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Advances in Plant Breeding for Climate Resilience

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ABSTRACT

Climate change poses unprecedented threats to global food security through increasing temperatures, erratic rainfall, rising salinity, and frequent extreme weather events. Traditional plant breeding methods, while foundational, are often too slow to address the accelerating pace of environmental change. This review examines recent advances in plant breeding technologies for developing climate-resilient crop varieties. Key innovations discussed include CRISPR/Cas9-mediated genome editing for targeted modification of stress-responsive genes, marker-assisted selection (MAS) for pyramiding abiotic stress tolerance traits, genomic selection (GS) for predicting complex trait performance, speed breeding protocols for accelerating generation cycles, and high-throughput phenotyping (HTP) for precision trait evaluation. The integration of these modern breeding approaches offers transformative potential for developing crop varieties with enhanced drought, heat, salinity, and flood tolerance. This paper highlights successful case studies and outlines future directions for achieving sustainable food production under changing climatic conditions.

Keywords: *Climate resilience; CRISPR/Cas9 genome editing; Marker-assisted selection; Speed breeding; Abiotic stress tolerance.*

INTRODUCTION

Climate change represents one of the most formidable challenges confronting global agriculture in the twenty-first century. The Intergovernmental Panel on Climate Change (IPCC, 2023) has projected that rising global temperatures, altered precipitation patterns, increased frequency of droughts and floods, and elevated atmospheric carbon dioxide concentrations will significantly reduce crop productivity in major agricultural regions worldwide. According to Zhao et al. (2017), each degree Celsius increase in global mean temperature could reduce global yields of wheat by 6.0%, rice by 3.2%, maize by 7.4%, and soybean by 3.1%.

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Plant breeding has historically been the cornerstone of crop improvement, enabling the development of high-yielding, disease-resistant, and stress-tolerant varieties that have sustained global food production (Collard & Mackill, 2008). However, conventional breeding approaches, which typically require 10 to 15 years to develop a new variety, are increasingly insufficient to keep pace with the rapid changes in climatic conditions (Hickey et al., 2019). The genetic gains achieved through traditional selection methods are further constrained by narrow genetic diversity in elite germplasm, complex inheritance patterns of stress tolerance traits, and the polygenic nature of most climate-adaptive characteristics (Varshney et al., 2021).

The emergence of new plant breeding techniques (NPBTs) has opened transformative avenues for accelerating crop improvement for climate resilience. These include CRISPR/Cas9-mediated genome editing, marker-assisted selection (MAS), genomic selection (GS), speed breeding, and high-throughput phenotyping (HTP) technologies (Watson et al., 2018). The integration of these technologies enables breeders to make precise genetic modifications, predict complex trait performance, and dramatically reduce breeding cycle times (Varshney et al., 2021). This review examines the current advances in these modern plant breeding approaches and their applications in developing climate-resilient crop varieties.

