BIOPENDIX: Jurnal Biologi, Pendidikan dan Terapan
Volume 13, Issue 2, October 2026
Pages: 125-134
https://doi.org/10.30598/biopendixvol13issue2page125-134
P-ISSN:2407-4969
E-ISSN:2684-8341

Original Article

Analysis of The Effectiveness of Marker-Assisted Selection (MAS) in Breeding High Yielding Plants

Nur Nazhifah Adyputri[1*], **Nanda Adrian Mursalim**[2], **Sri Mardawiyah**[3]
Yusminah Hala[4]

Departemen of Biology, Faculty of Mathematic and Natural Sciences Makassar State University, Makassar, Indonesia
**Corresponding author's e*-mail: yushala12@gmail.com

Submitted: March 26, 2026; Accepted:April 9, 2026; Available online: August 12, 2026; Published: October 31, 2026

Abstract. Global food security demands more precise and efficient plant breeding strategies to develop high-yielding varieties. Marker-Assisted Selection (MAS) is a molecular approach that utilizes genetic markers such as SSRs, SNPs, and InDels to identify superior genotypes from early growth stages. This study employs a Systematic Literature Review (SLR) method following PRISMA guidelines to analyze the effectiveness of MAS in enhancing crop productivity compared to conventional methods. Review results indicate that MAS can accelerate breeding cycles, improve selection accuracy, and support strategies such as foreground selection, background selection, and gene pyramiding across various commodities, including rice, maize, wheat, soybean, and alfalfa. Significant success is observed in improved disease resistance, abiotic stress tolerance, and yield stability. However, the implementation of MAS still faces challenges, including high operational costs, limited laboratory infrastructure, the complexity of quantitative traits, and the need for marker re-validation across different genetic backgrounds. Future prospects suggest that the integration of MAS with genomic selection, artificial intelligence, and CRISPR-Cas9 technology will strengthen data-driven predictive breeding systems. Consequently, MAS can be viewed as a strategic solution to accelerate the development of high-yielding superior varieties and support the global food security agenda.

Keywords: Marker-Assisted Selection (MAS); Plant Productivity; Molecular Breeding; Genetic Markers.

Check for updates
How to cite this article:
Adyputri, N. N., Mursalim, N. A., Mardawiyah, S., & Hala, Y. (2026). Analysis of the Effectiveness of Marker-Assisted Selection (MAS) in Breeding High-Yielding Plants. *BIOPENDIX*: *Jurnal Biologi, Pendidikan dan Terapan, 13*(2), 124-134. https://doi.org/10.30598/biopendixvol13issue2page125-134

Journal homepage: https://ojs3.unpatti.ac.id/index.php/biopendix
Journal e-mail: jbiopendix@gmail.com

INTRODUCTION

Global food security has become a paramount priority to meet the demands of a world population projected to reach unprecedented levels (Rajput et al., 2025). Ideally, plant breeding programs must significantly enhance Plant Productivity by developing high-yielding varieties resilient to various environmental stresses (Varshney et al., 2013). This is critical as the agricultural sector faces formidable challenges from climate change and land degradation, which threaten the stability of food production (Hafez et al., 2021). Increasing efficiency in identifying superior genotypes is an absolute prerequisite for accelerating breeding cycles and ensuring food availability for a rapidly expanding human population (Rajput et al., 2025).

Current realities indicate that the productivity of major food crops has tended to stagnate over the last five decades due to a reliance on conventional breeding methods (Varshney et al., 2013). These traditional methods possess significant limitations, as they depend heavily on phenotypic observations influenced by environmental variability and soil heterogeneity, which often mask the true genetic potential of the plant (Baidyussen et al., 2024; Schneider et al., 2026). Furthermore, the process of introgressing superior traits through conventional crossing is time-consuming, often taking years to stabilize desired characteristics (Rajput et al., 2025; Sathishkumar et al., 2025).

This productivity gap is driving a transition toward Molecular Breeding, which utilizes Genetic Markers as more precise and efficient selection tools. The primary mechanism of Marker-Assisted Selection (MAS) involves the use of DNA markers closely linked to quantitative trait loci (QTL) to identify high-yielding genotypes even at the seedling stage (Varshney et al., 2013; Sathishkumar et al., 2025). The utilization of molecular markers such as SSRs, SNPs, and InDels allows breeders to select for complex traits without waiting for plants to reach maturity or conducting extensive and costly field trials (Lin et al., 2024; Shen et al., 2026). Thus, a profound understanding of these marker utilization mechanisms is key to optimizing selection strategies for effective yield improvement (Rajput et al., 2025).

However, the effectiveness of MAS in significantly increasing Plant Productivity still faces major implementation challenges in the field. A problem statement arises regarding the extent to which this technology can truly surpass the efficiency of conventional methods, particularly in crops with complex genetic structures (Baidyussen et al., 2024). Technical hurdles such as linkage drag, high operational costs for genomic platforms like KASP, and the need for adequate laboratory facilities often limit technology adoption, especially in developing nations (Sathishkumar et al., 2025; Baidyussen et al., 2024). Moreover, low prediction accuracy for quantitative traits controlled by multiple genes remains a bottleneck in integrating MAS universally into practical breeding programs (Baidyussen et al., 2024).

