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REVIEW

Precision breeding in a changing climate: unlocking resilience through omics and gene editing

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Abstract

Climate change, rising global food demand, and shrinking resources require transformative innovations in crop breeding. This review outlines recent advances in new breeding technologies (NBTs), including molecular markers, genome-wide association studies (GWAS), genomic selection (GS), next-generation sequencing (NGS), and gene editing (GE) tools such as the clustered regularly interspaced short palindromic repeat (CRISPR/Cas), base editing, and prime editing. These methods enable the accurate improvement of traits, thereby accelerating the development of crops resistant to both abiotic and biotic stresses. The integration of multi-omics platforms, including genomics, transcriptomics, proteomics, metabolomics, and phenomics, provides a comprehensive framework for deciphering and manipulating complex trait architectures. Artificial intelligence (AI) and machine learning (ML) enhance precision breeding by providing data-driven insights and enabling the forecasting of traits. Emphasis is also placed on combining gene editing with other strategies, such as speed breeding, to accelerate the development of traits. This review underscores the importance of an integrated systems biology approach that combines multi-omics, gene editing, AI, and speed breeding to accelerate the development of climate-resilient, high-yielding, and nutritionally enhanced crops. The integration of these innovative technologies holds great promise for addressing global food security, environmental sustainability, and agricultural resilience in the face of climate change. A strategic framework for the future of plant breeding is outlined, emphasizing the importance of interdisciplinary collaboration in building a sustainable agricultural future.

Keywords Climate-resilient crops · Gene editing · CRISPR/Cas · Omics integration · Speed breeding · Precision breeding

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Introduction

Modern agriculture is experiencing an unprecedented convergence of global issues, largely driven by climate change, rising local food demand, and the need for sustainable production systems. Climate change intensifies the frequency of extreme weather events, alters precipitation patterns, and increases temperatures, all of which significantly reduce crop yields and threaten food security worldwide (Verma et al. 2025). Climate change effects on the agricultural sector are largely mediated by diverse extreme abiotic stressors that directly affect crop physiology and yield. The greatest of these stressors are extreme heat, long droughts, and soil salinity, which are increasingly becoming common (Zandalinas et al. 2024). High temperatures interfere with the fundamental physiological functions of photosynthesis, enzyme activity, and pollen viability, and increase yield loss and grain quality impairment, particularly during critical developmental periods (Mehmood et al. 2025). Drought stress limits plant growth by reducing water availability, which leads to stomatal closure and hinders nutrient uptake, ultimately decreasing overall biomass and productivity. Osmotic stress due to soil salinity also hampers a plant's ability to absorb water and nutrients, which are major limiting factors for crop production worldwide (Santos et al. 2022). It is estimated that in the global crop systems, with broad-scale adaptation by farmers, a high-carbon emission scenario would result in a net reduction of up to 24 per cent in calories in the global crop systems by 2100 relative to the world, with no climate change. This corresponds to an average of about 120 calories per person per day due to the global warming of 1 °C (Hultgren et al. 2025). Certain estimates also show that rice yields will drop by 3–22% and wheat yields by 2–19% by the century's end, due to further emissions of greenhouse gases (Ishaque et al. 2023; Gallé and Katzenberger 2025). Food and Agriculture Organization (FAO) of United Nations emphasizes that agriculture is the most impacted sector, as an average of 23% of the total economic losses of calamities between (Pearce 2007) and 2022, with droughts topping the losses that the agricultural sector suffered in the same period with over 65% of the losses being recorded, and the total estimated over 30 years of losses ranged at 3.8 trillion worth of crops and livestock (Raza et al. 2025).

As abiotic stressors increasingly impact crop productivity and the growing population leads to higher food demand, relying solely on conventional breeding methods is insufficient to meet food requirements. Therefore, it is essential to adopt advanced breeding technologies to ensure that agricultural systems can sustainably produce higher yields and improve resilience in response to escalating environmental and demographic pressures. Addressing these interconnected issues is essential for ensuring long-term agricultural productivity, environmental health, and global food security (Pretty et al. 2018). Over the centuries, plant breeding has consistently contributed to global food security by enhancing yields, disease resistance, and the quality of key crops (Hafeez et al. 2023). The past two decades have seen a blistering evolution of molecular biology and biotechnology that has redefined plant breeding, revolutionizing the older selection-based approach into a high-tech, more sophisticated process, enabling breeders to make more accurate and informed decisions (Lamichhane and Thapa 2022). Several practical case studies demonstrate that the current breeding technologies have already introduced agronomic benefits in terms of yield, stress resistance, and plant survival in harsh conditions, which are being measured. The CRISPR/Cas9-edited waxy maize, created to outperform conventional hybrids in the field, confirms the usefulness of precision editing even in real production conditions (Gao et al. 2020). Promoter editing of *OsNAS2* in rice resulted in significantly higher zinc accumulation, along with increased grain yield, in multi-location trials (Ludwig et al. linking omics-guided gene targeting to direct farmer-level benefits. Marker-assisted development of the rice cultivar Huhan-1516 resulted in improved resistance to drought, blast, and brown planthopper, yielding a recorded 2.2% yield gain compared to previous lines (Li et al. 2022). The development of improved varieties, such as Kamala, designed to enhance key agronomic traits like stress resilience and grain/fruit quality, and the CR Dhan series, known for targeted traits like drought and salinity tolerance, highlights the growing potential of genome-editing approaches in crop improvement. These varieties demonstrate how precision breeding tools can accelerate the development of cultivars with specific adaptation traits, enabling breeders to address challenges related to climate stress, productivity, and nutritional value. (https://icar.org.in/en/india-unveils-worlds-first-genome-edited-rice-varieties-3).

