

Trends in Maize Genomic Research: Past, Present, and Future

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Abstract Maize (*Zea mays*) is one of the most important food crops globally, playing a crucial role in agriculture, food security, and biofuel production. Due to its significance, maize genomics research has gradually become a focal point of scientific inquiry. From early genetic studies to modern molecular biology technologies, significant progress has been made in maize genome research, driving advancements in breeding and crop improvement. This study reviews the historical progress of maize genomics research and analyzes current trends in genomics, particularly breakthroughs in genome sequencing, functional genomics, gene editing, systems biology, and epigenomics. It also explores the impact of these studies on maize crop improvement, genetic diversity conservation, and addressing global challenges such as climate change and food security. The research indicates that technologies like maize genome sequencing and CRISPR gene editing have significantly accelerated the breeding process, enhancing stress resistance, yield, and nutritional value. Furthermore, multi-omics integration and the application of systems biology have revealed the complexity of the maize genome and regulatory networks, providing new opportunities for personalized agriculture and precision breeding. Maize genomics not only provides critical genetic information for crop improvement but also offers new solutions for tackling global issues like food security, climate change, and nutritional enhancement. By systematically summarizing past and current research achievements, this study lays the theoretical foundation for the broad application of maize genomics in agriculture and uncovers the potential for precision breeding and personalized agriculture.

Keywords Maize; Gene editing; Functional genomics; Crop improvement; Precision breeding

1 Introduction

Maize (*Zea mays* L.) is a cornerstone of global agriculture, serving as a vital source of food, feed, and fuel (Huang, 2024). Its significance is underscored by its extensive cultivation and the sheer volume of its production, which has reached over one billion tons annually (Yan and Tan, 2019). As a staple crop, maize is integral to the diets of millions, particularly in developing regions such as sub-Saharan Africa, where it constitutes a primary food source and a critical component of food security (Anami et al., 2009). The historical impact of maize research on agriculture and plant biology is profound. From its domestication from teosinte to its current status as a model organism in plant science, maize has been at the forefront of agricultural innovation and scientific discovery (Liu et al., 2019). The development of high-yielding, stress-tolerant varieties has been pivotal in meeting the growing global demand for food, feed, and bioenergy (Ortiz et al., 2010).

Genomic research in maize encompasses the study of its genetic makeup to understand and manipulate its traits for improved performance. This field has seen significant advancements, particularly with the advent of genomic tools and technologies. Key milestones include the sequencing of the maize genome, which has provided a comprehensive blueprint for genetic improvement (Muntean et al., 2022). The integration of genomic approaches with traditional breeding has accelerated the development of maize varieties with enhanced traits such as drought tolerance, disease resistance, and improved nutritional quality (Anami et al., 2009; Yang and Yan, 2021). The use of CRISPR/Cas9 technology and other genome editing tools has further revolutionized maize breeding, enabling precise modifications to meet specific agricultural needs (Dong et al., 2019; Kausch et al., 2021).

This study explores the development trends in maize genomics research, tracing its evolution from past achievements to current advancements and future prospects. By examining the trajectory of maize genomics, it highlights the key developments and emerging technologies that have shaped and influenced maize research. This

study contributes to a deeper understanding of how genomic research has transformed maize breeding and its potential to address future agricultural challenges. Through a comprehensive analysis of existing literature, this study provides insights into the ongoing efforts to enhance maize productivity and resilience, ultimately supporting global food security and sustainable agriculture.

2 Historical Perspectives: Early Maize Genomic Research

2.1 Beginnings of maize genetics

The study of maize genetics has its roots in the foundational principles of Mendelian genetics. Early geneticists utilized maize to test and validate Mendel's laws of inheritance, making it a cornerstone species in the field of genetics. The visible morphological mutants in maize, often referred to as "freaks," played a significant role in these early studies, providing clear phenotypic markers that facilitated the understanding of genetic inheritance (Richardson and Hake, 2022).