Previous research has made significant contributions by identifying various genetic markers for disease resistance and drought tolerance in commodities such as rice, wheat, and legumes (Lin et al., 2024; Han et al., 2025; Varshney et al., 2013). For instance, MAS has successfully introduced virus resistance genes into rice without compromising primary yield components (Lin et al., 2024). Other studies have demonstrated the successful development of Near Isogenic Lines (NIL) in melons and watermelons to map specific traits relevant to plant resilience (Chen et al., 2025). Nonetheless, these successes are often confined to laboratory scales or specific commodities and frequently fail when applied in heterogeneous field environments (Baidyussen et al., 2024).

There is a distinct research gap where, despite thousands of molecular markers being reported in the literature, only a few have been successfully recommended for broad practical application. Many prior studies focus on the technical aspects of marker development without sufficient functional verification of gene expression under actual stress conditions. This gap creates a "paradox" where genomic technological advancements do not correlate linearly with productivity increases at the farmer level (Baidyussen et al., 2024). Consequently, a comprehensive evaluation is required to align academic findings with the practical needs of field plant breeding (Han et al., 2025).

Given these conditions, a Systematic Literature Review is urgently needed to analyze the comprehensive effectiveness of MAS in breeding high-yielding crops. The primary objective of this study is to evaluate the successful application of genetic markers in enhancing productivity and to identify key factors hindering their efficiency (Baidyussen et al., 2024). To achieve this, the study is formulated around two main questions: 1) What are the mechanisms of utilizing Genetic Markers within the Marker-Assisted Selection (MAS) technique as a Molecular Breeding approach to identify and select high-yielding genotypes?, and 2) To what extent is the effectiveness of MAS in significantly increasing Plant Productivity compared to conventional methods, and what are the primary challenges in its application? By synthesizing data from various literature sources, this study will map the most effective and sustainable strategies, including the use of more affordable yet accurate alternative methods (Sathishkumar et al., 2025).

This systematic review serves as a crucial step in consolidating fragmented knowledge into practical guidelines for researchers and breeding practitioners (Han et al., 2025). The contribution of this study is expected to provide a strategic roadmap for the development of superior varieties to support future food security agendas. Theoretically, this study will enrich the literature on the correlation between molecular markers and tangible yield increases across diverse environments (Baidyussen et al., 2024). Practically, the results of this review will assist plant breeders in selecting appropriate technology platforms to minimize selection failure risks and reduce operational costs (Sathishkumar et al., 2025). Ultimately, this study aims to bridge the gap between molecular innovation and practical application, ensuring that modern breeding technology can deliver a real impact on global Plant Productivity (Rajput et al., 2025).

MATERIALS AND METHODS

This study employs a Systematic Literature Review (SLR) method adhering to the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines as outlined, complemented by a descriptive qualitative approach. A comprehensive literature search was conducted across several scientific databases, including Scopus, Web of Science, ScienceDirect, SpringerLink, PubMed, and Google Scholar, using the keywords “Marker-Assisted Selection”, “MAS”, “plant productivity”, and “genomic selection” for the 2022–2026 publication range. All search results were exported to a reference manager to remove duplicates (identification stage), followed by screening through titles and abstracts to exclude articles irrelevant to the focus of MAS in high-yielding plant breeding. Articles passing the screening phase underwent a full-text review to ensure eligibility, and the final inclusion stage determined the appropriate articles as primary sources for analysis. Data from the selected articles were subsequently synthesized using a descriptive qualitative technique to identify the effectiveness of MAS in enhancing crop yields, the types of markers utilized, target crops, and the prospects and challenges of implementing MAS in sustainable breeding programs.

RESULTS AND DISCUSSION

The results of the analysis of the effectiveness of marker-based selection (Marker-Assisted Selection/MAS) in breeding high-yielding plants have been studied by several researchers and are presented in Table 1.

Table 1. Summary of molecular marker applications and key findings across various crop species (2021–2026).

No.	Researcher	Research Title	Results	Year
1	S. Arockiasamy, et al.	Breeding and biotechnological efforts in Jatropha curcas L. for sustainable yields	Developed a high-density linkage map and identified 83 QTLs for yield and oil content, plus 3 minor QTLs for JMV resistance.	2021
2	J. Borella, et al.	Resistance to orange rust associated with the G1 molecular marker in parents of Brazilian RB sugarcane varieties	Validated G1 marker in 63 sugarcane lines with 71% selection accuracy for orange rust resistance in the field.	2022
3	Ahmed Mahmoud, et al.	Integrated Bulk Segregant Analysis, Fine Mapping, and Transcriptome Revealed QTLs and Candidate Genes Associated with Drought Adaptation in Wild Watermelon	Identified two major QTLs (qNLR_Dr. Chr01 and Chr02) and genes regulating root adaptation under drought stress.	2024
4	Louis McLeod, et al.	Multi-environment association study highlights candidate genes for robust agronomic quantitative trait loci in a novel worldwide Capsicum core collection	Identified 114 high-confidence QTLs and 31 candidate genes regulating agronomic traits through multi-environment GWAS.	2023
5	Noel Ndlovu, et al.	Linkage mapping and genomic prediction of grain quality traits in	Mapped QTLs for grain quality and demonstrated that genomic prediction efficiently	2024