Modern breeding tools such as Marker Assisted Selection (MAS) and Genomic Selection (GS) have greatly accelerated varietal improvement by enabling precise allele selection and early prediction of superior genotypes (Kumar et al. 2024). Transgenic approaches and, more recently, CRISPR/Cas-based editing have further expanded breeding possibilities by facilitating targeted genetic modification, including foreign-DNA–free edits that offer regulatory advantages (Ahmad et al. 2021; Tahakik et al. 2024). Advances in high-throughput phenotyping, bioinformatics, and speed breeding have simultaneously enhanced trait characterization and reduced generation time, allowing rapid introgression of climate-adaptive traits (York 2019; Sharma et al. 2023a). Likewise, multi-omics platforms provide deep insights into the molecular networks that govern stress responses and resource-use efficiency (Muttappagol et al. 2025). However, despite the maturity of these tools, current breeding frameworks and existing reviews often address them individually, without explaining how their strategic integration can more effectively tackle the complex, multilayered nature of climate resilience. This gap limits the translation of molecular discoveries into practical breeding outcomes. By emphasizing how multi-omics insights can guide precise gene editing, how AI and systems biology and ML can refine trait prediction, and how speed breeding can operationalize these improvements, this review highlights an integrated, end-to-end strategy for accelerating the development of climate-resilient crops, offering a perspective that extends beyond conventional technology-by-technology discussions(Cembrowska-Lech et al. 2023).

Although there is rapid development in the fields of molecular breeding, genome editing, multi-omics, and speed breeding, the majority of available reviews treat these technologies independently rather than as a unified concept of how they interrelate in a modern breeding pipeline. This reductionist methodology has constrained its practical usefulness, since the complexity of climate-resilient characteristics is inherently multilayered, with genetic, biochemical, and physiological networks that demand systems-level integration rather than tool-specific remedies. There is also an apparent gap in research on integrating these varied innovations into a systems-level model that not only describes the utility of each of them but also demonstrates how they can be combined effectively and strategically to accelerate and enhance crop improvement. The majority of available plant breeding reviews focus on a single type of molecular marker, gene editing, a multi-omics platform, or an AI application. Nevertheless, very little literature consolidates such developments into one unified framework. This review is unique compared to previous literature, as it combines multi-omics discovery pipelines with evolved gene editing (including CRISPR/Cas, base editing, and prime editing), systems biology modelling, AI/ML-based predictive breeding, and speed breeding technologies. Having taken these approaches jointly under the same platform, our review demonstrates the synergistic interactions among approaches- a factor that has received little attention in earlier studies. This integrative view not only encapsulates recent successes but also provides pipelines for methodologies, addressing the current challenge and future opportunities of using combined omics and editing approaches to accelerate the development of climate-hardy, high-performing crops.

The landscape of plant breeding research reviews primarily focuses on molecular markers, gene editing, and multi-omics individually; a significant gap remains in synthesizing these advancements into a single, cohesive framework. This fragmented approach often overlooks the synergistic potential of their integrated application. Therefore, this review aims to provide a comprehensive overview of modern plant breeding techniques, emphasizing the integration of multi-omics with gene editing and system biology, highlighting the synergistic potential of their integrated application in crop stress research. This integrative framework outlines significant accomplishments, technological innovations, and methodological pipelines, as well as challenges, knowledge gaps, and avenues for future research to harness the synergy between data-rich omics platforms and targeted gene-modulation tools in plant biotechnology, thereby accelerating the development of climate-resilient and high-performance crops for sustainable agriculture.

Traditional and modern breeding approaches for climate resilience

Traditional breeding

Traditional breeding, which has served as the fundamental basis of agriculture for millennia, involves the deliberate selection and cross-pollination of plants to cultivate improved varieties. This breeding leverages natural genetic recombination through methods such as mass selection, pure line selection, and various forms of hybridization. Mass selection, for example, has been shown to effectively improve the local crop varieties, both in terms of preferred traits, such as yield, resistance to disease, and more timely maturation, as well as in terms of genetic diversity within the populations (Nagaraja et al. 2024). Likewise, interspecific hybridization, including crosses among Triticum species, produces pentaploid hybrids with superior traits, including resistance to diseases and improved grain quality (Huang et al. 2024). Conventional breeding has successfully developed high-yielding maize varieties, such as hybrid maize and QPM; however, these methods are time-consuming and resource-intensive (Zhou and Xu 2024). Furthermore, Traditional breeding in sugarcane is insufficient because of its complex genome and long breeding cycle (Ali et al. 2024). Ultimately, these conventional methods are inherently slow, imprecise, and constrained by limited genetic diversity and environmental interactions, often leading to the doleful oversight of valuable genetic potential found in wild relatives (Lamichhane and Thapa 2022).

