

MODERN CROP IMPROVEMENT THROUGH GENOMIC SELECTION, MARKER-ASSISTED BREEDING, AND GENOME EDITING FOR CLIMATE RESILIENCE

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Abstract

Global agriculture is confronting an unprecedented crisis driven by climate change, characterized by rising temperatures, prolonged droughts, erratic precipitation, soil salinization, and unpredictable pest outbreaks. These environmental stressors severely compromise crop physiology, reducing yields of staple cereals such as wheat, rice, and sorghum. The narrow genetic base of elite cultivars and the limitations of conventional breeding including lengthy 10–12 year cycles, linkage drag, and poor selection efficiency for polygenic traits have necessitated a transition toward genomics-assisted precision breeding. This study synthesizes modern crop improvement strategies integrating Marker-Assisted Selection (MAS), Marker-Assisted Backcrossing (MABC), Genomic Selection (GS), CRISPR/Cas genome editing, and Speed Breeding (SB) to develop climate-resilient varieties. MAS enables early-generation selection of major-effect QTLs controlling drought, heat, and salinity tolerance, while MABC facilitates precise introgression and QTL pyramiding with minimal linkage drag. GS captures genome-wide additive and non-additive effects, making it effective for highly polygenic stress-adaptive traits through models such as gBLUP, Bayesian alphabetic methods, and deep learning algorithms. CRISPR/Cas systems enable targeted knockout or modification of negative regulators and signaling components, enhancing drought, heat, and salt tolerance. Integrating these tools with Speed Breeding and Doubled Haploid technology compresses breeding cycles from 10–12 years to 3–5 years. The study also examines global regulatory frameworks, contrasting product-based and process-based oversight, and addresses socio-economic barriers including intellectual property constraints and infrastructure gaps. Collectively, these integrated genomic approaches offer a

transformative pathway for accelerating climate-resilient crop development and ensuring global food security.

INTRODUCTION

Global agriculture faces an unprecedented crisis driven by the acceleration of climate change, characterized by rising ambient temperatures, prolonged droughts, erratic precipitation regimes, soil salinization, and unpredictable pest and pathogen outbreaks (Afzal et al., 2023). These environmental stressors induce multi-systemic physiological disruption in crops, compromising photosynthetic capacity, cell turgor, enzyme kinetics, and reproductive success. Major crop staples such as wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.), and sorghum (*Sorghum bicolor*) frequently experience terminal heat and moisture deficits during critical phenological stages like anthesis and grain filling, resulting in substantial yield reductions (Borgohain et al., 2026).

The vulnerability of modern agriculture is further heightened by the narrow genetic base of elite cultivars, which have been selected under high-input, static environmental conditions. As extreme weather events increase in frequency and intensity, historical yield gains achieved during the Green Revolution are stagnating (Budhlakoti et al., 2022). Consequently, bridging the gap between potential and realized crop yields under abiotic stress has become a primary mandate for global food security. Addressing these challenges requires crop varieties capable of enduring extreme climate fluctuations while maintaining stable, high-quality yields (Upadhyay et al., 2025).

Limitations of Conventional Breeding Paradigms

Traditional plant breeding relies on phenotypic selection and sexual hybridization to fix desirable alleles within breeding populations. Although

effective for simply inherited, high-heritability traits, classical approaches are inefficient for abiotic stress tolerance. Stress resilience traits such as root architecture, osmotic adjustment, canopy temperature maintenance, and stay-green physiology are polygenic, quantitative, and heavily influenced by complex Genotype-by-Environment ($G \times E$) interactions (Acquaah, 2024).

Conventional crop improvement pipelines operate on extended timeframes, typically requiring 10 to 12 years from initial hybridization to formal varietal release. This prolonged duration is driven by sequential cycles of phenotypic backcrossing, selfing, and multi-environment field testing necessary to stabilize yield and agronomic traits (Brescaghello & Coelho, 2013). Furthermore, conventional introgression of adaptive alleles from unadapted landraces or wild relatives is burdened by linkage drag the co-inheritance of deleterious loci physically linked to the target gene which requires extensive backcrossing to purge. Phenotypic selection under variable field conditions is also vulnerable to environmental noise, leading to low selection efficiency for low-heritability quantitative traits. Interspecific or wide sexual crosses face reproductive barriers, including pre- and post-zygotic incompatibilities and segregation distortion, which limit the available genetic diversity (Reshma et al., 2026).

