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FROM GENOMICS TO GENOME EDITING: MODERN BREEDING STRATEGIES FOR STRESS-RESILIENT MAIZE

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ABSTRACT

Climate change has intensified the occurrence of abiotic stresses such as drought, heat, salinity and waterlogging, posing serious challenges to maize production worldwide. Developing stress-resilient maize varieties has therefore become a major priority for sustainable agriculture and food security. Conventional breeding has contributed significantly to maize improvement, but the complex genetic nature of stress tolerance often limits the speed and precision of varietal development. Recent advancements in genomics, molecular breeding, genomic selection and genome editing have opened new possibilities for accelerating genetic improvement. Technologies such as quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), marker-assisted selection and CRISPR-Cas-based genome editing are helping researchers identify, select and modify genes associated with stress adaptation. Integrating these approaches with conventional breeding, advanced phenotyping and artificial intelligence can improve selection efficiency and genetic gain. This article highlights the role of modern breeding technologies in developing high-yielding, climate-resilient maize varieties for sustainable agricultural production.

Keywords: Stress-Resilient Maize, Molecular Breeding, Genome Editing

INTRODUCTION

Maize (*Zea mays L.*) is one of the world's most important cereal crops, contributing significantly to food, feed and industrial production. Its adaptability to diverse agro-climatic conditions makes it an essential component of global agricultural systems. However, changing climatic conditions have increasingly threatened maize productivity through irregular rainfall, prolonged drought, rising temperatures and increasing soil salinity. These environmental stresses

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affect crop growth, reproductive development and grain formation, ultimately reducing productivity and farmers' income. Drought during flowering can delay silk emergence and reduce successful pollination, while high temperatures may affect pollen viability, fertilisation and grain filling. Similarly, salinity interferes with water and nutrient uptake, restricting normal plant development. Waterlogging in poorly drained soils can also reduce root activity and disturb nutrient absorption. The simultaneous occurrence of these stresses makes maize improvement particularly challenging. Traditional breeding methods have been successful in developing high-yielding and locally adapted varieties. However, stress tolerance is generally governed by multiple genes and is strongly influenced by environmental conditions. Modern breeding technologies, particularly genomics and genome editing, provide opportunities to understand the genetic basis of stress tolerance and develop improved varieties more efficiently. The integration of these approaches with conventional breeding represents an important step towards sustainable and climate-resilient maize production.

1. GENOMICS: UNDERSTANDING THE GENETIC BASIS OF STRESS TOLERANCE

Genomics has transformed modern plant breeding by providing detailed information about the genetic composition and functioning of crop plants. Advanced DNA sequencing technologies enable researchers to identify genes, genetic variations and molecular pathways associated with important agronomic traits. In maize, genomic research has contributed substantially to understanding the mechanisms responsible for drought, heat and salinity tolerance. Quantitative trait locus (QTL) mapping and genome-wide association studies (GWAS) are important genomic approaches used to identify genomic regions associated with stress-related characteristics. These techniques help locate genes controlling traits such as root architecture, flowering behaviour, water-use efficiency and grain yield under adverse environmental conditions. Once identified and validated, favourable genomic regions can be utilised in breeding programmes to improve stress tolerance. Another important development is the application of multi-omics approaches, including genomics, transcriptomics, proteomics and metabolomics. While genomics identifies the genetic potential of a plant, transcriptomics helps understand changes in gene expression under stress conditions. Proteomics and metabolomics provide information about proteins and metabolic compounds involved in stress responses. Together, these approaches provide a comprehensive understanding of how maize plants perceive and respond to environmental challenges.

2. MOLECULAR BREEDING: FROM GENETIC DISCOVERY TO VARIETY DEVELOPMENT

Molecular breeding connects genomic discoveries with practical crop improvement. It uses DNA-based markers to identify desirable genetic characteristics and select superior plants during different stages of breeding.

Marker-assisted selection (MAS) is one of the most widely used approaches for improving stress-related traits. By identifying molecular markers linked to favourable genes or QTLs, breeders can select plants carrying desirable genetic variations without relying entirely on visible characteristics. Marker-assisted backcrossing is particularly useful for transferring stress-tolerance genes into popular high-yielding maize varieties while retaining their desirable agronomic features.

For complex traits controlled by several genes, genomic selection (GS) offers additional advantages. It uses genome-wide marker information to predict the genetic potential of breeding lines. This helps breeders identify promising genotypes at an early stage and reduce the time and resources required for repeated field evaluation.

Prasanna et al. (2021) highlighted the importance of integrating conventional breeding, molecular tools and stress-based selection strategies for developing climate-resilient maize in tropical rainfed environments. Such approaches are particularly relevant for regions where drought and other environmental stresses frequently affect crop productivity.

