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GENETIC APPROACHES FOR STRESS MANAGEMENT IN MAIZE: MECHANISMS, MOLECULAR BREEDING AND FUTURE PROSPECTS

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ABSTRACT

Climate change has increased the frequency and intensity of environmental stresses, including drought, heat, salinity and waterlogging, which significantly affect maize growth and productivity. Genetic stress management has emerged as an important strategy for developing maize varieties capable of maintaining stable performance under adverse environmental conditions. It involves understanding and utilising genetic mechanisms, stress-responsive genes, molecular pathways and genetic diversity to improve crop adaptability. Recent advancements in quantitative trait locus (QTL) mapping, marker-assisted selection, genomic selection, genome editing and multi-omics technologies have created new opportunities for improving stress tolerance. These approaches help identify favourable genes, understand plant defence mechanisms and accelerate the development of stress-resilient varieties. Integrating genetic improvement with physiological and molecular approaches can strengthen maize adaptation to changing climatic conditions. This article highlights the genetic mechanisms of stress management, modern breeding strategies and future opportunities for developing climate-resilient maize.

Keywords: Genetic Stress Management, Maize Stress Tolerance, Climate-Resilient Maize

INTRODUCTION

Maize (*Zea mays L.*) is one of the most important cereal crops worldwide, contributing significantly to food security, livestock nutrition and industrial production. However, its productivity is increasingly affected by environmental stresses associated with climate change. Irregular rainfall, prolonged drought, increasing temperatures, soil salinity and waterlogging create serious challenges for maize cultivation, particularly in rainfed agricultural systems. Abiotic stresses affect maize plants at different developmental stages. Drought during flowering can delay silk emergence

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and reduce pollination, whereas high temperatures affect pollen viability, fertilisation and grain development. Salinity interferes with water and nutrient absorption, while waterlogging restricts oxygen availability in the root zone. These stresses disturb normal physiological and metabolic activities, ultimately reducing grain yield and quality. Conventional breeding has contributed substantially to improving maize productivity. However, developing varieties with tolerance to multiple environmental stresses remains challenging because these characteristics are generally controlled by several genes and influenced by environmental conditions. Genetic stress management provides an effective approach by identifying and utilising favourable genetic variations responsible for stress adaptation. Modern molecular breeding, genomics and genome-editing technologies are further strengthening this approach and creating opportunities for developing high-yielding, climate-resilient maize varieties.

1. GENETIC MECHANISMS INVOLVED IN STRESS MANAGEMENT

Plants possess several genetic and molecular mechanisms that enable them to recognise and respond to environmental stresses. When maize plants experience drought, heat or salinity, specific stress-responsive genes become activated and regulate a series of physiological and biochemical processes. One important mechanism involves the regulation of stress-responsive transcription factors. Transcription factors are proteins that control the expression of other genes and play important roles in regulating plant responses to environmental changes. Important families, including NAC, MYB, bZIP, WRKY and heat shock transcription factors, participate in drought, heat and salinity responses. Their activity influences root development, stomatal regulation, antioxidant defence and cellular protection. Abscisic acid (ABA) signalling is another important mechanism, particularly under drought and salinity conditions. During water deficiency, ABA-related signalling regulates stomatal closure, reducing excessive water loss through transpiration. It also activates several stress-responsive genes involved in maintaining cellular water balance. Similarly, plants activate antioxidant defence systems to minimise oxidative damage caused by environmental stress. Enzymes such as superoxide dismutase, catalase and peroxidase help regulate reactive oxygen species (ROS) and protect cellular structures. The accumulation of compatible solutes, including proline, soluble sugars and certain amino acids, also helps maintain osmotic balance during water-deficit conditions. These genetic and biochemical mechanisms collectively contribute to the ability of maize plants to survive and maintain growth under adverse environments (Yang et al., 2023).

2. GENETIC MANAGEMENT OF MAJOR ABIOTIC STRESSES IN MAIZE

Drought Stress

Drought is one of the most important environmental constraints affecting maize production. Water deficiency reduces photosynthesis, restricts nutrient uptake and affects reproductive development. Genetic improvement for drought tolerance focuses on identifying plants capable of maintaining water balance, root development and reproductive stability under limited moisture conditions. Genes associated with root architecture, stomatal regulation, ABA signalling and osmotic adjustment are important targets for drought-tolerance breeding. Deep and well-developed root systems improve access to soil moisture, while efficient stomatal regulation helps reduce excessive water loss. Genetic improvement of flowering synchronisation is also important because drought during reproductive development can severely reduce kernel formation. Liu and Qin (2021) highlighted the importance of understanding the genetic architecture of drought tolerance at different maize developmental stages. QTL mapping, molecular markers and genomic approaches provide useful opportunities for identifying favourable genetic regions and incorporating them into improved breeding materials.

