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NEXT-GENERATION TECHNOLOGIES IN MAIZE BREEDING: GENOMIC SELECTION, HIGH-THROUGHPUT PHENOTYPING AND PRECISION GENOME EDITING

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ABSTRACT

Maize (*Zea mays L.*) is an important cereal crop worldwide; however, its productivity is increasingly challenged by climate change, emerging pests and diseases, and changing environmental conditions. Developing high-yielding and stress-resilient maize varieties requires faster, more accurate and efficient breeding approaches. Recent advancements in genomic selection, high-throughput phenotyping and precision genome editing are transforming conventional maize improvement programmes. Genomic selection enables the prediction of genetic potential using genome-wide molecular markers, while high-throughput phenotyping facilitates rapid and accurate assessment of important plant characteristics through advanced imaging and sensor technologies. Precision genome editing, particularly CRISPR/Cas-based approaches, provides opportunities to modify specific genes associated with desirable agronomic and stress-tolerance traits. Integrating these technologies with conventional breeding, artificial intelligence and advanced computational tools can accelerate genetic gain, improve selection accuracy and reduce breeding cycles. This article highlights the importance, applications, challenges and future prospects of next-generation technologies in developing productive, climate-resilient and sustainable maize varieties.

Keywords: Genomic Selection, High-Throughput Phenotyping, Precision Genome Editing

INTRODUCTION

Maize (*Zea mays L.*) is one of the world's leading cereal crops, contributing significantly to food security, livestock production and various industrial applications. Its wide adaptability and diverse uses make it an important component of agricultural production systems. However, increasing climatic variability, soil degradation, water scarcity and emerging production constraints are creating new challenges for maize cultivation. Drought, heat and salinity stress

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can adversely affect plant growth, reproductive development and grain yield, highlighting the need for improved varieties with greater adaptability and resilience. Conventional breeding has played a significant role in improving maize productivity through hybrid development, selection and genetic recombination. However, the increasing complexity of breeding objectives requires more efficient methods for identifying superior genotypes and improving desirable characteristics. Traditional selection often depends on extensive field evaluation, which is time-consuming and influenced by environmental variation. The development of genomic technologies, digital agriculture and genome-editing tools has introduced new opportunities for modern maize improvement. Genomic selection, high-throughput phenotyping and precision genome editing are emerging as three important components of next-generation breeding. Their integration enables breeders to understand genetic variation, evaluate plant performance and introduce targeted genetic improvements more efficiently. These approaches are expected to play a major role in developing high-yielding maize varieties capable of maintaining productivity under diverse environmental conditions.

1. GENOMIC SELECTION: PREDICTING THE GENETIC POTENTIAL OF MAIZE

Genomic selection (GS) is an advanced molecular breeding approach that uses genome-wide DNA marker information to predict the genetic potential of individual plants. Unlike conventional marker-assisted selection, which generally focuses on specific genes or quantitative trait loci (QTLs), genomic selection considers markers distributed throughout the genome. This makes it particularly useful for improving complex quantitative traits such as grain yield, drought tolerance, heat resilience and nutrient-use efficiency.

The basic principle of genomic selection involves developing a training population in which both molecular marker information and phenotypic observations are available. Statistical models are then developed to establish relationships between genetic markers and observed performance. These models are used to predict the genomic estimated breeding values (GEBVs) of untested individuals. Plants with higher predicted breeding values can be selected for subsequent breeding generations. One of the major advantages of genomic selection is that it enables early identification of promising breeding materials without waiting for repeated phenotypic evaluation across several locations and seasons. This can shorten breeding cycles, reduce evaluation costs and accelerate genetic improvement. In maize breeding, genomic selection has considerable potential for improving grain yield, flowering characteristics, plant height, kernel weight and tolerance to environmental stresses. It is also useful in hybrid breeding for identifying superior parental combinations and predicting the performance of potential hybrids. Gunundu et al. (2023) highlighted the importance of genomic selection and associated technologies in improving agronomic traits and accelerating maize breeding programmes. However, the accuracy of genomic selection depends on the quality of training populations, marker density, population structure and environmental representation. Therefore, continuous improvement of prediction models and integration of genomic information with field-based observations are necessary for achieving reliable breeding outcomes.