Considering the increasing difficulty of a rapidly shifting climate, the natural slowness, lack of precision, and limited access to genetic materials of traditional breeding approaches, there is an urgent necessity to adopt modern breeding technologies to produce climate-resistant crops, which ensure food security in the world in the shortest time possible (Altaf et al. 2024a). To enhance the effectiveness, efficiency, and speed of breeding programs, specific modern breeding methods are being developed. Some of these modern breeding methods are discussed below.

Transgenics

Transgenic technology, a foundational method that involves the stable integration of foreign DNA to introduce novel traits, marked a groundbreaking approach in the history of plant breeding. Insect-resistant crops like *Bacillus thuringiensis* (*Bt*) crops and herbicide-resistant crops like Roundup Ready crops, produced by this process, demonstrated the transformative potential of transgenic technology and have resulted in a remarkable improvement in agricultural productivity (Hallerman and Grabau 2016). Transgenic approaches have generated more resilient crops to mitigate abiotic stress. Drought-tolerant maize varieties were developed by overexpressing the NAC-domain transcription factor ZmNaC20, which enhances plant growth under water-stressed conditions (Liu et al. 2023). Similarly, overexpression of *SlARR1* in transgenic Micro-Tom tomatoes acts as a primary regulator of development, causing pleiotropic effects, including auxin-related growth variations and a significant reduction in lycopene and beta-carotene content (Fahad et al. 2023). Likewise, Flood-tolerant rice varieties were engineered to carry a specific gene that enables them to survive prolonged submergence. Despite this success, the technique raised concerns about integrating foreign DNA and attracted significant public and regulatory scrutiny. Consequently, the widespread adoption of these transgenic crops was often hindered, which created a strong impetus for the development of alternative, more precise gene modification technologies (Caradus 2023).

Marker-assisted selection (MAS)

MAS accelerates the development of climate-resilient crops by rapidly and precisely transferring desirable alleles from wild relatives into cultivated varieties, thereby enhancing resistance and improving quality (Misra and Singh 2025). Key molecular markers of MAS include restriction fragment length polymorphism (RFLP), extensively utilized in rice research to investigate intraspecific genetic variability and mapping studies, Amplified fragment length polymorphism (AFLP), revealing 88% polymorphism and 57% genetic differentiation within field in a study of 398 individual Moroccan sorghum landraces, Simple sequence repeat (SSRs) uncovering 27 rice genotypes aiding substantial Egyptian rice cultivars and single-nucleotide polymorphism (SNP), genotyping 359 sorghum plants showing 64.5% genetic variation and distinct peduncle shape (Enyew et al. 2022; Vieira et al. 2022; Medraoui et al. 2024; Salem et al. 2024). MAS significantly reduces traditional breeding time and enables precise selection, as demonstrated by the successful introgression of genes such as *Fhb1*, *Pm21*, and *Yr59* into elite wheat varieties for disease resistance (Song et al. 2023). The widespread availability of diverse DNA markers, such as Kompetitive allele-specific PCR (KASP) markers, namely TaDreb-B1 and 1-FEH w3, for wheat drought tolerance and Sequence-related amplified polymorphism (SRAP) markers like SC4-F/SC4-R and SC14-F/SC14-R for Fusarium-resistant banana germplasm, has streamlined MAS application (Eltaher et al. 2023; Qv et al. 2024). Additionally, SSR and inter-simple sequence repeat (ISSR) markers have been used to investigate genetic diversity and metabolite responses to heat stress in barley (Ghomi et al. 2021). Meta-quantitative trait loci (MQTL) analysis further supports MAS by identifying high-confidence candidate genes and markers that enhance stress tolerance, yield, and nutritional quality in wheat (Sharma et al. 2023b). Another specialized MAS technique, Marker-Assisted Backcross (MABC), utilizes marker strategies like Foreground Selection to track the desired trait, e.g., drought tolerance QTL using specific SSR markers and Background Selection to recover the recurrent parent's elite genome, as demonstrated in improving the drought tolerance of the rice restorer line RPHR-1005R (Sravanraju et al. 2024). Despite its advantages, it faces limitations with complex traits and multiple genes, and its effectiveness may diminish as crop productivity approaches genetic limits (Mapari and Mehandi 2024). Its application in (QTL) mapping studies is also challenging due to the influences of environmental and genetic backgrounds (Misra and Singh 2025).

Genomic selection (GS)