Several key discoveries in the early 20th century laid the groundwork for maize genomic research. The development of the first genetic and cytogenetic maps of maize was a pivotal milestone. These maps were instrumental in understanding the chromosomal basis of inheritance and paved the way for future genomic studies (Richardson and Hake, 2022). Additionally, the identification of transposable elements by Barbara McClintock in maize was a groundbreaking discovery that highlighted the dynamic nature of the genome and its ability to undergo structural changes (Kausch et al., 2021).

2.2 Development of classical genetic tools

Classical breeding techniques have been fundamental in maize research, particularly in the development of high-yielding and disease-resistant varieties. These techniques involved the selection and cross-breeding of plants with desirable traits, which led to significant improvements in maize productivity and adaptation to various environmental conditions. The advent of modern plant breeding in the 1930s marked a period of dramatic adaptation in North American maize, driven by high-input agricultural practices (Heerwaarden et al., 2012).

Early cytogenetic studies in maize involved the detailed examination of chromosome structure and behavior during cell division. These studies were crucial in constructing the first chromosome maps, which provided a visual representation of the genetic loci along the chromosomes. The alignment of physical and genetic maps further enhanced the understanding of genome organization and facilitated the identification of genes associated with important traits (Wei et al., 2007).

2.3 Transition to molecular genetics

The introduction of molecular tools revolutionized maize research by enabling more precise genetic manipulation and analysis. Techniques such as DNA sequencing, molecular markers, and genetic transformation systems allowed researchers to dissect the genetic basis of complex traits and improve maize varieties more efficiently. The development of maize transformation technology, including the use of CRISPR/Cas9 for genome editing, has significantly accelerated functional genomics research and genetic improvement strategies (Kausch et al., 2021).

One of the most notable milestones in maize molecular genetics was the discovery of transposable elements by Barbara McClintock. These mobile genetic elements, which can move within the genome, were first identified in maize and have since been recognized as a major force in genome evolution and diversity. This discovery not only provided insights into the mechanisms of genetic variation but also underscored the complexity of the maize genome (Jiao et al., 2017; Kausch et al., 2021).

2.4 Early genomic mapping efforts

The development of early genetic maps in maize was a significant achievement that laid the foundation for modern genomic research. These maps, constructed using molecular markers and linkage analysis, provided a framework for locating genes associated with important agronomic traits. The first-generation haplotype map of maize, for example, revealed the high chromosomal diversity and recombination rates that characterize the maize genome, highlighting the importance of genetic mapping in understanding trait inheritance (Gore et al., 2009).

Quantitative trait loci (QTL) mapping has been instrumental in dissecting the genetic architecture of complex traits in maize. By identifying regions of the genome associated with variation in traits such as yield, disease resistance, and stress tolerance, QTL mapping has provided valuable insights into the genetic basis of these traits. This approach has facilitated the development of marker-assisted selection strategies, enabling more efficient breeding of improved maize varieties (Li et al., 2012).

3 Present Trends: Advances in Maize Genomics

3.1 The sequencing of the maize genome

The first sequencing of the maize genome, particularly the B73 inbred line, marked a significant milestone in plant genomics. This project revealed the complexity and diversity of the maize genome, which is one of the most intricate plant genomes known to date. The sequencing provided insights into the diploid nature of maize following an ancestral chromosome doubling and highlighted the extensive presence of transposable elements, which constitute nearly 85% of the genome (Springer et al., 2018). This foundational work has paved the way for subsequent genomic studies and agricultural advancements.

Key findings from the maize genome sequencing include the identification of over 32 000 genes and the mapping of nearly 99.8% of these genes onto reference chromosomes. The genome's complexity is further underscored by the discovery of hundreds of families of transposable elements, which play a crucial role in gene regulation and genome evolution. Additionally, the sequencing of the W22 inbred line revealed significant structural heterogeneity compared to the B73 reference genome, providing a deeper understanding of genetic variation and its implications for functional genomics and transposon biology (Springer et al., 2018). These findings have significant implications for crop improvement, as they offer a comprehensive genetic framework for breeding programs and the development of sustainable agricultural technologies.

