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Marker Assisted Introgression to Develop New Generation Varieties in Crop Plants

Godwin Gilbert J.[1*], *Jaya Anjana Sunil*[1] *and K. Indira Petchiammal*[2]
[1]*Ph.D. Scholar, Division of Genetics and Plant Breeding, KITS, (Coimbatore), India.*
[2]*Assistant Professor and Head, Division of Genetics and Plant Breeding, KITS, (Coimbatore), India.*

(Corresponding author: Godwin Gilbert J.)*
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ABSTRACT: The growing global population and changing environmental conditions have intensified the demand for high-yielding, stress-resilient, and nutritionally enhanced crops. Conventional breeding, though historically impactful, is limited by dependence on phenotypic selection, long breeding cycles, and challenges in improving complex, low-heritability traits. Marker-assisted introgression (MAI) has emerged as a precise and efficient molecular breeding strategy to overcome these limitations. MAI enables the targeted transfer of genes or quantitative trait loci (QTLs) from donor lines into elite cultivars while retaining the desirable genetic background of the recurrent parent. The strategy relies on molecular markers, including functional markers, SNPs, SSRs, and multi-locus panels, to track alleles accurately, minimize linkage drag, and accelerate breeding cycles. MAI has been successfully applied across major crops, including rice, maize, wheat, and peanut, for improving disease resistance, abiotic stress tolerance, yield potential, and quality traits. Functional markers and multi-marker approaches have enhanced the precision of introgression, particularly for complex traits governed by multiple genes. Integration of high-throughput genotyping, phenotyping, and knowledge of marker-trait associations ensures reliable selection under diverse environmental conditions. This review highlights the concepts, methodologies, influencing factors, applications, and advantages of MAI, emphasizing its critical role in modern crop improvement programs aimed at developing climate-resilient and high-performing cultivars.

Keywords: Marker-assisted selection, introgression, backcross breeding, QTL mapping, crop improvement.

INTRODUCTION

The global agricultural sector faces mounting pressure to meet the food and nutritional needs of an exponentially growing population while grappling with increasingly challenging environmental conditions. The demand for enhanced crop productivity, superior quality traits, and increased stress resilience remains constant. While conventional breeding methods have made significant contributions in the past, they are limited by several factors. These include the reliance on phenotypic selection, the lengthy breeding cycles, the difficulty in accurately selecting for low heritability traits, and the challenges in pyramiding multiple genes controlling complex traits. Furthermore, phenotypic performance is often influenced by environmental variability, which can hinder conventional approaches from accurately capturing the true genetic potential of crops, thereby limiting genetic gains over successive breeding cycles (Zhou *et al*., 2012).

The integration of molecular genetics into crop improvement has unveiled new avenues for overcoming these limitations. DNA-based molecular markers have emerged as reliable and indispensable tools, enabling breeders to pinpoint, map, and transfer genes linked to agronomic traits with precision. This precision facilitates the tracking of specific genomic regions and accelerates the selection process (Chung *et al*., 2017). Marker-assisted introgression (MAI) has emerged as a highly efficient breeding strategy from these applications. MAI allows the transfer of one or more target genes from a donor parent to a recipient parent while preserving the elite genetic background of the recurrent parent. This approach saves time and ensures the maintenance of agronomic superiority (Chhabra *et al*., 2019).

MAI plays a crucial role in achieving complex breeding objectives, including enhancing stress tolerance, improving grain quality, and introducing disease resistance. The identification of functional single nucleotide polymorphisms (SNPs) in regulatory genes linked to stress responses has facilitated the introgression of abiotic stress tolerance traits, such as drought resistance (Assenov *et al*., 2013). The development of functional markers for nutritional quality traits has also enabled breeders to enhance biofortification in staple crops. In maize, for instance, the introgression of alleles associated with enhanced β-carotene accumulation has been achieved. Zhou *et al*. (2012) and Chhabra *et al*. (2019) demonstrates how MAI can contribute to addressing hidden hunger and consumer preference traits. The success of MAI is not limited to maize but extends across major cereals including wheat and rice. In wheat, molecular markers have been effectively used to introgress resistance genes against devastating diseases such as stem rust (Periyannan *et al*., 2014), providing durable and broad-spectrum resistance to breeding lines. In parallel, the application of PCR-based markers has allowed the identification of transcription factors like *DREB1*, which are crucial for improving tolerance to multiple abiotic stresses (Huseynova, 2018). These advancements underscore the potential of MAI to simultaneously address both biotic and abiotic stresses, thereby ensuring stable yields under varying climatic conditions. Rice, a staple food for over half of the global population, has also significantly benefited from MAI. The introgression of genes associated with erect panicle architecture, such as EP, has resulted in improved yield potential by increasing the number of grains per panicle (Wang *et al*., 2009). The utilization of wide-compatibility genes like *S5n* has been instrumental in developing fertile inter-subspecific hybrids, thereby overcoming hybrid sterility barriers and enhancing heterosis in rice breeding (Xin *et al*., 2012).

