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Plant Breeding, Genetics, and Genomics for Climate-Resilient and High-Yield Cereal Crop Improvement

Dr. Nadia Jabeen *
Department of Agriculture, Hazara University Mansehra, kpk
nadia_khan909090@yahoo.com
nadia.agri@hu.edu.pk
ORCID ID: 0000-0001-6617-8301

Mehwish Raza
Department: Plant Protection, Shanxi Agricultural University,030801, China
drmehwish512@gmail.com

Ameer Jan
Department of Botany, University of Makran, Panjgur
ameerjan@uomp.edu.pk

Talha
Department of Botany, University of Makran, Panjgur
Talha@uomp.edu.pk

Sadia Akbar
Department of Botany, University of Makran, Panjgur
sadiaakbar2003@gmail.com

ABSTRACT

Climate change poses a significant threat to global cereal production by increasing the frequency and intensity of drought, heat stress, salinity, flooding, and emerging pests and diseases. Ensuring food security for a growing global population requires the development of climate-resilient and high-yield cereal crop varieties through advanced plant breeding, genetics, and genomics. This review paper examines recent advances in plant breeding, genetics, and genomics for improving major cereal crops, including rice, wheat, maize, barley, sorghum, and millet. The study explores conventional breeding approaches alongside modern genomic technologies such as genome-wide association studies (GWAS), genomic selection, marker-assisted selection, quantitative trait loci (QTL) mapping, CRISPR-Cas genome editing, and multi-omics integration for identifying and manipulating genes associated with stress tolerance, yield potential, and grain quality. Furthermore, the review discusses the application of high-throughput phenotyping, artificial intelligence, bioinformatics, and precision breeding technologies

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in accelerating crop improvement and enhancing breeding efficiency. Recent developments demonstrate that integrating genomics with climate-smart breeding strategies can improve resilience against abiotic and biotic stresses while increasing productivity and resource use efficiency. However, challenges including complex trait inheritance, genotype-by-environment interactions, limited genetic diversity, regulatory constraints, and unequal access to advanced breeding technologies continue to influence breeding outcomes. This review synthesizes current developments and highlights the transformative role of plant breeding, genetics, and genomics in developing climate-resilient and high-yield cereal crops for sustainable agriculture and global food security.

Keywords— Plant Breeding, Genetics, Genomics, Climate-Resilient Crops, Cereal Crops, Genome-Wide Association Studies, Genomic Selection, Marker-Assisted Selection, CRISPR-Cas, Quantitative Trait Loci, High-Throughput Phenotyping, Precision Breeding, Abiotic Stress Tolerance, Crop Improvement, Food Security.

1. Introduction

Global food security is facing an unprecedented, multi-faceted challenge driven by the convergence of rapid anthropogenic climate change and an escalating global population. Demographic projections estimate that the global population will reach approximately 9.6 billion by the year 2050, requiring a corresponding increase in agricultural output of 70% to 100% to satisfy global caloric and nutritional demands (Wang et al., 2026). Simultaneously, climatic instability is severely undermining the productivity, quality, and environmental resilience of the primary staple cereal crops: rice (*Oryza sativa*), wheat (*Triticum aestivum*), maize (*Zea mays*), and barley (*Hordeum vulgare*), which collectively provide approximately 50% of the daily dietary energy and protein intake for the global human population (Naqvi et al., 2022).

Climate change manifests through intensified abiotic and biotic pressures, including extreme temperature fluctuations, prolonged droughts, unpredictable precipitation patterns, and rising sea levels that drive extensive soil salinization. Soil degradation, salinization, and desertification already affect more than one-third of global arable land, reducing crop yields in major cereal-growing regions (Mukherjee et al., 2024). The vulnerability of rainfed agricultural systems is particularly pronounced in developing regions, such as Sub-Saharan Africa, where rainfed agriculture predominates and adaptive capacity is constrained. In these regions, staple crop yields are projected to drop by 10% to 20% by 2050, including a 15% decline in Ethiopian maize production. Under severe terminal drought and heat stress, cereal yield potentials frequently decline by 20% to 60% due to impaired photosynthetic machinery, accelerated senescence, pollen sterility, and incomplete grain filling (Sinha et al., 2023).

To circumvent these losses and secure sustainable production, agricultural science must undergo a radical transformation. Traditional breeding methodologies, which rely on phenotypic selection of visible agronomic traits in late-generation segregating populations, are too slow and imprecise to keep pace with accelerating climate shifts. Developing a single elite cultivar via conventional pedigree breeding typically requires up to ten generation cycles of selection and stabilization (Chawla et al., 2023). To

