribute to phenotypic variation [5]. A genetic mapping method that isn't predicated on any physiological presumptions is frequently more successful in these situations.

1.2 Genetic Mapping and QTL Fine-mapping for complex traits

Major genes are located within broad chromosomal regions by combining phenotypic data with marker-assisted tracking of chromosomal inheritance in segregating families to map genes influencing a trait. These regions are identified by Quantitative Trait Loci (QTL) mapping and the candidate area is then narrowed by fine-mapping with additional markers and family lineages [6]. Recombination events aid in the refinement of QTL positions by examining identical-by-descent (IBD) genomic segments across generations. The region is cloned and sequenced to compare DNA between phenotypically different individuals in order to identify the causative genetic variation if no candidate gene is visible. This combined method connects accurate gene identification with early QTL detection [7].

2. Mechanisms of MAS in animal breeding

Marker-Assisted Selection (MAS) utilizes molecular markers to select animals with desirable genetic traits, enhancing the precision and efficiency of animal breeding programs. The mechanisms behind MAS involve several key steps that bridge molecular genetics and traditional breeding practices:

- **Identification of Genetic Markers:** The first step is to find DNA markers that are closely associated with quantitative trait loci (QTL) that affect economically significant traits like milk yield, growth rate, or feed efficiency. Examples of these markers include microsatellites, single nucleotide polymorphisms (SNPs), or insertions/deletions (indels) [8].
- **QTL Mapping:** To find the parts of the genome linked to desired traits, researchers use linkage analysis or genome-wide association studies (GWAS). This stage makes it possible to pinpoint the exact location of QTLs that cause phenotypic differences.
- **Genotyping of Animals:** Breeding animals are genotyped to find out which alleles they have at the marker loci after markers have been identified [9]. Time and money can be saved by using modern genotyping platforms that can evaluate thousands of markers at once.

- **Marker-Trait Association:** The genetic potential of an animal is predicted using markers that exhibit a strong correlation with the desired trait. Then, rather than depending only on observable traits (phenotypes) [10], selection decisions are made based on the presence or absence of advantageous alleles.

2.3 Integration with Breeding Programs

- MAS is integrated into breeding programs to:
- Select superior breeding stock at early age (e.g., at the embryo or young animal stage),
- Improve accuracy of selection
- Accelerate genetic gain by reducing the generation interval.

2.4 Selection Strategies: MAS can be used in:

- Introgression programs to introduce favorable alleles from one population to another
- Backcrossing to retain desired traits while recovering the background genome
- Pyramiding multiple QTLs to enhance complex traits like disease resistance or feed conversion efficiency.

3. Economic traits improved through MAS

By integrating molecular genetic information with conventional breeding, marker-assisted selection (MAS) in animals efficiently enhances a number of economically significant traits [11], increasing precision and speeding up genetic gain.

- **Milk production and composition:** MAS is frequently used to select genetic markers associated with these traits, which are otherwise influenced by the environment and have moderate heritability, in order to increase milk yield, protein content and fat percentage in dairy cattle.
- **Fertility and Reproductive Traits:** MAS has improved fertility traits such as bull fertility, litter size and reproductive efficiency. It is especially helpful for low heritability and sex-limited traits that are challenging to evaluate phenotypically [12, 23].
- **Growth and Carcass Traits:** By facilitating indirect selection based on markers connected to quantitative trait loci (QTLs), MAS has demonstrated improvements in growth rate [14], feed efficiency and carcass quality traits (such as marbling and tenderness in meat animals).
- **Disease Resistance:** By accurately identifying and selecting animals with genetic resistance to diseases, MAS offers financial advantages through lower veterinary expenses and morbidity [15].
- **Thermotolerance:** Cattle with increased resistance to heat stress have been bred using genetic markers connected to heat shock proteins, increasing productivity in arid environments.