3.2 Functional genomics and gene editing

Advances in functional genomics have been propelled by the development of high-throughput sequencing technologies and comprehensive genome annotations. For instance, the updated maize reference genome includes 111 000 full-length transcripts, which enhance the accuracy of gene annotations and facilitate the study of gene expression and regulation (Jiao et al., 2017). The integration of RNA-seq analysis, differential nuclease sensitivity profiling, and bisulfite sequencing has further enabled the mapping of open reading frames, chromatin accessibility, and DNA methylation profiles, respectively, providing a robust foundation for functional genomics research (Springer et al., 2018).

CRISPR and other gene-editing technologies have revolutionized maize research by enabling precise modifications of the genome. These tools allow for targeted gene knockouts, insertions, and modifications, which are essential for functional studies and trait improvement. The ability to edit specific genes has accelerated the pace of crop improvement by facilitating the development of maize varieties with enhanced traits such as disease resistance, drought tolerance, and increased yield (Xiao et al., 2017).

3.3 Systems biology and integrative approaches

Systems biology approaches have been instrumental in understanding the complex genetic networks in maize. By integrating data from various omics platforms, researchers can construct comprehensive models of gene interactions and regulatory networks. These models help elucidate the underlying mechanisms of key biological processes and traits, providing a holistic view of maize genetics (Xiao et al., 2017).

The integration of multi-omics approaches, including genomics, proteomics, and metabolomics, has significantly advanced maize research. For example, genome-wide association studies (GWAS) have linked genotypic variations to phenotypic traits, enhancing our understanding of complex traits and facilitating molecular breeding efforts (Xiao et al., 2017). Additionally, targeted sequencing of specific genomic regions has identified numerous single nucleotide polymorphisms (SNPs) and presence/absence variations (PAVs), which are crucial for dissecting the genetic basis of important agronomic traits (Muraya et al., 2015).

3.4 Epigenomics and regulatory networks

Epigenetic modifications, such as DNA methylation and histone modifications, play a critical role in gene regulation in maize. Studies have mapped DNA methylation profiles across the maize genome, revealing the dynamic nature of epigenetic regulation and its impact on gene expression and phenotypic variation (Springer et al., 2018). These insights are essential for understanding how environmental factors influence gene activity and trait development.

Research into the regulatory networks controlling key traits in maize has uncovered the intricate interactions between genes, transcription factors, and epigenetic modifications. For instance, the identification of open chromatin regions has highlighted the functional parts of the maize genome that are crucial for gene expression and recombination. These regions account for a significant portion of phenotypic variation in agronomic traits, underscoring their importance in crop improvement (Rodgers-Melnick et al., 2016). Understanding these regulatory networks enables the development of targeted strategies for enhancing desirable traits in maize.

4 Applications of Genomic Research in Maize

4.1 Crop improvement and breeding

Genomic research has significantly transformed maize breeding programs by introducing advanced tools and methodologies such as QTL mapping, GWAS, and genomic selection. These tools have enabled breeders to identify and select for desirable traits more efficiently, leading to the development of superior maize varieties (Hou et al., 2024). For instance, genomic selection has been shown to improve prediction accuracies for drought tolerance and other agronomic traits, thereby accelerating the breeding cycle and enhancing genetic gains (Shikha et al., 2017; Benavente and Giménez, 2021; Budhlakoti et al., 2022). Additionally, the integration of transgenic and genome editing technologies has provided more direct and precise approaches for trait improvement, further boosting the effectiveness of maize breeding programs (Simmons et al., 2021).

Genomic research has led to the improvement of several key traits in maize, particularly those related to abiotic stress resistance. For example, drought tolerance has been a major focus, with significant advancements achieved through the identification of drought-responsive genes and SNPs. Studies have demonstrated the potential of genomic tools to enhance traits such as water-use efficiency, nitrogen-use efficiency, and yield under drought conditions (Farfan et al., 2015; Nepolean et al., 2018; Benavente and Giménez, 2021). Specific examples include the identification of 22 validated gene leads that improve yield and drought tolerance in field-grown maize (Simmons et al., 2021), and the use of genome-wide association studies to pinpoint quantitative trait variants associated with grain yield and other important traits under drought stress (Farfan et al., 2015).

