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The Integration of Genetic Markers in Maize Breeding Programs

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Abstract The integration of genetic markers in maize breeding programs has revolutionized the field by enabling precise and efficient selection of desirable traits. This research explores the advancements and applications of molecular breeding techniques, including marker-assisted selection (MAS) and genomic selection (GS), in enhancing maize productivity and resilience. Key developments include the identification and mapping of functional genes related to agronomic traits, the establishment of cost-effective genotyping platforms, and the implementation of innovative breeding schemes. These advancements have facilitated the rapid genetic improvement of maize, particularly in developing regions, by addressing critical challenges such as disease resistance, stress tolerance, and nutritional quality. The research also highlights the importance of genomic tools in understanding complex traits and the potential of integrating these tools with conventional breeding methods to achieve sustainable genetic gains. The collaborative efforts and capacity-building initiatives are crucial for the successful adoption and impact of these technologies in maize breeding programs globally.

Keywords Marker-Assisted selection (MAS); Genomic selection (GS); Maize breeding; Genetic markers; Molecular breeding

1 Introduction

Maize (*Zea mays*) is one of the most significant crops globally, serving as a staple food, animal feed, and a key component in biofuel production. Its versatility and high yield potential make it a critical resource for addressing global food security and agricultural sustainability. Maize's importance is underscored by its extensive cultivation across diverse climatic regions, from temperate to tropical zones, and its role in supporting the livelihoods of millions of farmers worldwide (Ortiz et al., 2010; Nuss and Tanumihardjo, 2010; Wang et al., 2022). The crop's adaptability and productivity are vital for meeting the increasing demands driven by population growth and environmental challenges (Ortiz et al., 2010; Wang et al., 2022).

Genetic markers are specific sequences of DNA that can be used to identify particular genes or traits within an organism. These markers have revolutionized plant breeding by enabling the precise selection of desirable traits, thereby accelerating the development of improved crop varieties. The use of genetic markers in maize breeding has evolved significantly over the past few decades. Initially, simple sequence repeats (SSRs) and restriction fragment length polymorphisms (RFLPs) were commonly used. However, advancements in genomic technologies have led to the adoption of more sophisticated markers such as single nucleotide polymorphisms (SNPs) and the application of genome-wide association studies (GWAS) (Xu and Crouch, 2008; Prasanna et al., 2010; Vivodík et al., 2017). These tools have enhanced our understanding of the genetic architecture of important traits and facilitated marker-assisted selection (MAS) in breeding programs (Xu and Crouch, 2008; Prasanna et al., 2010; Baye et al., 2022).

This study provide a comprehensive overview of the integration of genetic markers in maize breeding programs, explores the historical context and technological advancements that have shaped current practices, highlight the key genetic markers used in maize breeding, and discuss their applications in improving yield, stress resistance, and other agronomically important traits. The study will also address the challenges and opportunities associated with the use of genetic markers, including the need for improved germplasm conservation and the potential of emerging technologies such as CRISPR-Cas for future breeding efforts. By synthesizing current knowledge and recent advancements, This study provides information and guidance for future research and breeding strategies to enhance maize productivity and sustainability.

2 Types of Genetic Markers and Their Applications in Maize Breeding

2.1 Simple sequence repeats (SSR) markers

Simple sequence repeats (SSRs), also known as microsatellites, are short, tandemly repeated DNA sequences that are highly polymorphic and distributed throughout the genome. They are co-dominant markers, meaning they can distinguish between homozygous and heterozygous states, which is particularly useful in breeding programs. SSRs are easy to score, highly abundant, and provide high-resolution genome coverage. For instance, a study identified 264 658 SSRs across 17 maize genomes, with an average marker density of one SSR every 15.48 kb, highlighting their abundance and utility in genetic studies (Xu et al., 2013). Additionally, SSR markers exhibit high levels of polymorphism, which is beneficial for assessing genetic diversity and relatedness among maize lines (Hamblin et al., 2007).