These findings underscore the pivotal role of MAI in overcoming genetic bottlenecks and expediting the development of high-yielding varieties. In today's climate change era, crops face more frequent droughts, salinity stress, pest outbreaks, and fluctuating temperature regimes. Conventional approaches alone are inadequate to meet the rapid adaptation demands of breeding programs.

Breeders can efficiently monitor target gene introgression and minimize linkage drag by incorporating molecular markers into backcross breeding strategies. Advancements in genomics, high-throughput sequencing, and bioinformatics have refined this process, enabling the identification of functional gene-based markers directly associated with trait expression (Assenov *et al*., 2013). As breeding programs continue to evolve, MAI stands as a powerful strategy for bridging the gap between classical approaches and advanced genomics.

In maize, Zhou *et al*. (2012) and Chhabra *et al*. (2019) demonstrated the use of MAI for nutritional and quality traits, while Periyannan *et al*. (2014) and Huseynova (2018) highlighted its effectiveness in disease resistance and stress tolerance in wheat. In rice, Wang *et al*. (2009) and Xin *et al*. (2012) showed how MAI can overcome hybrid sterility and improve yield potential. Nedunchezhiyan *et al*. (2025), stated that advanced molecular approaches, such as gene expression profiling, genome wide association studies, and marker-assisted selection, can be employed to identify and utilize key genes for expressing salinity tolerance.

Fundamentals and Implementation Strategies of Marker-Assisted Introgression in Plant Breeding

MAI is a molecular breeding strategy that allows the transfer of target genes or QTLs from donor lines into elite cultivars while maintaining the recurrent parent's desirable traits. Unlike conventional phenotypic selection, which is heavily influenced by environmental conditions, MAI enables precise tracking of specific alleles across generations. This approach reduces linkage drag and accelerates the development of improved cultivars (Monden *et al*., 2014). MAI is especially valuable for low heritability traits and complex polygenic traits such as disease resistance, stress tolerance, or quality attributes. For example, functional markers have been used to improve kernel sweetness in maize (Chhabra *et al*., 2019) and leaf rust and stripe rust resistance in wheat (Suenaga *et al*., 2003). By focusing on alleles that directly influence the trait, breeders can achieve more reliable genetic gains compared to conventional breeding (Ramirez-Prado *et al*., 2018).

The introgression process begins with selection of donor and recurrent parents based on the presence of target traits and overall agronomic performance. Molecular markers linked to target loci are identified and validated for polymorphism between the parents (Monden *et al*., 2014). Controlled crosses are performed, followed by successive backcrossing to recover the recurrent parent genome. At each generation, foreground selection ensures that progenies carry the desired allele(s), while background selection monitors genome recovery to minimize unwanted donor segments (Suenaga *et al*., 2003). Functional markers, which detect causative mutations rather than linked loci, improve selection accuracy and reduce recombination errors (Chhabra *et al*., 2019). The final step involves field evaluation to confirm that introgressed traits are expressed effectively without affecting yield or quality. In potato, mapping of resistance genes against Potato virus *Y* (Tian & Valkonen 2012) demonstrates how careful marker-assisted selection ensures successful introgression.

Factors Influencing Efficiency

The efficiency of marker-assisted introgression (MAI) is governed by a complex interplay of genetic, technical, and environmental factors, each of which can significantly impact the speed, precision, and overall success of breeding programs (Haberle *et al*., 2018). Understanding these factors is critical for designing introgression strategies that not only accelerate the transfer of desirable alleles but also ensure the retention of elite cultivar characteristics. Consideration of these variables enables breeders to optimize population size, choose appropriate marker systems, plan backcross generations strategically, and integrate phenotypic validation with molecular selection. Effective management of these factors allows MAI programs to achieve maximum genetic gain in a shorter timeframe while minimizing unwanted linkage drag, resource expenditure, and experimental inefficiencies.

Genetic Map Length

The distance between markers and target genes is a crucial determinant of MAI efficiency. Markers closely linked to the target gene minimize recombination events, thereby ensuring that the desired allele is reliably transmitted across generations (Sarris *et al*., 2016). For polygenic traits or genes located in recombination-poor regions, the use of flanking markers or multiple markers per locus increases precision and reduces the probability of losing the target gene during backcrossing (Chhabra *et al*., 2019). High-resolution genetic maps and functional markers that directly target causative mutations further improve selection efficiency by reducing linkage drag and unintended introgression of donor genome segments (Monden *et al*., 2014).

Breeders can monitor recombination more effectively and select individuals carrying the maximum number of desired alleles while minimizing donor genome fragments by incorporating multiple markers per QTL region. Additionally, combining marker information with phenotypic evaluation enhances the reliability of selection, especially for traits influenced by environmental interactions or minor-effect loci (Ashkani *et al*., 2011). Integrating fine-mapping data with genome-wide association studies (GWAS) can further aid in identifying optimal marker positions, enabling precise allele tracking, expediting the recovery of recurrent parent genomes, and ultimately ensuring the efficient fixation of target traits in superior breeding lines.

