# Genomics-Assisted Breeding in Maize: Techniques and Outcomes

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**Abstract** Genomics-assisted breeding (GAB) has revolutionized maize breeding by integrating advanced genomic techniques to enhance crop improvement. This study reviews the various techniques and outcomes of GAB in maize, focusing on the integration of genomic selection, genome optimization, and marker-assisted selection. Genomic selection leverages genome-wide marker data to predict breeding values, thereby increasing genetic gains with fewer breeding cycles. Genome optimization, incorporating doubled haploid production and computational simulations, aims to design optimized genomes for maximum genetic gain. Marker-assisted selection, facilitated by high-throughput genotyping platforms, provides cost-effective and efficient genotyping solutions. The outcomes of these techniques include the development of disease-resistant, climate-smart, and high-yielding maize cultivars. The integration of these genomic tools has transformed maize breeding from an empirical art to a data-driven science, promising significant advancements in crop productivity and sustainability

**Keywords** Maize; Genomics-assisted breeding; Genomic selection; Genome optimization; Marker-assisted selection

## 1 Introduction

Maize (*Zea mays* L.) is one of the most significant crops globally, serving as a crucial source of food, feed, and fuel. Its global production has seen a remarkable increase, with current annual production reaching approximately one billion tons (Yan and Tan, 2019). Maize's adaptability to diverse agro-climatic conditions and its high genetic yield potential have earned it the title "Queen of cereals" (Manoj et al., 2019). As a staple crop, maize plays a vital role in food security and the livelihoods of millions of people worldwide, particularly in regions like sub-Saharan Africa and Latin America (EIAR-Bako and Yadesa, 2021). The increasing global population, projected to reach 9 billion by 2050, underscores the need for continued advancements in maize production to meet the growing demand for food (Yan and Tan, 2019).

Traditional maize breeding has faced several challenges, including the lengthy time required for developing new varieties and the limitations in achieving desired traits such as disease resistance, drought tolerance, and nutritional quality (EIAR-Bako and Yadesa, 2021). Conventional breeding methods often involve extensive field trials and selection processes, which can be time-consuming and resource-intensive. Additionally, the genetic diversity within maize populations can complicate the breeding process, making it difficult to achieve consistent improvements in yield and other agronomic traits (Lal et al., 2021). The need to address these challenges has driven the exploration of more efficient and precise breeding techniques.

Genomics-assisted breeding has emerged as a promising approach to overcome the limitations of traditional breeding methods. This approach leverages advances in genomics technologies, such as genome sequencing, marker-assisted selection (MAS), and genomic prediction, to accelerate the breeding process and enhance the precision of trait selection (Thudi et al., 2020). By utilizing genomic information, researchers can identify and select for specific genes associated with desirable traits, thereby improving the efficiency and effectiveness of breeding programs (Yang and Yan, 2021). Genomics-assisted breeding also enables the exploration of novel genetic variations and the development of crops with enhanced stress tolerance, nutritional quality, and yield potential (Thudi et al., 2020).

The purpose of this study is to provide a comprehensive overview of the techniques and outcomes associated with genomics-assisted breeding in maize. By examining the current state of genomics technologies and their applications in maize breeding, this study highlights the potential benefits and challenges of integrating genomics into breeding programs. The expectations of this study include identifying key advancements in genomics-assisted breeding, evaluating the impact of these advancements on maize production, and providing insights into future directions for research and development in this field. Ultimately, this study seeks to contribute to the ongoing efforts to enhance maize breeding and ensure global food security in the face of growing population and climate change challenges.

## 2 Genomic Technologies in Maize Breeding

### 2.1 Genotyping-by-sequencing (GBS)

Genotyping-by-Sequencing (GBS) is a cost-effective, high-throughput genotyping method that utilizes restriction enzymes to reduce genome complexity, making it suitable for large-scale genetic studies in maize. GBS has been successfully applied to various maize populations, including association populations, backcross generations, double haploids, and recombinant inbred lines. This technique generates a substantial number of SNPs, although it often results in high rates of missing data, which can be mitigated through imputation methods. GBS is particularly beneficial for genetic diversity analysis, linkage mapping, and genomic prediction, making it a versatile tool in maize breeding programs (Elbasyoni et al., 2018; Wang et al., 2020; Munyengwa et al., 2021).