4.2 Understanding genetic diversity

Genomic research has played a crucial role in uncovering the genetic diversity of maize. By employing techniques such as genome-wide association studies and high-throughput SNP genotyping, researchers have been able to map the genetic variation present in maize populations. This has provided insights into the genetic architecture of important traits and facilitated the identification of novel alleles that contribute to trait diversity (Farfan et al., 2015; Shikha et al., 2017). The use of diverse maize inbred lines from different geographical regions has further highlighted the extent of genetic diversity and its potential for improving breeding programs (Farfan et al., 2015).

The conservation of genetic diversity in maize and its wild relatives is essential for maintaining the crop's adaptability and resilience to environmental changes. Genomic research has contributed to this effort by identifying and characterizing the genetic resources available in wild maize relatives. This information is critical for developing strategies to preserve these genetic resources and for incorporating beneficial alleles into cultivated maize varieties (Farfan et al., 2015; Li et al., 2023). Additionally, understanding the genetic basis of traits in wild relatives can provide valuable insights for breeding programs aimed at enhancing stress tolerance and other desirable traits in maize (Li et al., 2023).

Li et al. (2023) investigated the dynamic changes in gene expression throughout the process of modern maize breeding revealed by genomic analysis. The study found that breeding selection across different eras influenced

the expression patterns of specific genes, particularly those associated with stress resistance, yield, and other agronomic traits. Through clustering analysis, the research demonstrated the expression trends of genes across various breeding stages, which helps to identify key genetic diversity loci crucial for maize genetic improvement. The application of maize genomics offers new perspectives for further enhancing crop productivity and resistance, contributing to a deeper understanding of the genetic basis of complex traits.

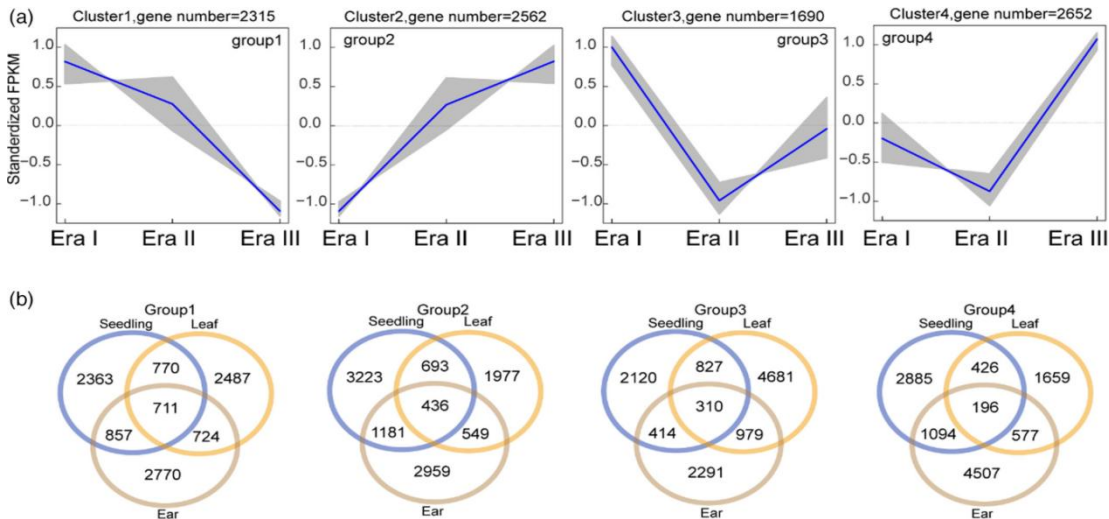


Figure 1 Gene Expression Patterns and Functional Enrichment Analysis in Modern Maize (*Zea mays* L.) Breeding (Adapted from Li et al., 2023)

Image caption: a: Gene expression patterns across different breeding eras, grouped using k-means clustering. Each line represents the expression pattern of a gene, with blue lines indicating the core expression trend for each group. Era I, Era II, and Era III represent different historical stages of maize breeding. b: Overlapping expression of different gene groups in seedlings, leaves, and ears, showing the distribution of gene expression across different tissues. A Venn diagram is used to illustrate the overlap of genes between the tissues (Adapted from Li et al., 2023).