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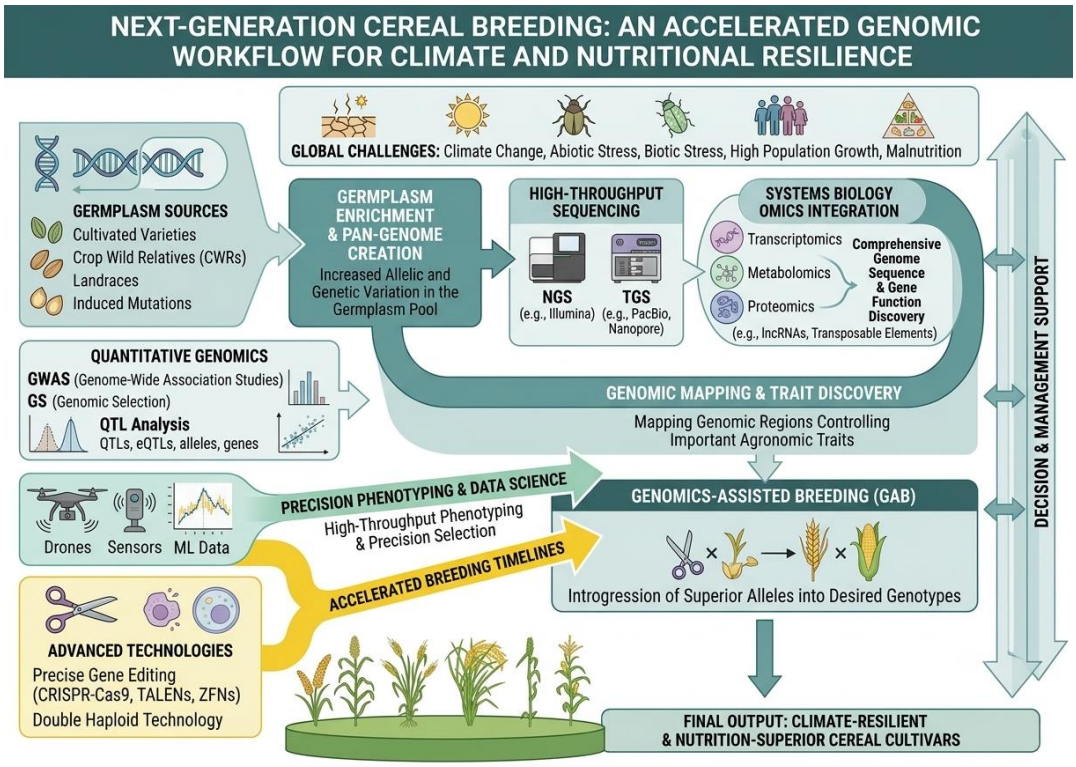
accelerate genetic gains, modern breeding programs must deploy an integrated, systems-level approach that merges quantitative genetics, precision genomics, high-throughput phenomics, and advanced computational modeling. Unifying these disciplines into a coherent, systems-level framework allows breeders to identify novel stress-adaptive alleles, unravel complex regulatory networks, and rapidly introgress resilient traits into elite agronomic backgrounds (Adhikari et al., 2023).

Figure 1. Integrated Next-Generation Cereal Breeding Workflow for Climate Resilience and Nutritional Trait Enhancement.



2. Physiological Adaptation and Molecular Signatures of Stress Resilience

2.1. Polygenic Control of Abiotic Stress Dynamics

Abiotic stress tolerance in cereals is a complex, polygenic trait characterized by intricate physiological, morphological, and biochemical adaptation mechanisms. When plants encounter soil moisture deficits or extreme temperatures, they activate complex signaling cascades that modulate root system architecture, stomatal conductance, osmotic adjustment, and reactive oxygen species (ROS) scavenging (Nawaz et al., 2026). Because these responses are governed by hundreds of minor-effect quantitative trait loci (QTLs) and are heavily influenced by genotype-by-environment (G x E) interactions, dissecting their genetic architecture requires high-density genomic mapping and functional genomics (Elankumaran et al., 2026).

A breakthrough in understanding chloroplastic ROS regulation and biogenesis under drought conditions occurred with the characterization of the rice gene *OsFeSOD3*. Discovered and validated in consecutive field trials, *OsFeSOD3* encodes a chloroplast-

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localized iron superoxide dismutase enzyme that neutralizes harmful ROS molecules that accumulate during water stress. Additionally, the encoded protein acts as an essential component of the plastid-encoded RNA polymerase complex, thereby facilitating chloroplast gene expression and maintaining photosynthetic capacity under severe stress (Zhang & Jiang, 2026). Overexpression of *OsFeSOD3* in rice lines led to a 33% to 42% grain yield increase under managed drought conditions, primarily due to enhanced grain filling and higher grain numbers per panicle. Conversely, CRISPR-Cas9 knockout mutants of *OsFeSOD3* exhibited severe chloroplast degradation, albino leaves, and arrested growth, underscoring its dual role in development and stress survival (Hafeez et al., 2023).

In parallel, haplotype-based studies have identified high-performing natural allelic variants that mitigate reproductive-stage drought stress, which is a highly vulnerable developmental window in cereals (Gao et al., 2025). Evaluation of over 450 rice lines identified superior haplotypes of the transcription factor *OsIRO2*. Introgression of the superior *OsIRO2* haplotype into the widely grown mega-variety DRR Dhan 44 from the ADT 12 donor parent resulted in up to a 27% increase in grain yield under drought conditions without compromising yield stability under well-watered environments (Kumar et al., 2022).

Furthermore, research has expanded flood tolerance pathways in rice beyond the classical *SUB1A* ethylene-responsive factor gene. Large-scale genomic screenings of 6,274 diverse accessions identified 89 elite genotypes possessing novel loci that confer tolerance to complete submergence and stagnant flooding (Raghunandan et al., 2025). Some of these lines surpassed the survival rate of standard *SUB1A* introgression lines by 40% to 50%. Deploying these novel resources through a "Transition from Trait to Environment" (TTE) breeding strategy facilitated a 65% genetic gain for flooding tolerance in regional trials in India and Bangladesh, highlighting the utility of expanding the functional genetic diversity of breeding pools (Saini et al., 2024).

Drought tolerance in rice is also regulated by other transcription factor families, such as the MYB family. For example, the R2R3-type MYB transcription factor *RRS1* acts as a negative regulator of root development by activating the expression of the *IAA3* gene in the indole-3-acetic acid (IAA) signaling pathway, which inhibits root growth and negatively impacts drought tolerance. Stomatal development and transpiration are regulated by the *OsFLP* gene, whereas *OsMYB60* participates in regulating the biosynthesis of epicuticular wax (Muntean et al., 2025). Other MYB transcription factors regulate the abscisic acid (ABA) synthesis pathway through post-translational modifications, such as *OsMYB48-1*. Additionally, *OsMYBR57* interacts with the homeobox transcription factor *OsHB22* to form the *OsFTIP6-OsHB22-OsMYBR57* module, which regulates the drought response. Similarly, *OsMFT1* enhances the binding ability of downstream drought-regulated promoters by interacting with *OsbZIP66* and *OsMYB26*, while *OsFTIP1* inhibits the nuclear mislocalization of *OsMFT1*, reversing its regulation (Cabusora, 2024). Under drought conditions, other critical genes that impact rice yield include *DROT1* (Drought-Responsive Oxidative Stress Tolerance 1), *RoLe1* (Root Length Estimation 1), and *OsZIP23*. The overexpression of the *OsPR10A* protein, which increases during tillering and later stages, is linked to the activation of the jasmonic acid (JA) and ABA signaling

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pathways, enhancing drought tolerance (Qiao et al., 2026).