### 2.2 Single nucleotide polymorphism (SNP) arrays

SNP arrays are another powerful tool for maize breeding, providing high-quality genotyping data. Although SNP arrays are more expensive per sample compared to GBS, they offer high accuracy and consistency. SNP arrays have been used to develop high-density genetic maps and perform genome-wide association studies (GWAS) in maize. These arrays facilitate the identification of genetic patterns and population structures, which are crucial for genomic selection and marker-assisted selection、

### 2.3 Whole-genome sequencing (WGS)

Whole-Genome Sequencing (WGS) provides comprehensive genotyping data by sequencing the entire genome. This method is highly accurate and can identify millions of genetic markers, making it ideal for fine mapping and high-resolution GWAS. However, WGS is costly, especially when applied to large populations. Despite its expense, WGS is invaluable for constructing high-density genetic maps and understanding the genetic basis of complex traits in maize (Elbasyoni et al., 2018; Rice and Lipka, 2021; Chen et al., 2021).

### 2.4 Marker-assisted selection (MAS)

Marker-Assisted Selection (MAS) involves using molecular markers linked to desirable traits to select individuals in breeding programs. MAS has been widely used in maize breeding to improve traits such as yield, disease resistance, and abiotic stress tolerance. The integration of MAS with other genomic technologies, such as QTL mapping and RNA-sequencing, has enhanced the efficiency of selecting superior genotypes. MAS is particularly effective for traits controlled by major QTLs, providing a targeted approach to breeding (Torkamaneh et al., 2021).

### 2.5 Genomic selection (GS)

Genomic Selection (GS) is a cutting-edge approach that uses genome-wide marker data to predict the breeding values of individuals. GS has revolutionized maize breeding by increasing genetic gains and reducing the number of breeding cycles required to develop new varieties. This method captures both major and minor genetic effects, making it suitable for complex traits. GS models have been refined to account for non-additive genetic effects, genotype-by-environment interactions, and other factors, further improving prediction accuracy. The integration of high-throughput phenotypic and genotypic data has made GS a powerful tool for accelerating maize breeding programs. By leveraging these genomic technologies, maize breeders can achieve significant improvements in crop performance, ensuring food security and sustainability in agriculture (Guo et al., 2019; Rice and Lipka, 2021; Merrick et al., 2022).

## 3 Techniques in Genomics-Assisted Breeding

### 3.1 Quantitative trait loci (QTL) mapping

QTL mapping is a fundamental technique used to identify genomic regions associated with specific phenotypic traits. This method involves crossing two genetically distinct lines to produce a mapping population, which is then genotyped and phenotyped to detect QTLs. For instance, QTL mapping has been instrumental in identifying loci associated with yield-related traits in maize, such as kernel weight and ear length (Zhao and Su, 2019). Additionally, meta-analysis of QTLs has been used to identify stable QTLs for traits like popping quality and disease resistance, which are crucial for marker-assisted selection (Kaur et al., 2021; Akohoue and Miedaner, 2022).

### 3.2 Genome-wide association studies (GWAS)

GWAS is a powerful approach that scans the entire genome to find genetic variants associated with traits of interest. This method utilizes high-density SNP arrays and large, diverse populations to detect associations between genetic markers and phenotypic traits. For example, GWAS has been used to identify SNPs linked to yield-related traits and kernel micronutrient concentrations in maize (Hindu et al., 2018; Zhang et al., 2020). Multi-trait GWAS approaches have also been effective in uncovering pleiotropic QTLs that influence multiple traits simultaneously, enhancing our understanding of complex trait architecture (Rice et al., 2020).

### 3.3 Transcriptomics and RNA-seq

Transcriptomics, particularly RNA-Seq, provides insights into gene expression patterns and regulatory networks underlying phenotypic traits. This technique involves sequencing the RNA transcripts in a sample to quantify gene expression levels. RNA-Seq has been used to validate candidate genes within QTL regions and to understand the genetic basis of traits such as kernel width and disease resistance (Zhao et al., 2022). By integrating transcriptomic data with QTL mapping, researchers can identify differentially expressed genes that contribute to trait variation.

### 3.4 CRISPR/Cas9 and gene editing

CRISPR/Cas9 is a revolutionary gene-editing technology that allows precise modifications of the genome. This technique has been applied to create targeted knockouts and insertions in maize, facilitating the study of gene function and the improvement of complex traits. For instance, the BREEDIT pipeline combines CRISPR/Cas9-mediated multiplex genome editing with traditional breeding to enhance traits like yield and drought tolerance (Lorenzo et al., 2022) (Figure 1). This approach accelerates the development of improved maize varieties by enabling the precise manipulation of multiple genes simultaneously.