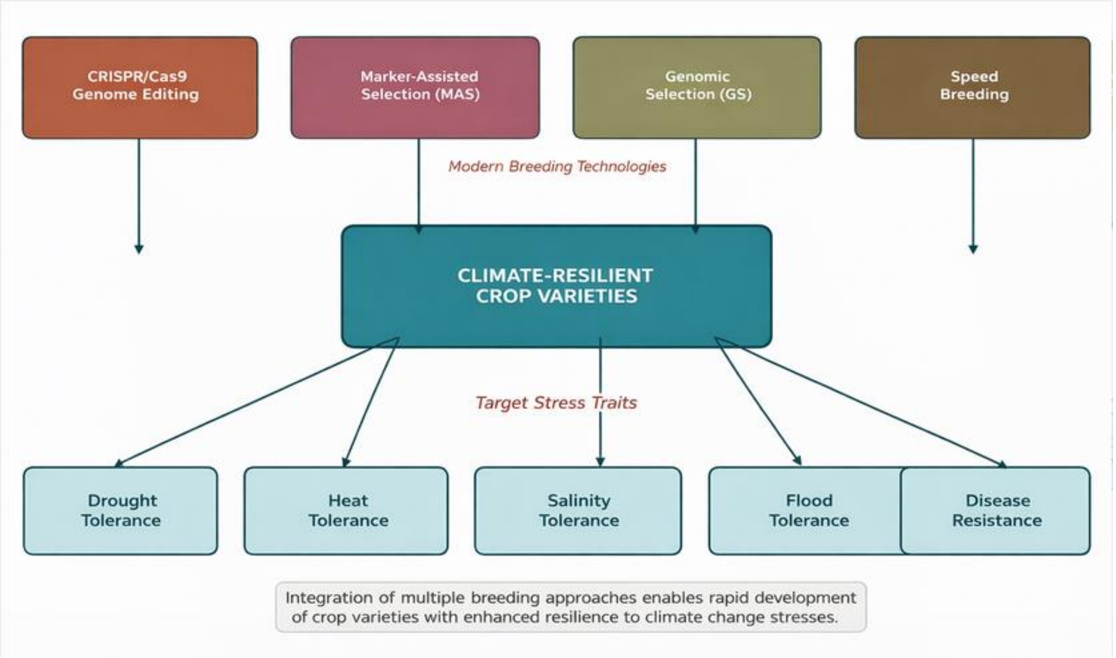


Figure 1: Integrated Modern Plant Breeding Approaches for Climate Resilience

2. CRISPR/Cas9 Genome Editing for Climate Resilience

The clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) system has revolutionized crop improvement by enabling precise, targeted modifications of plant genomes (Zafar et al., 2023). Unlike conventional genetic engineering, CRISPR/Cas9 allows researchers to make specific alterations in stress-responsive genes without introducing foreign DNA, making it a powerful tool for developing climate-resilient varieties (Rathore et al., 2023).

2.1 Drought Tolerance

Drought stress is the most devastating abiotic factor affecting crop productivity worldwide. CRISPR/Cas9-mediated genome editing has demonstrated remarkable success in enhancing drought tolerance across multiple crop species. In rice, the knockout of negative regulators of drought tolerance, including OsDST (drought and salt tolerant protein 1), OsDIS1 (drought-induced SINA protein 1), and OsSRFP1 (stress-related ring finger protein 1), resulted in enhanced antioxidant enzyme levels, reduced hydrogen peroxide concentrations, and improved drought tolerance (Santosh Kumar et al., 2020). Shi et al. (2017) demonstrated that CRISPR/Cas9-mediated editing of the ARGOS8 gene in maize produced variants with enhanced grain yield under drought field conditions.

In tomato, Liu et al. (2020) showed that CRISPR/Cas9-mediated knockout of SlLBD40, a lateral organ boundaries domain transcription factor, significantly enhanced drought tolerance. Furthermore, Li et al. (2019) confirmed that editing of the pathogenesis-related gene SlNPR1 in tomato regulated drought response mechanisms, offering multiple variant possibilities for broad-spectrum drought tolerance.

2.2 Heat and Salinity Tolerance

CRISPR/Cas9 has also been successfully applied to improve heat stress tolerance in crops. Bouzroud et al. (2023) demonstrated that CRISPR-edited mutant plants exhibited improved agronomic characteristics and enhanced resilience to heat stress. The BRZ1 gene, which positively regulates reactive oxygen species formation in the tomato apoplastic area, was confirmed through CRISPR/Cas9-based bzr1 mutants as a key component of heat tolerance mechanisms (Li et al., 2023). For salinity tolerance, CRISPR/Cas9-mediated editing of genes involved in ABA signalling pathways, including OsSAPK2 and OsERA1, has shown promising results in rice (Ogata et al., 2020; & Lou et al., 2017).