		tropical maize (Zea mays L.)	accelerates high-nutrition maize breeding.	
6	Aleksandra Noweiska, et al.	Multiplex PCR assay for the simultaneous identification of race specific and non-specific leaf resistance genes in wheat (Triticum aestivum L.)	Optimized 13 multiplex PCR protocols to simultaneously detect multiple leaf rust resistance genes (Lr19, Lr24, etc.).	2023
7	V. Sagwal, et al.	Discovery of miRNAs and development of miRNA-SSR markers in response to N and P use in wheat	Validated novel miRNA-SSR markers to differentiate wheat lines based on Nitrogen and Phosphorus utilization efficiency.	2022
8	Arun Kumar Singh, et al.	Improving blast resistance of maintainer line DRR 9B by transferring broad spectrum resistance gene Pi2 by marker assisted selection in rice	Successfully introgressed the Pi2 gene into maintainer line DRR 9B, enhancing blast resistance without compromising grain quality.	2023
9	Gagandeep Singh, et al.	Genetic Enhancement for Biotic Stress Resistance in Basmati Rice through Marker-Assisted Backcross Breeding	Developed Basmati lines (PB1509) by pyramiding genes against bacterial leaf blight and blast using MABC.	2023
10	Lovepreet Singh, et al.	Validation of DNA marker-assisted selection for forage biomass productivity under deficit irrigation in alfalfa	Validated markers for biomass productivity in Medicago sativa under deficit irrigation, highlighting donor allele effects.	2022
11	Wei Zhou, et al.	Integrative machine learning approach for identifying genes associated with quantitative traits: A soybean (Glycine max) yield case study	Used LightGBM algorithm to isolate predictive SNP markers and identify genes associated with soybean yield stability.	2026

Concepts of Marker-Assisted Selection (MAS) and Genetic Markers

Marker-Assisted Selection (MAS) is a plant selection method that utilizes DNA markers linked to target loci as a tool to predict plant phenotypes (Cahyo, 2023). This method aims to increase the efficiency of selection for agronomic traits that are difficult to observe visually (Abbas et al., 2017). Breeders can identify the presence of superior genes at very early stages of plant development, such as the seedling stage (Fitriyah & Siregar, 2025). This selection procedure offers significant advantages because it is not affected by environmental factors that often mask original genetic potential (Baidyussen et al., 2024). These technical advantages make MAS a primary strategy for accelerating the duration of plant breeding programs (Sathishkumar et al., 2025). The speed of this selection process is largely determined by the availability of genetic markers with a high level of accuracy in detecting target genes.

Genetic markers used in the MAS system include various types of molecular markers such as SSR, SNP, and InDel (Prayoga et al., 2022). Simple Sequence Repeats (SSR) markers are often chosen by researchers because they have a very high level of polymorphism (Prayoga et al., 2022). On the other hand, Single Nucleotide Polymorphism (SNP) markers have become the new standard in modern breeding because they are very abundant throughout the genome (Sathishkumar et al., 2025). In addition to SNPs, Insertion-Deletion (InDel) markers have also been shown to be effective in tracking the introgression of specific resistance genes in rice plants (Lin et al., 2024). These various types of molecular markers function as indicators of gene position on chromosomes during the crossing process (Manisa et al., 2026). The precise positioning of markers on the genetic map makes it easier for breeders to implement more specific selection strategies.

Selection strategies in MAS generally involve foreground selection techniques to ensure the presence of target genes in offspring (Lin et al., 2024). Additionally, breeders employ background selection to accelerate the recovery of the genetic background of desired parents (Chen et al., 2025). The simultaneous application of these two selection techniques can drastically increase genetic gain in a shorter time (Fitriyah & Siregar, 2025). The integration of genetic marker technology also facilitates the combination of several superior genes simultaneously, a process known as gene pyramiding (Prayoga et al., 2022). Therefore, mastering the concepts of MAS and genetic markers is a crucial step in producing high-yielding plant varieties (Cahyo, 2023).

Marker-Assisted Selection (MAS) Mechanism in Increasing Crop Productivity

The MAS mechanism for increasing productivity begins with the identification of quantitative trait loci (QTL) that control yield components (Baidyussen et al., 2024). Breeders conduct genetic mapping to find molecular markers located very close to target genes on chromosomes (Manisa et al., 2026). This process allows early detection of plants carrying potential genes for high yields without having to wait for the harvest phase (Fitriyah & Siregar, 2025). The use of these DNA markers provides much higher accuracy because genetic data is stable and not affected by environmental fluctuations (Luca et al., 2024). Through this precise selection mechanism, breeders can discard unproductive genotypes early in the laboratory (Cahyo, 2023). The integration of these markers in parent selection is a crucial initial step before carrying out further crossing procedures.

Once the target marker is identified, the next step is the application of Marker-Assisted Backcrossing (MABC) to transfer superior genes into commercial varieties (Lin et al., 2024). This strategy involves foreground selection to maintain the presence of the target gene from the donor parent in each generation of the cross (Lin et al., 2024). Simultaneously, breeders apply background selection to restore the entire genome of the recipient parent to maintain its original agronomic traits (Lin et al., 2024). The use of molecular markers in this process drastically reduces the number of backcross generations required compared to conventional methods (Sathishkumar et al., 2025). The success of gene introgression through MABC has been shown to increase plant resistance to biotic stresses, directly securing yield potential (Lin et al., 2024). The efficiency of this gene transfer is then enhanced by techniques that combine multiple genetic advantages simultaneously.

