



Molecular Breeding a Sustainable Tool for Maize Improvement

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Maize is one of the most important cereal crops worldwide and serves as a major source of food, feed and industrial raw material. However, maize productivity is severely affected by various biotic and abiotic stresses, including drought, salinity, diseases, insect pests and climate change. Conventional breeding methods have significantly contributed to crop improvement, but they are often time-consuming and less efficient for complex traits controlled by multiple genes. Molecular breeding has emerged as a powerful approach that integrates molecular markers and genomic tools with conventional breeding techniques to accelerate the development of improved maize varieties. Techniques such as marker-assisted selection (MAS), quantitative trait loci (QTL) mapping, genomic selection and gene editing have enhanced breeding precision and efficiency. Molecular breeding has played a major role in improving yield, nutritional quality, stress tolerance and disease resistance in maize. The integration of modern genomic technologies with conventional breeding strategies offers significant opportunities for sustainable maize production and global food security under changing climatic conditions.

Introduction

Maize (*Zea mays*) is one of the most important cereal crops cultivated throughout the world and occupies a significant position in global agriculture due to its high productivity and wide adaptability under diverse agro-climatic conditions (Prasanna, 2003). It is commonly referred to as the "queen of cereals" because of its highest genetic yield potential among cereal crops (Moose and Mumm, 2008). Maize is used extensively as human food, livestock feed and industrial raw material for the production of starch, oil, ethanol and several processed products. In developing countries maize contributes substantially to food and nutritional security while in developed countries it serves mainly as feed for the livestock industry (Tester and Langridge, 2010).

The global demand for maize is increasing continuously due to rapid population growth, urbanization and changing food habits. However maize productivity is adversely affected by several biotic and abiotic stresses including drought, salinity, extreme temperatures, insect pests and diseases (Tester and Langridge, 2010; Meng et al., 2024). Climate change has further intensified these stresses by increasing the frequency of drought and heat stress conditions (Raza et al., 2022). Conventional breeding approaches have contributed significantly to the development of improved maize cultivars but these methods require long breeding cycles and are highly influenced by environmental factors (Xu and Crouch, 2008). Furthermore several economically important traits such as yield and stress tolerance are quantitatively inherited and controlled by multiple genes making their improvement through conventional breeding more difficult (Collard and Mackill, 2008).

Recent advancements in molecular biology and genomics have revolutionised crop improvement strategies (Varshney et al., 2019; Bohra et al., 2024). Molecular breeding has emerged as an efficient and reliable approach for improving complex traits in maize through

the use of molecular markers and genomic tools (Moose and Mumm, 2008). It enables precise selection of desirable genes and accelerates the development of superior cultivars with improved yield potential, stress tolerance and nutritional quality (Xu and Crouch, 2008). Therefore molecular breeding has become an essential component of modern maize improvement programs worldwide (Prasanna, 2003; Gunundu et al., 2023).

Molecular Breeding and Its Importance

Molecular breeding is a modern breeding approach that integrates molecular biology techniques with conventional plant breeding for efficient crop improvement (Moose and Mumm, 2008). It involves the identification and utilization of molecular markers linked to desirable genes or quantitative trait loci associated with important agronomic traits (Collard and Mackill, 2008). Molecular markers are segments of DNA that help identify genetic differences among plant genotypes and facilitate indirect selection of desired traits at an early stage of crop development (Xu and Crouch, 2008). The introduction of molecular breeding has significantly improved the efficiency and precision of plant breeding programs (Prasanna, 2003). Unlike conventional breeding molecular breeding allows breeders to select plants based on their genetic makeup rather than relying solely on phenotypic performance (Collard and Mackill, 2008). This reduces the influence of environmental factors on selection and improves breeding accuracy. Molecular breeding also shortens the breeding cycle by enabling early selection of superior genotypes (Xu and Crouch, 2008). Several types of molecular markers such as Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR), Amplified Fragment Length Polymorphism (AFLP) and Single Nucleotide Polymorphism (SNP) markers have been widely used in maize breeding programs (Prasanna, 2003). Among these SNP markers are highly preferred because of their abundance and high-throughput genotyping capability (Varshney et al., 2019; Gao et al., 2021). Molecular breeding has become an important tool for improving grain yield, nutritional quality, disease resistance and abiotic stress tolerance in maize (Moose and Mumm, 2008; Gunundu et al., 2023).