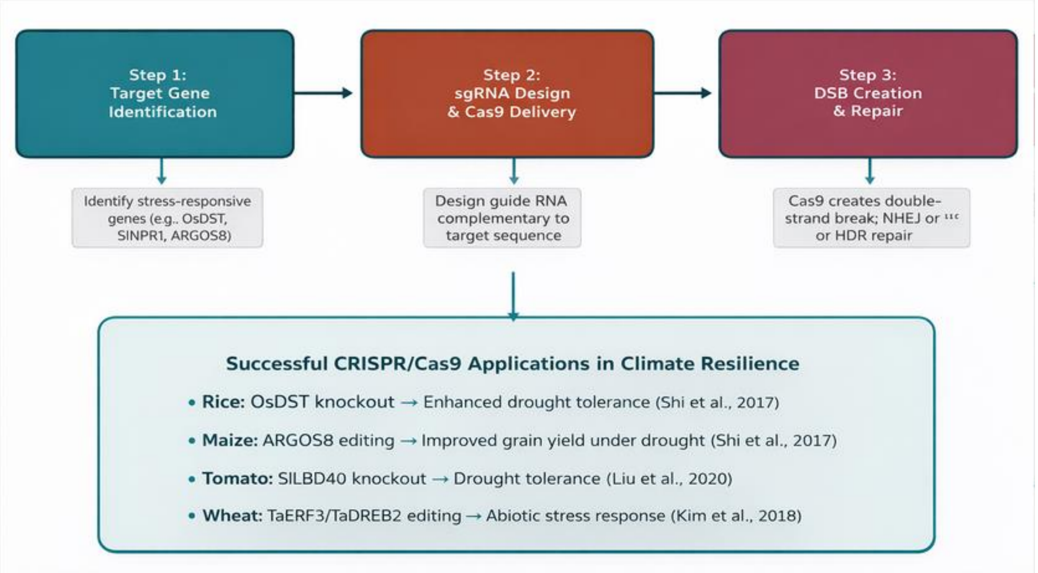


Figure 2: CRISPR/Cas9-Mediated Genome Editing for Abiotic Stress Tolerance in Crops

3. Marker-Assisted Selection for Climate Adaptation

Marker-assisted selection (MAS) employs DNA markers linked to quantitative trait loci (QTLs) to identify and select individuals carrying desirable alleles for stress tolerance traits. Collard and Mackill (2008) highlighted that MAS offers significant advantages over conventional phenotypic selection, including the ability to select for traits at the seedling stage, pyramid multiple resistance genes, and accelerate backcrossing programmes.

Recent advances in genome-wide association studies (GWAS) and QTL mapping have identified numerous genomic regions associated with drought, heat, and salinity tolerance in major cereal crops (Garcia-Oliveira et al., 2024). The integration of MAS with modern genotyping platforms has enabled cost-effective deployment of molecular markers in breeding programmes targeted at developing climate-smart cultivars (Frontiers in Plant Science, 2025). MAS has been particularly successful in pyramiding multiple stress tolerance genes within single elite varieties, allowing breeders to develop cultivars with combined resistance to multiple abiotic stresses simultaneously (Varshney et al., 2021).

4. Genomic Selection for Complex Stress Traits

Genomic selection (GS) represents a paradigm shift in breeding for complex quantitative traits, including abiotic stress tolerance. Unlike MAS, which targets individual QTLs of large effect, GS utilizes genome-wide marker data to predict the breeding value of individuals based on their total genetic merit (Meuwissen et al., 2001). This approach is particularly valuable for climate resilience traits, which are typically governed by numerous small-effect genes distributed across the genome.

GS enhances yield stability by enabling breeders to predict performance across diverse environments using multi-environment trial (MET) data (Biochemical Journal, 2025). Integration of GS with high-throughput phenotyping strengthens selection for stability indices, resilience trajectories, and stress-adaptive growth patterns. Recent studies have demonstrated that GS can increase genetic gain per unit time by 1.5 to 2.0 times compared with conventional phenotypic selection methods, particularly for stress-related traits (Hickey et al., 2019).

5. Speed Breeding for Accelerated Crop Development

Speed breeding is an innovative approach that dramatically shortens generation times by optimizing photoperiod, temperature, and light intensity conditions in controlled environments. Watson et al. (2018) demonstrated that speed breeding can achieve up to six generations per year for spring wheat, durum wheat, barley, chickpea, and pea, and four generations per year for canola, compared with two to three generations under normal glasshouse conditions.