A more complex productivity improvement mechanism is implemented through gene pyramiding techniques to combine multiple yield-controlling genes into a single genotype (Abbas et al., 2017). This technique allows the accumulation of various resistance and productivity genes derived from different parental sources. Breeders monitor the presence of each marker representing these genes through PCR analysis in the laboratory (Prayoga et al., 2022). This approach ensures that new varieties have dual protection against pests and diseases while also having maximum production capacity (Abbas et al., 2017). Ultimately, this entire series of MAS mechanisms can significantly accelerate the achievement of genetic progress (genetic gain) compared to phenotype-based breeding (Fitriyah & Siregar, 2025). In Figure 1 you can see a flow diagram of genome-based plant breeding.

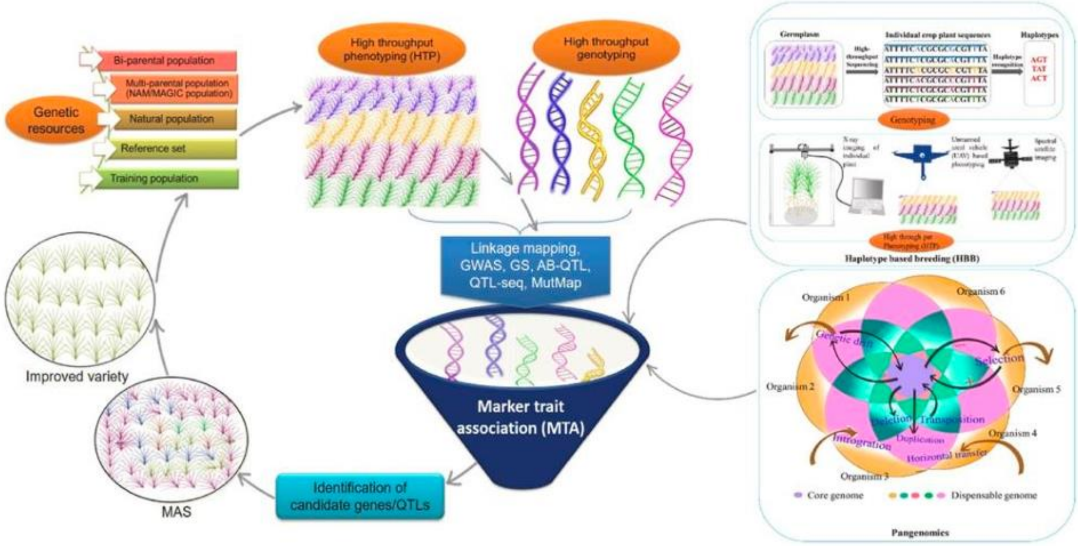
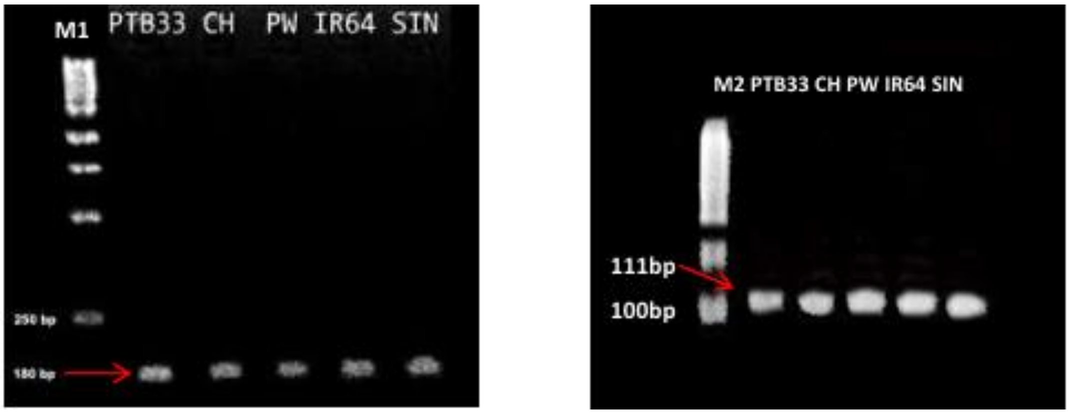


Figure 1. Flowchart of genome-assisted plant breeding.
(Source: Manisa et al, 2026)

Analysis of the Effectiveness of Marker-Assisted Selection (MAS) for High-Yielding Crops

The effectiveness of MAS in creating high-yielding plants is measured by its ability to significantly increase genetic gain (Fitriyah & Siregar, 2025). The application of this method has been proven to reduce costs and time required in the plant breeding program cycle. The analysis of this effectiveness is based on the strong level of linkage *disequilibrium (* LD) between markers and causative genes (Luca et al., 2024). The use of precise molecular markers allows breeders to select complex yield traits with a higher level of accuracy than visual selection (Baidyussen et al., 2024). This success is seen in the accelerated development of superior varieties that have yield stability under various environmental conditions (Prasetya et al., 2025). This increase in selection accuracy is highly dependent on the selection of the type of molecular marker that is most representative of the plant genome.