To overcome these constraints, modern crop improvement has transitioned toward a genomics-assisted precision breeding framework. By combining marker-assisted backcrossing, genomic selection, CRISPR-based site-directed mutagenesis, and speed breeding protocols, breeders can precisely target complex traits and accelerate varietal deployment (Podevin et al., 2013).

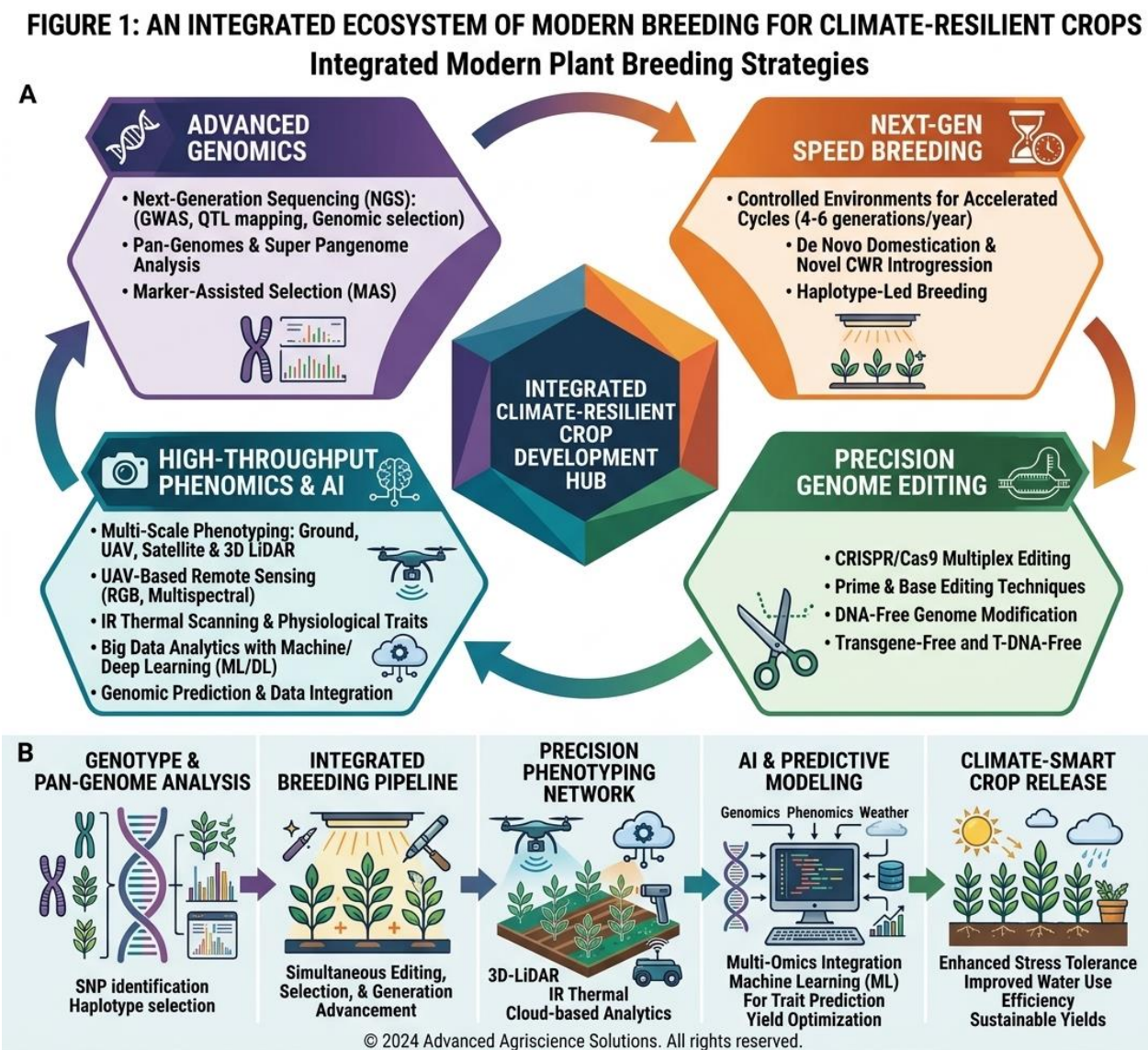


Figure 1: An Integrated Ecosystem and Multi-Tiered Framework for Climate-Resilient Crop Improvement

Table 1: Comparison of Traditional vs. Genomics-Assisted Plant Breeding Paradigms