Population size

Population size is a critical determinant of the efficiency and success of marker-assisted introgression (MAI). Larger populations increase the probability of capturing favourable recombination events, which is particularly important for complex traits governed by multiple genes or minor-effect loci (Saijo *et al*., 2018). Inadequate population sizes may result in the loss of targ*et al*leles, insufficient recovery of the recurrent parent genome, or reduced chances of identifying progeny carrying the desired allele combinations.

Large populations facilitate more effective background selection, enabling breeders to select individuals with maximal recurrent parent genome recovery at early backcross generations (Ramirez-Prado *et al*., 2018). They also increase the likelihood of detecting rare recombinants, which is essential when introgressing genes located in recombination-poor regions or in clusters with tightly linked undesirable alleles. Optimal population sizes allow for better representation of genetic diversity and increase the probability of pyramiding multiple favourable alleles within a single genotype.

Balancing operational feasibility with population scale is critical, as excessively large populations may pose logistical challenges, whereas very small populations reduce the effectiveness of selection and slow down the breeding process (Wenke *et al*., 2015). Careful planning of population size in conjunction with marker density and selection strategy ensures that breeding programs achieve maximum efficiency and genetic gain while maintaining cost-effectiveness and resource management.

Backcross Duration

The number of backcross generations plays a crucial role in determining how effectively the recurrent parent genome is restored while preserving the target allele(s). While increasing the number of backcrosses generally improves genome recovery, it also results in increased time, labour, and financial costs. Marker-assisted background selection has been demonstrated to significantly reduce the number of backcross generations by facilitating the early identification of progeny that carry the highest proportion of the recurrent parent genome (Sarris *et al*., 2016).

Optimizing backcross duration is crucial not only for efficiency but also to minimize linkage drag, in which undesirable donor genomic segments remain linked to the target gene, potentially affecting agronomic performance. The use of functional markers that directly target causative mutations, along with flanking markers around the target locus, allows precise monitoring of both the allele of interest and adjacent genomic regions (Chhabra *et al*., 2019). By combining marker-assisted selection with strategic planning of backcross cycles, breeders can achieve rapid introgression, ensure the fixation of desired alleles, and maintain the elite background of the recurrent parent. Then, integrating high-density genetic maps and genotyping data can provide additional insight into optimal backcross timing and the selection of progeny with maximal recovery of the recurrent parent genome in fewer generations, thus improving both precision and efficiency of MAI programs.

Marker Polymorphism and Type

The effectiveness of marker-assisted introgression (MAI) is strongly influenced by the level of polymorphism between the donor and recurrent parent at the selected marker loci. Highly polymorphic markers allow greater discrimination between alleles, improving selection accuracy and reducing the risk of retaining unwanted donor segments.

Functional markers that target causative nucleotide changes directly associated with the trait offer higher precision than markers linked to the gene, as they avoid uncertainties from recombination events near the locus (Chhabra *et al*., 2019). The choice of marker type SSR, SNP, or InDel affects genotyping throughput and costefficiency. SNPs are abundant and suitable for high-throughput automated platforms, making them ideal for large-scale breeding programs, while SSRs, though highly informative, require more labour-intensive genotyping. Combining multiple markers or using panels of tightly linked markers enhances selection resolution and minimizes the loss of targ*et al*leles during backcrossing.

Careful consideration of marker polymorphism, type, and genomic location is essential for efficient MAI strategies that maximize precision, reduce linkage drag, and accelerate recovery of the recurrent parent genome (Deshmukh *et al*., 2020).

Trait Complexity and Heritability

Traits with simple inheritance, controlled by a single gene, are more straightforward to introgress compared to complex polygenic traits influenced by multiple genes and their interactions. Polygenic traits often exhibit additive and epistatic effects, making the selection of favourable alleles more challenging and requiring careful planning of marker-assisted introgression (Ramirez-Prado *et al*., 2018). Traits with low heritability are highly affected by environmental factors, which can obscure the expression of targ*et al*leles and complicate phenotypic evaluation.

The successful introgression of these traits often necessitates the use of QTL mapping to identify key genomic regions, multiple linked markers to track alleles accurately, and larger population sizes to capture rare favourable recombinants (Steiner *et al*., 2017). A thorough understanding of the genetic architecture and inheritance patterns is critical for selecting the most effective markers, designing appropriate backcross schemes, and ensuring that desired alleles are reliably transmitted across generations. This strategic approach enhances precision in introgression programs and maximizes the recovery of recurrent parent traits while integrating the target genes effectively.

Genotyping and Phenotyping Accuracy

High-throughput genotyping platforms allow rapid screening of large breeding populations, significantly reducing the labour, time, and errors associated with manual marker analysis (Monden *et al*., 2014). These platforms facilitate the simultaneous evaluation of numerous loci across hundreds or thousands of individuals, ensuring precise identification of progeny carrying the desired alleles.

Accurate phenotyping is equally critical, as it verifies that the introgressed traits are expressed as intended, preventing the selection of false positives and confirming the functional impact of target alleles. Integration of molecular marker data with phenotypic evaluations provides a comprehensive assessment of each progeny's genetic and agronomic potential, thereby enhancing selection accuracy and program reliability (Boeven *et al*., 2016).