Selection accuracy in high-yielding breeding programs is greatly influenced by the abundance and distribution of markers such as *Single Nucleotide Polymorphisms* (SNPs) within the genome (Sathishkumar et al., 2025). SNP markers are considered highly effective because they can be analyzed rapidly through *high-throughput platforms* at a relatively affordable cost (Sathishkumar et al., 2025). Furthermore, the use of molecular markers allows for the precise identification of homozygous and heterozygous plants in the early generations of crosses (Manisa et al., 2026). This technical effectiveness provides breeders with assurance that high-yielding traits are maintained throughout the gene introgression process (Lin et al., 2024). This superior genotype differentiation automatically minimizes the risk of selection failure due to phenotypic observation errors in the field (Prayoga et al., 2022). This genetic certainty then becomes the primary basis for evaluating the final yield performance of selected plants. The DNA banding profile resulting from amplification using SSR markers in five rice cultivars can be seen in Figure 2.



(a) (b)

Figure 2. DNA band profile resulting from amplification using SSR markers in five rice cultivars.

(Source: Prayoga et al, 2022)

The implementation of MAS has also demonstrated remarkable effectiveness in transferring resistance genes, indirectly securing maximum yield potential (Lin et al., 2024). The gene pyramiding technique, assisted by molecular markers, has been shown to combine multiple yield-controlling genes into a single cultivar (Abbas et al., 2017). Through this approach, the resulting varieties not only have high yields but also exhibit resistance to pests and diseases (Prayoga et al., 2022). Operationally, the MAS method can reduce the duration of annual plant breeding from decades to a much shorter time (Cahyo, 2023). Therefore, a comprehensive analysis indicates that MAS is the most effective solution to address the challenge of stagnant global food crop productivity (Baidyussen et al., 2024).

Challenges and Limitations of Using Marker-Assisted Selection (MAS)

The use of *Marker-Assisted Selection* (MAS) in breeding programs still faces significant challenges related to high initial operational investment costs. The cost of introducing resistance genes into selected lines through MAS is often considered prohibitively expensive for institutions with limited budgets. This limitation is even more pronounced when breeders use KASP-based genotyping methods, which require expensive laboratory equipment (Sathishkumar et al., 2025). In addition to financial challenges, the effectiveness of MAS is also severely limited by the availability of markers that are strongly linked to the target trait (Baidyussen et al., 2024). These technical challenges mean that the selection process does not always produce the expected accuracy in every plant population (Baidyussen et al., 2024). Therefore, economic and technical factors are major obstacles to the widespread adoption of MAS technology in developing countries.

Another technical limitation relates to the genetic complexity of quantitative traits controlled by numerous minor genes (Fitriyah & Siregar, 2025). MAS has low effectiveness when used to select traits that are strongly influenced by non-linear genetic interactions and epistasis (Fitriyah & Siregar, 2025). Furthermore, genetic recombination can cause linkages between molecular markers and target genes to be broken during the crossing process (Manisa et al., 2026). This problem often forces breeders to revalidate markers used in different genetic backgrounds (Baidyussen et al., 2024). These constraints indicate that MAS cannot fully replace the role of phenotypic evaluation under highly diverse environmental conditions (Luca et al., 2024). The inability of markers to predict all genetic variation requires integration with more sophisticated technological approaches.

Operational challenges also arise in terms of the need for information technology infrastructure and bioinformatics expertise to manage genomic data (Fitriyah & Siregar, 2025). Reliance on standard laboratory facilities often hinders the acceleration of genotype analysis on a large population scale (Sathishkumar et al., 2025). Furthermore, the limited number of functional markers for perennial crops makes the selection process require a long validation time (Cahyo, 2023). Breeders often face constraints regarding interspecific sexual compatibility, which limits the source of superior genes that can be transferred through MAS (Abbas et al., 2017). The low availability of dense genetic maps for some local commodities also poses a serious obstacle to the effectiveness of marker-based selection (Manisa et al., 2026). Overall, the integration of cost, genetic diversity, and infrastructure remains a central issue in the development of high-yielding varieties in the future (Fitriyah & Siregar, 2025). The DNA banding profile resulting from amplification using SSR markers in five rice cultivars can be seen in Figure 3.

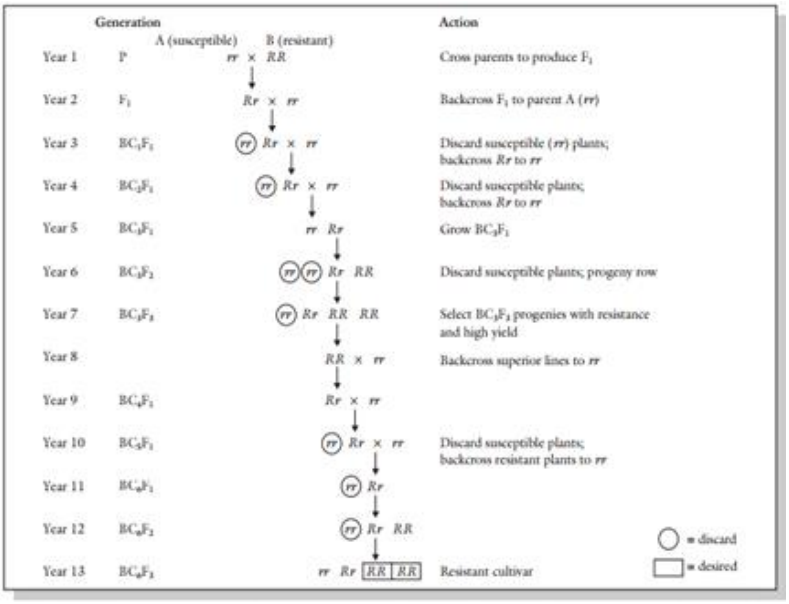


Figure 3. DNA band profile resulting from amplification using SSR markers in five rice cultivars.
(Source: Manisa et al, 2026)