2. HIGH-THROUGHPUT PHENOTYPING: RAPID AND ACCURATE PLANT EVALUATION

Phenotyping is the process of measuring observable plant characteristics resulting from interactions between genetic factors and environmental conditions. Conventional phenotyping generally involves manual observations of plant height, leaf characteristics, flowering time, biomass and grain yield. Although useful, these methods are labour-intensive and may not capture complex changes in plant growth over time. High-throughput phenotyping (HTP) has emerged as an important technological advancement that enables rapid, automated and non-destructive assessment of plant characteristics. It uses advanced imaging systems, sensors, robotics and computational technologies to collect large amounts of phenotypic information from individual plants and field trials. In maize breeding, high-throughput phenotyping can be performed through ground-based platforms, greenhouse imaging systems, drones and satellite-based observations. Different sensors provide information about plant growth, canopy temperature, vegetation indices, chlorophyll status and biomass accumulation.

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- **Drone-based phenotyping:** Unmanned aerial vehicles (UAVs) equipped with RGB, multispectral and thermal cameras can monitor large maize breeding fields within a short period. These systems help assess plant growth, canopy development, vegetation health and responses to drought and heat stress. Repeated observations throughout the growing season provide valuable information about crop performance under changing environmental conditions.

- **Thermal imaging:** Thermal cameras measure canopy temperature and provide indirect information about plant water status and transpiration. Under drought conditions, changes in canopy temperature can help identify genotypes with better water-use efficiency and stress adaptation.

- **Multispectral and hyperspectral imaging:** These technologies capture information across different wavelengths of light and help evaluate chlorophyll content, photosynthetic activity, nutrient status and plant stress responses. They can support the identification of promising maize genotypes before visible symptoms become severe.

- **Root phenotyping:** Root architecture plays an important role in water and nutrient absorption. Advanced imaging and sensor-based methods help evaluate root length, depth, branching and distribution, providing useful information for selecting drought-adaptive maize genotypes.

The integration of high-throughput phenotyping with genomic selection improves the accuracy of breeding decisions. Herr et al. (2023) highlighted the potential of unoccupied aerial systems for generating dynamic phenotypic information in major field crops, including maize. Such technologies can strengthen the selection of superior genotypes under diverse field environments.

3. PRECISION GENOME EDITING: TARGETED GENETIC IMPROVEMENT

Precision genome editing represents a major advancement in modern crop improvement by enabling targeted modifications of specific DNA sequences. Among available technologies, CRISPR/Cas systems have gained considerable attention because of their flexibility, efficiency and potential for modifying genes associated with important agronomic traits. In maize, precision genome editing can be used to investigate and improve genes associated with grain yield, plant architecture, flowering behaviour, disease resistance and abiotic stress tolerance. For example, genes involved in stomatal regulation, root development, stress signalling and antioxidant defence can be explored to improve adaptation under drought and heat conditions. The CRISPR/Cas9 system uses a guide RNA to identify a specific DNA sequence, while the Cas9 enzyme introduces a targeted cut. The plant's DNA repair mechanisms then produce genetic changes at the selected location. Depending on the editing strategy, this can result in gene disruption or other targeted modifications. Recent developments have further expanded the scope of genome editing. Base editing enables specific nucleotide changes without requiring conventional double-strand DNA breaks, while prime editing offers opportunities for more flexible and precise genetic modifications. Multiplex genome editing can target several genes simultaneously, which is particularly useful for improving complex traits controlled by multiple genetic components. Precision genome editing also provides opportunities to modify regulatory regions that influence gene expression. This is important because many agronomic traits depend not only on the presence of particular genes but also on the level, timing and location of their expression. However, the successful application of genome editing requires reliable gene identification, efficient transformation, plant regeneration and careful evaluation of edited plants. Li et al. (2024) highlighted the rapid development of targeted genome-modification technologies, including base editing and prime editing, and their potential applications in precision crop breeding.