Combining high-throughput genotyping with standardized phenotyping protocols enables breeders to track both major and minor-effect alleles efficiently, facilitating the introgression of complex traits while maintaining the elite background of the recurrent parent. This integrated approach ensures that MAI programs achieve rapid genetic gains with precision and consistency across generations.

Environmental Interactions

Molecular markers reliably track the presence of target alleles, but the expression of traits, especially quantitative traits, can be significantly influenced by environmental conditions. Factors such as temperature, soil fertility, water availability, and biotic stress can alter the phenotypic manifestation of introgressed genes, even when the alleles are present in the genome (Ramirez-Prado *et al*., 2018).

Marker-assisted introgression programs must therefore incorporate strategies to account for genotype × environment interactions, ensuring that selected alleles perform consistently under the conditions for which the crop is intended. Multi-environment trials of introgressed lines allow breeders to evaluate the stability and effectiveness of marker-assisted selection across diverse locations and seasons (Andersson *et al.,2015*). These trials help identify progeny that combine the desired genetic traits with resilience to environmental variability, supporting stable genetic gains and enhancing the reliability of breeding outcomes. Integrating environmental considerations into MAI programs ensures that introgressed traits contribute effectively to yield, quality, and stress adaptation, reinforcing the practical utility of molecular breeding strategies in real-world agricultural settings.

Marker-Trait Associations

Marker-trait associations form the backbone of marker-assisted introgression (MAI), enabling breeders to precisely identify and select alleles linked to desirable agronomic, quality, or stress-resistance traits (Wang *et al*., 2021). These associations allow the tracking of target genes across generations, reducing reliance on phenotypic selection, which can be strongly influenced by environmental conditions. A thorough understanding of marker-trait relationships is essential for improving the efficiency, accuracy, and reliability of breeding programs, particularly for traits with low heritability or complex polygenic inheritance. The effectiveness of marker-assisted selection is determined by the type and strength of the association between molecular markers and target loci (Kim *et al.,* 2015). Markers tightly linked to the trait gene or located within regions of high linkage disequilibrium can reliably predict trait presence, facilitating precise introgression and minimizing the risk of recombination events that could separate the marker from the gene.

Functional markers, which directly target causative mutations, enhance selection accuracy by reducing linkage drag and avoiding unintended donor genome segments. For complex quantitative traits, multi-marker strategies or marker panels are applied to capture the cumulative effects of multiple QTLs, enabling the pyramiding of favourable alleles into a single elite genotype (Kamdar *et al.*, 2022). In cereals, marker-assisted introgression has contributed to improved disease resistance, abiotic stress tolerance, and grain quality. For instance, bacterial blight resistance in rice was successfully introgressed using markers linked to the *Xa21* gene, demonstrating that MAI can introduce target traits while retaining the elite background of cultivars (Gao *et al.*, 2013). Leaf rust and stripe rust resistance in wheat were similarly enhanced using markers associated with resistance genes, enabling rapid development of resistant cultivars through backcross breeding (Shanti *et al*., 2010).

In legumes, particularly groundnut (*Arachis hypogaea* L.), marker-trait associations have supported improvements in yield, oil quality, and disease resistance. Molecular markers integrated with conventional breeding approaches have been instrumental in enhancing productivity under diverse cropping systems. Marker-assisted approaches complemented agricultural interventions, including direct cash transfer schemes, improving groundnut cultivation outcomes in Karnataka (Kavitha *et al.*, 2021). Breeding programs optimizing intercropping systems and yield stability have also benefited from marker-trait associations, ensuring efficient capture of favourable alleles while maintaining resource-use efficiency (Hussainy *et al*., 2020).

Evaluations of the groundnut value chain highlight the role of molecular marker-assisted selection in strengthening production systems and supporting global food security (Sakha *et al*., 2022). Marker-trait associations provide the foundation for precision breeding. By combining functional markers, multi-locus selection strategies, and knowledge of genetic architecture, breeders can accelerate the development of superior cultivars with target traits while maintaining the genetic integrity of elite lines (Zongo *et al*., 2017). Integrating molecular data with field performance evaluation ensures that MAI strategies deliver both genetic precision and agronomic effectiveness across variable environmental conditions.

Linkage vs. Linkage Disequilibrium Linkage

The physical proximity of a molecular marker to a target gene on a chromosome, which reduces the probability of recombination events separating them during meiosis. Markers that are tightly linked to a trait gene can reliably indicate the presence of the desired allele across generations, allowing breeders to track and select for the trait with high precision (Ashkani *et al.*, 2011). The closer the marker is to the gene, the lower the chance of recombination, making linkage-based selection particularly effective for monogenic traits or QTLs located in recombination-rich regions. In practical breeding, flanking markers are often used to further minimize the risk of losing the targ*et al*lele, especially for traits with low heritability or polygenic inheritance (Hossain *et al.*, 2018) Linkage disequilibrium (LD), Linkage refers to the physical proximity of a molecular marker to a target gene on a chromosome, which reduces the likelihood of recombination events separating them during meiosis.