Future Prospects of Molecular Breeding

The future prospects of molecular breeding point to a paradigm shift from conventional methods to predictive breeding strategies (Fitriyah & Siregar, 2025). This transformation is driven by the integration of molecular marker technology with artificial intelligence (Fitriyah & Siregar, 2025). The use of large-scale genomic data allows breeders to predict an individual's genetic potential with a higher degree of accuracy (Prasetya et al., 2025). This future technology is designed to address various environmental constraints caused by global warming, which increasingly threaten food security (Cahyo, 2023). Therefore, the development of future crop varieties will depend heavily on the ability of computing systems to process genetic information (Fitriyah & Siregar, 2025). Advances in data processing will strengthen the effectiveness of selection through a more comprehensive genomic selection approach.

The implementation of Genomic Selection (GS) is predicted to become the new standard to overcome the limitations of traditional MAS methods (Fitriyah & Siregar, 2025). This strategy allows breeders to predict individual breeding outcomes without the need for repeated marker validation in each generation (Fitriyah &

Siregar, 2025). Furthermore, the use of cheaper and more efficient SNP genotyping platforms will facilitate the adoption of molecular technology by various research institutions (Sathishkumar et al., 2025). Technological innovations such as CRISPR-Cas9 will also be synergized with molecular markers to produce specific mutations that benefit plant productivity (Abbas et al., 2017). The combination of these cutting-edge technologies aims to create a faster and more precise breeding ecosystem (Fitriyah & Siregar, 2025). This technological synergy will ultimately lead to the concept of data-driven intelligent breeding.

The concept of data-driven smart breeding will be a key pillar in producing superior cultivars that are adaptive to climate change. Future breeding will integrate genomic data with high -throughput phenotyping. This hybrid approach is expected to increase genetic progress many times over compared to traditional methods (Fitriyah & Siregar, 2025). Digital management of genetic resources will also facilitate the identification of rare genes with high yield potential (Prasetya et al., 2025). With the support of adequate technological infrastructure, molecular breeding will continue to evolve into a fundamental solution for global food security (Baidyussen et al., 2024).

ACKNOWLEDGEMENTS

The author would like to express his gratitude to all parties who are friends who have contributed ideas and thoughts in writing the systematics of literature in this manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest and take full responsibility for the content of the article, including the implications of AI-generated content

CONCLUSION

Marker-Assisted Selection (MAS) is a molecular approach capable of accelerating and increasing the accuracy of high-yielding plant breeding. The mechanism of MAS operates through the identification of Quantitative Trait Loci (QTL) and the utilization of genetic markers, such as SSR, SNP, and InDel, to detect target genes during the early growth stages. Foreground selection strategies ensure the presence of superior genes, while background selection accelerates the recovery of the recipient parent's genome, and gene pyramiding facilitates the simultaneous integration of multiple resistance and productivity genes.

Compared to conventional methods, MAS has proven more effective by reducing breeding durations from decades to just a few generations, enhancing yield stability across diverse environmental conditions, and minimizing field testing costs. Significant success has been demonstrated in major commodities, including rice, maize, wheat, soybean, and alfalfa, where MAS has successfully improved disease resistance, abiotic stress tolerance, and biomass productivity.

However, the application of MAS still faces substantial challenges, such as high operational costs, limited laboratory infrastructure, the genetic complexity of quantitative traits controlled by numerous minor genes, and the necessity for marker re-validation across different genetic backgrounds. Furthermore, genetic recombination phenomena and the limited availability of dense genetic maps for local commodities remain significant obstacles. Consequently, while MAS is highly effective, it cannot yet fully replace phenotypic evaluations in the field. Future prospects indicate that integrating MAS with genomic selection, artificial intelligence, and CRISPR-Cas9 technology will provide a strategic solution to overcome these limitations while strengthening data-driven predictive breeding systems. Thus, MAS serves as a vital bridge toward sustainable smart breeding, supporting the global food security agenda amidst climate change and the growing needs of the world population.

REFERENCES

Abbas, B., Mawikere, NL, Dasnarebo, SSH, Yuliati, TI, Kurung, S., Rumi, HS (2025). *Textbook of Biotechnological Perspectives in Plant Breeding.* Cirebon: Greenbook Publishing Indonesia.