SSRs have been extensively used in maize breeding for various applications, including genetic diversity analysis, germplasm characterization, and marker-assisted selection. They are particularly effective in clustering germplasm into populations and measuring genetic distances based on allele-sharing (Hamblin et al., 2007). SSR markers have also been employed to map quantitative trait loci (QTLs) and to assist in the selection of desirable traits in breeding programs. For example, SSR markers have been used to estimate genetic diversity among maize inbred lines, providing valuable information for breeding strategies (Shehata et al., 2009). Moreover, SSRs have been integrated into high-density genetic linkage maps, facilitating the identification of genomic regions associated with important agronomic traits (Daware et al., 2016).

2.2 Single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are single base-pair variations in the DNA sequence that occur throughout the genome. SNPs are the most abundant type of genetic variation and can be detected using high-throughput genotyping technologies. They offer several technical advantages, including higher data repeatability, lower levels of missing data, and the ability to detect expected alleles in hybrids and DNA pools. For instance, SNP marker data showed more than a fourfold lower level of missing data compared to SSRs and higher repeatability rates (Jones et al., 2007). These characteristics make SNPs highly suitable for large-scale genotyping and genetic studies.

SNPs have been increasingly used in hybrid maize development due to their high density and the ability to provide detailed genetic information. They are particularly useful in assessing genetic diversity and relatedness among maize lines, which is crucial for hybrid breeding. Although SSRs performed better at clustering germplasm into populations, SNPs can compensate for their lower polymorphism by increasing the number of loci analyzed (Hamblin et al., 2007). SNP markers have been successfully used to genotype maize inbreds and hybrids, providing valuable insights into the genetic makeup and aiding in the selection of parent lines for hybrid development (Jones et al., 2007).

2.3 Other molecular markers

Other molecular markers, such as random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP), have also been used in maize breeding. RAPD markers are based on the amplification of random DNA segments, while AFLP markers involve the selective amplification of restriction fragments. These markers are generally dominant, meaning they cannot distinguish between homozygous and heterozygous states. However, they are useful for generating a large number of markers quickly and can be applied to a wide range of species without prior sequence information.

RAPD and AFLP markers have been used in specific breeding scenarios where rapid and cost-effective genotyping is required. They are particularly useful in early-stage breeding programs for preliminary genetic mapping and diversity studies. For example, RAPD markers have been employed to assess genetic diversity in maize germplasm collections, providing initial insights into the genetic structure of the populations. AFLP markers have been used for high-resolution mapping and the identification of QTLs associated with important traits. Although these markers are less commonly used than SSRs and SNPs in modern breeding programs, they still offer valuable tools for specific applications where their unique characteristics are advantageous.

By integrating various types of genetic markers, maize breeding programs can leverage the strengths of each marker system to enhance the efficiency and precision of breeding efforts.

3 Integration of Marker-Assisted Selection (MAS) in Maize Breeding

3.1 Basic principles of marker-assisted selection (MAS)

Marker-Assisted Selection (MAS) is a process that uses molecular markers to select desirable traits in plant breeding. The fundamental principle of MAS involves identifying and using DNA markers that are closely linked to genes controlling important agronomic traits. These markers can be used to track the presence of these genes in breeding populations, thereby accelerating the selection process and improving the accuracy of breeding programs (Mohan et al., 1997; Collard et al., 2005; He et al., 2014). MAS integrates molecular genetics with traditional phenotypic selection, allowing breeders to make more informed decisions and achieve genetic gains more efficiently (Lande and Thompson, 1990; Francia et al., 2005).

3.2 Application of MAS in quality improvement

Quality Protein Maize (QPM) is a notable example of MAS application in improving maize quality. QPM contains the *opaque2* (*o2*) gene, which enhances the levels of essential amino acids like lysine and tryptophan, addressing the nutritional deficiencies of normal maize (Babu et al., 2005; Kaur et al., 2020).

In a study, a two-generation marker-based backcross breeding program was employed to incorporate the *o2* gene into an early maturing normal maize inbred line, V25. This program utilized flanking markers to optimize population size and ensure the recovery of the recurrent parent genome. The resulting BC2F3 lines showed significant enhancement in tryptophan concentration, demonstrating the effectiveness of MAS in developing QPM with desirable agronomic and biochemical traits (Babu et al., 2005).