Markers closely linked to a trait gene ensure the desired allele is transmitted across generations, allowing precise tracking and selection (Ashkani *et al*., 2011). Tighter linkage lowers recombination probability, which is especially effective for monogenic traits or QTLs in recombination-rich regions.

Flanking markers are commonly employed to reduce the risk of losing the targ*et al*lele, particularly for low heritability or polygenic traits. LD involves the non-random association of alleles at different loci within a population. LD can occur between loci that are not physically adjacent, enabling marker-trait associations to be captured across broader genomic regions. This property underpins genome-wide association studies (GWAS) to detect QTLs controlling complex traits (Freeland, 2017). LD patterns depend on population size, mating structure, selection pressure, and recombination rates, and they vary across species and populations.

Understanding LD decay over physical distance guides the required marker density in GWAS and MAS programs to maintain accurate allele tracking. LD facilitates identification of genomic regions controlling quantitative traits influenced by multiple small-effect genes. High-density marker panels combined with LD data allow detection of favourable alleles even without knowledge of causal genes. Functional markers and high-throughput genotyping platforms enhance the precision of marker-assisted introgression (MAI), accelerating the development of improved cultivars. For instance, polyphenols from finger millet seed coat improved oxidative stability in peanut oil (Balasubramaniam *et al*., 2020), and studies on fatty acid metabolism emphasize selecting alleles with beneficial nutritional effects (Mariamenatu & Abdu 2021).

Functional markers in Precise introgression

Functional markers (FMs) target causative polymorphisms that are directly responsible for phenotypic variation, offering a significant advantage over markers merely linked to a trait locus. By detecting the actual functional allele, these markers reduce errors arising from recombination between the marker and the gene of interest and minimize linkage drag, thereby preserving the genetic background of elite cultivars (Jadhav *et al.*, 2021). The use of FMs allows breeders to distinguish between progeny carrying the favourable allele and those carrying closely linked but non-functional donor segments, which is particularly important for traits with low heritability or controlled by multiple loci (Salgotra *et al*., 2020).

In rice, marker-assisted backcross breeding using functional markers for the bacterial blight resistance gene *Xa21* has enabled precise transfer of the resistance allele into elite cultivars while retaining agronomic performance, demonstrating the reliability and efficiency of FMs in breeding programs (Gao *et al*., 2013). Similarly, in peanut (*Arachis hypogaea*), functional markers targeting fatty acid desaturase mutant alleles have been used to improve oleic acid content, resulting in stable expression of high oleic acid across successive generations and minimal impact on other seed traits (Bera *et al*., 2019). Beyond disease resistance and quality traits, functional markers have been successfully applied to stress tolerance, nutrient content, and yield-related traits in cereals and legumes (Sagar *et al*., 2018).

For complex quantitative traits, FMs can be combined with multi-locus or haplotype-based selection to capture favourable allele combinations across multiple loci simultaneously. Integrating functional markers with high-throughput genotyping platforms accelerates the selection process, enabling early generation screening and more efficient recovery of the recurrent parent genome (Bera *et al*., 2019). These approaches enhance both the precision and speed of marker-assisted introgression, ensuring that desired traits are fixed rapidly while maintaining overall cultivar performance.

Multi-Marker Approaches for QTLs

Complex traits such as stress tolerance, yield potential, and quality attributes are frequently governed by multiple quantitative trait loci (QTLs), each contributing partially to the overall phenotype. Single-marker selection often fails to capture all beneficial alleles for such traits due to recombination events or incomplete linkage between the marker and causative gene. Multi-marker strategies address this challenge by employing flanking markers, haplotype blocks, or panels of tightly linked markers for each QTL, thereby improving selection precision and reducing the probability of losing desirable alleles during backcrossing (Lou *et al.*, 2017). In rice, Lou *et al.* (2017) used multiple markers around the *OsSAPK2* locus to improve drought tolerance, enabling precise selection of progeny carrying favourable alleles while minimizing unwanted donor genome segments.

You *et al*. (2023) applied multi-marker panels to pyramid several traits, combining yield-related and quality traits across different loci, showing how multiple markers facilitate simultaneous selection of complex traits. In peanut, Jadhav *et al.* (2021) employed functional and flanking markers to enhance oleic acid content, stabilizing the trait across generations. Bera *et al*. (2019) achieved steady expression of high oleic acid in peanut by using multiple markers per QTL, reducing recombination errors and ensuring efficient introgression of the desired alleles. These studies illustrate that multi-marker strategies allow breeders to capture the cumulative effects of minor-effect QTLs, improve the precision of selection for complex traits, and minimize the introgression of unwanted donor genome segments (Khanna *et al*., 2015). Multi-marker approaches also accelerate pyramiding of multiple desirable traits within a single genotype, enhancing both stress tolerance and quality attributes while maintaining the recurrent parent background. The application across different crops, including rice and peanut, underscores the versatility and effectiveness of using multiple markers for QTL-based selection and trait improvement in both cereals and legumes.