The protocol typically employs an extended photoperiod of 22 hours of light at controlled temperatures (22°C day/17°C night) with supplemental LED lighting to accelerate photosynthesis, growth, and seed maturation (Watson et al., 2018). The RapidGen technology developed at ICRISAT has reduced the breeding cycle by 40%, demonstrating the scalability of speed breeding for large-scale crop improvement programmes (Bioingene, 2021). When integrated with marker-assisted selection, genomic selection, and genome editing, speed breeding offers a powerful platform for rapidly developing climate-resilient varieties, reducing the time from initial cross to varietal release from 10–12 years to as few as 3–4 years (Hickey et al., 2019).

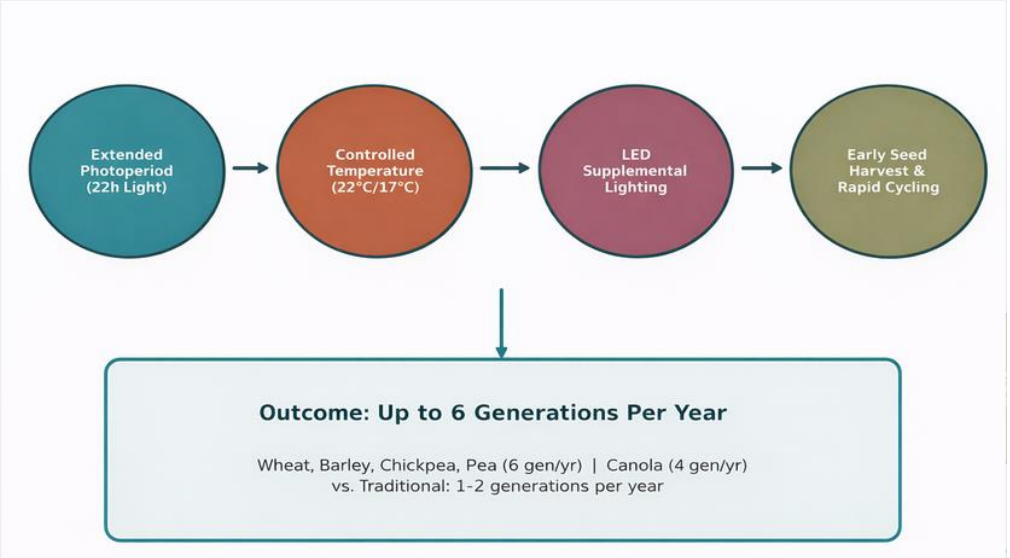
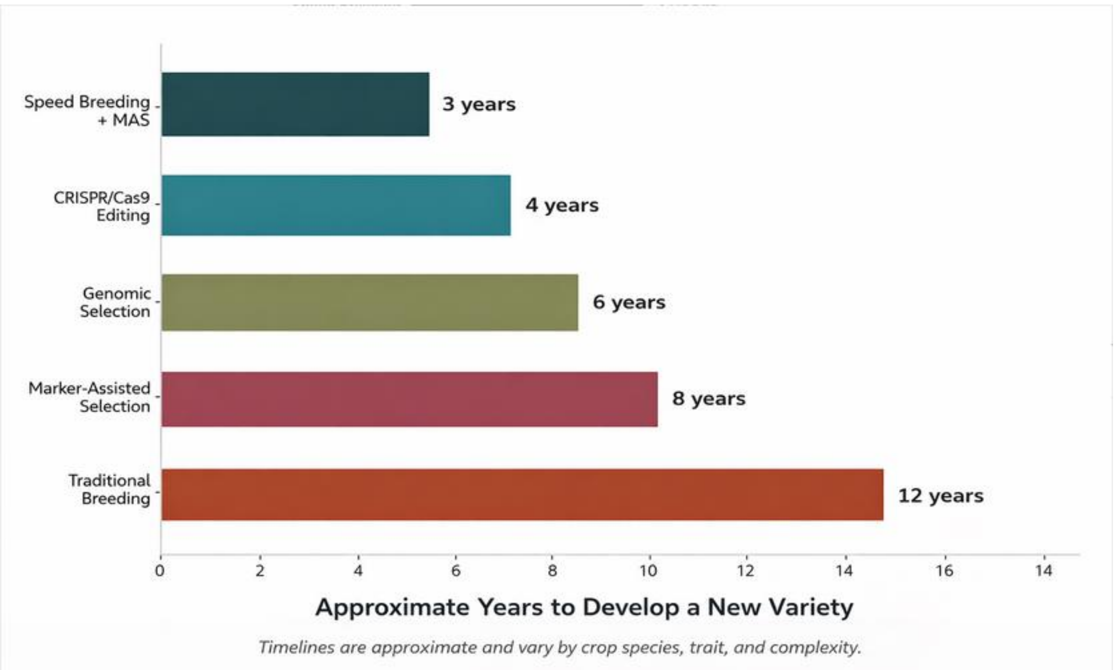