Lorenzo et al. (2022) presents an innovative CRISPR/Cas9 multiplex genome editing pipeline designed to enhance maize growth by targeting 48 growth-related genes (GRGs). It employs a sophisticated approach that combines multiple gRNAs into vectors (SCRIPTs) and transforms Cas9-expressing lines (EDITOR lines) to create supertransformed plants. These plants undergo various crossing schemes to maximize the diversity of gene edits. High-throughput sequencing and bioinformatics workflows monitor gene edits, classify them into loss-of-function (LOF) categories, and facilitate genotype-to-phenotype associations. This method enables the systematic evaluation of the effects of multiple gene edits on plant growth, ultimately identifying key genes that significantly influence growth traits. The study demonstrates the potential of this pipeline to generate a large collection of higher-order mutants, providing a valuable resource for future research and trait improvement in maize.

### 3.5 Epigenomics

Epigenomics involves the study of heritable changes in gene expression that do not involve changes to the DNA sequence. These changes can be influenced by environmental factors and can affect traits such as stress tolerance and disease resistance. Epigenomic studies in maize have the potential to uncover novel regulatory mechanisms and epigenetic markers that can be used in breeding programs. Although specific studies on epigenomics in maize are less prevalent, integrating epigenomic data with other genomic techniques can provide a comprehensive understanding of trait regulation and inheritance.

In summary, genomics-assisted breeding in maize employs a suite of advanced techniques to dissect the genetic basis of important traits and to accelerate the development of improved varieties. By integrating QTL mapping,

GWAS, transcriptomics, CRISPR/Cas9, and epigenomics, researchers can enhance the precision and efficiency of breeding programs, ultimately contributing to increased crop productivity and resilience.
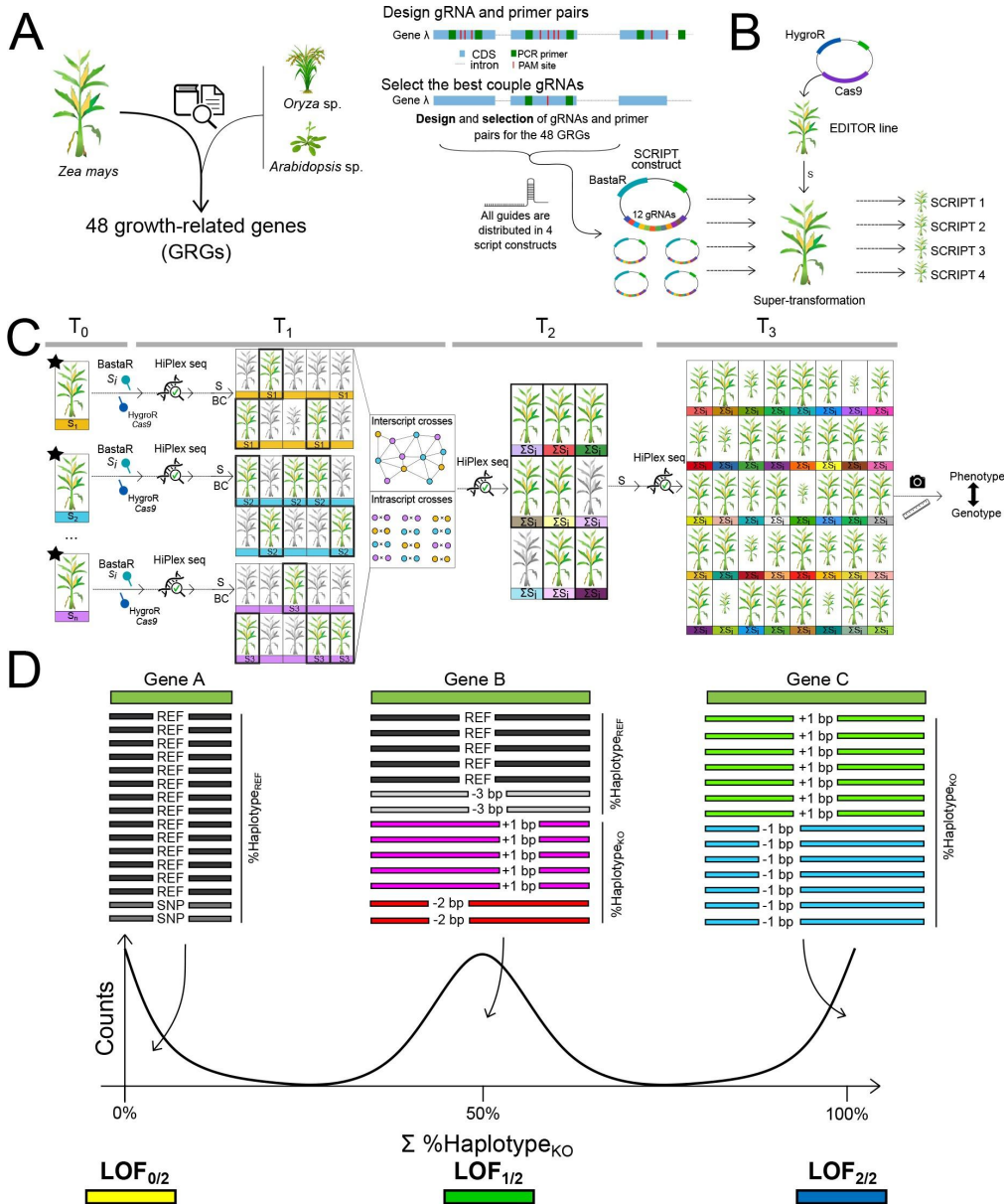