2.2. Master Regulators of Growth and Survival Trade-Offs

One of the most persistent hurdles in breeding for climate resilience is the evolutionary trade-off between growth and defense. High-yielding varieties are frequently highly sensitive to environmental fluctuations, whereas stress-tolerant genotypes often display reduced stature, delayed development, or lower yield potential under optimal conditions (Bhanu et al., 2026).

Recent structural and functional genomic analyses have identified master transcriptional regulators that coordinate this delicate balance. In bread wheat, the WRKY transcription factor *TaWRKY58*, located on chromosome 1A, was identified as a key repressor coordinating plant architecture and drought response (Rathod et al., 2026). *TaWRKY58* is a nuclear-localized subgroup Ia protein that directly binds to the consensus W-box element (YTGACY) in the promoters of two critical target genes: *TaLRR* (encoding a leucine-rich repeat signaling receptor protein) and *TaBCS1* (encoding a mitochondrial AAA+ ATPase energy regulator) (Mba & Ogbonnaya, 2022).

Loss-of-function mutants of *TaWRKY58* (delta-tawrky58), characterized by a premature stop codon (T4-2223, C1593T), display increased plant height, early flowering mediated by elevated gibberellin levels, and significantly enhanced drought tolerance via increased soluble sugar accumulation. Conversely, overexpression of *TaWRKY58* represses both signaling and mitochondrial energy metabolic pathways, leading to dwarfism and drought hypersensitivity (Maity et al., 2025). The transcriptional expression of *TaWRKY58* is induced by ultraviolet radiation, salicylic acid (10 mM), PEG6000 (20%), sodium chloride (200 mM), and *Fusarium graminearum* infection. Other wheat WRKY genes, such as *TaWRKY2* and *TaWRKY19*, regulate abiotic stress tolerance positively; transgenic plants overexpressing *TaWRKY2* exhibit salt and drought tolerance by binding to the promoters of *STZ* and *RD29B*, while *TaWRKY19* binds to and activates *DREB2A*, *RD29A*, *RD29B*, and *Cor6.6* promoters (Molla et al., 2025).

In wheat, terminal heat stress exceeding 30 to 35 degrees Celsius alters pollen viability, fertilization, and kernel development, shortens the grain-filling period, and reduces yield by 20% to 40%. Salinity stress, impacting more than 20% of irrigated lands globally, reduces wheat yields by 30% to 50% (Phogat et al., 2024). To counter these impacts, breeders utilize landraces like Aragon 03 (Spain), which exhibits durable drought tolerance and higher pre-anthesis biomass, and cultivars harboring specific genes such as *TaDREB1* and *TaDREB2* for drought resilience, and *TaHKT1;5-D* for salinity tolerance. Landraces like Norin 10 contain the *Rht1* and *Rht2* dwarfing genes, and Aka Komugi harbors the *Rht8c* dwarfing allele, both contributing to improved harvest index and drought adaptation (Murtaza et al., 2026).

Barley displays high tolerance to abiotic stresses, utilizing tissue-specific transcriptomic networks. Roots significantly upregulate *HvNAC2* and *HvNAC6* during salt and drought stress, whereas leaves show minimal expression changes (Lutege et al., 2026). Under temperature stress, leaves upregulate *HvNAC4*, *HvNAC5*, and *HvNAC3* during heat, while roots upregulate *HvNAC6* and *HvNAC6-C* during cold stress. Candidate genes HORVU2Hr1G091030 (encoding CPL1, a negative regulator

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of ABA and osmotic stress) and HORVU2Hr1G091170 (encoding expansin B3, which regulates spikelet development under drought) have been identified from spring barley accessions (Kumar et al., 2022). Barley's adaptation is also regulated by flowering time genes (vernalization *VRN-H1*, photoperiod, and circadian clock) to escape terminal stress. Its cellular protection systems include dehydrins (*HVA1*, *HVA22*, *Dhn3*, and *Dhn9*), which bind to membrane phospholipids, and antioxidant enzymes (*HvAPX1*, *HvMT-2*, and *HvGST1*) and heat shock proteins (*HSP17.8*) (George & Darshana, 2024). In maize, drought during the jointing or tasseling periods for more than 30 days prevents recovery, and extreme heat exceeding 30 degrees Celsius causes up to a 7.4% yield decline for every 1 degree Celsius increase in mean temperature (Gatica-Arias & Hernández-Soto, 2025). Under these conditions, the transgenic Event MON 87460 (*CspB*, encoding cold shock protein B; DroughtGard) has been evaluated in Kenya, South Africa, and Uganda. It has shown positive and significant yield effects of 36% to 62% in specific hybrids (e.g., CML312/CML445, WMA8101/CML445, and CML312/S0125Z) under managed drought, with no yield penalties under optimal moisture (Ravuri et al., 2026). Additionally, the adapted DroughtTEGO hybrids provide robust protection against yield loss. In selecting for combined drought and heat stress (CDHS), the stress tolerance indices YI (Yield Index), GMP (Geometric Mean Productivity), MP (Mean Productivity), HM (Harmonic Mean), and STI (Stress Tolerance Index) serve as the most effective selection criteria (Nandakumar et al., 2025).