4. Genotyping and Infrastructure Costs for Dairy Animals in India

- Although there is a lack of direct specific MAS genotyping cost data for dairy animals in Indian rupees (INR), comparable genotyping services in India can cost up to INR 450,000 for the sequencing technology used to genotype 96 samples, which translates to an approximate cost of INR 4,700 per sample, though costs can vary by provider and scale [16].
- In addition to genotyping costs, dairy farming infrastructure costs include Breeding (AI) costs of

approximately ₹2,500 for five services per buffalo and additional insurance costs of approximately ₹12,000 per animal per year. These inform budgetary considerations but are more related to general dairy breeding investments than MAS-specific infrastructure.

- In other countries, the cost of genotyping an animal varies greatly; for instance, in European programs with some early subsidies, the cost of a sample is €18 (roughly ₹1,600). This suggests that, if scaled and subsidized similarly, the costs of MAS genotyping in India could be competitive.

5. Economic Costs of Reproductive Problems in Indian Dairy Animals:

- Reproductive problems cause significant economic losses, estimated at approximately INR 2,425 (around USD 36) per dairy animal annually, which is about 4.1% of the average dairy animal value (INR 58,966).
- Major cost drivers include extended calving intervals due to repeat breeding and abortion, resulting in prolonged management costs for feed ^[17], labor and utilities, accounting for nearly half the total losses.
- Loss from salvage selling of unproductive animals and decreased milk production form other significant components of these costs.
- The economic burden is higher in states like Bihar (INR 2,912 per animal) compared to Assam (INR 1,060 per animal), reflecting differences in herd composition, management and reproductive health.
- These reproductive issues reduce fertility, milk yield and overall lifetime productivity, posing substantial cost impacts on dairy farmers in India.

6. Impact on Smallholder vs. Commercial production systems

Smallholder dairy farming adds resilience, food security and income to rural livelihoods. Smallholder farmers, on the other hand, usually have limited resources, animals with low genetic potential and a reliance on conventional feeding methods, all of which limit their capacity to quickly adopt cutting-edge technologies like MAS. On the other hand, commercial dairy production frequently entails bigger herd sizes, more stringent management and easier access to improved breeds ^[18], all of which enable more efficient use of MAS for genetic improvement. Although there are obstacles such as limited infrastructure and lower technical capacity, the use of MAS in smallholder systems can improve milk yield and reproductive characteristics ^[19]. Better integration of MAS with reproductive technologies and genomic selection results in higher genetic gains for commercial systems. The trends in herd composition also show the disparities in productivity, with improved buffalo and crossbred cattle predominating in commercial and peri-urban dairy production while native breeds continue to exist in smallholder systems with lower yields.

- **Affordability and Accessibility of MAS:** One of the main obstacles to smallholders' widespread adoption of MAS is still affordability. Smallholder farmers with limited resources find it challenging to obtain these advantages without subsidies or group programs due to the comparatively high costs of genotyping and the technological infrastructure needed for MAS. Small SNP panels are one example of an innovation that has been developed to improve potential uptake by lowering

testing costs and making it more accessible for small-scale farmers. Additionally, smallholder dairy farmers frequently experience poor veterinary service quality and a lack of technical support, while commercial dairy farmers typically have better access to veterinary, breeding and extension services that support MAS implementation ^[20]. Small-scale farmers also face greater barriers to credit and market connections, which restricts their capacity to invest in MAS technologies.

- **Economic Disparities and Scalability:** MAS scalability is impacted by the economic differences between commercial and smallholder dairy production systems. Due to their typically smaller herds (1-2 milk animals) and lower incomes, smallholders are less able to independently fund MAS-based breeding improvements. Commercial producers, on the other hand, are able to invest in genomics and infrastructure that support MAS because of their larger herds and higher incomes. The ability of MAS to close these gaps determines its scalability in the dairy industry of India. The growth of the nation's milk supply depends on the expansion of crossbred and improved buffalo herds with higher productivity. The development of cost-effective genotyping techniques, improved farmer training and strengthened institutional support for smallholders are all necessary to enable MAS scalability across all production scales. Collective breeding programs and cooperative models can also help distribute MAS benefits among smallholders by sharing costs and knowledge.