GS is transforming plant breeding by enabling early and accurate predictions of genetic values, including genomic estimated breeding values (GEBVs), using genome-wide marker data. This practice leads to tremendous increases in genetic gains (Anilkumar et al. 2023). Increasing genetic enhancement of breeding populations by offering the possibility to select high-quality clones and new parents to cross and not to directly examine phenotypes (Zhang and Li 2024a; Costa et al. 2024). GS is an effective method for using genome-wide marker data to map QTLs and enhance complex traits such as yield and stress tolerance (Anilkumar et al. 2023). Popular prediction models in GS studies, including RR-BLUP (ridge regression best linear unbiased prediction) and G-BLUP (genomic best linear unbiased prediction), can be successfully applied in the analysis of quantitative traits with thousands of small genes, as they consider all the effects of loci as common (Parveen et al. 2023). Multi-trait genomic selection models (e.g., Random Forest, Multilayer Perceptron) based on machine and deep learning showed significantly higher predictive accuracy of complex traits in wheat than traditional methods (GBLUP, Bayesian) by up to 28.5% and make them a better predictor of genetic gain in breeding programs (Sandhu et al. 2021). Consequently, GS has become one of the most important approaches for simulating crop yield under different climatic conditions, addressing the challenge of production in a changing climate (Budhlakoti et al. 2022). The current GS and MAS are hastening peanut breeding because it is now feasible to predict, with high accuracy and high throughput, multiple breeding traits such as yield, disease resistance, and oil content using molecular markers (Umer et al. 2025). As a promising tool to enhance drought tolerance in cassava, genetic gain in winter wheat, and yield in soybean, GS relies on multiple prediction models and SNP-based data (Ficht et al. 2023; Miller et al. 2023; Costa et al. 2024). Meanwhile, integration of GS with GWAS accelerates genomic hybrid breeding in maize and enables the study of agronomic traits in rice (Zhang et al. 2023, 2025). Despite its significant advantages, the application of GS and other modern breeding tools is often constrained by factors such as high genotyping costs, the need for large, well-structured training populations, complex polygenic architectures, and economic or regulatory constraints. These challenges can be progressively addressed through integration with emerging technologies, including AI-driven analytics, high-throughput phenotyping, improved data-sharing frameworks, and optimized resource allocation, thereby enhancing precision, scalability, and efficiency in breeding pipelines (Kouser et al. 2024). A comprehensive and comparative summary of major breeding approaches, their utilities, strategic advantages, limitations, and integration potential across traditional, molecular, and genomics-assisted methods is presented in Table 1.

Advances in genomics: expanding the breeding toolbox

Genome-wide association studies (GWAS)

The primary advantage of GWAS over conventional breeding is that it utilizes high-density genomic markers, including SNPs, to pinpoint specific genomic regions and even candidate genes directly associated with a trait. The traditional GWAS involves compiling a series of samples, determining their SNPs across the genome using high-throughput sequencing or gene chip technology, statistically analyzing the data to identify relationships between characteristics, and finally validating the results (Xiao et al. 2022). At the same time, phenotypic data are ideally collected across multiple environments to measure differences associated with stress. Quality control is used to exclude poor-quality SNPs and to estimate population structure and kinship using principal component analysis or kinship matrices (Sahito et al. 2024). After preparing the data, statistical analysis is conducted to test the strength of the relationship between each SNP and the trait using linear regression, Mixed linear models (MLMs), or multi-locus models. Lastly, the researchers validate and interpret the results, which may verify the biological significance of the identified SNPs through functional experiments (Jiang 2024). Research on the genome-wide expression of the aldo-keto reductase gene family in cotton identified 249 genes across four cotton species and highlighted their potential for stress tolerance (Liu et al. 2025a). GWAS has been applied to enhance the understanding of the genetic basis of yield, stress tolerance, nutrient efficiency, and quality (Prabhu et al. 2023). One notable study on cotton identified 25 genomic loci using 27 SNPs, each showing strong relationships with three salt-stress tolerance phenotypes across many chromosomes. This analysis identified possible genes responding to salt stress, such as protein kinases and aquaporins, that could make a significant contribution to salt stress resistance in cotton (Xu et al. 2021). A GWAS of 125 rice lines identified important QTLs for traits related to false smut resistance, including the number of smut balls per plant, the number of smut panicles per plant, and the disease score, on chromosomes 2, 3, 4, 6, 8, 9, and 11. The research has identified resistant germplasm and potential genomic areas for marker-assisted breeding (Hiremath et al. 2021). Following this line, GWAS was used to identify candidate genes regulating germination performance under salt stress in bread wheat and to enhance drought and salt tolerance in watermelon using GBS (Javid et al. 2025; Nyirahabimana and Solmaz 2025). Genetic markers of salinity stress have also been detected by GWAS using diversity array technology sequencing (DArTseq) markers across different chickpea germplasms (Ahmed et al. 2021). In wheat, GWAS with five models, Compressed Mixed Linear Model (CMLM), Settlement of MLM Under Progressively Exclusive Relationship (SUPER), Multi-locus Mixed Model (MLMM), Fixed and Random Model Circulating Probability Unification (FarmCPU), and Bayesian Information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) have aided in identifying the genetic basis of spot blotch resistance (Singh et al. 2023). However, even with considerable progress, GWAS faces several imminent limitations, including difficulties in acquiring high-quality genetic

Table 1 Overview of plant breeding approaches, their advantages, disadvantages and strategic application