One of the major examples of molecular breeding in maize is the development of drought-tolerant hybrids through marker-assisted selection and QTL mapping (Collard and Mackill, 2008; Raza et al., 2022). Several genomic regions associated with drought tolerance, root architecture and water-use efficiency have been identified and incorporated into elite maize lines for improving adaptation under water-deficit conditions (Prasanna, 2003; Liu et al., 2020). Molecular breeding has also played an important role in improving resistance against diseases such as maize streak virus, northern leaf blight and downy mildew through the transfer of resistance genes into high-yielding cultivars (Xu and Crouch, 2008; Meng et al., 2024).

Major molecular breeding techniques used in maize improvement

Marker-Assisted Selection (MAS): Marker-assisted selection is one of the most widely used molecular breeding techniques in crop improvement programs (Collard and Mackill, 2008; Ndjondjop et al., 2023). It involves the use of molecular markers tightly linked to genes or QTLs controlling desirable traits (Xu and Crouch, 2008). MAS allows breeders to identify plants carrying favourable alleles without waiting for the expression of traits under field conditions. This approach increases selection efficiency and reduces the time required for developing improved cultivars (Prasanna, 2003). In maize breeding MAS has been extensively used for improving resistance against diseases such as downy mildew, leaf blight, maize streak virus and rust diseases (Prasanna, 2003; Bohra et al., 2024). It has also been successfully applied for enhancing tolerance against drought and salinity stress (Tester and Langridge, 2010; Raza et al., 2022). Through marker-assisted backcross breeding desirable genes from donor parents can be transferred into elite cultivars while retaining the genetic background of the recurrent parent (Xu and Crouch, 2008). MAS is particularly useful for traits that are difficult to evaluate phenotypically or highly influenced by environmental conditions (Collard and Mackill, 2008). It also facilitates pyramiding of multiple resistance

genes into a single genotype to achieve durable resistance against pathogens (Xu and Crouch, 2008). The application of MAS has greatly accelerated maize breeding programs and improved the efficiency of developing stress-tolerant and high-yielding hybrids (Moose and Mumm, 2008; Ndjiondjop et al., 2023).

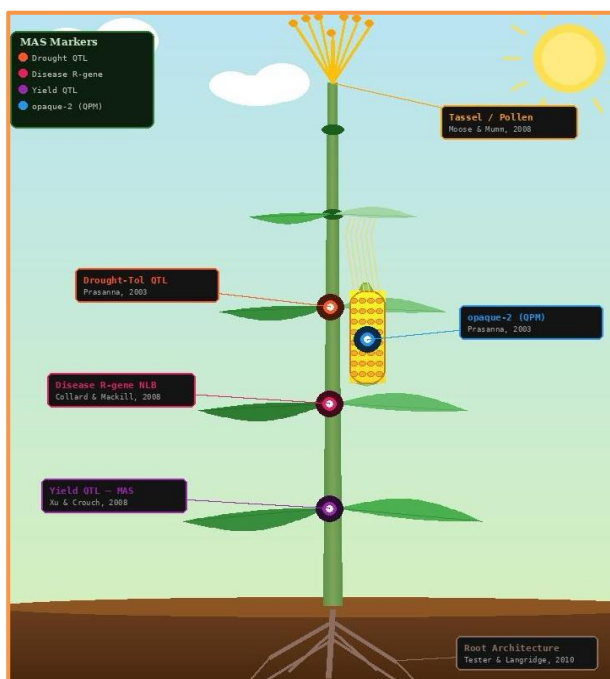
Quantitative Trait Loci (QTL) Mapping:

Many economically important traits in maize such as grain yield, drought tolerance, nutrient-use efficiency and kernel quality are quantitatively inherited and controlled by several genes with small individual effects (Varshney et al., 2019). Quantitative trait loci mapping is an important molecular breeding approach used to identify genomic regions associated with such complex traits (Collard and Mackill, 2008; Jiang et al., 2024). QTL mapping involves the identification of statistical associations between molecular markers and phenotypic traits in segregating populations.

Once QTLs associated with desirable traits are identified molecular markers linked to these regions can be used in breeding programs for indirect selection (Xu and Crouch, 2008). QTL mapping has helped researchers understand the genetic basis of several agronomic and physiological traits in maize (Moose and Mumm, 2008). Numerous QTLs associated with drought tolerance, root architecture, stay-green character and disease resistance have been identified in maize (Prasanna, 2003; Jiang et al., 2024). Identification of these genomic regions has facilitated the development of stress-tolerant maize hybrids through marker-assisted breeding. QTL mapping has also contributed significantly to improving grain quality traits such as protein content, oil content and provitamin A concentration in maize kernels (Varshney et al., 2019; Maqbool et al., 2021).