Table 1. High-Priority Climate Resilience Genes and Allelic Variants in Cereal Crops

Crop	Locus / Gene	Physiological Mechanism	Agronomic / Breeding Impact
Rice	*OsFeSOD3*	Chloroplastic iron superoxide dismutase; ROS scavenging; plastid-encoded RNA polymerase complex cofactor.	33% to 42% yield increase under drought; essential for chloroplast biogenesis.
Rice	*OsIRO2*	Transcriptional regulator of iron homeostasis and reproductive stress pathways.	Up to 27% higher grain yield under reproductive drought in elite backgrounds.
Rice	*RRS1*	R2R3-type MYB transcription factor; activates *IAA3* and inhibits root elongation.	Negative regulator of root development; target for inactivation to increase rooting depth.
Wheat	*TaWRKY58*	Transcriptional repressor of growth signaling (*TaLRR*) and energy metabolism (*TaBCS1*).	Loss-of-function mutation (delta-tawrky58) enhances drought tolerance and

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			plant height.
Wheat	*TaHKT1;5-D*	Sodium transporter facilitating selective exclusion of Na+ from shoots.	Confers high salinity tolerance and protects photosynthetic tissues in sodic soils.
Maize	MON 87460 (*CspB*)	RNA-binding chaperone; stabilizes translation machinery during water deficit.	36% to 62% yield gain under managed drought in Sub-Saharan Africa.
Barley	*HvNAC2* / *HvNAC6*	Root-specific NAC transcription factors driving stress-responsive cellular networks.	Significantly upregulated in roots to adapt to salinity and osmotic stress.
Barley	HORVU2Hr1G091030	CPL1 (C-terminal domain phosphatase-like 1); negative regulator of ABA signaling.	Loss of function enhances tolerance to osmotic and oxidative stresses.

3. Advancements in Cereal Epigenomics and Precision Genome Editing

3.1. Technical Platforms for Targeted Mutation and Epigenetic Control

The progression of site-directed nucleases has transformed plant breeding from empirical selection into a highly precise engineering science. Historically, cereal crop improvement depended on imprecise methods like random chemical or physical mutagenesis and conventional recombination, which carry high off-target mutation risks and linkage drag (Waqar et al., 2024). Early target-specific systems like Zinc Finger Nucleases (ZFNs) and Transcription Activator-Like Effector Nucleases (TALENs) laid the groundwork for precision engineering. ZFNs were successfully deployed to edit complex loci in maize and rice, but their applications were constrained by design complexity and high off-target risks (Totawara et al., 2026).

A major biological constraint in plant genetic engineering is that homologous recombination operates at very low frequencies in somatic cells, limiting the efficiency of direct gene insertions and gene replacements. The development of the CRISPR-Cas system has bypassed this bottleneck. Modern CRISPR platforms include Cas9, Cas12, Cas13, base editors, and prime editors (Huang et al., 2026). Base editors (cytosine and adenine base editors, CBEs and ABEs) facilitate single-nucleotide transitions without inducing double-strand breaks (DSBs), enabling the targeted introduction of naturally occurring adaptive alleles. Prime editors write new genetic code directly into target sites by utilizing a Cas9 nickase fused to a reverse transcriptase guided by a prime editing guide RNA (pegRNA), circumventing both DSBs and the requirement for exogenous donor templates (Cooper & Messina, 2023).

The utility of CRISPR-mediated targeted mutagenesis was demonstrated in the dissecting of chlorophyll biosynthesis in barley. By targeting the *Ycf54* gene, which is involved in the magnesium-protoporphyrin IX monomethyl ester cyclase enzyme complex, researchers evaluated the phenotypes of resulting mutations (Fahad et al., 2021). Mutants carrying homozygous 1 or 2 base pair deletions caused translational

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reading frame shifts and premature truncation of the Ycf54 protein, resulting in a lethal, chlorophyll-deficient yellow xantha phenotype. Conversely, in-frame deletions of 6 and 27 base pairs did not disrupt chlorophyll synthesis or plant viability, providing genetic evidence of the essential regions of the *Ycf54* gene (Ndlovu, 2020).

Beyond genomic editing, CRISPR-based epigenome editing platforms allow for targeted modulation of DNA methylation and chromatin states, providing tools to regulate endogenous genes without altering the primary sequence. This is complemented by the analysis of non-coding RNAs, particularly microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), which function as regulators of developmental pathways and stress-adaptive networks (Anusha & Amir, 2024).

Figure 2. Comparative CRISPR-Cas Genome Editing Strategies and Mechanisms for Trait Customization and De-Novo Crop Domestication.