Applications of Marker-Assisted Introgression in Major Crops

Rice has served as a model crop for demonstrating the effectiveness of marker-assisted introgression (MAI) in transferring disease resistance and other agronomically important traits. For instance, breeding programs targeting bacterial leaf blight resistance have successfully incorporated the *Xa21* gene, along with additional resistance loci, into elite cultivars using closely linked molecular markers (Shanti *et al*., 2010). These programs illustrate how functional markers and precise foreground and background selection strategies can minimize linkage drag while retaining the elite characteristics of the recurrent parent. In peanut (*Arachis hypogaea*), marker-assisted backcross breeding has been employed to improve seed quality traits, such as high oleic acid content.

Functional markers targeting fatty acid desaturase mutant alleles (*ahFAD2A* and *ahFAD2B*) enabled stable trait expression over successive generations while maintaining other seed and plant traits (Pasupuleti *et al*., 2016). The use of multiple markers per QTL region in these programs facilitated the pyramiding of beneficial alleles and improved selection accuracy, highlighting the importance of multi-marker strategies for complex or quantitative traits. These instances illustrate that integrating functional markers, multi-locus marker panels, and high-throughput phenotyping enhances the efficiency and precision of MAI programs. Similar strategies have been applied to other cereals and legumes for disease resistance, stress tolerance, and quality improvement, indicating that marker-assisted introgression can accelerate genetic gains across diverse crop species (Janaki *et al*., 2021).

The careful selection of markers, combined with rigorous genotypic and phenotypic evaluation, ensures that target traits are incorporated reliably without compromising overall cultivar performance.

CONCLUSIONS

Marker-assisted introgression has emerged as a transformative strategy in modern plant breeding, bridging the gap between conventional phenotypic selection and molecular approaches. By enabling the precise transfer of target genes or QTLs from donor to elite cultivars, MAI speeds up genetic improvements while keeping the desirable traits of the recurrent parent. Its efficiency depends on factors as genetic map length, population size, backcross duration, marker type and polymorphism, trait complexity, and environmental conditions. Using multiple markers helps improve accuracy and reduces the chance of unwanted traits being transferred. MAI has shown effectiveness across major crops, including rice, maize, wheat, and peanut, for improving disease resistance, stress tolerance, yield, and quality traits. It contains introgression of *Xa21* in rice for bacterial blight resistance, *β-carotene* and kernel sweetness alleles in maize, and high oleic acid alleles in peanut highlight its value in addressing challenges, improving nutrition, and supporting climate-resilient farming. It provides a precise and efficient way to develop improved crop varieties. Combining marker information with careful field evaluation allows breeders to produce high-performing, stress-tolerant, and nutritionally enhanced crops that meet the demands of a growing population (Suen *et al*., 2003).

FUTURE SCOPE

MAI holds immense potential for the future by seamlessly integrating cutting-edge genomic technologies, high-throughput phenotyping, and bioinformatics. This integration enables the precise and efficient development of improved crop varieties that are not only resilient but also high-yielding and nutritionally enhanced. By expanding MAI to include orphan and minor crops, along with multi-trait pyramiding and considering environmental adaptation, its impact on food security and global agriculture will be significantly amplified. As the field continues to evolve, collaborative data sharing and a deeper comprehension of gene regulatory networks will further enhance the accuracy and scope of breeding programs. Consequently, MAI will emerge as a pivotal tool to address the challenges posed by climate change, population growth, and evolving consumer preferences.

REFERENCES

Andersson, R., Chen, Y., Core, L., Lis, J. T., Sandelin, A. & Jensen, T. H. (2015). Human gene promoters are intrinsically bidirectional. *Molecular cell*, *60*(3), 346-347.

Assenov, B., Andjelkovic, V., Ignjatovic-Micic, D. & Pagnotta, M. A. (2013). Identification of SNP mutations in *MYBF-1* gene involved in drought stress tolerance in maize. *Bulgaria Journal of Agricultural Science*, *19*, 181–185.

Ashkani, S., Rafii, M., Sariah, M., Akmar, A. S., Rusli, I., Rahim, H. A. & Latif, M. (2011). Analysis of simple sequence repeat markers linked with blast disease resistance genes in a segregating population of rice (*Oryza sativa*). *Gesnetics and Molecular Research*, *10*(3), 1345–1355.

Balasubramaniam, V. G., Sathvika, S., Ayyappan, P. & Antony, U. (2020). Improved oxidative stability of peanut oil through addition of finger millet (*Eleusine coracana*) seed coat polyphenols. *Journal of Food Process Engineering*, *43*(3), e13194.

Bera, S. K., Kamdar, J. H., Kasundra, S. V., Patel, S. V., Jasani, M. D., Maurya, A. K., ... & Varshney, R. K. (2019). Steady expression of high oleic acid in peanut bred by marker-assisted backcrossing for fatty acid desaturase mutant alleles and its effect on seed germination along with other seedling traits. *PloS one*, *14*(12), e0226252.

Boeven, P. H., Longin, C. F. H. & Würschum, T. (2016). A unified framework for hybrid breeding and the establishment of heterotic groups in wheat. *Theoretical and Applied Genetics*, *129*(6), 1231–1245.