Figure 3: Speed Breeding Protocol for Accelerated Generation Advancement

6. High-Throughput Phenotyping for Stress Tolerance

High-throughput phenotyping (HTP) has emerged as a critical component of modern breeding programmes, addressing the phenotyping bottleneck that has historically limited the pace of genetic improvement for stress tolerance traits. HTP platforms utilize advanced sensor technologies, including RGB imaging, infrared thermography, near-infrared spectroscopy, hyperspectral imaging, and chlorophyll fluorescence measurement, to non-destructively assess plant responses to abiotic stresses at unprecedented scale and resolution (Kim et al., 2021).

The integration of HTP with machine learning algorithms has further enhanced the accuracy of phenotypic predictions, enabling breeders to identify drought-tolerant genotypes through canopy temperature analysis, water-use efficiency assessment, and stress-adaptive growth pattern evaluation (Das et al., 2025). Christopher et al. (2015) demonstrated the efficacy of combining phenotyping and speed breeding to promote root adaptation in changing environments, advancing over 1,000 recombinant inbred lines of wheat within 18 months. These approaches have been extensively applied in rice, wheat, and maize breeding programmes to develop varieties capable of tolerating abiotic stresses such as drought and salinity (High-throughput Plant Phenotyping, 2025).



Timelines are approximate and vary by crop species, trait, and complexity.

Figure 4: Comparison of Breeding Timelines for Developing Climate-Resilient Crop Varieties

CONCLUSION

The development of climate-resilient crop varieties is imperative for ensuring global food security in the face of accelerating climate change. This review has highlighted the transformative potential of modern plant breeding technologies, including CRISPR/Cas9 genome editing, marker-assisted selection, genomic selection, speed breeding, and high-throughput phenotyping, in addressing the limitations of conventional breeding approaches. CRISPR/Cas9 has demonstrated remarkable precision in modifying stress-responsive genes, enabling targeted enhancement of drought, heat, and salinity tolerance in major crop species. Marker-assisted selection and genomic selection have expanded the capacity to identify, track, and combine beneficial alleles for complex stress tolerance traits across diverse germplasm.

Speed breeding has dramatically reduced generation cycle times, enabling up to six generations per year and accelerating the pace of genetic improvement. High-throughput phenotyping has resolved the phenotyping bottleneck, providing non-destructive, high-resolution assessment of stress tolerance traits at scale. The synergistic integration of these technologies represents the most promising pathway for developing climate-resilient crop varieties capable of sustaining productivity under increasingly challenging environmental conditions. Future research should focus on expanding the application of these technologies to underutilized crops, enhancing regulatory frameworks for genome-edited varieties, and ensuring equitable access to these innovations for smallholder farmers in climate-vulnerable regions. Collaborative efforts across disciplines, including genomics, bioinformatics, agronomy, and policy, will be essential for translating these scientific advances into tangible improvements in food security and agricultural sustainability.

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All authors reviewed and approved the manuscript.

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