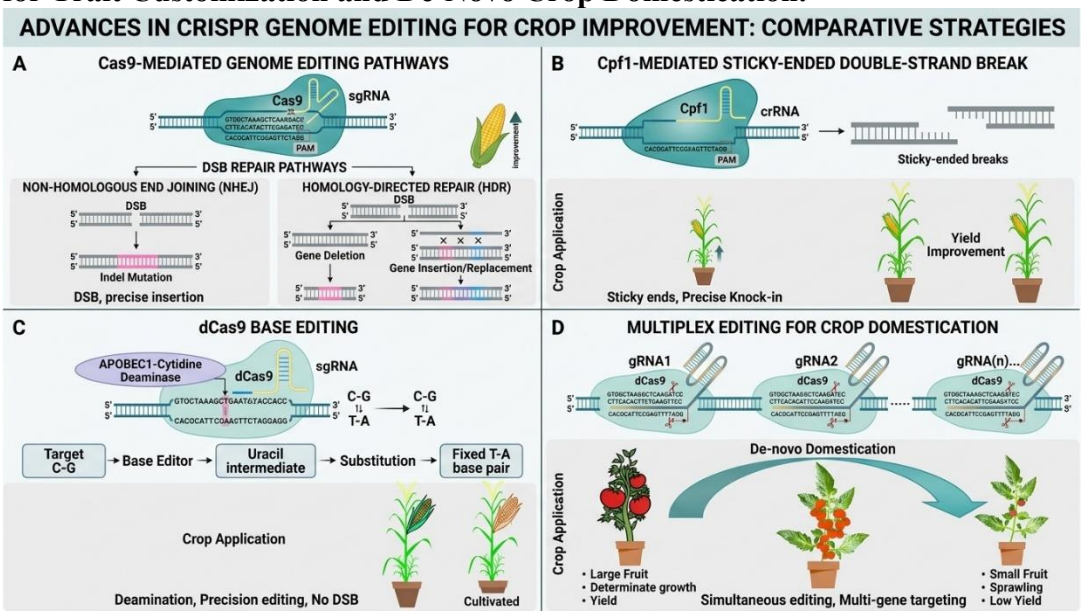

Table 2. Technical Capabilities of Precision Breeding and Gene Editing Platforms

Platform	Editing Mechanism	Advantages in Cereal Breeding	Primary Constraints
ZFNs	Zinc-finger proteins fused to FokI cleavage domain; DSB generation.	Historical proof-of-concept; successfully engineered loci in maize and rice.	Complex protein design; high off-target cleavage rates; difficult to multiplex.
CRISPR-Cas9	sgRNA-guided cleavage; generates double-strand breaks upstream of PAM site.	High cleavage efficiency; simple design; robust multiplexing of several target genes.	Off-target risks; depends on low-frequency HDR pathways for gene knock-ins.
CRISPR-Cas12a	sgRNA-guided cleavage; creates	Enhances targeting precision in AT-rich	Staggered cleavage can lead to complex

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	staggered DSBs; targets T-rich PAM sites.	promoter and regulatory regions.	insertion-deletion profiles.
Base Editors	Deaminase fused to Cas9 nickase; direct transitions (C to T or A to G).	High-precision single-base transitions without inducing double-strand breaks.	Restricted to transition mutations; restricted by genomic PAM spacing.
Prime Editors	Cas9 nickase fused to reverse transcriptase guided by pegRNA.	Writes any point mutation, small insertion, or deletion without donor DNA.	Large construct sizes; lower delivery efficiency in recalcitrant monocot tissues.

4. Speed Breeding and Integrated Genomic Selection Pipelines

4.1. Genomic Prediction and Statistical Models

For complex quantitative traits like grain yield under climate stress, marker-assisted selection (MAS) targeting major QTLs has limited efficacy because these traits are governed by many minor-effect genes (Aggarwal et al., 2025). Genomic Selection (GS) addresses this limitation by utilizing genome-wide molecular markers to calculate Genomic Estimated Breeding Values (GEBVs) for all individuals within a segregating population. By training statistical models on a reference training population that has been both genotyped and phenotyped, breeders can predict the performance of untested candidates based solely on their genotypic profiles (Chawla et al., 2025).

Univariate GS models can achieve yield prediction accuracies of 0.5 to 0.6 in highly stressed environments. To improve prediction accuracy under variable environments, breeders deploy Integrated Genomic Selection (IGS). IGS couples marker-based models with speed breeding, machine learning, and environmental/weather data (Phogat et al., 2024). It incorporates environmental covariates, such as relative humidity, solar radiation, temperature variations, and soil moisture, directly into the prediction models, capturing G x E interactions and improving predictive ability by up to 67% over univariate models (Mondal et al., 2023).

4.2. Environmental Controls in Speed Breeding

While genomic prediction accelerates selection, the physical generation time required to achieve homozygosity remains a key bottleneck in crop breeding. Speed Breeding (SB) addresses this generation-time constraint by manipulating environmental parameters within controlled growth chambers to accelerate vegetative growth and floral induction (Rehman et al., 2025). The conceptual roots of speed breeding lie in NASA-funded research on plant cultivation under extended artificial photoperiods in closed growth systems, which was adapted for field crop breeding by a research team at the University of Queensland in 2003 (Tejasree et al., 2024).

Standard speed breeding protocols rely on a multi-factor environmental control strategy:

- **Photoperiod Extension:** Long-day crops such as spring wheat, barley, and chickpeas are exposed to an extended photoperiod of 20 to 22 hours of daily

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light.

- **Spectral Optimization:** Utilizing customized LED light sources optimized for the active absorption spectra of chlorophyll and photoreceptors to accelerate development (Rajan & Kumari, 2025).
- **Temperature and Carbon Dioxide Regulation:** Precise diurnal temperature controls paired with elevated carbon dioxide concentrations to maximize photosynthetic efficiency (Roy et al., 2021).
- **Dormancy Breaking:** Harvesting immature seeds approximately two to three weeks post-anthesis, followed by desiccation or chilling treatments, to bypass seed dormancy and accelerate generation turnover (Barmukh et al., 2024).

By combining these interventions, speed breeding protocols can reduce generation times from 2.5 to 5 times compared to conventional glasshouse or field methods. This enables the generation of up to six generations of wheat and barley per year. For short-day or day-neutral species like rice, amaranth, hemp, and soybean, modified LED-based protocols utilizing short photoperiods prevent the delay of floral induction, enabling four to five generations per year (Hao et al., 2020).

4.3. Genomics-Assisted Speed Breeding Synergy

Integrating Genomic Selection directly with Speed Breeding (Genomics-assisted SB) represents a major advancement in accelerated crop breeding. Instead of selecting parents in the field, breeders perform multiple cycles of genomic prediction and selection under the controlled, accelerated conditions of speed breeding (Srivastava et al., 2025).

This combined pipeline reduces the time required to develop near-homozygous, agronomically stable lines (F5 to F6) to just 15 months, compared to five to seven years using traditional pedigree breeding (Kopeć, 2024). In an integrated wheat breeding scenario, a population of 350 selection candidates was developed by inter-crossing 20 individuals, followed by five generations of selfing under SB. To optimize selection, principal components derived from SB vegetative/physiological traits (SB-PCs), such as days to anthesis and plant height under controlled environments, were incorporated into multivariate GS models. This significantly improved yield prediction accuracy under field conditions, in some cases doubling the predictive ability of univariate GS models (Kpoviessi et al., 2024).