Figure 1 The multiplex gene editing strategy of BREEDIT (Adopted from Lorenzo et al., 2022)

Image caption: A: Selection of growth-related genes (GRGs) is based on published and in-house research in Arabidopsis, rice, or maize; B: Guide RNAs (gRNAs) with NGG protospacer adjacent motif (PAM) sites are chosen for each gene, PCR primer pairs are designed to resequence gRNA target sites and flanking regions using HiPlex amplicon sequencing; The best sets of gRNAs and primer pairs are selected, and twelve gRNAs are cloned into multiplex gene editing vectors (SCRIPTs); These SCRIPT constructs are then transformed into a Cas9-expressing maize line (EDITOR); C: Vigorous T0 plants containing both the SCRIPT (BASTA resistant) and the Cas9 EDITOR construct (hygromycin resistant) are genotyped using HiPlex amplicon sequencing. Based on the genotypes, plants are selected for various crosses: backcrosses with B104 (BC), intra-script crosses with plants having complementary mutations, and inter-script crosses with plants having different SCRIPTs and mutations in different gene families or pathways; These crosses aim to maximize mutation diversity; Self-crosses (S) produce segregating progeny for high-throughput phenotyping of selected traits, which are then associated with gene combinations; D: Sequencing reads are mapped to the B104 reference loci, deriving two read categories: haplotypeREF (aggregated reads with only SNPs, in-frame indels, or reference haplotype) and haplotypeKO (aggregated reads with out-of-frame indels). HaplotypeKO is divided into three loss-of-function (LOF) genotypic classes based on their tri-modal distribution: LOF0/2 (no out-of-frame indels, 0 chromosomes edited), LOF1/2 (one chromosome edited), and LOF2/2 (both chromosomes edited). (Adapted from Lorenzo et al., 2022)

## 4 Applications and Case Studies

### 4.1 Drought and heat tolerance

Drought and heat stress are significant challenges in maize production, particularly in tropical and subtropical regions. Genomics-assisted breeding has been pivotal in developing drought-tolerant maize varieties. Techniques such as rapid DNA and RNA sequencing, high-throughput SNP genotyping, and genomic selection have accelerated the breeding cycle and improved the genetic gain under stress conditions (Nepolean et al., 2018; Yuan et al., 2019; Liu and Qin, 2021) (Figure 2). For instance, a study involving genome-wide association mapping and genomic prediction analyses identified key genomic regions associated with grain yield and flowering time under drought stress, providing valuable insights for breeding stress-tolerant maize germplasm. Additionally, QTL analysis across multiple environments has revealed promising chromosome regions associated with yield-related traits under drought conditions, supporting marker-assisted breeding efforts.
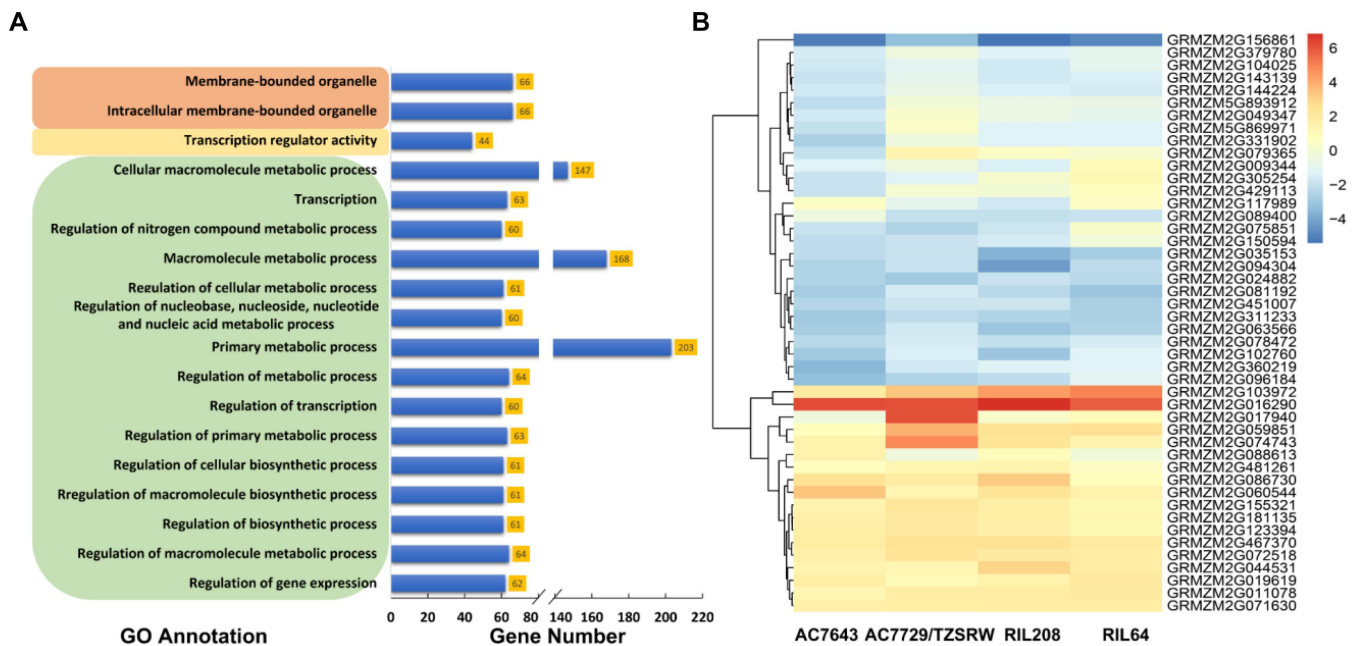