Approach	Tools & markers used	Purpose in pipeline	Advantages	Limitations	Notable Crop-specific outcome	Integration with other tools	References
Traditional Breeding	Morphological traits, pedigree selection	Develops base varieties via phenotypic selection	Broad genetic variability; natural adaptation	Slow, environment-dependent; low precision	Wheat: high-yielding, Rice: salt tolerance	Provides raw material for MAS, GS, and gene editing	(Pearce 2021; Padmavathi et al. 2024)
Backcross Breeding (BCB)	Foreground and background SSR markers, field screening	Transfers desired trait into elite lines	Efficient trait stabilization in superior backgrounds	Requires multiple generations; limited to known traits	Wheat: salt tolerance, Tomato: heat tolerance	MAS-enabled backcross pipelines for disease traits	(Sharma et al. 2024; Bashary et al. 2024)
Recurrent Selection (RS)	Half-sib, full-sib testing, phenotyping	Improves polygenic traits through population cycles	Cumulative gain across cycles	Labour-intensive; sensitive to environmental variance	Maize: drought tolerance, Rice: high yield	Precursor to GS and hybrid parent pools	(Musimwa et al. 2023; Castro et al. 2023)
Nested Association Mapping (NAM)	GBS, SNP array, R/qtl2	High-resolution mapping across diverse structured families	Combines GWAS and linkage mapping strengths	Requires structured populations; high cost	Maize: cold tolerance, Wheat: drought and heat tolerance	Supports GS model training and marker discovery	(Chidzanga et al. 2022; Revilla et al. 2023)
MAS (Marker-Assisted Selection)	SSRs, SNPs, InDel markers linked to QTLs, CAPS, SCAR, STS, ISSR, KASP, DArT	Selects known QTLs using molecular markers	Fast, highly precise trait introgression	Limited for polygenic traits; needs validated markers	Rice: Heat tolerance, Pearl millet: drought tolerance	Used with Speed Breeding and QTL pyramiding	(Rani et al. 2022; V et al. 2024)
GWAS (Genome-Wide Association Studies)	SNP markers, GBS, SNP chips, PCa, MLM, Farm CPU models, DArT, KASP	Identifies alleles associated with traits from natural diversity	High-resolution trait mapping	Requires large germplasm panels; confounded by population structure	Maize: drought tolerance, Tomato: cold resilience	Guides GS and CRISPR; linked to HTP platforms	(Zhu et al. 2023; Chen et al. 2023)
Genomic Selection (GS)	Genome-wide SNPs, GBLUP, Bayesian LASSO, RR-BLUP,	Predicts breeding values from genome-wide markers	Enables early selection, boosts gain per cycle	Needs large training populations; high genotyping cost	Maize: drought, heat, and salinity tolerance, rice: salinity tolerance	Enhanced by HTP, Speed Breeding, and ML	(Prasanna et al. 2021; Bartholomé et al. 2023)
Genomic Pyramiding	Linked QTLs, trait-specific markers, background selection	Combines multiple resistance loci into elite lines	Durable and broad-spectrum stress resistance	Technically complex; requires tightly linked markers	Cotton: heat tolerance, Tomato: drought and salinity tolerance	Integrates with MAS and GS	(Raja et al. 2022; Saleem et al. 2024)
Double Haploids (DH)	Anther culture, flow cytometry	Fixes homozygosity in one generation	Major reduction in breeding time	Not suitable for all crops; requires lab expertise	Barley: salt tolerance, Rice: high-yielding, drought tolerance	Combined with MAS and GS pipelines	(Tripathy and Maharana 2024; Xu et al. 2025)
Polyploidy Breeding	Colchicine, flow cytometry, meiotic screening	Induces whole-genome duplication for trait enhancement	Increased vigor and tolerance	Genome instability; fertility issues	Wheat: drought and salinity tolerance, Brassica: drought tolerance	Serves as a donor in MAS and GS; supports pre-breeding	(Wang et al. 2022; Yoo et al. 2024)
Hybrid Breeding	Anther culture, CMS, flow cytometry	Exploits heterosis by crossing genetically diverse parents	Superior yield and stability	CMS systems may limit applicability; high seed cost	Rice: salinity tolerance, Maize: heat and drought resistance	Supported by DH lines, MAS, and GS	(Patil et al. 2025; Sun et al. 2025)
Mutation Breeding	EMS, gamma rays, TILLING	Creates novel variation through induced mutagenesis	Generates unique alleles not found in nature	Random mutations; need for large screening population	Rice: drought tolerance, Wheat: salt tolerance	Used upstream of TILLING, functional genomics	(Karimzadeh et al. 2023; Fatima et al. 2024)
Transgenic Breeding	Gene constructs, Agrobacterium, selectable markers	Introduces foreign genes for novel traits	Enables trait addition beyond species boundaries	Regulatory hurdles; limited public acceptance	Potato: drought and salt tolerance, Soybean: salt tolerance	Paves the way for gene editing (CRISPR)	(Ye et al. 2025; Fu et al. 2025)

data and accurately characterizing complex traits (Xiao et al. 2022). Moreover, GWAS requires large collections of germplasm, such as Multiparent Advanced Generation Intercross (MAGIC) and Nested Association Mapping (NAM) populations, which are more labor-intensive due to the multiple successive crosses compared to a single germplasm sample (Susmitha et al. 2023).

Next-generation sequencing (NGS)

NGS has transformed the field of plant genomics, enabling fast, cost-effective sequencing of complex genomes and the identification of genetic variation, including SNPs, for genomics-assisted breeding to increase crop resistance and yield (Tyagi et al. 2024). Whole-genome resequencing