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3. GENOMIC SELECTION AND ADVANCED PHENOTYPING

Genomic selection is emerging as an effective strategy for improving complex traits such as grain yield, drought tolerance and environmental adaptability. Unlike conventional marker-assisted selection, which generally focuses on specific genomic regions, genomic selection considers information from markers distributed across the entire genome. This allows breeders to estimate the breeding value of individual plants and select promising parents for future generations. However, genomic information alone is not sufficient to identify the best stress-tolerant genotypes. Accurate phenotypic evaluation is equally important. Advanced phenotyping technologies, including drone-based imaging, remote sensing, thermal cameras and automated field-monitoring systems, can assess plant growth, canopy temperature, chlorophyll status and water stress responses. For example, canopy temperature measurements can provide useful information about plant water status, while imaging technologies can help monitor changes in leaf area and crop growth. Integrating these observations with genomic data improves the accuracy of selection and helps identify maize genotypes that maintain productivity under adverse conditions. Artificial intelligence (AI) and machine learning are further strengthening this approach by analysing large genomic, environmental and phenotypic datasets. These technologies can identify complex relationships between genetic characteristics and environmental responses, supporting faster and more informed breeding decisions.

4. GENOME EDITING: A NEW ERA OF PRECISION BREEDING

Genome editing represents one of the most promising developments in modern crop improvement. Among the available technologies, CRISPR-Cas systems have gained considerable attention because of their ability to modify specific regions of DNA with high precision. Unlike conventional breeding, which involves selecting and combining genetic variations over successive generations, genome editing enables targeted changes in genes associated with desirable traits. In maize, this technology offers opportunities to improve drought, heat and salinity tolerance by modifying genes involved in stress perception, signalling and physiological regulation. For instance, genes associated with stomatal regulation can be investigated to improve water-use efficiency and reduce excessive water loss during drought. Similarly, modifications in genes controlling root development may help plants explore deeper soil layers and access water during prolonged dry periods. Other potential targets include genes involved in antioxidant defence, osmotic adjustment and cellular protection under high-temperature and salinity stress. Genome editing also includes advanced approaches such as base editing and prime editing, which offer opportunities for making more specific genetic changes. Multiplex genome editing can potentially modify multiple target genes simultaneously, an important advantage when improving complex traits controlled by several genetic components. Nevertheless, the successful application of genome editing requires careful identification of target genes, efficient transformation systems and evaluation of the resulting plants under field conditions. The edited plants must also be assessed for genetic stability, yield performance, environmental safety and compliance with applicable regulatory requirements.

5. INTEGRATING GENOMICS, MOLECULAR BREEDING AND GENOME EDITING

The greatest opportunity for developing stress-resilient maize lies in combining different breeding technologies rather than applying them independently. Genomics helps identify favourable genes and genetic regions, molecular breeding facilitates their selection and transfer, and genome editing enables targeted modification of specific genes. For example, genomic studies may identify genes associated with drought tolerance, which can subsequently be validated through molecular and physiological studies. Promising genetic variations can then be incorporated into breeding populations using marker-assisted or genomic selection. Where appropriate, genome editing may be used to modify specific target genes to improve particular stress-related characteristics. The integration of these technologies with conventional breeding can also help maintain desirable characteristics such as high grain yield, maturity duration, grain quality and disease resistance. Multi-location field testing remains essential to confirm that improved genotypes perform consistently under different climatic and soil conditions. This integrated approach is particularly important

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for developing maize varieties capable of tolerating combined stresses, such as drought and heat, which frequently occur together in rainfed agricultural systems.

6. CHALLENGES AND FUTURE PROSPECTS

Despite considerable progress, several challenges remain in developing stress-resilient maize. Abiotic stress tolerance is a complex trait influenced by multiple genes, environmental conditions and interactions between different physiological processes. Identifying reliable genetic targets and maintaining high grain yield under stress conditions are major priorities for future breeding programmes. Another important challenge is the translation of laboratory-based research into practical field-level improvements. Genotypes showing promising responses under controlled conditions may not always perform similarly under natural environments. Therefore, extensive field evaluation across different locations and seasons is necessary. Future breeding programmes should focus on developing maize varieties with multiple stress tolerance, improved water-use efficiency, stable grain production and adaptability to diverse agro-climatic conditions. Greater use of genetic diversity from traditional landraces and existing germplasm collections can also provide valuable sources of stress-adaptive traits. The combination of speed breeding, genomic selection, genome editing, artificial intelligence and high-throughput phenotyping is expected to further accelerate maize improvement. Strengthening collaboration among plant breeders, molecular biologists, geneticists and farmers will be essential to ensure that these scientific innovations reach agricultural fields.

CONCLUSION

Modern maize breeding is moving beyond conventional selection towards a more precise, data-driven and technology-supported approach. Genomics provides a deeper understanding of the genetic basis of stress tolerance, molecular breeding improves the efficiency of selection, and genome editing offers opportunities for targeted genetic improvement. Their integration with advanced phenotyping, artificial intelligence and conventional breeding can accelerate the development of high-yielding and stress-resilient maize varieties. Although challenges related to complex genetic interactions, field performance and regulatory requirements remain, continued research and technological innovation will play a crucial role in overcoming these limitations. Ultimately, integrating genomics with precision breeding will be essential for developing climate-resilient maize varieties and ensuring sustainable food production under changing climatic conditions.

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