Arockiasamy, S., Kumpatla, J., Hadole, S., Yepuri, V., Patil, MS., Shrivastava, V., Rao, J., Kancharla, N., Jalali, S., Varshney, A., Madan, NS, Pothakani, S., Nair, V., Peyyala, S., Kumar, A., Gomaruri, A. NS, Pachiyannan, J., Seelamanthula, S., … Dasgupta, S. (2021). Breeding and biotechnological efforts in Jatropha curcas L. for sustainable yields. *Oil Crop Science*, *6*(4), 180–191. https://doi.org/10.1016/j.ocsci.2021.10.004

Baidyussen, A., Khassanova, G., Utebayev, M., Jatayev, S., Kushanova, R., Khalbayeva, B., Amangeldiyeva, A., Yerzhebayeva, Y., Bulatova, K., Schramm, C., Anderson, P., Jenkins, C. L. D., Soole, K. L., & Shavrukov, Y. (2024). Assessment of molecular markers and marker-assisted selection for drought tolerance in barley (*Hordeum vulgare* L.). *Journal of Integrative Agriculture*, *23*(1), 20–38. https://doi.org/10.1016/j.jia.2023.06.012

Borella, J., Brasileiro, B. P., de Azeredo, A. A. C., Ruaro, L., de Oliveira, R. A., & Bespalhok Filho, J. C. (2022). Resistance to orange rust associated with the G1 molecular marker in parents of Brazilian RB sugarcane varieties. Genetics and Molecular Research, 21(1). https://doi.org/10.4238/gmr18980

Cahyo, AN (2023). The Importance of Marker-Assisted Selection Application in the Selection of Drought-Tolerant Rubber Clones. *Warta Perkaretan, 42*(2). https://doi.org/10.22302/ppk.wp.v42i2.939

Chen, Y., Zhou, Y., Yan, W., Li, Q., Liang, X., Wang, J., Cao, L., Zhang, X., Liu, Y., Mao, W., Luo, C., Li, Development of near isogenic lines for the glabrous gene *Cmgl* by marker assisted selection and transcriptome analysis in melon. *Scientia Horticulturae*, *353*, 114505. https://doi.org/10.1016/j.scienta.2025.114505

Fitriyah, F & Siregar, HA (2025). Transforming Oil Palm Plant Breeding Through Genomic Selection and Artificial Intelligence Towards Data-Driven Smart Breeding. *Warta PPKS,* 30(3), 197-210. https://doi.org/10.22302/iopri.war.warta.v30i3.242

Hafez, M., Mohamed, A. E., Rashad, M., & Popova, A. I. (2021). The efficiency of application of bacterial and humic preparations to enhance of wheat (*Triticum aestivum* L.) plant productivity in the arid regions of Egypt. *Biotechnology Reports*, *29*, 1-5. https://doi.org/10.1016/j.btre.2020.e00584

Han, G., Yan, H., Li, L., & An, D. (2025). Advancing wheat breeding using rye: A key contribution to wheat breeding history. *Trends in Biotechnology*, *43*(9), 2170–2182. https://doi.org/10.1016/j.tibtech.2025.03.008

Lin, F., Jing, D., Zhang, J., Sun, Y., Du, L., Li, C., Lan, Y., & Zhou, T. (2024). Introgression of *OsAP47* by marker-assisted selection enhanced resistance against southern rice black-streaked dwarf virus disease. *Virology*, *594*, 110060. https://doi.org/10.1016/j.virol.2024.110060

Luca, L. P., Guardio, M. D., Bennici, S., Ferlito, F., Nicolosi, E., Malfa, S. L., Gentile, A., Distefano, G. (2024). Development of An Efficient Molecular-Marker Assisted Selection Strategy For Berry Color In Grapevine. *Scentia Horticulturae, 337,* 1-8. https://doi.org/10.1016/j.scienta.2024.113522

Mahmoud, A., Qi, R., Chi, X., Liao, N., Malangisha, G. K., Ali, A., Moustafa-Farag, M., Yang, J., Zhang, M., & Hu, Z. (2024). Integrated Bulk Segregant Analysis, Fine Mapping, and Transcriptome Revealed QTLs and Candidate Genes Associated with Drought Adaptation in Wild Watermelon. *International Journal of Molecular Sciences*, 25(1). https://doi.org/10.3390/ijms25010065

McLeod, L., Barchi, L., Tumino, G., Tripodi, P., Salinier, J., Gros, J., Boyaci, H.F., Özalp, R., Borovsky, Y., Schafleitner, R., Barchenger, D.W., Finkers, R., Brouwer, M., Stein, N., Rabance-Wallace, G.M., Giuliano, G.M. Voorrips, R.E., Paran, I., & Lefebvre, V. (2023). Multi-environment association study highlights candidate genes for robust agronomic quantitative trait loci in a novel worldwide Capsicum core collection. *Plant Journal* , 116(5), 1508–1528. https://doi.org/10.1111/tpj.16425

Manisa, T., Zuyasna, Saniaty, A., Sapareng, S. (2026). *Introduction to Plant Genetics.* Padang: CV Hey Publishing Indonesia

Ndlovu, N., Kachapur, R. M., Beyene, Y., Das, B., Ogugo, V., Makumbi, D., Spillane, C., McKeown, P. C., Boddupalli, P. M., & Gowda, M. S. (2024). Linkage mapping and genomic prediction of grain quality traits in tropical maize (*Zea mays* L.). *Frontiers in Genetics*, 15. https://doi.org/10.3389/fgene.2024.1353289