4.3 Addressing global challenges

Maize genomic research addresses global challenges such as food security and climate change by developing crop varieties that are more resilient to abiotic and biotic stresses. By improving traits like drought tolerance, heat tolerance, and nitrogen-use efficiency, genomic research helps ensure stable maize production under changing environmental conditions (Nepolean et al., 2018; Benavente and Giménez, 2021; Cooper and Messina, 2022). These advancements contribute to increased yield and productivity, which are essential for meeting the growing global demand for food (Budhlakoti et al., 2022; Cooper and Messina, 2022). Moreover, the integration of genomic tools in breeding programs enables the rapid development of climate-resilient maize varieties, thereby supporting sustainable agriculture (Nepolean et al., 2018; Budhlakoti et al., 2022).

Several case studies highlight the success of genomic solutions in addressing global challenges. For instance, the long-term improvement of temperate maize for the US corn belt has demonstrated the effectiveness of genomic selection in breeding drought-resistant varieties (Cooper and Messina, 2022). Another example is the discovery and validation of gene leads that enhance yield and drought tolerance in maize, which have been field-tested and shown to outperform existing varieties (Simmons et al., 2021). Additionally, the use of genome-wide association studies to identify SNPs associated with drought tolerance and other agronomic traits has provided valuable genetic markers for breeding programs aimed at improving maize resilience to environmental stresses (Farfan et al., 2015; Shikha et al., 2017).

4.4 Genomics in stress resistance

Genomic research has significantly contributed to the development of stress-resistant maize varieties by identifying key genes and regulatory networks involved in stress responses. Techniques such as QTL mapping, GWAS, and genomic selection have been pivotal in understanding the genetic basis of stress tolerance. These methods have enabled the identification of genetic variations linked to traits such as drought and heat tolerance,

which are crucial for improving maize resilience to abiotic stresses (Labuschagne, 2020; Benavente and Giménez, 2021; Kamali and Singh, 2023). Additionally, transcriptomic approaches, including RNA-seq, have provided insights into the gene expression dynamics under stress conditions, revealing novel stress-responsive genes and pathways (Li et al., 2017; Kamali and Singh, 2023). The integration of these genomic tools with advanced breeding techniques, such as CRISPR-Cas9, has further enhanced the precision and efficiency of developing stress-tolerant maize cultivars (Kamali and Singh, 2023).

Research has extensively focused on both biotic and abiotic stress resistance in maize. For abiotic stresses, studies have highlighted the importance of transcription factors (TFs) in regulating stress responses. Specific TF families and their downstream target genes have been identified as crucial players in enhancing maize's tolerance to drought, salinity, heat, and cold (Li et al., 2017; Kimotho et al., 2019). For instance, RNA-seq analysis has identified differentially expressed genes (DEGs) involved in hormone metabolism, transcription regulation, and lipid signaling, which are common to multiple abiotic stresses (Li et al., 2017).

In terms of biotic stress resistance, maize has been studied for its responses to arthropod herbivory and diseases. The physiological, biochemical, and molecular responses to these biotic factors involve complex defense mechanisms, including inducible and constitutive defenses. The simultaneous occurrence of abiotic and biotic stresses poses additional challenges, necessitating a comprehensive understanding of the interplay between different stress factors (Chávez-Arias et al., 2021).

4.5 Nutritional enhancement through genomics

Genomic research has also been directed towards enhancing the nutritional quality of maize. Efforts have included the identification and manipulation of genes involved in nutrient biosynthesis and accumulation. Techniques such as marker-assisted selection and genomic selection have been employed to improve traits related to nutritional quality, such as increased vitamin and mineral content (Benavente and Giménez, 2021; Prasanna et al., 2021). The use of transcriptomics and other omics technologies has further facilitated the understanding of the molecular mechanisms underlying nutrient biosynthesis, enabling targeted breeding for enhanced nutritional traits (Kamali and Singh, 2023).

Biofortification efforts in maize have led to the development of varieties with increased levels of essential vitamins and minerals. For example, genomic approaches have been used to enhance the content of provitamin A, iron, and zinc in maize kernels. These biofortified varieties aim to address micronutrient deficiencies in populations that rely heavily on maize as a staple food. The integration of genomic tools with traditional breeding methods has accelerated the development of nutritionally enhanced maize varieties, contributing to improved food security and public health (Benavente and Giménez, 2021; Prasanna et al., 2021).