Feature / Dimension	Conventional Breeding	Marker-Assisted Selection (MAS)	Genomic Selection (GS)	CRISPR/Cas Genome Editing	Integrated Speed-GS-CRISPR Pipeline
Genetic Basis	Visual phenotypes; unmapped polygenes	Linked molecular markers to major QTLs	Genome-wide markers capturing additive effects	Targeted site-specific gene modifications	Multi-omic, genome-wide predictive and targeted edits
Trait Architecture Targeted	Monogenic & high-heritability	Major QTLs ($R^2 > 10 - 15\%$) and	Highly polygenic traits	Known negative/positive gene regulators	Simple and complex

	quantitative traits	oligogenic traits	controlled by small-effect loci		polygenic trait complexes
Breeding Cycle Duration	10–12 Years	6–8 Years	4–6 Years	2–4 Years (trait integration)	3–5 Years (end-to-end varietal release)
Linkage Drag Risk	High; requires extensive backcrossing	Moderate; mitigated by recombinant marker selection	Low; genome-wide background monitoring	Zero; precise target editing without donor genome	Minimal to zero
$G \times E$ Confounding Impact	High; dependent on field environment stability	Moderate; sensitive to environmental QTL expression	Low; explicitly modeled in multi-environment GS	Trait-dependent; edit target must be functionally robust	Low; minimized via predictive environmental modeling
Primary Limitation	Labor-intensive, low selection intensity	Ineffective for polygenic traits with minor QTLs	High initial genotyping costs, complex bioinformatics	Tissue culture/recalcitrant transformation barriers	High infrastructure capital requirements

2. Marker-Assisted Selection and Backcrossing for Abiotic Stress Tolerance

2.1 Principles and Evolution of Molecular Markers

Marker-Assisted Selection (MAS) utilizes DNA molecular markers linked to target quantitative trait loci (QTLs) to indirectly select for phenotypes. Selection at the DNA level allows breeders to screen individuals at early seedling stages, independent of environmental fluctuations or gene expression timing, bypassing the need for destructive field testing (Hasan et al., 2021).

The evolution of marker systems has driven advancements in molecular breeding over recent decades. First-generation systems, such as Restriction Fragment Length Polymorphisms (RFLPs) and Random Amplified Polymorphic DNA (RAPDs), established the initial framework for genetic mapping and polygenic trait dissection. However, their reliance on hybridization techniques, high DNA quantity requirements, and poor laboratory reproducibility limited their deployment in large-scale breeding programs (Kumari et al., 2024). The introduction of second-generation markers specifically Amplified

Fragment Length Polymorphisms (AFLPs) and Simple Sequence Repeats (SSRs or microsatellites) improved genotyping efficiency through high polymorphic information content (PIC), co-dominant inheritance, and PCR-based automation. SSRs became the standard for QTL mapping and marker-assisted backcrossing (Parihar & Shiwani, 2022).

Third-generation marker systems, dominated by Single Nucleotide Polymorphisms (SNPs), represent the current standard for high-throughput plant genotyping. Distributed densely across crop genomes, SNPs enable base-pair level resolution (Gantait et al., 2019). Coupled with array platforms and sequencing-by-synthesis technologies such as Genotyping-by-Sequencing (GBS), SNP technologies allow automated, cost-effective screening of thousands of individuals across millions of genomic loci. This high marker density enables precise QTL mapping, fine-scale genome-wide association studies (GWAS), and background genome tracking during introgressions (Gupta et al., 2010).

2.2 Dissecting Stress-Responsive Quantitative Trait Loci (QTLs)

Abiotic stress tolerance is governed by complex genetic networks. Genetic mapping studies differentiate between constitutive QTLs which are stably expressed across diverse moisture and thermal regimes and adaptive QTLs, whose expression is triggered by specific environmental stress thresholds or growth stages. Identifying these loci provides specific molecular targets for marker-assisted breeding and gene discovery (Goud et al., 2026).

Targeting root system architecture (RSA) represents an effective strategy for drought adaptation. In rice, the identification and positional cloning of the *DEEPER ROOTING 1* (*DRO1*) locus demonstrated that modifying root growth angles to steer roots downward into deeper, moisture-retentive soil layers preserves leaf water potential and prevents drought-induced floral sterility during severe moisture stress (Pauli et al., 2026). Similarly, osmotic adjustment and canopy microclimate maintenance are regulated by distinct genomic regions. In wheat, meta-QTL analyses have resolved major loci controlling canopy temperature depression, normalized difference vegetation index (NDVI), and proline accumulation under heat and water deficits (Meckes et al., 2018).