Heat Stress

Increasing temperatures, particularly during flowering and grain filling, negatively affect maize productivity. Heat stress can reduce pollen viability, disturb fertilisation and accelerate leaf senescence. Genetic management of heat stress involves identifying genes associated with heat-shock proteins, antioxidant defence and cellular stability. Heat-

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shock proteins protect cellular proteins from damage under elevated temperatures, while heat-responsive transcription factors regulate the expression of several protective genes. Improving these molecular mechanisms may help maize plants maintain physiological activities and reproductive performance during heat stress. The development of heat-tolerant varieties should also focus on maintaining pollen viability, synchronised flowering and grain-filling capacity under high-temperature conditions.

Salinity Stress

Soil salinity is an increasing concern in agricultural regions affected by excessive salt accumulation. High salt concentrations create osmotic stress and ionic imbalance, restricting water absorption and plant growth. Genetic management of salinity focuses on improving ion homeostasis, particularly the regulation of sodium and potassium concentrations within plant tissues. Genes associated with ion transport, membrane stability, osmotic adjustment and antioxidant defence are important targets for improving salt tolerance. Recent research has identified several salt-responsive genes and molecular pathways in maize that may be useful for developing improved breeding materials. Integrating genomic, transcriptomic and metabolomic information can help identify promising candidate genes for salinity-tolerance improvement (Qu et al., 2026).

Waterlogging Stress

Waterlogging occurs when excess water saturates the soil and reduces oxygen availability around plant roots. This condition restricts root respiration, affects nutrient absorption and may cause severe growth reduction. Genetic management of waterlogging involves identifying traits associated with root adaptation, oxygen sensing, anaerobic metabolism and antioxidant protection. Stress-responsive genes involved in ethylene signalling and metabolic adjustment are particularly important for understanding plant responses to oxygen deficiency. Developing maize varieties with improved root functioning and tolerance to temporary waterlogging is important for regions experiencing heavy rainfall and poor drainage.

3. MOLECULAR BREEDING: UTILISING FAVOURABLE GENETIC VARIATIONS

Molecular breeding is an important component of genetic stress management because it enables the identification and selection of desirable genetic characteristics through DNA-based technologies. Marker-assisted selection (MAS) helps identify plants carrying favourable genes or quantitative trait loci associated with drought, heat and salinity tolerance. Once suitable molecular markers are identified, breeders can select promising plants at early growth stages without depending entirely on visible stress symptoms. Marker-assisted backcrossing is useful for transferring favourable stress-tolerance genes into high-yielding maize varieties while retaining their desirable agronomic characteristics. This approach can improve the genetic background of popular varieties and reduce the time required for conventional selection. Genomic selection further strengthens molecular breeding by using genome-wide molecular markers to predict the genetic potential of breeding materials. It is particularly useful for complex traits controlled by several genes, such as grain yield, drought tolerance and environmental adaptability. These approaches, when combined with conventional field evaluation, provide opportunities to improve selection accuracy and accelerate the development of stress-resilient maize varieties.

4. GENOME EDITING: PRECISION GENETIC IMPROVEMENT

Genome editing has introduced new possibilities for modifying genes associated with stress tolerance. Among available technologies, CRISPR/Cas9 has gained considerable attention because of its ability to make targeted changes in specific DNA sequences. In maize, CRISPR/Cas-based approaches can be used to investigate and modify genes involved in drought response, heat tolerance, salinity resistance and plant development. One important example is the ARGOS8 gene, where CRISPR/Cas9-mediated promoter replacement improved grain yield under flowering-stage drought conditions (Shi et al., 2017). Other potential targets include genes involved in stomatal regulation, root

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development, antioxidant defence and stress-responsive signalling. Advanced genome-editing approaches, including base editing and prime editing, provide additional opportunities for making precise genetic modifications.However, the successful application of genome editing requires careful selection of target genes, evaluation of genetic stability and assessment of possible effects on grain yield and quality. Field-level testing and compliance with applicable biosafety and regulatory requirements are also essential.