Another study focused on improving four maize inbred lines by introgressing the *o2* allele using marker-assisted backcross breeding. The converted QPM lines exhibited high tryptophan content and maintained grain yield comparable to the original hybrids, highlighting the potential of MAS in tackling protein-energy malnutrition in developing countries (Kaur et al., 2020).

3.3 Application of MAS in resistance breeding

MAS has been extensively used in breeding for disease and pest resistance in maize. By identifying markers linked to resistance genes, breeders can efficiently select for these traits, reducing the reliance on phenotypic screening, which can be time-consuming and less accurate (Moreau et al., 1997; Francia et al., 2005; Gupta et al., 2010).

For instance, MAS has been applied to improve resistance to various pathogens and pests by incorporating resistance genes into elite maize lines. This approach not only accelerates the breeding process but also ensures the stability and durability of resistance traits across different environments (Moreau et al., 1997; Gupta et al., 2010).

3.4 Economic benefit analysis of MAS

The economic benefits of MAS in maize breeding are significant. While the initial costs of developing and implementing MAS, including genotyping and marker development, can be high, the long-term benefits often outweigh these costs. MAS can substantially reduce the time required to develop new varieties, leading to faster commercialization and increased profitability (He et al., 2014; Francia et al., 2005; Hasan et al., 2021).

MAS also enhances the precision of selection, reducing the number of breeding cycles needed to achieve desired traits. This efficiency translates into cost savings in terms of labor, field trials, and other resources (Lande and Thompson, 1990; Moreau et al., 2004). Additionally, the ability to stack multiple traits using MAS can lead to the development of superior varieties with combined resistance to diseases, pests, and improved nutritional quality, further increasing the economic returns (Moreau et al., 1997; Gupta et al., 2010).

Several case studies illustrate the economic benefits of MAS in maize breeding. For example, the development of QPM using MAS not only improved the nutritional quality of maize but also demonstrated cost-effectiveness by reducing the breeding cycle time and minimizing genetic drag (Figure 1) (Babu et al., 2005; Kaur et al., 2020).