(WGRS) methods are necessary for mapping traits and localizing QTLs using computational programs, while techniques such as RNA sequencing and whole-genome bisulfite sequencing provide information on the regulation of genes under stress (Altaf et al. 2024b). NGS approaches such as WGS, GBS, and RAD-seq facilitate the detection of SNPs, InDels, and structural variants, improving the accuracy of trait mapping and attributing QTLs to traits like early development and nutrient acquisition in barley and maize (Capo-chichi et al. 2021; Zhang et al. 2020). For example, RAD-seq was used to develop 113 InDel markers in tobacco for plant height association in MAS breeding (Li et al. 2022). Furthermore, the availability of complete wheat genomes and WGS has led to the discovery of over 260 million SNPs, which are used in large-scale, cost-effective genotyping with arrays and KASP assays to characterize genetic loci for traits such as rust resistance and advanced breeding (Geethanjali et al. 2024). Likewise, GBS of proso millet mutants revealed yield-related SNPs, creating critical molecular resources for breeding (Francis et al. 2023) and RNA-Seq data from maize, which helped to develop 71,311 high-density KASP markers valuable for fine mapping QTL and efficient MAS (Chen et al. 2021). Precisely, RNA-seq has revealed stress-responsive regulatory networks, including stress-related families of transcription factors (TFs), such as DREB, NAC, bZIP, and WRKY, which regulate the oxidative stress response and abscisic acid signalling (Kaya 2025).

These mechanistic insights are increasingly applied to inform genomic prediction and CRISPR/Cas-based gene editing strategies. The integration of NGS data into breeding pipelines is increasingly streamlined, primarily due to the well-maintained genomic databases such as Ensembl Plants, Gramene, Sol Genomics, and the Rice SNP-Seek platform (Ambrosino et al. 2020). The use of NGS in climate-resilient breeding is further enhanced by incorporating pan-genomic and epigenomic techniques, providing a more comprehensive understanding of genetic and regulatory variations crucial for adaptation.

Pan-genomics

Pan-genomics is radically transforming crop genomics by demonstrating the impressive diversity of species genomes. Crops such as soybean, maize, wheat, and tomato have been the subject of pan-genome studies that have revealed major presence-absence and copy-number variations that are vital to local adaptation (Sarawad et al. 2025). A recent pan-genome investigation of pearl millet identified 424,085 structural variants, accompanied by a proliferation of RWP-RK transcription factors, which make it more heat-adaptive during domestication (Yan et al. 2023). In the same way, an in-depth pan-genome map of rice revealed the most important salt-tolerance regulators using the integrated QTL/GWAS methods (Wei et al. 2024). In Maize, the Pan-Genome method identified 75 abiotic stress-associated GATA TF family members, providing useful new resources for functional analysis of ZmGATA (Zhao et al. 2025a).

Epigenomics

Epigenomic profiling has revealed heritable methylation changes associated with stress adaptation, providing a crucial avenue for identifying novel targets and strategies for developing climate-resilient crop varieties. Bisulfite sequencing of *Gossypium hirsutum* whole-genome data showed that heat stress causes an apparent change in DNA methylation across subgenomes (reducing CG/CHG methylation and increasing CHH methylation), affecting hormone biosynthesis and metabolism genes, providing new data on the enhancement of heat tolerance (Gong et al. 2024). Likewise, genome-wide bisulfite sequencing revealed drought-memory differentially methylated regions (DMRs) in rice, providing insights into how rice copes with repeated short-term drought stress at the global methylome level and highlighting the potential future use of epigenetic markers to breed drought-resistant rice varieties (Kou et al. 2022).

High-throughput phenotyping (HTP)

HTP platforms exceed the limit of traditional methods, significantly advancing genetic research by enhancing trait discovery, parental selection, and hybridization optimization. Hyperspectral imaging precisely quantifies key traits, such as chlorophyll content and photosynthetic efficiency, helping breeders identify genotype-specific responses to abiotic stresses, such as drought and salinity (Angidi et al. 2025). Simultaneously, thermal infrared imaging has been particularly effective for identifying heat-tolerant cereals and legume lines by enabling cooler canopies to be maintained even when water is scarce (Brewer et al. 2022; Poudel et al. 2024). Recent studies have focused on the flexibility of these tools through their integration with ground sensors and UAV-based systems, which enable field-level HTP at massive spatial and temporal scales (Ninomiya 2022). Hyperspectral UAV imagery has also been used to quantify the extent of wheat breeding trials' responses to drought and nitrogen, accelerating the screening of phenotypes (Yang et al. 2020). The integration of HTP data with genomics and gene editing would produce a robust pipeline that would help breeders to locate and manipulate more targeted genes that carry favorable traits. High-throughput genotypic and high-density markers have a strong positive effect on the identification of QTL and candidate genes, speeding up GAB and germplasm (Bhat and Yu 2021). Integration of HTP with GWAS and QTL mapping has dramatically enhanced our understanding of the genetics of complex traits, and has helped to accelerate the production of climate-resilient wheat by utilizing phenomics and genomic selection (Kaushal et al. 2024; Yang et al. 2020). GWAS combined with HTP has demonstrated significant benefits for drought resistance in wheat and maize (Wu et al. 2021; Zhang et al. 2024b). Additionally, the combination of HTP and GE or AI can reveal multidimensional trends and help create predictive models of trait selection (Huang et al. 2024; Sheikh et al. 2024). For example, by using UAV-based HTP and machine learning models namely Random Forest and XGBoost can accurately predict underground peanut yield for efficient genotype screening (Pugh et al. 2024). The systematic progress in crop breeding methods, highlighting the shift from traditional selection techniques to high-throughput, data-driven approaches, is shown in Fig. 1.