Figure 2 The results of gene ontology (GO)-based functional enrichment analysis (A) and the expression profiling analysis (B) (Adopted from Yuan et al., 2019)

Image caption: The GO terms in brown, yellow, and green colored boxes are cellular component, molecular function, and biological process categories, respectively. AC7643 and RIL208 are drought tolerance maize inbred lines, AC7729/TZSRW and RIL64 are drought sensitive maize inbred lines, and RIL 208 and RIL64 are derived from the cross of AC7643 and AC7729/TZSRW (Adopted from Yuan et al., 2019)

Yuan et al. (2019) focuses on identifying and analyzing candidate genes in maize that contribute to drought stress tolerance. Through gene ontology (GO) functional enrichment analysis, it highlights significant enrichment of genes involved in metabolic processes, cellular components, and transcription regulation. The expression profiling under drought conditions revealed 46 differentially expressed genes (DEGs) with notable changes in expression levels, correlating with drought tolerance across different maize lines. These findings emphasize the crucial role of specific genes, particularly transcription factors, in responding to drought stress. The research provides essential insights into the genetic basis of drought tolerance, which can inform breeding programs aimed at enhancing crop resilience.

### 4.2 Disease resistance

Genomics-assisted breeding has also been instrumental in enhancing disease resistance in maize. By leveraging genomic data, researchers can accelerate the resistance breeding process through family or population mapping and genomic selection (Miedaner et al., 2020). For example, significant progress has been made in breeding maize resistant to diseases such as Gibberella ear rot, Fusarium ear rot, and Northern corn leaf blight. These diseases are controlled by numerous QTL scattered across the genome, often located in hotspots (Miedaner et al., 2020).

Furthermore, genomic studies have identified SNPs associated with resistance to multiple diseases, including maize lethal necrosis, gray leaf spot, and turcicum leaf blight, facilitating the development of disease-resistant maize lines (Sadessa et al., 2022).

### 4.3 Nutritional quality improvement

Improving the nutritional quality of maize is another critical application of genomics-assisted breeding. Advances in genomic technologies have enabled the identification and manipulation of alleles associated with higher nutritional value. For instance, genomic breeding strategies aim to optimize crop genomes by accumulating beneficial alleles and purging deleterious ones, thereby enhancing the nutritional profile of maize cultivars (Varshney et al., 2021). This approach is expected to play a crucial role in breeding climate-smart crops with higher nutritional value in a cost-effective and timely manner.

### 4.4 Yield enhancement

Yield enhancement remains a primary goal in maize breeding. Genomics-assisted breeding has significantly contributed to this objective by identifying genomic regions associated with yield-related traits and developing high-yielding maize varieties. For example, a study on genomic prediction models demonstrated that effective genomic prediction of hybrid performance could be achieved with a small training set, enabling efficient exploration of genetic combinations for yield improvement (Guo et al., 2019). Additionally, QTL analysis has identified key chromosome regions associated with yield traits under various environmental conditions, supporting marker-assisted selection for yield enhancement (Hu et al., 2020).