Chhabra, R., Hossain, F., Muthusamy, V., Baveja, A., Mehta, B. K. & Zunjare, R. U. (2019). Development and validation of breeder-friendly functional markers of *sugary1* gene encoding starch-debranching enzyme affecting kernel sweetness in maize (*Zea mays*). *Crop & Pasture Science*, *70*(10), 868–875.

Chung, Y. S., Choi, S. C., Jun, T. H. & Kim, C. (2017). Genotyping-by-sequencing: A promising tool for plant genetics research and breeding. *Horticulture, Environment, and Biotechnology*, *58*(5), 425–431.

Deshmukh, D. B., Marathi, B., Sudini, H. K., Variath, M. T., Chaudhari, S., Manohar, S. S. ... & Pasupuleti, J. (2020). Combining high oleic acid trait and resistance to late leaf spot and rust diseases in groundnut (*Arachis hypogaea* L.). *Frontiers in Genetics*, *11*, 487438.

Freeland, J. R. (2017). The importance of molecular markers and primer design when characterizing biodiversity from environmental DNA. *Genome*, *60*(4), 358–374.

Gao, L., Cao, Y., Xia, Z., Jiang, G., Liu, G., Zhang, W. & Zhai, W. (2013). Do transgenesis and marker-assisted backcross breeding produce substantially equivalent plants?-A comparative study of transgenic and backcross rice carrying bacterial blight resistant gene Xa21. *BMC genomics*, *14*(1), 738.

Haberle, V. & Stark, A. (2018). Eukaryotic core promoters and the functional basis of transcription initiation. *Nature reviews Molecular cell biology*, *19*(10), 621-637.

Hossain, F., Muthusamy, V., Pandey, N., Vishwakarma, A. K., Baveja, A., Zunjare, R. U., ... & Gupta, H. S. (2018). Marker-assisted introgression of opaque2 allele for rapid conversion of elite hybrids into quality protein maize. *Journal of genetics*, *97*(1), 287-298.

Huseynova, I. M. (2018). Application of PCR-based functional markers for identification of *DREB1* genes in *Triticum aestivum* L. *SF Biotechnology & Bioengineering Journal*, *1*(1), 1.

Janaki Ramayya, P., Vinukonda, V. P., Singh, U. M., Alam, S., Venkateshwarlu, C., Vipparla, A. K., ... & Kumar, A. (2021). Marker-assisted forward and backcross breeding for improvement of elite Indian rice variety

Naveen for multiple biotic and abiotic stress tolerance. *PLoS One*, *16*(9), e0256721.

Jadhav, M. P., Patil, M. D., Hampannavar, M., Venkatesh, Dattatreya, P., Shirasawa, K. ... & Bhat, R. S. (2021). Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. *Crop Science*, *61*(4), 2435-2443.

Kamdar, J. H., Jasani, M. D., Chandrashekar, A. B., Janila, P., Pandey, M. K., Georrge, J. J., ... & Bera, S. K. (2022). Does improved oleic acid content due to marker-assisted introgression of ahFAD2 mutant alleles in peanuts alter its mineral and vitamin composition?. *Frontiers in Plant Science*, *13*, 942617.

Kavitha, H. N., Kumar, P., Anbukkani, P. & Burman, R. R. (2021). Impact of direct cash transfer scheme on production and efficiency of groundnut. [Journal/Publisher not specified]

Khanna, A., Sharma, V., Ellur, R. K., Shikari, A. B., Gopalakrishnan, S., Singh, U. D., … Singh, A. K. (2015a). Development and evaluation of near-isogenic lines for major blast resistance gene(s) in Basmati rice. *Theoretical and Applied Genetics*, *128*(7), 1243–1259.

Kim, T. K. & Shiekhattar, R. (2015). Architectural and functional commonalities between enhancers and promoters. *Cell*, *162*(5), 948-959.

Lou, D., Wang, H., Liang, G. & Yu, D. (2017). OsSAPK2 confers abscisic acid sensitivity and tolerance to drought stress in rice. *Frontiers in Plant Science, 8*, 993.

Mariamenatu, A. H. & Abdu, E. M. (2021). Overconsumption of omega-6 polyunsaturated fatty acids (PUFAs) versus deficiency of omega-3 PUFAs in modern-day diets: The disturbing factor for their “balanced antagonistic metabolic functions” in the human body. *Journal of Lipids, 2021*, 8848161.

Monden, Y., Fujii, N., Yamaguchi, K., Ikeo, K., Nakazawa, Y., Waki, T. & Tahara, M. (2014). Efficient screening of long terminal repeat retrotransposons that show high insertion polymorphism via high-throughput sequencing of the primer binding site. *Genome, 57*(5), 245–252.

Ni, T., Corcoran, D. L., Rach, E. A., Song, S., Spana, E. P., Gao, Y. ... & Zhu, J. (2010). A paired-end sequencing strategy to map the complex landscape of transcription initiation. *Nature methods*, *7*(7), 521-527.