Noweiska, A., Bobrowska, R., Spychała, J., Tomkowiak, A., & Kwiatek, M. T. (2023). Multiplex PCR assay for the simultaneous identification of race specific and non-specific leaf resistance genes in wheat (*Triticum aestivum* L.). *Journal of Applied Genetics*, *64*(1), 55–64. 10.1007/s13353-022-00745-5

Prasetya, MGA, Hayati, SA, Khuzniah, A., Hamdiyah, Aulia, A., & Sasmita, TD (2025). Integrating Molecular Breeding, Plant Biotechnology, and Genetic Resource Management to Support Food Security under Climate Change: A Systematic Literature Review. *Indonesian Journal of Multidisciplinary Studies*, 1(3)

Prayoga, GI, Sari, S., Dono, D., & Carsono, N. (2022). Correlation Analysis of Simple Sequence Repeats Molecular Markers with Brown Planthopper Resistance Characteristics in Five Rice Cultivars. *Journal of Agriculture, 33*(3), 331-341. https://doi.org/10.24198/agrikultura.v33i3.41024

Rajput, R., Boone, B. A., Mandlik, R., Islam, M. T., Qi, Y., Wang, J., Barrangou, R., Sozzani, R., Eckert, C. A., Tuskan, G. A., Chen, J. G., & Yang, X. (2025). Multigene engineering in plants: Technologies, applications, and future prospects. *Biotechnology Advances*, *85*, 1 - 17.https://doi.org/10.1016/j.biotechadv.2025.108697

Sagwal, V., Sihag, P., Singh, Y., Mehla, S., Kapoor, P., Balyan, P., Kumar, A., Mir, R. R., Dhankher, O. P., & Kumar, U. (2022). Development and characterization of nitrogen and phosphorus use efficiency responsive genic and miRNA derived SSR markers in wheat. *Heredity,* 128(6), 391–401. https://doi.org/10.1038/s41437-022-00506-4

Sathishkumar, R., Darpan Mohanrao, M., Geethanjali, S., Santha Lakshmi Prasad, M., & Senthilvel, S. (2025). A simple and cost-effective SNP genotyping assay for marker-assisted selection of wilt resistance in castor breeding. *Industrial Crops & Products*, *226*, 1-11. https://doi.org/10.1016/j.indcrop.2025.120693

Schneider, H. M., Ben-Gal, A., Furtado, B., Cicek, N., Dalmaris, E., Atzori, G., & Bazihizina, N. (2026). Going underground: The importance of soil heterogeneity in shaping plant productivity and responses to saline soils. *Environmental and Experimental Botany*, *243*, 1 - 10. https://doi.org/10.1016/j.envexpbot.2026.106321

Shen, J., Ye, Y., Zhou, Y., & Rong, X. (2026). Genomic SSR markers elucidate genetic architecture and phenotypic trait associations in *Rhododendron* Linnaeus. *Journal of Genetic Engineering and Biotechnology*, *24*(1), 1-11. https://doi.org/10.1016/j.jgeb.2025.100631

Singh, A. K., Revathi, P., Srinivas Prasad, M., Sundaram, R. M., Hari Prasad, A. S., Senguttuvel, P., Kempa Raju, K. B., & Sruthi, K. (2023). Improving blast resistance of maintainer line DRR 9B by transferring broad spectrum resistance gene Pi2 by marker assisted selection in rice. Physiology and Molecular Biology of Plants, 29(2), 253–262. https://doi.org/10.1007/s12298-023-01291-y

Singh, G. P. I., Singh, N., Ellur, R. K., Balamurugan, A., Prakash, G., Rathour, R., Mondal, K. K., Bhowmick, P. K., Gopala Krishnan, S., Nagarajan, M., Seth, R. K., Vinod, K. K., Singh, V. P., Bollinedi, H., & Singh, A. K. (2023). Genetic Enhancement for Biotic Stress Resistance in Basmati Rice through Marker-Assisted Backcross Breeding. *International Journal of Molecular Sciences*, *24*(22).1 - 18. https://doi.org/10.3390/ijms242216081

Singh, L., Pierce, C. A., Santantonio, N., Steiner, R. L., Miller, D., Reich, J., & Ray, I. M. (2022). Validation of DNA marker-assisted selection for forage biomass productivity under deficit irrigation in alfalfa. *Plant Genome*, *15*(1). 1-14. https://doi.org/10.1002/tpg2.20195

Varshney, R. K., Mohan, S. M., Gaur, P. M., Gangarao, N. V. P. R., Pandey, M. K., Bohra, A., Sawargaonkar, S. L., Chitikineni, A., Kimurto, P. K., Janila, P., Saxena, K. B., Fikre, A., Sharma, M., Rathore, A., Pratap, A., Tripathi, S., Datta, S., Chaturvedi, S. K., Mallikarjuna, N., ... & Gowda, C. L. L. (2013). Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. *Biotechnology Advances*, *31*(7), 1120–1134. https://doi.org/10.1016/j.biotechadv.2013.01.001

Zhou, W., Ouyang, H., Yan, Z., Song, J., Li, Y., Tang, Z., & Zhao, C. (2026). Integrative machine learning approach for identifying genes associated with quantitative traits: A soybean (Glycine max) yield case study. *Plant Genome*, *19*(1). 1-25. https://doi.org/10.1002/tpg2.70178