Furthermore, to reduce the cost of large-scale field trials, breeders utilize High-Throughput Phenotyping (HTP) and genomic prediction in small plot (SP) trials to predict grain yield in later-stage big plot (BP) trials. SP models using genomic plus hyperspectral (G+H) data achieve accuracies of 0.43 to 0.51, while genomic plus metabolomic (G+M) models reach 0.53 to 0.58 within a year (Yadav, 2020). A Random Forest Regression (RFR) model achieved an accuracy of 0.47 in predicting 2023 BP yields using 2022 SP data. The top 25% specificity (coincide index) showed up to 47% to 51% within-year overlap and 43% to 45% between-years overlap in the highest predicted-yielding lines, proving that SP datasets can facilitate early selection and reduce breeding costs (Borgohain et al., 2026).

Despite these technical successes, implementing genomic selection and speed breeding faces infrastructural and economic barriers in developing regions like Pakistan. These barriers include high genotyping costs, limited high-throughput phenotyping capacity,

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insufficient training population sizes, and the need for localized statistical models adapted to native germplasm (Wang et al., 2026).

5. Multi-Omics Integration and Deep Phenotyping via Artificial Intelligence

5.1. Pangenomics and Structural Variations

The understanding of genetic variation within cereal crops has expanded beyond the traditional single-reference genome model. Single-reference assemblies fail to capture a significant proportion of the genetic diversity present within a species, as they overlook structural variations that are often critical for environmental adaptation. This limitation led to the development of the pan-genome, which characterizes the collective genome of a species by sequencing and aligning diverse accessions (Mishra, 2025).

Pan-genomics categorizes genes into three functional fractions:

- **Core Genome:** Housekeeping genes present in all accession lines, primarily responsible for fundamental cellular processes (Mukhtar & Arif, 2024).
- **Dispensable (Accessory) Genome:** Loci present in some but not all accessions, which are highly enriched for genes involved in biotic defense and abiotic stress response (Yashavanthakumar et al., 2025).
- **Unique Genome:** Genes restricted to specific genotypes, driving specialized local adaptations (Kumari et al., 2026).

By building graphical pangenomes and examining presence-absence variations (PAVs) and copy-number variations (CNVs) in the dispensable and unique regions, researchers can identify novel, stress-tolerant alleles that were lost during domestication or conventional breeding bottlenecks (Cao & Tan, 2026).

The transition to pangenomics is supported by improvements in sequencing throughput and quality. Reference genomes are now available for over 800 plant species, with de novo assemblies generated via third-generation sequencing (Sukumaran et al., 2021). However, near-complete, chromosome-level assemblies represent fewer than 300 assemblies out of an estimated 0.5 million species in the green plant clade. Large-scale genomic resequencing has been completed for over 6,000 soybean accessions and 10,000 rice accessions, providing rich genetic resources for genomic breeding. Structural variations (SVs) identified through these pangenomes have been directly associated with environmental adaptation, flowering time, plant architecture, and pod dehiscence (Ali et al., 2025).

Table 3. Structural and Functional Comparison of Cereal Genomes and Resequencing Efforts

Crop Species	Diploid / Polyploid State	Estimated Genome Size (Gb)	Chromosome-Scale Assemblies / Resequenced Accessions	Key SVs and Domestication Loci Identified
Rice (*O. sativa*)	Diploid (2n=2x=12)	0.39	Chromosomal level; >10,000 accessions resequenced.	Loci regulating submergence survival (*SUB1A*), root

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				angle (*DRO1*), and panicle branching (*Gn1a*).
Soybean (*G. max*)	Palaeopolyploid (2n=2x=40)	1.10	Chromosomal level; >6,000 accessions resequenced.	SVs associated with oil content, photoperiod insensitivity, and cyst nematode resistance.
Bread Wheat (*T. aestivum*)	Allohexaploid (2n=6x=42)	17.00	Haplotype-resolved assemblies; thousands of elite lines.	Homoeologous loci regulating plant height (*Rht1*, *Rht2*, *Rht8c*) and disease resistance (*Lr34*).
Wild Barley (*H. brevisubulatum*)	Halophytic Diploid (2n=2x=14)	2.90	De novo chromosome-scale; 38 diploid germplasms resequenced.	Duplication of CaBP-NRT2 and horizontal transfer of the fungal gene *Fhb7*.

To build a comprehensive, systems-level model of plant stress response, researchers integrate pangenomics with transcriptomics, proteomics, metabolomics, and epigenomics, creating a multi-dimensional map of plant biology.

5.2. HTP Sensors and Deep Learning Implementations

Analyzing the multi-dimensional datasets generated by multi-omics and high-throughput phenotyping (HTP) requires advanced computational modeling. HTP platforms utilize ground and aerial systems with multiple sensors to capture morphological and physiological traits throughout crop development, helping to reduce the phenotyping bottleneck (Ngongolo & Mmbando, 2024).

Deep learning (DL) models are transforming image-based high-throughput phenotyping into a quantitative science. Using RGB or multispectral images captured by Unmanned Aerial Vehicles (UAVs), deep semantic segmentation networks (such as DeepLabV3+ or Segment Anything Model, SAM) categorize plants at pixel-level resolution. This allows breeders to separate foliage from complex backgrounds, enabling precise, non-destructive measurements of canopy coverage, leaf area index, and organ-level development (Mwamahonje et al., 2024).

Under complex field conditions, 3D point cloud segmentation networks like PSegNet segment individual organs in tall, dense cereal plantings (e.g., maize and wheat),

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allowing researchers to measure structural traits like leaf insertion angles that influence light interception (Tahakik et al., 2024). These AI-derived phenomic metrics are integrated with genotypic markers in Random Forest (RF) regression models to predict complex traits. Studies show that incorporating multiple omics layers into RF or deep learning networks can increase wheat grain yield prediction accuracy from 0.32 to 0.43 (and up to 0.58 in specific G+M models), helping to bridge the genotype-to-phenotype gap (Agho et al., 2025).