5. INTEGRATION OF MULTI-OMICS APPROACHES IN GENETIC STRESS MANAGEMENT

Modern genetic stress management increasingly depends on the integration of different omics technologies to understand the complex responses of maize plants to environmental stress. Genomics helps identify genes and genetic variations associated with stress tolerance, while transcriptomics reveals changes in gene expression under different environmental conditions. Proteomics identifies stress-responsive proteins involved in cellular protection and metabolism, whereas metabolomics provides information about compounds such as proline, sugars and antioxidants that contribute to stress adaptation. Combining these approaches helps researchers understand the relationship between genetic variation, gene expression and physiological performance. For example, the identification of drought-responsive genes through genomics can be supported by transcriptomic studies, while metabolomic analysis can reveal the biochemical mechanisms responsible for maintaining cellular water balance. High-throughput phenotyping and artificial intelligence can further strengthen this approach by connecting molecular information with field-level plant performance. Such integration can help identify promising genetic resources and develop improved maize varieties with multiple stress tolerance.

6. CHALLENGES AND FUTURE PROSPECTS

Despite considerable progress, several challenges remain in genetic stress management. Abiotic stress tolerance is a complex characteristic influenced by multiple genes, environmental conditions and interactions among different physiological processes. Therefore, improving a single gene or trait may not provide sufficient tolerance under all environmental conditions. Another major challenge is the transfer of laboratory-based genetic discoveries into practical breeding programmes. Promising genotypes must be evaluated under different soil, climatic and management conditions to confirm their performance. The cost of advanced molecular technologies, limited access to genomic facilities and the need for skilled researchers may also restrict their wider application. Future maize improvement programmes should focus on integrating molecular breeding, genomic selection, genome editing, multi-omics and advanced phenotyping. Greater utilisation of diverse germplasm resources, including traditional landraces and stress-adapted varieties, will be important for identifying valuable genetic variations. Special attention should be given to developing maize varieties with combined tolerance to drought, heat and salinity while maintaining high grain yield, nutritional quality and disease resistance. Strengthening collaboration among geneticists, plant breeders, biotechnologists and farmers will be essential for translating scientific discoveries into practical agricultural benefits.

CONCLUSION

Genetic stress management offers an important pathway for improving maize adaptability and productivity under changing environmental conditions. Understanding stress-responsive genes, molecular signalling pathways and genetic variations provides a strong foundation for developing stress-tolerant varieties. Molecular breeding, genomic selection and precision genome editing can accelerate the identification, selection and utilisation of favourable genetic traits. Their integration with multi-omics approaches and advanced phenotyping can further improve the efficiency of modern maize improvement programmes. Although challenges related to complex genetic interactions and field-level validation remain, continued advances in plant genetics and biotechnology will strengthen the development of climate-resilient maize. Ultimately, effective genetic stress management will contribute to stable crop productivity, sustainable agriculture and future food security.

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REFERENCES

1. Yang, Z., Cao, Y., Shi, Y., Qin, F., Jiang, C., and Yang, S. (2023). Genetic and molecular exploration of maize environmental stress resilience: Toward sustainable agriculture. *Molecular Plant*, 16(10), 1496–1517. https://doi.org/10.1016/j.molp.2023.07.005

2. Liu, S., and Qin, F. (2021). Genetic dissection of maize drought tolerance for trait improvement. *Molecular Breeding*, 41, 8. https://doi.org/10.1007/s11032-020-01194-w

3. Peer, L. A., Bhat, M. Y., Lone, A. A., Dar, Z. A., and Mir, B. A. (2024). Genetic, molecular and physiological crosstalk during drought tolerance in maize (*Zea mays*): Pathways to resilient agriculture. *Planta*, 260, 81. https://doi.org/10.1007/s00425-024-04517-9

4. Qu, Y., Zhang, J., Zhang, Y., Xie, Y., Cao, X., Li, J., Yin, Z., Luo, J., Long, Y., Zaidi, P. H., and Wan, X. (2026). Molecular mechanisms and genic resources responsive to salinity stress and their applications in maize and other crop breeding. *Science Bulletin*, 71(8), 2094–2114. https://doi.org/10.1016/j.scib.2026.03.023