4. INTEGRATION OF GENOMICS, PHENOTYPING AND GENOME EDITING

The greatest potential of next-generation maize breeding lies in integrating genomic selection, high-throughput phenotyping and precision genome editing into a coordinated breeding strategy. Genomic selection helps predict the

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genetic potential of breeding materials, while high-throughput phenotyping provides accurate information about their performance under different environmental conditions. Genome editing can then be used to introduce targeted modifications in validated genes associated with desirable traits. For example, genomic studies may identify genetic regions associated with drought tolerance, while high-throughput phenotyping helps evaluate related characteristics such as canopy temperature, root development and flowering behaviour. Based on this information, promising candidate genes can be investigated through genome editing. The resulting materials can subsequently be evaluated using genomic and phenotypic tools to identify superior plants. Artificial intelligence (AI) and machine learning further strengthen this integrated approach by analysing large genomic, phenotypic and environmental datasets. Predictive models can identify relationships between genetic variation, environmental conditions and crop performance, supporting more accurate selection decisions. The combination of these technologies can help develop maize varieties with improved grain yield, stress tolerance, resource-use efficiency and environmental adaptability. It can also reduce the time and resources required for breeding by improving the precision of selection at different stages of crop improvement.

5. APPLICATIONS IN CLIMATE-RESILIENT MAIZE BREEDING

Next-generation technologies have considerable importance in developing maize varieties adapted to changing climatic conditions. Drought tolerance can be improved by identifying and selecting genotypes with favourable root architecture, better water-use efficiency and stable reproductive development. High-throughput imaging can help identify plants that maintain canopy growth and physiological activity under limited water availability. Similarly, genomic selection and advanced phenotyping can support the identification of heat-tolerant genotypes with improved pollen viability, flowering synchronisation and grain-filling capacity. Precision genome editing may provide additional opportunities to modify genes associated with heat-stress responses. Salinity tolerance can also be improved by identifying genetic variations associated with ion transport, osmotic adjustment and cellular protection. In addition, these technologies can support the development of maize varieties with improved nitrogen-use efficiency, disease resistance and grain quality. For tropical and subtropical agricultural regions, the integration of these approaches is particularly important because crops frequently experience multiple environmental stresses during the growing season. Developing varieties that combine high yield potential with stable performance under variable climatic conditions will be essential for sustainable maize production.

6. CHALLENGES AND FUTURE PROSPECTS

Despite significant technological progress, several challenges remain in the practical application of next-generation breeding approaches. Genomic selection requires high-quality reference populations, reliable phenotypic data and suitable prediction models. Similarly, high-throughput phenotyping generates large datasets that require advanced computational facilities, standardised measurement procedures and skilled personnel. Precision genome editing also faces challenges related to transformation efficiency, genotype dependency, off-target modifications and regulatory requirements. Furthermore, improving one desirable characteristic may sometimes negatively influence other agronomic traits. Therefore, careful evaluation of genetic interactions and field performance is essential. Future maize breeding programmes should focus on integrating multi-omics approaches, genomic prediction, artificial intelligence, speed breeding and precision genome editing. Greater use of diverse germplasm resources will also be important for identifying novel genetic variations associated with stress tolerance and yield improvement. Collaboration among plant breeders, geneticists, biotechnologists, data scientists and farmers will be essential for translating technological innovations into practical agricultural benefits. The development of affordable phenotyping systems and accessible genomic tools will further strengthen their application in public-sector and farmer-oriented breeding programmes.

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CONCLUSION

Next-generation technologies are transforming maize breeding from conventional selection towards a more precise, predictive and data-driven approach. Genomic selection enables early prediction of genetic potential, high-throughput phenotyping provides rapid and accurate assessment of plant performance, and precision genome editing offers opportunities for targeted genetic improvement. Their integration with conventional breeding, artificial intelligence and advanced computational tools can accelerate genetic gain and improve the development of high-yielding, stress-resilient maize varieties. Although challenges related to cost, technical capacity, field validation and regulatory requirements remain, continued research and technological innovation will strengthen their contribution to crop improvement. Ultimately, the successful application of these technologies will be essential for enhancing maize productivity, climate resilience and sustainable agricultural development.

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