### 4.5 Hybrid breeding

Hybrid breeding has benefited immensely from genomics-assisted approaches. The integration of genomic selection and other advanced breeding techniques has optimized the prediction of hybrid performance, leading to the development of superior hybrid maize varieties. For instance, genomic prediction models have been validated in multiple crops, including maize, demonstrating their effectiveness in predicting hybrid performance and facilitating the breeding of high-yielding hybrids (Guo et al., 2019) (Figure 3). Moreover, the identification of genomic regions associated with agronomic traits and disease resistance has further supported the development of robust hybrid maize lines (Sadessa et al., 2022).

Guo et al. (2019) explores the genomic relationships and phenotypic variations in maize by examining 24 inbred lines and 276 hybrids. Using principal component analysis (PCA) and hierarchical clustering, the research identifies distinct separation patterns between temperate and mixed (TM) and tropical and subtropical (TS) germplasm. The phenotypic evaluation of hybrids for traits like flowering time, ear height, and grain yield shows that inter-group hybrids (TM×TS) generally exhibit intermediate values for flowering time and ear height but display higher grain yield, indicating a heterosis effect. The variance component analysis reveals that additive genetic variance is more influential for flowering time and ear height, while dominance variance plays a larger role in grain yield. These findings highlight the potential of leveraging genomic diversity and specific hybrid combinations to enhance desirable traits in maize breeding programs.

In summary, genomics-assisted breeding has revolutionized maize breeding by providing advanced tools and techniques to address critical challenges such as drought and heat tolerance, disease resistance, nutritional quality improvement, yield enhancement, and hybrid breeding. The integration of genomic data and breeding strategies continues to accelerate the development of superior maize varieties, ensuring sustainable agricultural practices and food security.

## 5 Outcomes and Impact

### 5.1 Success stories in maize breeding

Genomics-assisted breeding (GAB) has led to significant advancements in maize breeding, particularly in developing disease-resistant and high-yielding varieties. For instance, the integration of genomic data has facilitated the breeding of maize varieties resistant to Gibberella ear rot (GER) and Fusarium ear rot (FER), which are major threats to maize production (Miedaner et al., 2020). Additionally, the use of genomic selection has enabled the prediction and selection of superior hybrids, significantly enhancing breeding efficiency and outcomes

(Cui et al., 2019). The development of affordable genotyping platforms, such as genotyping by target sequencing (GBTS), has further democratized access to advanced breeding technologies, benefiting small- and medium-sized breeding programs (Guo et al., 2019).
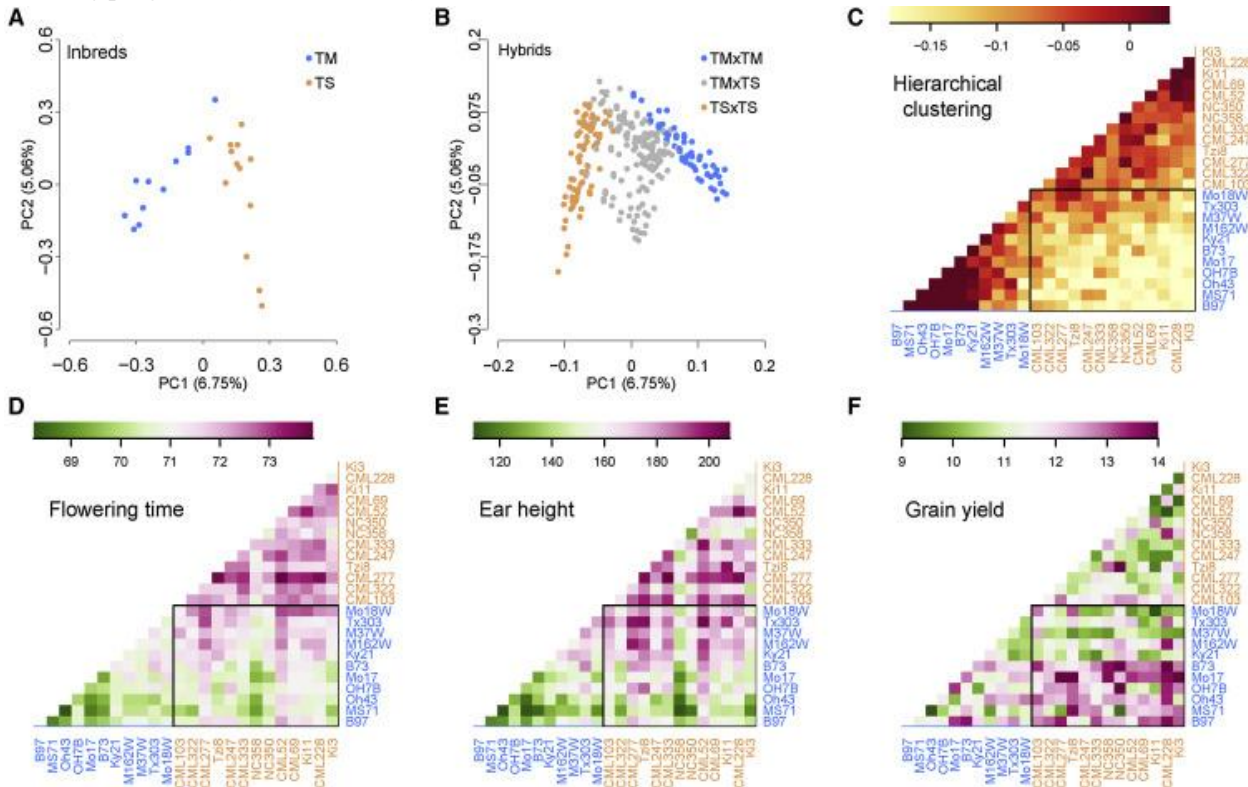