Table 4. HTP Sensor Modalities and Deep Learning Network Implementations

Sensor Technology	Measured Wavelengths / Data Types	Analytical Deep Learning Model	Extracted Phenotypic Metrics
RGB Imaging	400 to 700 nm (Red, Green, Blue visible spectra).	DeepLabV3+, SAM, YOLO models.	Morphological traits; plant height; leaf area; canopy coverage; germination rate.
Multispectral / Hyperspectral	400 to 1000+ nm (Narrowband visible and near-infrared reflectance).	Random Forest, Deep Neural Networks.	Chlorophyll concentration; nitrogen-use efficiency; water index; disease detection (e.g., maize streak virus).
Thermal Infrared (TIR)	7500 to 14000 nm (Long-wave infrared thermography).	Regression algorithms; convolutional neural networks.	Canopy temperature depression; transpiration rate; stomatal conductance.
3D LiDAR	Spatial laser coordinates (point clouds).	PSegNet, 3D instance segmentation networks.	Volumetric biomass; plant height; leaf angle; organ-level morphology.

Despite these advancements, drone-based UAV phenotyping faces operational limitations. UAVs rely on top-view or oblique-view observations of the canopy, making them susceptible to occlusion in dense plantings or tall crops (Ahmad et al., 2023). This limits their ability to stably measure lower-canopy and organ-level traits. Furthermore, under challenging field conditions, such as abrupt illumination changes, wind-induced leaf motion, muddy terrain, and weed interference, substantial weaknesses persist in perception robustness and online data processing (Kim et al., 2026). Ground-based mobile robots provide an alternative by operating below the canopy to perform high-resolution 3D phenotyping of individual organs, helping to bridge macro-scale remote sensing and leaf-level physiological analysis (Kim et al., 2026).

These digital phenotyping platforms are also used to analyze plant-associated microbiomes. Plant-associated microbiomes contribute to stress tolerance and soil health through the application of bioinoculants and synthetic microbial communities,

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buffering plants against osmotic and nutritional stresses (Mir et al., 2022).

6. Crop Wild Relatives, Halophytic Genomics, and Synthetic Allopolyploidy

6.1. Genomic Discoveries in Halophytic Relatives

As genetic diversity declines within elite breeding pools due to selection pressure, crop wild relatives (CWRs) represent invaluable reservoirs of adaptive variation for abiotic and biotic stress resistance. Halophytic wild relatives are especially valuable for studying saline-alkaline tolerance, as they have evolved distinct mechanisms to maintain cellular homeostasis under extreme osmotic conditions (Sarfraz et al., 2025).

A milestone in understanding these adaptations was the publication in March 2025 of the chromosome-scale genome assembly of *Hordeum brevisubulatum* (a wild grass relative with the I-genome, 2n=2x=14). Resequencing 38 diploid lines across the *Hordeum* I-genome complex revealed that the species' evolutionary adaptation is driven by genomic structural variations, copy-number variations, and specific gene duplications (Sandhu et al., 2021). Phylogenetic analysis indicates that *H. brevisubulatum* split from *H. marinum* (sea barleygrass) approximately 5.34 million years ago during the late Miocene, and it has a lower transposable element content (83.60%, 2.90 Gb) than both *H. marinum* and *H. vulgare*, making it the smallest diploid *Hordeum* sequenced (Mallikarjuna et al., 2022).

Two key tolerance mechanisms were identified in the *H. brevisubulatum* genome (Sadhukhan, 2025):

- **Duplication of the CaBP-NRT2 Stress Sensor-Responder Module:** Duplication of this calcium-binding protein and nitrate transporter module enhances nitrate uptake efficiency and maintains ion balance under alkaline stress (Manzoor et al., 2022).
- **Horizontal Gene Transfer of *Fhb7*:** The presence of the horizontally transferred fungal gene *Fhb7* reduces oxidative stress in high-salinity environments (Naveed et al., 2026).

Additionally, functional characterization of specific transcription factors and transporters in *H. brevisubulatum* has resolved downstream regulation pathways. The transcription factor *HbERF6* induces the expression of the kinase *AtCIPK24* (*SOS2*) to regulate potassium retention (K+/Na+ homeostasis) under salinity stress. Similarly, the transcriptional coactivator *HbMBF1a* regulates salt tolerance and abscisic acid (ABA) sensitivity by coordinating downstream stress-responsive genes (Ladumor et al., 2026).

6.2. Synthetic Polyploidy and Subgenome Engineering

To transfer these wild alleles into cultivated backgrounds, researchers utilize synthetic polyploidy to overcome hybridization barriers. Combining wild genomes with cultivated crops allows for the synthesis of new allopolyploid species with enhanced stress tolerance (Reynolds et al., 2021).

The potential of this approach was demonstrated by replacing the D-subgenome of wheat with the I-genome of *H. brevisubulatum* to synthesize hexaploid Tritordeum (AABBII). This synthetic hexaploid exhibited a 48% increase in nitrate uptake and a 28% increase in grain yield under salt/alkaline stress compared to conventional wheat (Wang et al., 2025).

Phylogenomic and comparative structural analyses of polyploids, such as Tritordeum and hybrid wheatgrass (*Elymus hoffmannii*, StStStStHH), reveal complex subgenome

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dominance and chromosomal rearrangements. In these synthetic grasses, specific subgenomes display biased gene retention and upregulation of functionally important stress genes (Mwamahonje et al., 2026). Resolving these genomic trajectories provides breeders with a roadmap for targeted subgenome engineering, enabling the development of resilient, high-yielding synthetic cereals designed to thrive in degraded soils (Saha et al., 2025).

Table 5. Agronomic Performance of Synthetic Allopolyploids and CWR Introgression Lines

Synthetic Combination	Genomic Constitution	Chromosome Number (2n)	Targeted Physiological Traits	Demonstrated Yield / Biomass Gains
Tritordeum	AABBII (Wheat x *H. brevisubulatum*)	42	High nitrate assimilation; salinity and alkaline tolerance.	48% increase in nitrate uptake; 28% increase in grain yield under stress.
Hybrid Wheatgrass	StStStStHH	42	Deep rooting; persistent osmotic adjustment.	Enhanced forage biomass under prolonged drought and high salinity.
SUB1A Introgressions	*O. sativa* backcross lines	24	Submergence survival via metabolic dormancy.	40% to 50% survival gains over standard varieties in flood-prone zones.
MON 87460 Hybrids	Transgenic *CspB* introgression	20	RNA chaperoning under moisture deficit.	36% to 62% yield gains under dryland conditions in South Africa.