Post-flowering drought tolerance in *Sorghum bicolor* is linked to the stay-green phenotype, which delays foliar senescence and maintains active photosynthetic output during the grain filling phase. Map-based cloning and QTL mapping have identified key stay-green loci including *Stg1*, *Stg2*, *Stg3*, *Stg4*, *Stg3A*, and *Stg3B* that modulate stem lodging resistance, preserve functional transpiration, and maintain seed weight under terminal drought conditions (Li et al., 2019). Beyond drought, cloned loci regulating ion homeostasis under toxicity stress have been deployed in breeding programs. Notably, the *ALMT1* locus (encoding an aluminum-activated malate transporter) and the *HKT1* locus (mediating selective sodium exclusion) preserve root apical meristem viability and cytosolic

potassium balance in acidic and saline soils, respectively (Kujur et al., 2013).

2.3 Marker-Assisted Backcrossing (MABC) and QTL Pyramiding in Practice

Marker-Assisted Backcrossing (MABC) accelerates the transfer of major-effect loci or QTLs from an unadapted donor line into an elite, high-yielding recurrent parent while minimizing donor genome contamination. MABC employs a three-tiered marker selection protocol across backcross generations:

- **Foreground Selection:** Confirms the presence of the target stress-tolerance allele using linked diagnostic markers, eliminating offspring lacking the donor gene (Goud et al., 2026).
- **Recombinant Selection:** Deploys polymorphic markers flanking the target locus to identify crossover events close to the target gene, breaking unwanted linkage drag and removing linked donor sequences.
- **Background Selection:** Screens genome-wide markers across all non-target chromosomes to select individuals with maximum recovery of the Recurrent Parent Genome (RPG), compressing the traditional 6–8 generation backcross timeline into 2–3 generations (Pauli et al., 2016).

In wheat (*Triticum aestivum* L.), Marker-Assisted Backcross Breeding (MABB) was successfully used to introgress drought-tolerant QTLs into the elite cultivar 'HD3086'. Foreground selection targeted loci controlling Biomass (BIO), Canopy Temperature (CT), Thousand Kernel Weight (TKW), Normalized Difference Vegetation Index (NDVI), and overall Yield (YLD) under moisture deficits (Collins et al., 2008). By monitoring background genome recovery across BC₁F₁ to BC₂F₅ generations, breeders achieved 78% to 91% RPG recovery. Two-year field evaluations under managed drought stress confirmed that the improved lines maintained lower canopy temperatures, higher green leaf area (NDVI), increased kernel mass, and significantly higher grain yields compared to the unimproved recurrent parent (Meckes et al., 2018).

Similarly, MABC facilitates QTL pyramiding, combining multiple major genes controlling

complementary stress mechanisms into a single elite background. Introgressing combinations of stay-green loci (*Stg1–Stg4*) in sorghum and submergence tolerance loci (*Sub1*) in rice has produced multi-stress resilient cultivars. However, because MABC targets major loci ($R^2 > 10 - 15\%$), it is less effective for highly polygenic traits controlled by hundreds of minor-effect loci. This limitation led to the development of Genomic Selection (Cao et al., 2022).

3. Genomic Selection and Predictive Breeding Frameworks

3.1 Statistical Models and Algorithmic Innovations

Genomic Selection (GS) estimates the genetic merit of candidate plants across the entire genome using dense marker coverage. Rather than tracking individual major-effect QTLs, GS estimates Genomic Estimated Breeding Values (GEBVs) by capturing all additive and non-additive locus effects simultaneously, making it well-suited for polygenic traits influenced by small-effect loci (Chafai et al., 2023).

The basic linear additive model for genomic prediction is expressed as:

$$y_i = \mu + \sum_{j=1}^p x_{ij} \beta_j + e_i$$

Where y_i is the observed phenotype of individual i , μ is the population mean, p is the total number of genome-wide SNP markers, x_{ij} represents the numerical genotype at locus j (coded as 0, 1, or 2

for allele dosage), β_j is the estimated effect of marker j , and e_i is the residual error term (Amin et al., 2025).

Because the number of marker loci (p) typically far exceeds the number of phenotyped individuals (n) the $p \gg n$ dimensionality problem standard ordinary least squares regression cannot be applied. Advanced statistical and machine learning models are used to address this issue:

- **Genomic Best Linear Unbiased Prediction (gBLUP):** Uses a Genomic Relationship Matrix (GRM) derived from SNP data to model polygenic variance. gBLUP assumes that all markers contribute equally to genetic variation with small additive effects drawn from a normal distribution (Jeon et al., 2023).