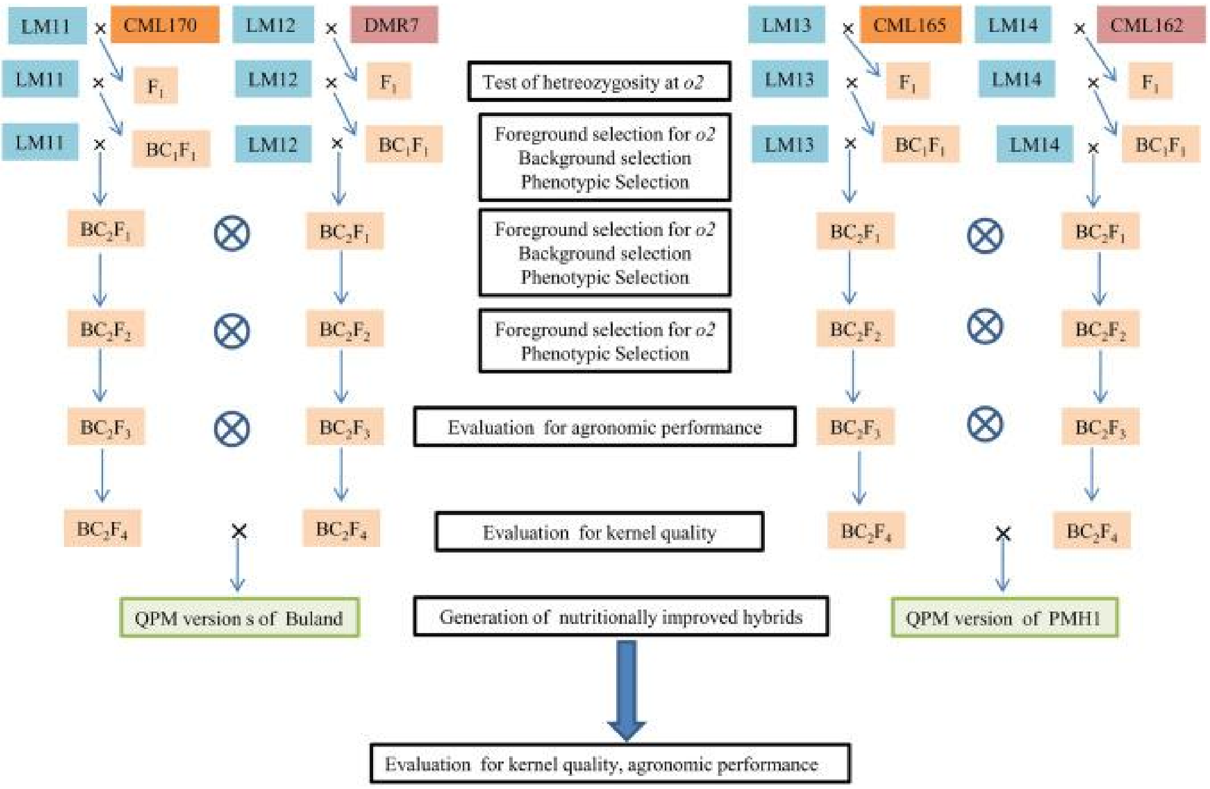

Figure 1 A schematic representation of simultaneous conversion of four normal inbreds to QPM versions and development of QPM hybrids (Adapted from Kaur et al., 2020)

Image caption: This diagram illustrates the process of improving maize varieties to obtain Quality Protein Maize (QPM) versions through marker-assisted selection (MAS). The diagram shows the backcross breeding process (BC) using different inbred lines (e.g., CML170, CML165, etc.), with foreground selection for the *o2* gene, background selection, and phenotypic selection. After several generations of backcrossing, the diagram also shows the generation of hybrids and the evaluation of kernel quality and agronomic traits, ultimately leading to the development of improved QPM varieties (Adapted from Kaur et al., 2020)

Another case study compared the efficiency of MAS and conventional phenotypic selection in maize. The study found that MAS significantly increased the rate of genetic gain and selection efficiency, particularly when combined with phenotypic selection. Although the initial costs of MAS were higher, the overall economic benefits, including increased yield and improved trait stability, justified the investment (Moreau et al., 2004).

In conclusion, the integration of MAS in maize breeding programs offers substantial economic benefits by enhancing the efficiency and accuracy of selection, reducing breeding cycle times, and improving the overall quality and resilience of maize varieties. These advantages make MAS a valuable tool in modern plant breeding, with the potential to address both agronomic and nutritional challenges in maize production.

4 Challenges in the Integration of Genetic Markers

4.1 Technical challenges

One of the primary technical challenges in integrating genetic markers is the accuracy of these markers. While platforms like genotyping by target sequencing (GBTS) have shown high consistency in marker genotypes and phylogenetic relationships, there are still limitations. For instance, the effectiveness of certain markers can be influenced by genetic background and environmental factors, which can lead to inaccuracies in marker-assisted selection (MAS) (Guo et al., 2019; Chen et al., 2022). Additionally, the complexity of the maize genome, with its high level of duplication and repetitive sequences, can impede the development of true single nucleotide polymorphism (SNP) markers, further complicating the accuracy of genetic markers (Mammadov et al., 2014).

The genetic diversity and complexity of maize present another significant challenge. Maize breeding programs often deal with a wide range of genetic backgrounds, which can affect the performance and reliability of genetic markers. For example, the genetic structure of early and extra-early maturing maize germplasm in sub-Saharan Africa is highly complex, making it difficult to classify inbred lines into heterotic groups solely based on molecular markers (Badu-Apraku et al., 2021). This complexity necessitates the use of comprehensive genotyping and phenotyping to ensure accurate selection and breeding outcomes (Romay et al., 2013; Gedil and Menkir, 2019).

4.2 Cost and resource limitations

The integration of genetic markers into breeding programs requires significant infrastructure and resources. High-throughput genotyping platforms, such as those used for developing SNP marker panels, demand advanced laboratory facilities and technical expertise (Guo et al., 2019). The cost of these technologies, although decreasing, can still be prohibitive, especially for large-scale breeding programs. Additionally, the need for extensive field trials and phenotyping to validate marker effectiveness adds to the resource burden (Cooper et al., 2014).