7. Global Regulatory Harmonization, Policy Divergence, and Commercial Deployment Trends

7.1. Diverging Governance of Genetically Engineered Crops

The translation of gene-edited cereal crops from laboratory proof-of-concept to commercial field deployment is highly dependent on global regulatory frameworks. Historically, agricultural biotechnology has been governed by disparate legal systems, leading to high commercialization costs and complex international trade dynamics (Kumar et al., 2022). Nearly three decades after genetically modified (GM) crops first

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entered global agriculture in 1996, the world remains divided over how they should be governed. Today, more than 209 million hectares of GM crops are cultivated globally, concentrated primarily in soybean (105.1 million hectares, ~50%), maize (68.4 million hectares, ~32.5%), cotton (24.2 million hectares, ~11.8%), and canola (10.4 million hectares, ~5%) (Ghimire et al., 2025).

The core scientific and political debate centers on whether regulatory oversight should target the product itself (focusing on the biosafety of the final phenotype) or the process (focusing on the molecular methods used for trait introduction) (Al-Tawaha et al., 2022). In product-based systems like the United States, gene-edited crops are exempt from strict GMO oversight if the genetic modifications could have occurred naturally through mating or natural recombination. This lowers the regulatory hurdle, facilitating fast-track commercialization (Albertsen et al., 2026).

In contrast, process-based systems like the European Union historically subjected all gene-edited crops to strict GMO regulations. However, the European regulatory landscape shifted following legislative developments in mid-2026. Under the European Parliament's New Genomic Techniques (NGT) regulation, plants edited using CRISPR are categorized into two regulatory streams (Nagaraja et al., 2024):

- **Category 1 NGTs (NGT1):** Plants containing fewer than 20 genetic modifications (such as single-nucleotide substitutions, small insertions up to 20 nucleotides, or deletions of any size) that are deemed equivalent to conventionally bred varieties (Ali et al., 2026). NGT1 crops are exempt from the risk assessments of the 2001 GMO Directive, requiring only standard variety registration. Researchers estimate that 94% of NGT plants developed in the EU would fall under this category (Ahmed et al., 2026).
- **Category 2 NGTs (NGT2):** Plants with complex, multi-site genomic alterations exceeding the 20-modification threshold. These remain subject to strict environmental risk assessment and post-market monitoring analogous to transgenic GMOs (Ameen et al., 2023).

7.2. State-Directed Biotech Programs in Asia

China has integrated gene editing and agricultural biotechnology directly into its national crop security strategies. In December 2024, the Chinese Ministry of Agriculture and Rural Affairs (MARA) approved the first gene-edited rice event for local cultivation, targeting resistance to devastating diseases like rice blast (*Magnaporthe oryzae*) (Ngalamu et al., 2023). Supported by state-directed research, China expanded its genetically engineered and edited corn and soybean production to roughly three million hectares in 2025, which represents a fourfold expansion compared to 2024 (Tefera & Debele, 2026). China's National Smart Agriculture Action Plan and seed security documents highlight the development of precision gene-editing tools, genome selection, and intelligent design as top priorities to foster high-quality varieties with independent intellectual property rights (Prasanna et al., 2021).

These diverging global policies create critical regulatory considerations for international grain trade. Export markets must reconcile importing gene-edited grain that may be regulated differently across jurisdictions (Ghorbanzadeh et al., 2025). Tools like the Genome Editing Regulations Tracker help researchers and policymakers monitor these changing regulations, supporting trade and collaborative crop

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improvement programs (Yali, 2026).

Table 6. Global Regulatory Architectures for New Genomic Techniques (NGTs)

Jurisdiction	Regulatory Category	Legal Classification	Safety Assessment Requirement	Impact on Commercialization Pathways
United States	Product-based.	Exempt from GMO labeling if changes occur naturally.	Standard USDA and FDA crop clearance; no additional GMO assessments.	Highly streamlined; lowers regulatory costs; accelerates product release.
European Union	Process-based (split).	NGT1: Equivalent to conventional plants (<20 edits).	Exempt from 2001 Directive; standard variety register; no specific risk analysis.	Accelerates commercial development of 94% of native CRISPR projects.
European Union	Process-based (split).	NGT2: Regulated under GMO Directive (>20 edits).	Full environmental and toxicity risk assessment.	High regulatory testing burdens; restricts commercial cultivation.
China	Dual system.	Streamlined, product-specific gene editing safety track.	Streamlined biosafety certificate processing via MARA.	Facilitates large-scale adoption; approved first edited rice event in late 2024.

Conclusion

In conclusion, plant breeding, genetics, and genomics have become indispensable components of modern cereal crop improvement for addressing the challenges of climate change and increasing global food demand. The integration of conventional breeding methods with advanced genomic technologies, including genomic selection, GWAS, marker-assisted breeding, CRISPR-Cas genome editing, and multi-omics approaches, has significantly accelerated the development of cereal varieties with enhanced yield, stress tolerance, nutritional quality, and resource use efficiency. These innovations provide valuable opportunities to strengthen crop resilience against drought, heat, salinity, flooding, and emerging diseases while supporting sustainable agricultural production. Nevertheless, challenges such as the complex genetic architecture of adaptive traits, environmental variability, limited genetic resources,

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regulatory barriers, and the need for greater accessibility of advanced breeding technologies continue to impede widespread implementation. Future research should focus on integrating artificial intelligence, predictive breeding models, high-throughput phenotyping, and climate-resilient genomics into breeding programs while promoting international collaboration and the conservation of genetic diversity. Overall, continued advances in plant breeding, genetics, and genomics will play a pivotal role in developing resilient, productive, and sustainable cereal cropping systems capable of ensuring long-term global food and nutritional security.

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