- **Bayesian Alphabetic Models (BayesA, BayesB, BayesC, LASSO):** Model variation by allowing locus-specific variances. BayesB, for instance, assumes that many genomic regions have zero effect while a small subset carries non-zero effects, reflecting genetic architectures that contain major QTLs alongside polygenic backgrounds.

- **Non-Parametric Machine and Deep Learning (DL):** Approaches such as Multilayer Perceptrons (MLP), Convolutional Neural Networks (CNNs), and Random Forests capture non-linear relationships, complex epistatic gene interactions, and high-order $G \times E$ dynamics without requiring explicit assumptions about genetic architecture (Zhang et al., 2025).

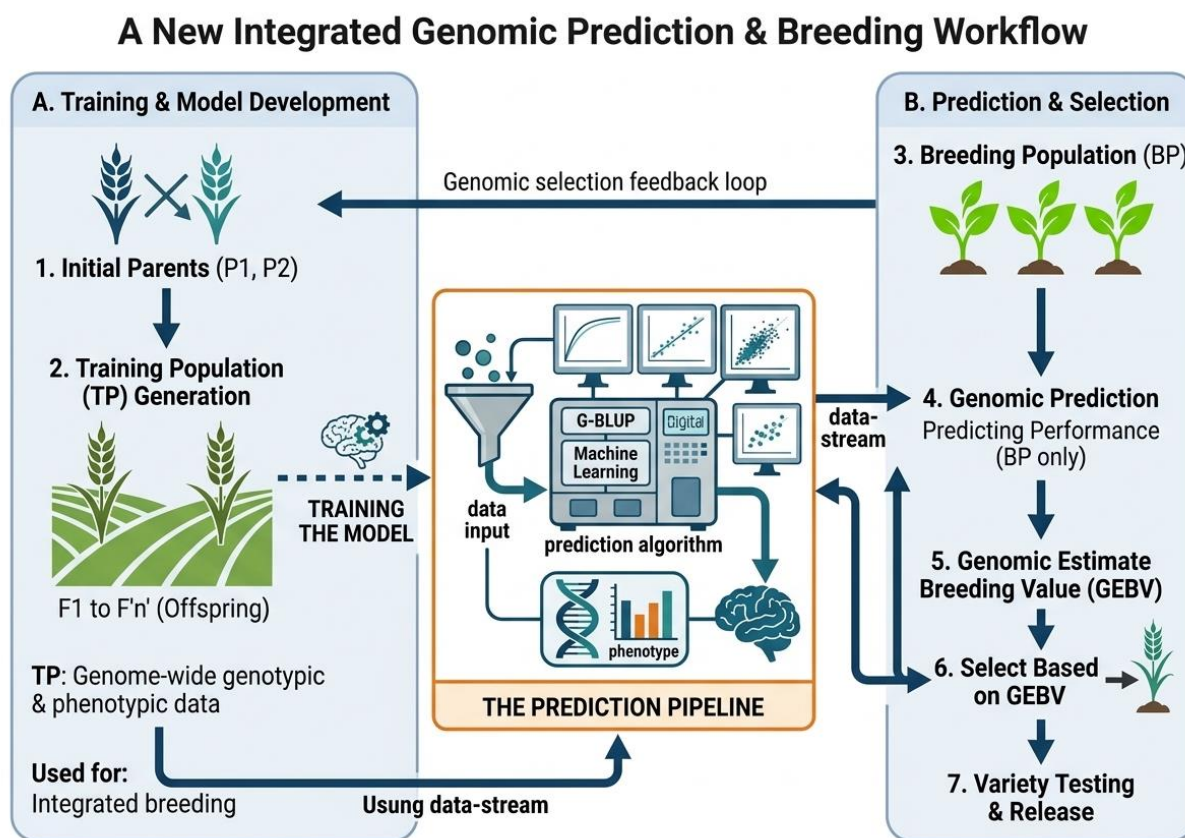


Figure 2: End-to-End Workflow for Model Development, Genomic Prediction, and Selection in Breeding Populations

4. Genome Editing Technologies for Precision Climate Adaptation

4.1 CRISPR/Cas Systems and Targeted Mutagenesis

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated endonucleases (e.g., Cas9, Cas12a) enable precise sequence modifications within plant genomes without integrating persistent foreign DNA. Guided by a synthetic single-guide RNA (sgRNA) matching a 20-nucleotide genomic target sequence, the Cas protein introduces a site-specific double-strand DNA break (DSB) at the target locus (Angon et al., 2026).