Figure 3 Patterns in Genomic Relationship and Phenotypes in Maize (Adopted from Guo et al., 2019)

Image caption: (A) PCA plot for 24 parental inbreds. TM, temperate and mixed; TS, tropical and subtropical. (B) PCA plot for 276 hybrids. Hybrids are color coded into TM × TM, TS × TS, and TM × TS. (C) Genomic relationship between inbreds in hierarchical cluster order. (D) Phenotypic values of hybrids for flowering time (days). (E) Ear height (cm). (F) Grain yield (Mg ha−1). For each hybrid in (D–F), inbred parents were ordered by hierarchical clustering. Inter-group hybrids (from factorial) were boxed in (D–F), and the corresponding genomic relationship section in (C). (Adopted from Guo et al., 2019)

## 5.2 Economic benefits
The economic benefits of genomics-assisted breeding in maize are substantial. By accelerating the breeding cycle and improving the accuracy of selection, GAB reduces the time and cost associated with developing new maize varieties. For example, the use of genomic selection models has been shown to increase genetic gains with fewer breeding cycles, translating to cost savings and higher productivity (Rice and Lipka, 2021). Moreover, the reduction in yield losses due to disease-resistant varieties, such as those resistant to ear rots, directly contributes to increased profitability for farmers (Gaikpa and Miedaner, 2019). The cost-benefit analysis of GBTS also indicates that genotypic selection is more cost-effective than traditional phenotypic selection, making advanced breeding technologies accessible to a broader range of breeding programs (Guo et al., 2019).

## 5.3 Environmental Sustainability
Genomics-assisted breeding contributes to environmental sustainability by enabling the development of maize varieties that are more resilient to biotic and abiotic stresses. For instance, breeding for drought tolerance using genomic tools helps ensure stable maize production in regions prone to water scarcity, thereby supporting sustainable agriculture (Nepolean et al., 2018). Additionally, the development of multi-disease resistant varieties reduces the need for chemical inputs, such as fungicides, thereby minimizing the environmental impact of maize cultivation (Miedaner et al., 2020). The integration of genomic data in breeding programs also facilitates the selection of climate-smart crop cultivars, which are better adapted to changing environmental conditions (Varshney et al. 2022).

### 5.4 Challenges and Limitations

Despite the successes, several challenges and limitations remain in the application of genomics-assisted breeding in maize. One major challenge is the need for large, well-characterized populations for accurate genomic selection, which can be resource-intensive to develop and maintain (Miedaner et al., 2020). Additionally, the complexity of quantitative traits, which are often controlled by multiple genes with small effects, poses a challenge for effective selection and breeding (Gaikpa and Miedaner, 2019). The integration of diverse data types, such as phenotypic, genotypic, and environmental data, into genomic selection models also requires sophisticated computational tools and expertise, which may not be readily available in all breeding programs (Rice and Lipka, 2021). Finally, the adoption of advanced genomic technologies in developing countries is often hindered by limited infrastructure and funding, highlighting the need for international collaboration and support (Guo et al., 2019).

While genomics-assisted breeding has revolutionized maize breeding with notable successes and economic benefits, ongoing efforts are needed to address the challenges and ensure the broad adoption and sustainability of these advanced breeding technologies.