Small and medium-sized breeding companies face unique challenges in adopting genetic marker technologies. The high initial investment in infrastructure and the ongoing costs of genotyping and phenotyping can be a significant barrier. However, affordable genotyping platforms like GBTS have shown promise in making marker-assisted breeding more accessible to these companies (Guo et al., 2019). Despite this, the integration of these technologies into existing breeding programs requires substantial training and capacity building, which can be a limiting factor for smaller enterprises (Gedil and Menkir, 2019).

4.3 Social and ethical issues

The use of genetic markers in breeding programs often intersects with the broader debate on genetic modification (GM). While marker-assisted selection does not necessarily involve the creation of genetically modified organisms (GMOs), the public perception of genetic technologies can influence the acceptance and adoption of these methods. Concerns about the safety and ethical implications of genetic modification can lead to resistance from consumers and regulatory bodies, impacting the implementation of marker-assisted breeding (Chen et al., 2022).

There are also concerns about the environmental impact of using genetic markers in breeding programs. The introduction of new traits through marker-assisted selection can potentially affect biodiversity and ecosystem balance. For instance, the development of drought-tolerant maize hybrids involves the integration of multiple traits, which could have unforeseen ecological consequences (Cooper et al., 2014). Ensuring that these breeding practices do not negatively impact the environment requires careful consideration and ongoing monitoring.

In conclusion, while the integration of genetic markers in maize breeding programs offers significant potential for improving crop traits and productivity, it is accompanied by a range of challenges. Addressing these challenges requires a multifaceted approach that includes technical innovation, resource investment, and consideration of social and ethical implications. By navigating these complexities, breeding programs can harness the full potential of genetic markers to achieve sustainable agricultural advancements.

5 Case Studies and Success Stories

5.1 Quality protein maize (QPM) breeding programs

Quality Protein Maize (QPM) has been a significant breakthrough in addressing protein malnutrition, particularly in developing countries. The genetic basis of QPM involves the *opaque-2* (*o2*) mutation, which increases lysine and tryptophan content in maize endosperm. However, the initial *o2* mutation resulted in undesirable agronomic traits such as soft, chalky kernels that were prone to damage and poor germination. To overcome these challenges, breeders combined the *o2* allele with genetic modifiers to develop QPM genotypes with hard kernels and high nutritional quality (Tripathy et al., 2017).

In India, the development of Vivek QPM-9, a hybrid of two QPM introgression lines, has been a notable success. This hybrid, developed through marker-assisted selection (MAS), has been widely adopted for commercial cultivation. Vivek QPM-9 not only retains high lysine and tryptophan content but also exhibits early maturity and high yield, making it suitable for various agro-climatic conditions (Gupta et al., 2009). Similarly, in sub-Saharan Africa, QPM hybrids have played a crucial role in combating malnutrition. The development of early maturing yellow-endosperm QPM inbreds and their evaluation under multiple environments, including Striga-infested and drought conditions, has led to the identification of stable and high-yielding hybrids (Badu-Apraku et al., 2015).

5.2 Success stories in hybrid development

The integration of genetic markers in maize breeding programs has significantly accelerated the development of QPM hybrids. Marker-assisted backcrossing has been employed to rapidly convert normal maize lines to QPM. For instance, a two-generation marker-based backcross breeding program successfully incorporated the *o2* gene into an early maturing normal maize inbred line, resulting in QPM lines with enhanced tryptophan concentration and desirable agronomic traits (Babu et al., 2005).

Another success story involves the pyramiding of the *o2* and novel *opaque16* (*o16*) genes to further enrich lysine and tryptophan content in sub-tropical maize. This approach led to the development of QPM hybrids with significantly higher nutritional quality compared to their original versions. The reconstituted hybrids showed an average enhancement of 49% and 60% in lysine and tryptophan content, respectively, while maintaining similar grain yield and agronomic traits (Sarika t al., 2018).

In the Democratic Republic of Congo, a QPM breeding program developed 137 inbred lines adapted to various agro-ecological conditions. These lines exhibited high genetic variability and were selected based on agro-morphometric characteristics and molecular markers. The program is developing QPM varieties with high grain yield and resistance to local diseases and pests, contributing to increased grain production and improved nutritional security (Mbuya et al., 2012).