Cellular repair of this double-strand break occurs through two primary repair pathways, which define the regulatory category of the edited crop:

- **Site-Directed Nuclease-1 (SDN-1):** Endogenous Non-Homologous End Joining (NHEJ) repairs the

DSB, frequently introducing small random insertions or deletions (indels). This causes frameshift mutations that lead to targeted gene knockouts without requiring foreign donor DNA constructs (Garcia-Oliveira et al., 2025).

- **Site-Directed Nuclease-2 (SDN-2):** Homology-Directed Repair (HDR) uses a short synthetic DNA template containing specific sequence alterations to introduce precise, base-pair level modifications or micro-edits at the target cleavage site.

- **Site-Directed Nuclease-3 (SDN-3):** Delivers larger DNA constructs or multi-gene expression cassettes into defined target locations via HDR (Sharma et al., 2025).

4.2 Engineering Abiotic Stress Resistance Pathways

CRISPR/Cas technologies facilitate climate adaptation by enabling targeted modifications of negative regulators, signal transduction factors, and metabolic pathways.

Knocking out negative regulators of stress pathways has proven effective for improving drought tolerance (Zafar et al., 2020). In rice (*Oryza sativa*), CRISPR/Cas9-mediated knockout of the *OsDST* (*Drought and Salt Tolerant*) gene reduces leaf stomatal density while increasing stomatal sensitivity to abscisic acid (ABA), enhancing drought survival without compromising vegetative biomass. Similarly, disabling *OsDIS1* (*Drought-Induced SINA Protein 1*, an E3 ubiquitin ligase) and *OsSRFP1* (*Stress-Related RING Finger Protein 1*) stabilizes protective intracellular proteins, improving drought tolerance under field conditions (Vinocur & Altman, 2005).

CRISPR systems have also been deployed to address heat and salinity stress. High temperatures cause severe cellular damage through apoplastic Reactive Oxygen Species (ROS) accumulation. Editing the brassinosteroid-responsive transcription factor *BRZ1* in tomato (*Solanum lycopersicum*) regulates apoplastic ROS dynamics, protecting photosystem II complexes during heat stress (Bhatnagar-Mathur et al., 2008). For salinity mitigation, knocking out negative regulators within the ABA signaling cascade such as *OsSAPK2* (Stress-Activated Protein Kinase 2) and *OsERA1* (Enhanced Response to ABA 1) improves osmotic adjustment and salt exclusion in saline soils. Direct editing of agronomic traits in elite hybrids, such as generating waxy maize by targeting the *WAXY* locus, demonstrates that gene editing can bypass years of traditional backcrossing (Zhang et al., 2000).

Table 2: Validated Genes, QTLs, and Molecular Targets for Abiotic Stress Adaptation

Crop Species	Target Stress	Targeted Locus / Gene	Strategy / Editing Method	Physiological & Molecular Mechanism	Primary Agronomic Outcome
Wheat (<i>Triticum aestivum</i>)	Drought & Heat	Biomass, CT, TKW, NDVI, Yield QTLs	Marker-Assisted Backcross Breeding (MABB)	Recurrent parent genome recovery (78–91%) with introgressed root and canopy loci	Higher kernel weight, reduced canopy temperature, yield preservation under stress
Sorghum (<i>Sorghum bicolor</i>)	Post-Flowering Drought	<i>Stg1</i> , <i>Stg2</i> , <i>Stg3</i> , <i>Stg4</i> , <i>Stg3A</i> , <i>Stg3B</i>	Marker-Assisted Backcrossing (MABC)	Maintenance of green leaf area, deferred foliar senescence, active filling phase	Canopy collapse prevention, stable grain filling under severe moisture deficit
Rice (<i>Oryza sativa</i>)	Severe Drought	<i>DEEPER ROOTING 1</i> (<i>DRO1</i>)	Marker-Assisted Selection (MAS)	Downward steepening of root growth angle into deeper, moist soil horizons	Water access preservation, avoided drought-induced floral sterility
Rice (<i>Oryza sativa</i>)	Drought & Salinity	<i>OsDST</i>	CRISPR/Cas9 Knockout (SDN-1)	Reduction in leaf stomatal density; altered stomatal guard cell movement	Water loss reduction, enhanced drought and salt tolerance