Genomic Selection: Genomic selection is an advanced molecular breeding strategy that uses genome-wide marker information to predict the breeding value of individuals. Unlike marker-assisted selection which focuses on a few major genes genomic selection considers the cumulative effect of thousands of markers distributed throughout the genome (Varshney et al., 2019). This approach improves the prediction accuracy for complex quantitative traits controlled by multiple genes. In genomic selection statistical models are developed using both genotypic and phenotypic data from a training population. These models are then used to predict the performance of breeding lines without extensive field evaluation. Genomic selection accelerates breeding progress by reducing the time and cost associated with phenotypic screening (Tester and Langridge, 2010). The application of genomic selection in maize has shown promising results for improving grain yield, stress tolerance and hybrid performance (Varshney et al., 2019; Gunundu et al., 2023). It has become particularly useful in hybrid breeding programs where rapid selection of superior parental lines is essential (Moose and Mumm, 2008; Xu et al., 2022). Genomic selection is expected to play a major role in future maize improvement programs due to advancements in high-throughput sequencing and computational biology (Tester and Langridge, 2010).

CRISPR/Cas: CRISPR/Cas precision editing optimizes maize by making targeted micro-adjustments directly within the plant's native genome, enhancing key physiological pathways without inserting foreign DNA. To improve nitrogen-use efficiency, scientists edit the promoters of native ammonium and nitrate transporter genes or disable negative regulatory transcription factors. This forces roots to absorb nitrate more aggressively and accelerates its metabolic conversion into essential amino acids via glutamine synthetase, allowing maize to



sustain high kernel yields even under low-fertilizer conditions. For heat and drought tolerance, CRISPR re-engineers stress-signaling circuits—such as swapping the promoter of the endogenous ARGOS8 gene—to dampen stress-induced ethylene production, maintaining active ear development and delaying leaf senescence during severe thermal stress. Beyond nutrient efficiency and climate resilience, CRISPR significantly strengthens pathotype and disease resistance by disabling native susceptibility genes that pathogens exploit to infect host cells. Furthermore, because transient delivery methods allow the editing machinery to degrade after modifying the genome, the resulting maize plants carry zero foreign transgenic constructs.

Technique	Application	Improved Traits	Key References / Recent Advancements
Marker-Assisted Selection (MAS)	Targeted introgression of major effect loci via backcrossing	Protein quality enhancement (opaque2 introgression for elevated lysine/tryptophan); major disease resistance loci	Collard & Mackill, 2008; Swaran Lata et al., 2022
QTL Mapping	Identification of genomic loci underlying complex traits	Grain yield potential, drought tolerance parameters, root architecture phenotypes	Prasanna, 2003; Varshney et al., 2019
Genomic Selection (GS)	Genome-wide prediction of breeding values (GEBVs)	Heterosis prediction, hybrid performance estimation, stover quality, and silage yield	Moose & Mumm, 2008; Varshney et al., 2019
Doubled Haploid (DH) Breeding with Markers	Accelerated production of completely homozygous inbred lines	Reduces inbred line development cycle from 6–7 generations down to 2 generations	Prasanna et al., 2012; Chaikam et al., 2019
Expression QTL (eQTL) Mapping	Integration of transcriptomic variation with genomic sequence data	Mapping gene regulatory networks controlling drought and temperature stress survival	Zhang et al., 2025
Base Editing (C-to-T & A-to-G)	Precise single-nucleotide conversions without double-stranded DNA breaks	Non-transgenic herbicide tolerance via targeted mutations in native ALS genes	Sony et al., 2023

Challenges and Future Prospects

Despite remarkable progress molecular breeding still faces several challenges including high costs of genotyping, requirement of advanced laboratory facilities and limited availability of skilled manpower in developing countries. The genetic complexity of quantitative traits and genotype environment interactions also limit breeding efficiency. Furthermore, regulatory concerns regarding genetically modified crops may affect the adoption of advanced breeding technologies in some regions. However rapid advancements in genomics, bioinformatics, next-generation sequencing and high-throughput phenotyping are continuously improving the effectiveness of molecular breeding. Integration of artificial intelligence and machine learning with genomic data analysis is expected to further accelerate crop improvement programs. Future maize breeding strategies will focus on developing climate-smart cultivars with higher productivity, improved nutritional quality and enhanced resilience against

multiple stresses. Integration of molecular breeding with conventional breeding approaches will continue to play a crucial role in ensuring sustainable maize production and global food security.

Conclusion

Molecular breeding has emerged as a revolutionary approach for maize improvement by enhancing the precision, speed and efficiency of breeding programs. Techniques such as marker-assisted selection, QTL mapping and genomic selection have significantly contributed to the development of high-yielding, stress-tolerant and nutritionally enriched maize varieties. These advanced molecular tools have enabled breeders to overcome limitations associated with conventional breeding and improve complex traits more effectively.

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