5.3 Successful practices in different regions and countries

The success of QPM breeding programs varies across regions and countries, depending on local agro-climatic conditions and breeding strategies. In India, the use of SSR markers has been effective in differentiating QPM inbred lines and analyzing their genetic relationships. This has facilitated the utilization of elite QPM germplasm in breeding programs, leading to the development of high-yielding and nutritionally enriched hybrids (Bantte and Prasanna, 2003).

In southern Africa, the heritability and associations among grain yield and quality traits in QPM and non-QPM hybrids have been studied to inform breeding decisions. The findings suggest that ear aspect, ears per plant, and starch content are major traits contributing to grain yield. However, the negative association between grain yield and tryptophan content poses a challenge in developing hybrids with both high yield and high nutritional quality. Gene pyramiding is recommended to address this challenge (Figure 2) (Amegbor et al., 2022).

Despite the successes, the adoption of QPM varieties has been limited in some regions due to challenges such as the need for isolation from normal maize and minimal collaboration between breeders, farmers, and other stakeholders. To enhance adoption, participatory plant breeding (PPB) and participatory variety selection (PVS) approaches are recommended. These approaches involve farmers and other stakeholders in the breeding process, ensuring that the developed varieties meet local needs and preferences (Tandzi et al., 2017).

In conclusion, the integration of genetic markers in maize breeding programs has led to significant advancements in the development of QPM hybrids. Success stories from different regions highlight the potential of QPM to address protein malnutrition and improve food security. However, continued efforts are needed to overcome adoption challenges and ensure the widespread cultivation of QPM varieties.

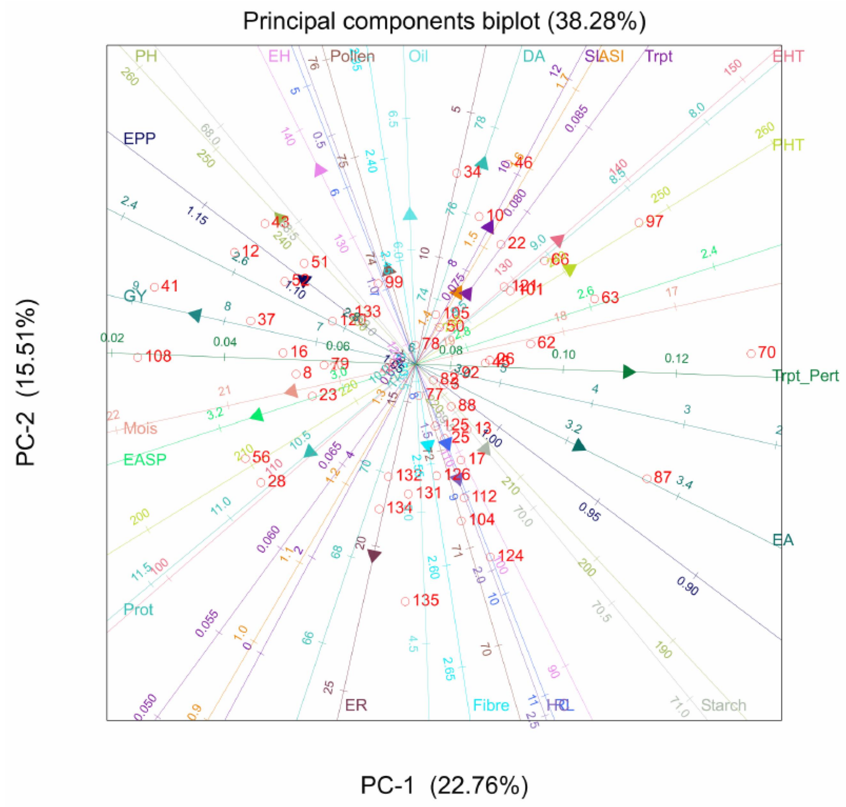

Figure 2 Principal component analysis biplot of genotype by quality traits of 135 QPM and non-QPM hybrids evaluated across six locations (Adopted from Amegbor et al., 2022)

Image caption: Trypt_Pert: tryptophan; Prot: protein (Adopted from Amegbor et al., 2022)

6 Future Directions and Prospects

6.1 Advances in technology and emerging marker technologies

The integration of genetic markers in maize breeding programs has been significantly advanced by recent technological innovations. One notable development is the genotyping by target sequencing (GBTS) platform, which offers high-throughput genotyping with high quality, flexibility, and affordability. This platform can handle a range of marker numbers, from a few to 45 000, through multiplex PCR and in-solution capture methods. The GBTS platform has demonstrated high consistency in marker genotypes and phylogenetic relationships, making it a reliable and cost-effective tool for marker-assisted breeding (Guo et al., 2019).