5 Challenges in Maize Genomic Research

5.1 Technical and methodological challenges

Maize genomics faces significant technical challenges due to the complexity of its genome. The maize genome is characterized by a high content of repetitive elements, which complicates sequencing and assembly processes. For instance, the assembly of the maize genome using single-molecule real-time sequencing revealed over 130 000 intact transposable elements, highlighting the intricate nature of the genome (Jiao et al., 2017). Additionally, the presence of structural variations and methylation patterns across different maize lines adds another layer of complexity to data analysis, as demonstrated by the comparative analysis of 26 diverse maize genomes (Figure 2) (Hufford et al., 2021).

Assembling and annotating the maize genome is particularly challenging due to its large size and repetitive sequences. Efforts to create gapless assemblies of maize chromosomes using long-read technologies have shown promise, but the process remains arduous. For example, a study achieved gapless assemblies of certain maize chromosomes, yet the overall assembly still required merging multiple contigs and dealing with highly repetitive regions (Liu et al., 2020). Moreover, the annotation of gene models and transposable elements requires integrating various data types, such as RNA-seq and bisulfite sequencing, to achieve accurate results (Springer et al., 2018).



Figure 2 Analysis of UMR (Unmethylated Region) Variations in the NAM Founding Genomes (Adapted from Hufford et al., 2021)
 Image caption: A: Annotation of the Miniature Seed1 gene in the maize inbred line Mo18W; green, gray, red, and blue represent different superfamilies of transposable elements (TEs), with gray vertical lines indicating 2.5 kbp intervals. B: Annotation and methylation data of the Miniature Seed1 gene in the maize inbred line B73; insertion of a Gypsy element has moved part of the UMR from 14 kbp upstream of the TSS to other locations, showing different methylation types CG, CHG, and CHH. C: Comparison of the relationship between UMR methylation status and gene expression; red indicates methylated regions, turquoise indicates unmethylated regions, and the y-axis represents the proportion of transcripts per million (TPM) (Adapted from Hufford et al., 2021).

5.2 Ethical considerations

The use of genetic modification in maize raises several ethical concerns. One major debate centers around the potential long-term impacts on biodiversity and ecosystem balance. Genetic modifications can lead to unintended consequences, such as the creation of superweeds or the disruption of local flora and fauna. Additionally, there are concerns about the ownership and control of genetically modified organisms (GMOs), which can lead to monopolies and limit the accessibility of these technologies to small-scale farmers.

Public perception of genetically modified maize varies widely, with some viewing it as a solution to food security and others as a potential health risk. Regulatory frameworks for GMOs differ across countries, influencing the adoption and commercialization of genetically modified maize. For instance, stringent regulations in the European Union have slowed the acceptance of GMOs, while other regions, such as the United States, have more lenient policies. These regulatory differences can create barriers to the global trade of genetically modified maize and affect research and development efforts.

5.3 Economic and accessibility challenges

The cost of advanced genomic technologies remains a significant barrier to widespread adoption in maize research. High-quality genome assemblies and annotations require substantial financial investment in sequencing technologies and computational resources. For example, the de novo assembly of the Chinese maize elite inbred line RP125 using Nanopore long-read sequencing and Hi-C scaffolding involved considerable expenses (Nie et al., 2021). Similarly, targeted sequencing approaches to identify sequence polymorphisms in maize candidate genes for biomass production also incur high costs (Muraya et al., 2015).

Developing countries often face challenges in accessing genomic resources and technologies due to financial constraints and lack of infrastructure. This disparity limits their ability to participate in cutting-edge maize genomic research and benefit from its advancements. Efforts to democratize access to genomic data and technologies are crucial for ensuring that the benefits of maize genomics are equitably distributed. For instance, the creation of community reference genomes, such as the W22 reference genome, aims to provide a foundation for functional genomics and transposon biology, potentially aiding researchers in resource-limited settings (Springer et al., 2018).