Pasupuleti, J., Pandey, M., S. Y., Variath, M. & Pawan, S. M. (2016). Molecular breeding for introgression of fatty acid desaturase mutant alleles (ahFAD2A and ahFAD2B) enhances oil quality in high and low oil containing peanut genotypes. *Plant Science, 242*, 203–213.

Periyannan, S., Bansal, U., Bariana, H., Deal, K., Luo, M., Dvorak, J. & Lagudah, E. (2014). Identification of a robust molecular marker for the detection of the stem rust resistance gene Sr45 in common wheat. *Theoretical and Applied Genetics, 127*(4), 947–955.

Ramirez-Prado, J. S., Abulfaraj, A. A., Rayapuram, N., Benhamed, M. & Hirt, H. (2018). Plant immunity: From signalling to epigenetic control of defence. *Trends in Plant Science, 23*(9), 833–844.

Sagar, V., Gopala Krishnan, S., Dwivedi, P., Mondal, K. K., Prakash, G., Nagarajan, M. & Singh, A. K. (2018). Development of Basmati rice genotypes with resistance to both bacterial blight and blast diseases using marker assisted restricted back cross breeding. *Indian Journal of Genetics, 78*, 36–47.

Salgotra, R. K. & Stewart Jr, C. N. (2020). Functional markers for precision plant breeding. *International journal of molecular sciences*, *21*(13), 4792.

Sarris, P. F., Cevik, V., Dagdas, G., Jones, J. D. G. & Krasileva, K. V. (2016). Comparative analysis of plant immune receptor architectures uncovers host proteins likely targeted by pathogens. *BMC Biology, 14*(1), 8.

Shanti, M. L., Shenoy, V. V., Devi, G. L., Kumar, V. M., Premalatha, P., Kumar, G. N., ... & Freeman, W. H. (2010). Marker-assisted breeding for resistance to bacterial leaf blight in popular cultivar and parental lines of hybrid rice. *Journal of plant pathology*, 495-501.

Steiner, B., Buerstmayr, M., Michel, S., Schweiger, W., Lemmens, M. & Buerstmayr, H. (2017). Breeding strategies and advances in line selection for Fusarium head blight resistance in wheat. *Tropical Plant Pathology, 42*(3), 165–174.

Suenaga, K., Singh, R. P., Huerta-Espino, J. & William, H. M. (2003). Microsatellite markers for genes Lr34/Yr18 and other quantitative loci for leaf rust and stripe rust resistance in bread wheat. *Phytopathology, 93*(7), 881–890.

Tian, Y. P. & Valkonen, J. P. T. (2012). Mapping of the a-virulence determinant of Potato virus Y strain O corresponding to the gene Ny for hypersensitive resistance in potato. *Molecular Plant-Microbe Interactions*, *26*(3), 297–305.

Vasudev Ramaraj, Jegadeeswaran Mokkaraj, Thirugnanakumar Sivagurunathan, Geetha S., Vinothini Nedunchezhiyan, Sathees Kumar Kathirvel, Susi Sivakumar and Tamilarasan Arikrishnan (2025). Assessment of Salinity Tolerance in Barnyard millet (*Echinochloa frumentacea* Roxb.) Genotypes using Dendrogram and PCA Biplot. *Biological Forum, 17*(7), 148-154.

Wang, J., Nakazaki, T., Chen, S., Chen, W., Saito, H., Tsukiyama, T., ... & Tanisaka, T. (2009). Identification and characterization of the erect-pose panicle gene EP conferring high grain yield in rice (Oryza sativa L.). *Theoretical and Applied Genetics*, *119*(1), 85-91.

Wang, X., Guo, X., Ma, X., Luo, L., Fang, Y., Zhao, N., ... & Li, R. (2021). Development of new rice (oryza. sativa l.) breeding lines through marker-assisted introgression and pyramiding of brown planthopper, blast, bacterial leaf blight resistance, and aroma genes. *Agronomy*, *11*(12), 2525.

Wenke, T., Seibt, K. M., Döbel, T., Muders, K. & Schmidt, T. (2015). Inter-SINE amplified polymorphism (ISAP) for rapid and robust plant genotyping. In *Plant Genotyping* (pp. 183–192). Humana Press, New York.

You, F. M., Khan, N., Shazadee, H. & Cloutier, S. (2023). QTL mapping: Strategy, progress, and prospects in flax. *The Flax Genome*, 69-99.

Zhou, Y., Han, Y., Li, Z., Fu, Y., Fu, Z., Xu, S. ... & Yang, X. (2012). ZmcrtRB3 Encodes a Carotenoid Hydroxylase that Affects the Accumulation of α-carotene in Maize Kernel F. *Journal of integrative plant biology*, *54*(4), 260-269.

Zongo, A., Khera, P., Sawadogo, M., Shasidhar, Y., Sriswathi, M., Vishwakarma, M. K., ... & Desmae, H. (2017). SSR markers associated to early leaf spot disease resistance through selective genotyping and single marker analysis in groundnut (*Arachis hypogaea* L.). *Biotechnology reports*, *15*, 132-137.

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