Gene editing (GE)

GE technologies have driven a revolution in plant breeding, providing unprecedented accuracy, efficiency, and flexibility compared to conventional approaches. Whereas Zinc Finger Nucleases (ZFNs) and Transcription Activator-Like Effector Nucleases (TALENs) provided a framework to perform gene editing, the CRISPR/Cas system has overshadowed them because of its simplicity, cost-efficiency, and programmability to locate the DNA target (Hwarari et al. 2024).

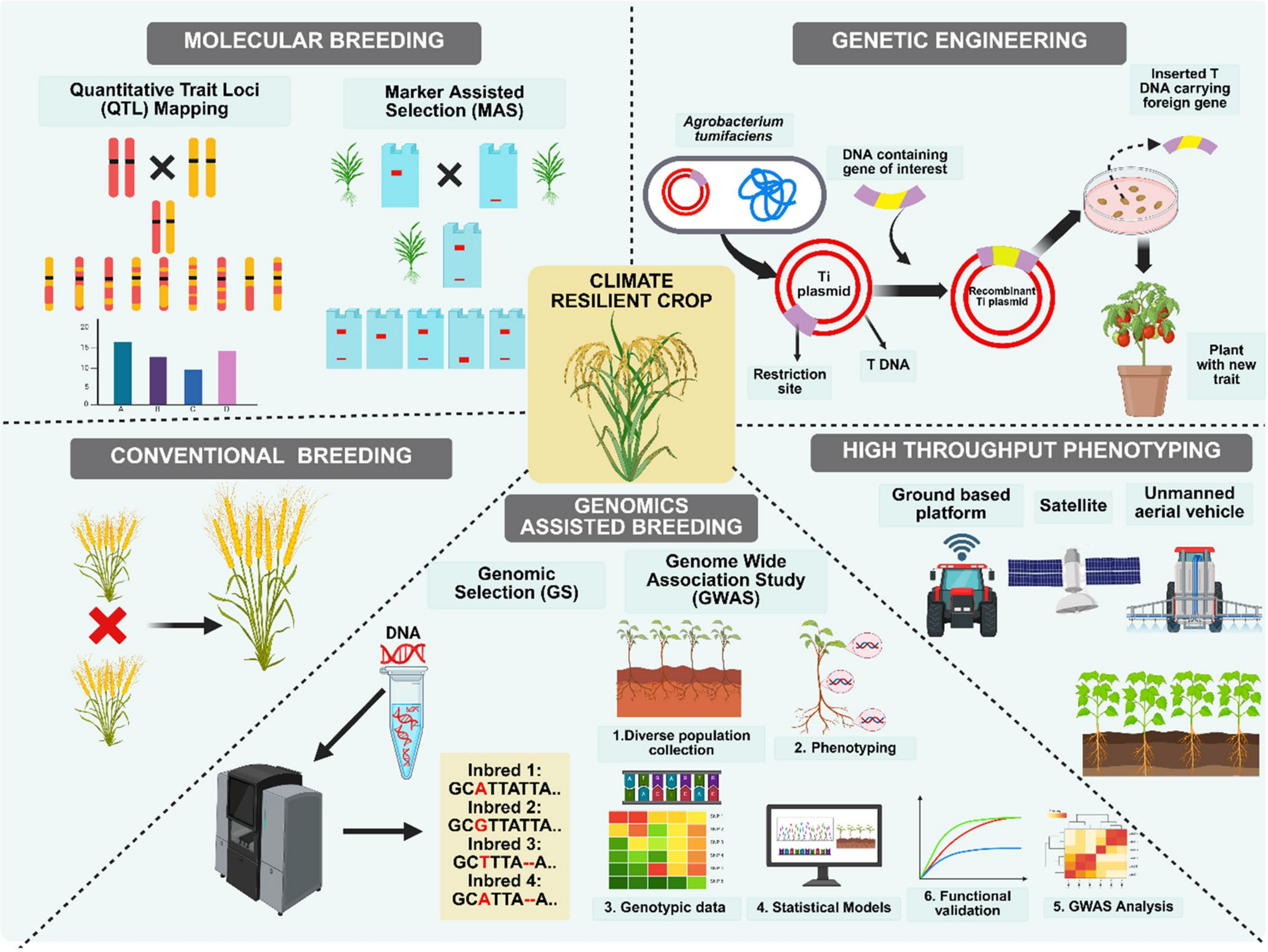

Fig. 1 Systematic advancements of crop breeding techniques. This figure illustrates the workflow and how various breeding paradigms contribute to developing stress-tolerant crops. From conventional breeding to advanced molecular breeding and data-driven genomics-assisted breeding, these methods aim to fortify plants against environmental and biological threats. The diagram also highlights the precision of genetic engineering for direct genetic modification. All strategies are enhanced by high-throughput phenotyping to efficiently identify and select resilient varieties. This figure was created BioRender (https://www.biorender.com/), and some elements were adapted from BioRender templates