6 Future Directions in Maize Genomic Research

6.1 Emerging technologies in genomics

The future of maize genomic research is poised to be significantly influenced by emerging technologies such as long-read sequencing and artificial intelligence (AI). Long-read sequencing technologies, like Single Molecule Real-Time (SMRT) sequencing, have already demonstrated their potential by providing more complete and accurate reference genomes. For instance, the assembly of a maize reference genome using SMRT sequencing resulted in a 52-fold increase in contig length and improved assembly of complex regions such as intergenic spaces and centromeres (Jiao et al., 2017). These advancements enable a more detailed understanding of genetic and functional variations, which is crucial for crop improvement.

AI in genomics is another promising frontier. AI and machine learning algorithms can analyze vast amounts of multiomics data, integrating genomics, transcriptomics, proteomics, and metabolomics to uncover complex biological insights. This integration is essential for understanding the genotype-phenotype relationships in maize, which can lead to more precise breeding strategies (Xiao et al., 2017; Wang et al., 2022). The expected impact of these technologies includes accelerated discovery of genetic variations, improved crop traits, and enhanced resilience to environmental stresses.

6.2 Personalized agriculture and precision breeding

Personalized agriculture refers to the customization of agricultural practices based on the specific genetic makeup of crops and environmental conditions. In maize production, this concept can be realized through precision breeding, which utilizes genomic information to develop crop varieties tailored to specific needs. Precision breeding techniques, such as CRISPR/Cas9-mediated genome editing, allow for targeted modifications in the maize genome, leading to the development of varieties with desired traits such as increased yield, drought tolerance, and pest resistance (Andorf et al., 2019; Kausch et al., 2021).

The revolution in maize cultivation through precision breeding is evident in the ability to manipulate genetic diversity and predict hybrid performance more accurately. By leveraging genomic data, breeders can create inbred lines and hybrid seeds with optimized traits, significantly enhancing productivity and sustainability in maize farming (Andorf et al., 2019). This approach not only improves crop performance but also reduces the reliance on chemical inputs, promoting environmentally friendly agricultural practices.

6.3 Ethical and societal implications

The application of advanced genomic technologies in maize research raises several ethical considerations. One major concern is the potential for unintended consequences of genetic modifications, which could impact biodiversity and ecosystem balance. Ensuring the safety and efficacy of these technologies is paramount, and rigorous regulatory frameworks must be established to address these issues (Kausch et al., 2021).

Societal impacts of advancements in maize genomics include the potential for increased food sovereignty and security. By developing maize varieties that are more resilient to climate change and other environmental stresses, genomic research can contribute to stable food supplies in vulnerable regions. However, there is also the risk of exacerbating inequalities if access to these technologies is limited to certain groups or regions. It is crucial to promote equitable access to genomic advancements to ensure that the benefits are widely shared (Moose et al., 2004; Yang and Yan, 2021).

6.4 Climate change and sustainability

Climate change poses significant challenges to agricultural productivity, necessitating the development of climate-resilient crops. Genomic research plays a crucial role in this endeavor by enabling the identification and manipulation of genes associated with stress tolerance. Advances in genomics, such as high-throughput sequencing and genome editing technologies, have facilitated the development of maize varieties that can withstand various abiotic stresses, including drought, heat, and salinity (Kole et al., 2015; Pourkheirandish et al., 2020; Thudi et al., 2020). For instance, genomics-assisted breeding (GAB) has been instrumental in enhancing the stress adaptation of maize by identifying and incorporating beneficial alleles from wild relatives and landraces (Kole et al., 2015; Zenda et al., 2021). Additionally, the integration of genomic data with phenotypic information through bioinformatics tools has accelerated the breeding of climate-smart maize varieties (Marsh et al., 2021).

To enhance the sustainability of maize agriculture, several genomic strategies can be employed. One approach is the use of marker-assisted selection (MAS) and genomic prediction to accelerate the breeding process and improve the accuracy of selecting desirable traits (Abberton et al., 2015; Thudi et al., 2020). Another strategy involves the exploitation of crop wild relatives (CWRs) and underutilized species to broaden the genetic base and introduce novel alleles for stress tolerance and nutritional quality. Furthermore, the application of genome editing technologies, such as CRISPR-Cas9, allows for precise modifications of specific genes to enhance stress resilience and yield stability (Pourkheirandish et al., 2020; Zenda et al., 2021). The integration of machine learning and artificial intelligence in genomics can also optimize breeding programs by predicting gene-to-phenotype associations and tailoring plants for specific environmental conditions (Thudi et al., 2020; Zenda et al., 2021).