Additionally, genomic selection (GS) has emerged as a powerful tool in maize breeding. GS uses genome-wide marker data to estimate breeding values, leading to increased genetic gains with fewer breeding cycles. The sophistication of high-throughput phenotypic, genotypic, and other -omic level data currently available allows for more accurate predictions of breeding values. This technology is particularly beneficial in developing superior maize inbreds and hybrids (Rice and Lipka, 2021).

Moreover, advancements in molecular marker-assisted breeding have shown promise in improving maize production in regions like sub-Saharan Africa and Asia. These technologies have been used for DNA fingerprinting, genetic diversity analysis, QTL analysis, and marker-assisted selection (MAS) to address biotic and abiotic stresses, thereby enhancing the productivity and value of maize germplasm (Stevens, 2008).

6.2 Future challenges and solutions for marker integration

Despite the promising advancements, several challenges remain in the integration of genetic markers into maize breeding programs. One major challenge is the need for cost-effective and scalable genotyping platforms that can be widely adopted by small- and medium-sized breeding companies and in developing countries. The GBTS platform addresses this challenge by offering a lower genotypic selection cost compared to phenotypic selection, making it an affordable option for marker-assisted breeding (Guo et al., 2019).

Another challenge is the complexity of coordinating multiple targets within a single breeding program. The identification and validation of quantitative trait loci (QTLs) associated with key traits such as grain quality and yield are crucial. Meta-QTL analysis and genome-wide association studies (GWAS) have been used to identify breeding-friendly QTLs, which can be further utilized to model plant architecture and enhance desirable traits through marker-assisted breeding, genetic engineering, and genome editing (Figure 3)(Sethi et al., 2023).

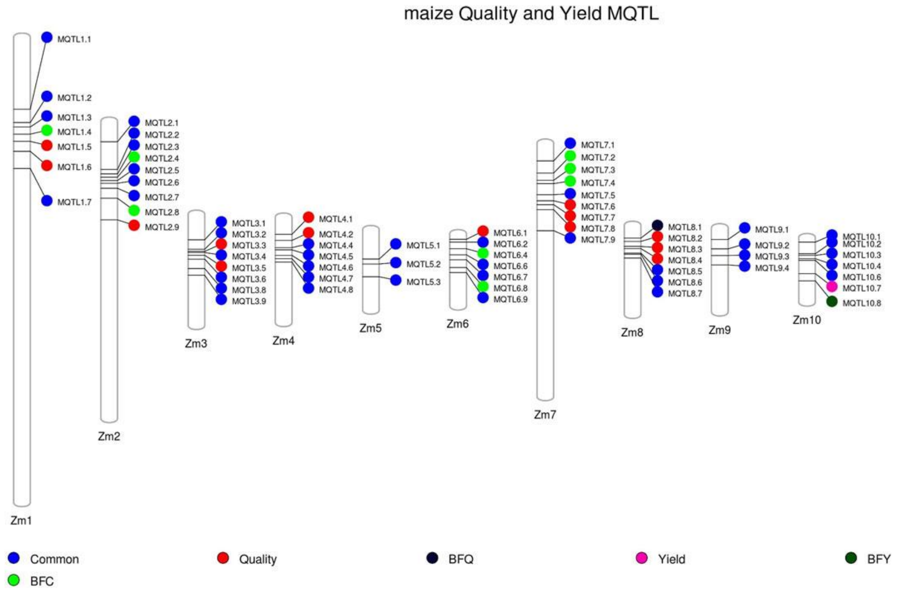

Figure 3 Distribution of MQTLs on different maize chromosomes (Adopted from Sethi et al., 2023)

Image caption: MQTLs associated with both quality and yield-associated traits, BFQ: breeder-friendly quality trait MQTLs, BFY: breeder-friendly yield trait MQTLs, BFC: breeder-friendly common MQTLs (involving both quality and yield-related traits) (Adopted from Sethi et al., 2023)

Furthermore, the successful implementation of molecular marker-assisted breeding requires innovative models for resource-pooling and intellectual-property-respecting partnerships. These models are essential for enhancing the level and scope of molecular marker-assisted breeding, particularly in regions with limited resources (Prasanna et al., 2010).