Rice (<i>Oryza sativa</i>)	Drought Stress	OsDIS1 & OsSRFP1	CRISPR/Cas9 Knockout (SDN-1)	Disruption of E3 ubiquitin ligase-mediated degradation of stress-protective proteins	Cellular survival enhancement, reduced drought-induced biomass loss
Tomato (<i>Solanum lycopersicum</i>)	Heat Stress	BRZ1	CRISPR/Cas9 Edit (SDN-1/SDN-2)	Regulation of apoplastic reactive oxygen species (ROS) accumulation dynamics	Thermal shock tolerance, structural protection of Photosystem II
Rice (<i>Oryza sativa</i>)	Salinity Stress	OsSAPK2 & OsERA1	CRISPR/Cas9 Targeted Edit (SDN-1)	Sensitizing ABA signaling cascades controlling cell turgor and osmotic adjustments	Preserved vegetative growth and seed setting under saline water regimes

5. Systemic Integration and Acceleration Protocols

5.1 Speed Breeding and Controlled Environment Generation Advancement

Speed Breeding (SB) utilizes controlled environments to accelerate plant growth and flowering, shortening the generation time required in crop improvement programs. By manipulating photoperiod, light quality, temperature, and moisture, SB enables multiple generation advances per year (Potts et al., 2023). SB protocols optimize several environmental parameters:

- **Extended Photoperiods:** Delivering 20 to 22 hours of daily illumination using light-emitting diode (LED) arrays tailored to Photosynthetically Active Radiation (PAR) spectra accelerates vegetative growth and triggers early floral transition in long-day and day-neutral crops (Pathania et al., 2025).
- **Temperature and Humidity Cycling:** Diurnal temperature regimes matched with controlled atmospheric humidity maximize photosynthetic rates while preventing thermal stress.
- **Early Seed Harvest and Dormancy Breaking:** Harvesting immature embryos or seeds followed by physical or chemical treatments (such as cold stratification, drying, or gibberellic acid

application) bypasses seed dormancy stages (Indurthi et al., 2026).

In long-day cereal crops like wheat and barley, speed breeding achieves 4 to 7 generations per year compared to 1 to 2 under conventional field conditions. In short-day crops like rice, modified daylength and temperature cycling enable 3 to 5 generations annually (Verma et al., 2026).

5.2 Fast Backcross (FB) Pipelines and Integrated Breeding Systems

Combining Speed Breeding, Marker-Assisted Backcrossing, Doubled Haploid (DH) production, and Genomic Selection establishes Fast Backcross (FB) platforms (Samantara et al., 2022).

In an integrated pipeline, targeted mutations generated via CRISPR/Cas editing are introduced into elite genetic backgrounds. These modified plants are advanced under speed breeding conditions to accelerate cross-pollination cycles. Early-stage SNP genotyping screens for target edits while background genomic prediction models calculate GEBVs to select individuals with optimal recurrent parent genome recovery. Doubled Haploid (DH) technology via microspore culture or haploid inducer lines then fixes complete homozygosity in a single generation, eliminating multiple cycles of selfing (Zhao et al., 2026).

Through these integrated pipelines, the total breeding cycle from initial target identification to multi-environment field validation is compressed from 10–12 years down to 3–5 years (Cha et al., 2024).

6. Global Regulatory Landscapes and Socio-Economic Implementation

6.1 Regulatory Frameworks: Product- vs. Process-Based Oversight

The commercialization and global trade of gene-edited crops depend on evolving regulatory frameworks that distinguish between transgenic organisms (traditional GMOs) and transgene-free gene-edited plants (Kho et al., 2025).

Global regulatory policies have split into two primary frameworks:

- **Product-Based Frameworks:** Adopted by nations including the United States, Argentina, Brazil, and Japan, these frameworks evaluate crops based on the final plant traits and risk profiles rather than the technology used. Under the USDA SECURE (Sustainable, Ecological, Consistent, Uniform, Responsible, and Efficient) rule, gene-edited crops containing SDN-1 or SDN-2 modifications that could occur through

conventional breeding are exempt from classical GMO oversight (Vengadesen et al., 2025).

- **Process-Based Frameworks:** Historically, the European Union regulated all gene-edited plants under Directive 2001/18/EC, subjecting SDN-1 and SDN-2 edited crops to the same risk assessments as transgenic organisms. However, recent legislative proposals for New Genomic Techniques (NGTs) aim to create a differentiated pathway. Under Category 1 NGT provisions, transgene-free SDN-1 and select SDN-2 crops with minor edits would be treated similarly to conventionally bred varieties, bypassing traditional GMO authorization steps (Mbaya et al., 2022).