7. Challenges and Limitations of MAS in Economic Terms in animal production

- **High Cost of Genotyping and Infrastructure:** The high expense of animal genotyping and setting up the necessary infrastructure for extensive molecular data collection and analysis is one of the main financial limitations of MAS ^[21]. Because it is frequently too costly to genotype entire populations in commercial breeding programs, MAS use is restricted to subsets of animals or families within populations. The financial burden is further increased by expenses for sample collection, data management and computational resources, especially for smaller or resource-constrained breeding operations.
- **Cost-Benefit Trade-offs and Profitability:** When used for traits like disease resistance, fertility, or carcass quality that are costly, time-consuming, or difficult to measure phenotypically, MAS is more economical. Depending on the trait, MAS can boost genetic gain by 10% to 20%; however, unless the implementation is carefully optimized, the initial costs may exceed the short-term economic benefits. According to economic models, MAS schemes need to significantly increase genetic merit or decrease generation intervals in order to be financially viable.
- **Dependency on Marker-QTL Linkage and Trait Architecture:** Strong linkage disequilibrium between markers and quantitative trait loci (QTLs) is essential for MAS effectiveness. Recombination events may erode this connection over generations, decreasing the accuracy of MAS and possibly raising long-term expenses if new markers need to be continuously found and verified. Additionally, MAS works better for traits that are regulated by a small number of key QTLs. MAS's economic advantage over genomic selection or

conventional breeding is diminished by complex polygenic traits with small-effect loci that restrict its gains.

- **Limited Genetic Data and Accuracy:** The lack of complete genotypic and phenotypic data in many populations is a major economic constraint. The reliability of MAS for estimating breeding values is compromised by the lack of complete genotype data, which could result in an overestimation of QTL effects and lower economic returns ^[22]. Furthermore, uncertainty is introduced by the variation in QTL expression among populations and environments, which may reduce cost-effectiveness.
- **Scale and Resource Constraints:** Due to its high cost, MAS is less available to small-scale and resource-constrained breeders, which can aggravate economic inequality in the animal production industry. Due to herd size and organizational capacity, large-scale commercial operations are better able to absorb the investments required for MAS infrastructure and realize financial gains. This restricts the economic impact and scalability of MAS across various production systems.

8. Other Economic Challenges

- Managing the risk of inbreeding caused by intensive selection focused on a limited number of markers requires additional genetic management, which adds cost.
- Implementation requires skilled personnel and training, which can raise operational costs and delay adoption.
- Potential ethical and regulatory issues may introduce indirect economic costs related to public acceptance and market access.

9. Conclusion

A revolutionary development in animal breeding, Marker-Assisted Selection (MAS) uses molecular genetics to improve accuracy, productivity and genetic gain. Breeders can make early, data-driven selections by using MAS to find and use DNA markers associated with economically significant traits, such as growth performance, disease resistance and milk production, which lessens the need for phenotypic assessments alone. Modern approaches like SNP genotyping and QTL fine-mapping have improved MAS applications, enabling targeted introgression, trait pyramiding and accelerated breeding cycles, even though more conventional approaches like RFLPs established the groundwork for genomic mapping. MAS continues to support traditional breeding, providing long-term solutions for enhancing livestock productivity, resilience and overall agricultural sustainability, despite difficulties in identifying genes for complex polygenic traits.

Although there are obstacles to adoption, marker-assisted selection (MAS) presents a promising approach to improve dairy breeding in India. Accessibility is restricted by high genotyping costs and infrastructure requirements, particularly for resource-poor smallholder farmers. Commercial farms can use MAS more efficiently, but increasing its use calls for policy support, farmer training, and cost reductions. Long-term success is also impacted by issues like inbreeding risks, trait complexity, and gaps in genetic data. Affordably priced solutions and inclusive breeding initiatives are crucial for MAS to benefit India's diverse dairy industry. Small farmers might be left behind if its potential is limited to large-scale operations in the absence of these.

Conflict of Interest

Not available

Financial Support

Not available

Reference

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