6.3 Prospects and Potential in Global Maize Breeding Programs

The prospects for integrating genetic markers in global maize breeding programs are promising. In Africa, the integration of molecular and conventional breeding schemes has led to remarkable genetic gains, addressing critical issues such as drought, diseases, and parasitic weeds. The use of genomic tools for genetic dissections of complex traits and the implementation of marker-aided selection and genome-wide selection schemes are expected to accelerate genetic gains and improve the resilience and nutritional quality of maize (Gedil and Menkir, 2019).

In Asia, molecular marker-assisted breeding has the potential to meet the growing demand for maize by enhancing the productivity and value of maize germplasm. Efforts in DNA fingerprinting, genetic diversity analysis, and QTL analysis are crucial for developing commercially viable cultivars that can address the most important constraints to maize production in the region (Prasanna et al., 2010).

Globally, the use of genome-wide selection (GWS) for quantitative traits in maize has shown superior results compared to traditional marker-assisted recurrent selection (MARS). GWS allows for marker-based selection without the need to identify a subset of markers with significant effects, leading to larger responses to selection and more efficient breeding processes (Bernardo and Yu, 2007).

In conclusion, the integration of genetic markers in maize breeding programs holds great potential for improving maize production worldwide. Advances in technology, innovative breeding schemes, and collaborative efforts will be key to overcoming challenges and realizing the full benefits of marker-assisted breeding in maize.

7 Concluding Remarks

The integration of genetic markers in maize breeding programs has shown significant promise in enhancing the efficiency and effectiveness of breeding efforts. The development of high-throughput genotyping platforms, such as genotyping by target sequencing (GBTS), has made marker-assisted breeding more affordable and accessible, particularly for small- and medium-sized enterprises and developing countries. The identification of quantitative trait loci (QTLs) and meta-QTLs (MQTLs) associated with grain quality and yield-related traits has provided valuable insights into the genetic framework of maize, enabling the selection of breeding-friendly MQTLs for future breeding programs. Genomic selection (GS) has emerged as a powerful tool, leveraging genome-wide marker data to estimate breeding values and accelerate genetic gains. The characterization of functional genes and their integration into breeding programs has further enhanced the ability to improve important agronomic traits. Additionally, the modernization of breeding programs through the integration of molecular and conventional breeding techniques has shown potential in addressing the challenges faced by maize production in regions such as West and Central Africa.

The long-term impact of integrating genetic markers in maize breeding programs is profound. The use of molecular markers has enabled more precise and efficient selection processes, leading to the development of superior maize varieties with enhanced yield, quality, and stress tolerance. The ability to identify and utilize specific genetic regions associated with desirable traits has accelerated the breeding cycle, reducing the time required to develop new varieties. Furthermore, the integration of genomic tools and high-throughput phenotyping has facilitated the understanding of complex traits and their genetic architecture, enabling the development of maize varieties that are better adapted to diverse environmental conditions. The continuous improvement of genotyping platforms and the increasing availability of genomic data will further enhance the ability to achieve genetic gains and address future challenges in maize production.

Future research should focus on expanding the catalog of functional genes and QTLs associated with important agronomic traits in maize. This includes the identification and characterization of new genetic markers and the development of high-throughput genotyping platforms to reduce the cost and increase the efficiency of MAS and GS. Additionally, integrating advanced genomic tools such as genome editing and genetic engineering with traditional breeding methods will enable the precise manipulation of target genes, further enhancing the genetic improvement of maize. Collaborative efforts between public and private sectors will be crucial in translating these advancements into practical breeding applications, ultimately leading to the development of superior maize varieties that can meet the growing demands of the global population.

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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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