Other regions, including India, Australia, and several APEC member economies, are establishing tiered frameworks that exempt SDN-1 and SDN-2 edits from strict biosafety trials while maintaining oversight for transgenic SDN-3 edits. Removing SDN-1 and SDN-2 edits from strict GMO oversight significantly reduces regulatory costs and development timelines, enabling public institutions and small-to-medium enterprises (SMEs) to commercialize climate-resilient varieties (Koščik & Vladíková, 2022).

Table 3: Comparative Global Regulatory Frameworks for Genome-Edited Crops

Country / Region	Regulatory Framework Type	Primary Governing Body / Legislation	Classification of SDN-1 & SDN-2 Edits	Impact on Innovation & Commercialization
United States	Product-Based	USDA-APHIS (SECURE Rule)	Exempt from GMO oversight if achievable via conventional breeding	Accelerates entry; reduces regulatory costs for SMEs and academic developers
European Union	Process-Based (Transitioning to Differentiated)	EFSA / Proposed NGT Regulation	Historically strict GMO rules; NGT Category 1 proposal aims to exempt SDN-1/SDN-2	Legacy rules delayed field deployment; proposed reforms aim to restore competitiveness
Argentina & South America	Trait/Product-Based	MAGyP Resolution 173/2015	Non-transgenic SDN-1/SDN-2 evaluated on case-by-case basis; exempt if	Established early regulatory clarity, leading to increased local private and public breeding projects

			foreign DNA is absent	
India	Product-Based (Tiered)	Ministry of Environment, Forest and Climate Change (MoEFCC)	SDN-1 and SDN-2 exempted from biosafety assessment; SDN-3 remains regulated	Facilitates public-sector trait development for regional stresses
Japan	Product-Based	Ministry of Agriculture, Forestry and Fisheries (MAFF)	Endogenous gene edits (SDN-1) require notification only; exempt from GMO laws	Enables commercial sale of gene-edited crops with improved quality and stress traits

6.2 Socio-Economic Barriers, Seed Systems, and Intellectual Property

Deploying advanced breeding technologies in resource-constrained agricultural systems presents structural challenges. Broad access to CRISPR and genomic selection tools is restricted by complex intellectual property (IP) licensing environments. Securing access to core gene-editing patents can be cost-prohibitive for public breeding programs in developing nations. Establishing open-access technologies, humanitarian licensing frameworks, and international consortia (such as CGIAR centers) is essential to ensure equitable access to precision breeding tools (Ajates, 2023).

Additionally, resource-constrained regions often lack high-throughput genotyping facilities, bioinformatic capacity, computational power, and automated phenotyping infrastructure. Building regional technical capacity and open-data platforms is critical to prevent a technology divide between high-income and low-income agricultural systems (Pandey & Mishra, 2026). Finally, new crop varieties must reach farmers through functional formal and informal seed systems. Institutional partnerships between national agricultural research systems (NARS), private seed companies, and local farmer cooperatives are necessary to deliver climate-resilient varieties to farming communities (Pandey, 2025).

Conclusion

Climate change poses an escalating threat to global food security, demanding urgent transformation of crop improvement strategies. This review

demonstrates that the integration of Marker-Assisted Selection, Genomic Selection, CRISPR/Cas genome editing, and Speed Breeding offers a powerful and cohesive framework for developing climate-resilient crop varieties. Conventional breeding, constrained by extended timelines, linkage drag, and limited efficiency for polygenic traits, cannot alone meet the demands of rapidly shifting agro-climatic conditions. MAS and MABC provide precise tools for transferring and pyramiding major-effect QTLs controlling drought, heat, and salinity tolerance, while GS enables prediction of genomic estimated breeding values for complex, quantitatively inherited traits governed by numerous small-effect loci. CRISPR/Cas technologies, particularly SDN-1 and SDN-2 edits, enable targeted modification of stress-responsive genes without foreign DNA integration, accelerating trait deployment in elite backgrounds. The systemic integration of these approaches with Speed Breeding and Doubled Haploid technology has compressed varietal development cycles from over a decade to just 3–5 years. However, realizing this potential requires addressing regulatory disparities, intellectual property constraints, infrastructure limitations, and seed system gaps, particularly in resource-constrained regions. Product-based regulatory frameworks, capacity building, open-access technologies, and multi-stakeholder partnerships are essential to ensure equitable deployment. Ultimately, the convergence of genomics, genome editing, and accelerated breeding platforms represents a paradigm shift in crop improvement

offering a sustainable pathway toward climate-resilient agriculture and long-term global food security.

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