6.5 Integration with global food systems

Maize genomics has the potential to significantly contribute to global food security by increasing crop yields and improving nutritional quality. Genomic tools enable the identification of genes controlling critical agronomic traits, which can be manipulated to develop high-yielding and nutrient-rich maize varieties (Pourkheirandish et al., 2020; Steinwand and Ronald, 2020). The development of climate-resilient maize varieties ensures stable production under adverse environmental conditions, thereby reducing the risk of food shortages (Abberton et al., 2015; Pourkheirandish et al., 2020). Additionally, genomics can facilitate the diversification of crop production by improving minor and newly established crop species, thus enhancing the overall resilience of the food supply (Abberton et al., 2015; Yuan et al., 2019).

In the future, maize genomics will play a pivotal role in integrated global food systems by enabling sustainable intensification of agriculture. The convergence of low-cost genome sequencing, high-throughput phenotyping, and advanced bioinformatics will provide breeders with the tools needed to develop maize varieties tailored to specific environments and management practices (Marsh et al., 2020; Steinwand and Ronald, 2020). Moreover, the integration of genomic data with agronomic and climatic information will allow for the optimization of crop management strategies, further enhancing productivity and sustainability (Marsh et al., 2020; Rizzo et al., 2022). As genomic technologies continue to evolve, they will facilitate the rapid development of maize varieties that can meet the growing food demands while mitigating the impacts of climate change (Yuan et al., 2019; Pourkheirandish et al., 2020).

7 Concluding Remarks

Maize genomic research has undergone significant transformations over the decades, driven by technological advancements and a deeper understanding of genetic mechanisms. Historically, maize has been a pivotal crop both in agriculture and as a genetic model organism. Early efforts in maize breeding were primarily focused on phenotypic selection and hybridization techniques. The advent of next-generation sequencing (NGS) technologies and genome-wide association studies (GWAS) has revolutionized our ability to link genotypic variations to phenotypic traits, thereby enhancing our understanding of maize genetics. The development of genetic transformation systems, including CRISPR/Cas9-mediated genome editing, has further accelerated functional genomics research and genetic improvement strategies. Additionally, the assembly of high-quality reference

genomes using single-molecule real-time (SMRT) sequencing has provided comprehensive tools for characterizing genetic and functional variations in maize. These advancements have collectively contributed to the current state of maize genomic research, characterized by sophisticated breeding methodologies and a robust understanding of genetic diversity and hybrid performance.

The future of maize genomic research holds promising potential for addressing global agricultural challenges. Emerging trends such as multiomics approaches, which integrate genomics, transcriptomics, proteomics, and metabolomics, are expected to provide a holistic understanding of maize biology and its response to environmental stresses. The continuous improvement of genome editing technologies, particularly CRISPR/Cas9, will likely lead to more precise and efficient genetic modifications, enabling the development of maize varieties with enhanced traits such as drought tolerance and disease resistance. Furthermore, advancements in bioinformatics and computational tools will facilitate the analysis and integration of large-scale genomic data, thereby accelerating the breeding process and the discovery of novel genetic variations. These ongoing and emerging research trends are poised to significantly impact maize breeding programs, ultimately contributing to global food security and sustainable agriculture.

The trends in maize genomic research underscore the critical role of advanced genetic tools and technologies in modern agriculture. The integration of genomics into maize breeding has not only enhanced our understanding of the crop's genetic architecture but also enabled the development of high-performance hybrids with improved yield and resilience to environmental stresses. The ability to manipulate genetic diversity through genome editing and transformation technologies represents a significant leap forward in crop improvement strategies³. As the global population continues to grow and climate change poses new challenges to food production, the advancements in maize genomic research will be instrumental in ensuring food security and sustainable agricultural practices. The collaborative efforts of the scientific community in harnessing these technologies will pave the way for innovative solutions to meet the demands of future agriculture.

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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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