## 6 Future Prospects

### 6.1 Advances in genomic technologies

The future of genomics-assisted breeding in maize is poised to benefit significantly from advances in genomic technologies. High-throughput sequencing technologies (HSTs) have revolutionized crop breeding by enabling the identification of beneficial quantitative trait loci (QTL), genes, and alleles for crop improvement (Farooqi et al., 2022). The integration of doubled haploid production, genomic selection, and genome optimization is expected to facilitate the evolution of maize breeding from an art to a science, and eventually to intelligence, in the Breeding 4.0 era (Jiang et al., 2019). These advancements will allow for the precise manipulation of allelic variation, creating novel diversity and facilitating rapid incorporation into crop improvement programs (Varshney et al., 2021).

### 6.2 Integration of multi-omics data

The integration of multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics, is crucial for enhancing the predictive ability of hybrid performance and improving crop traits (Schrag et al., 2018). Multi-omics approaches have been successfully implemented in various crops, including maize, to elucidate growth, senescence, yield, and responses to biotic and abiotic stress (Yang et al., 2021). The combination of different omics data can improve the prediction of hybrid performance, thereby contributing to more efficient selection of hybrid candidates. This integration is expected to address the challenges of abiotic stresses and enhance maize productivity (Farooqi et al., 2022).

### 6.3 Precision breeding

Precision breeding techniques, such as genome editing and synthetic biology, are set to play a pivotal role in the future of maize breeding. These techniques enable the precise assembly of desired alleles, allowing for the development of climate-resilient and nutrient-sufficient crops (Mahmood et al., 2022). The use of genomic tools and bioinformatics will further aid in the development of high-performance and well-adapted maize hybrids (Muntean et al., 2022). The concept of genomic design breeding, which incorporates genomic selection and genome optimization, will facilitate the creation of optimized genomes expressing optimal phenotypes (Jiang et al., 2019).

### 6.4 Regulatory and ethical considerations

As genomic technologies and precision breeding techniques advance, regulatory and ethical considerations will become increasingly important. The manipulation of genetic material raises questions about the safety and ethical implications of genetically modified organisms (GMOs). It is essential to establish robust regulatory frameworks to ensure the safe and responsible use of these technologies. Additionally, ethical considerations regarding the equitable distribution of benefits and access to advanced breeding technologies must be addressed to prevent disparities between different regions and communities.

## 6.5 Global collaboration and data sharing

Global collaboration and data sharing are vital for the success of genomics-assisted breeding in maize. The integration of multi-disciplinary technologies, including Big Data and artificial intelligence, requires extensive collaboration among researchers, breeders, and institutions worldwide (Jiang et al., 2019). Sharing genomic and phenotypic data across borders will accelerate the breeding process and enhance the development of superior maize cultivars. Collaborative efforts will also facilitate the exchange of knowledge and resources, ensuring that advancements in genomic technologies benefit a wide range of stakeholders.

In conclusion, the future of genomics-assisted breeding in maize is promising, with significant advancements in genomic technologies, multi-omics integration, precision breeding, and global collaboration. Addressing regulatory and ethical considerations will be crucial to ensure the responsible and equitable use of these technologies. By leveraging these advancements, maize breeding can achieve greater efficiency, resilience, and productivity, ultimately contributing to global food security.

# 7 Concluding Remarks

Genomics-assisted breeding (GAB) has revolutionized maize breeding by leveraging modern genomic tools to enhance germplasm and develop superior cultivars. The integration of genomic selection, genome optimization, and advanced phenotyping has significantly accelerated the breeding process, enabling the development of climate-resilient and high-yielding maize varieties. Key advancements include the use of high-density marker arrays for genomic selection, the incorporation of doubled haploid production and genome optimization, and the development of cost-effective genotyping platforms. These technologies have collectively improved the efficiency and accuracy of breeding programs, resulting in substantial genetic gains and the creation of maize cultivars with enhanced disease resistance, yield, and nutritional quality.

The future of maize breeding lies in the continued evolution and integration of genomics-assisted breeding techniques. The next phase, often referred to as GAB 2.0, will focus on the targeted manipulation of allelic variation to create novel diversity and optimize crop genomes. This will involve the use of advanced computational models and artificial intelligence to predict and design optimal genotypes. Additionally, the incorporation of multi-disease resistance (MDR) QTL and the development of climate-smart cultivars will be crucial in addressing the challenges posed by global climate change. The use of affordable and high-throughput genotyping platforms will further democratize access to advanced breeding technologies, enabling smaller breeding programs and developing countries to participate in the global effort to enhance food security. Overall, the future of maize breeding will be characterized by a more precise, efficient, and inclusive approach to developing superior maize cultivars.

**Conflict of Interest Disclosure**

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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