Precise and targeted genetic modifications by Cas9, Cas12 and Cas13

The CRISPR/Cas system comprises a heterogeneous group of enzymes, including Cas9, Cas12, and Cas13. Cas9 is an endonuclease in a single-guide RNA (sgRNA) that directs the specific cut of DNA at particular sites of the genome next to a protospacer adjacent motif (PAM) site. This leads to the formation of double-strand breaks (DSBs), which can be repaired by non-homologous end joining (NHEJ) or homology-directed repair (HDR). Such repair usually results in the insertion or deletion of target genes. Recent applications have demonstrated the practical utility of CRISPR/Cas9 in other areas, including improving protein production in rice and soybean by promoting the *NF-YC4* gene and in wheat by targeting the *TaRPK1* gene, a root architecture gene (Rahim et al. 2024; Wang et al. 2025a). Additionally, it has been used to improve the multi-stress resistance of tomatoes by targeting the *SlHyPRP1* and *SlDEA1* genes (Saikia et al. 2024). In parallel, Cas12a (Cpf1) is a popular variant of Cas12 that targets DNA by recognizing T-rich PAM sequences (TTTV) at the 5’ end, generating staggered DSBs. Others, including Cas12b (C2c1), Cas12c (C2c3), and Cas12f, are also beneficial for specific gene integration in a particular gene-editing process. CRISPR/Cas12a has been shown to improve the rapid and efficient detection of pathogens greatly and has been applied to amplification-free detection of tomato leaf curl Karnataka virus (Shashikala et al. 2025). Also, compared to conventional Cas12a, PAM-relaxed and temperature-tolerant CRISPR-Mb3Cas12a are more versatile for editing rice, maize, and tomatoes (Liu et al. 2025b). Another benefit of Cas13, in particular, compared to DNA-targeting CRISPR, is that it targets RNA. This enables the temporary and reversible modification of gene expression without altering the genome permanently. Cas13 can be utilised in various perspectives, including as an RNA diagnostic, for gene regulation, and for biotechnological applications in the agricultural field. In transgenic tobacco plants, Cas13 reduces damage, mild oxidative stress, and viral particle accumulation when challenged with Tobacco mosaic virus (TMV) infection (Yu et al. 2024). CRISPR/Cas13 offers a promising approach to enhance plant resistance by precisely targeting and modulating non-coding RNAs at the RNA level. Further research into this Cas13-mediated RNA editing in plants is essential for its successful application in future crop improvement (Kavuri et al. 2022).

Advanced editing capabilities through base and prime editing

Beyond traditional CRISPR, base editing and prime editing are advanced CRISPR-based tools that offer an effective alternative to HDR for precise crop gene editing by chemically altering target nucleobases and modifying single nucleotides without breaking the nucleic acid backbone. DNA base editors, Cytosine base editing (CBE) and Adenine base editing (ABE), have been successfully used to rapidly enhance crops by correcting point mutations and restoring key agricultural traits lost due to SNPs in the genome. In contrast, RNA base editors, such as RNA editing for programmable A-to-I replacement (REPAIR) and RNA editing for specific C-to-U exchange (RESCUE), have not yet been utilized in plants (Hillary and Ceasar 2024). For example, base editing of the *OsNAS2* gene promoter in rice has simultaneously increased zinc uptake and grain yield, addressing both yield and nutritional improvement in a single genetic modification (Ludwig et al. 2024a). Correspondingly, prime editing is a reverse-transcriptase-based genome-editing tool that revolutionizes gene editing by enabling all types of mutations without relying on DSBs. This innovation significantly reduces off-target edits, thereby overcoming major bottlenecks that limit the biotechnological applicability of producing designer crops (Vats et al. 2024). Dual prime editing precisely replaces large DNA fragments in wheat (51.5% efficiency) and in dicots like tobacco and tomato (72.7% efficiency), significantly expanding precision GE capabilities for crop improvement (Zhao et al. 2025b).

Gene regulation and spatiotemporal control

Using a dead Cas9 (dCas9) enzyme, CRISPR/Cas systems can be repurposed to either activate (CRISPRa) or suppress (CRISPRi) the expression of specific genes, offering fine-tuned control over plant development and response. In Rice, the dCas9-based CRISPR-Act2.0 system was developed to enhance the transcription of multiple genes synthetically. Meanwhile, CRISPR/dCas12a-mediated activation of *SlPAL2* has been shown to enhance tomato resistance to bacterial canker (Pramanik et al. 2021; Rivera-Toro et al. 2025). Spatiotemporal regulation further refines gene editing by enhancing heritability and efficiency of targeted mutagenesis, thereby minimizing off-target effects and mitigating the negative impacts associated with constitutive expression (Rahman et al. 2022). In rice, tissue-specific inhibition of brassinosteroid signaling regulates panicle branching and grain yield (Islam et al. 2025), whereas callus-specific promoters generate transgenic lines with strong callus specificity (Ma and Wu 2025).

CRISPR/Cas-based gene editing has transformed plant breeding by enabling precise, efficient, and targeted genetic modifications that enhance yield, stress tolerance, and disease resistance, surpassing earlier tools like ZFNs and TALENs. Advanced tools like base and prime editing improve accuracy and minimize off-target effects, while CRISPRa/i and spatiotemporal control systems fine-tune gene regulation and heritability. As CRISPR-edited crops lack foreign DNA, unlike traditional GMOs, they enhance biosafety and public acceptance, establishing this technology at the forefront of sustainable agriculture.

The ethical and regulatory landscape of CRISPR-Cas-based genome editing in crops designed for climate resilience is highly complex and varies around the world. While some countries (e.g., USA, Australia) exempt these crops from strict GMO regulations, others (e.g., EU) enforce full GMO scrutiny (Ahmad et al. 2021). This divergence creates significant trade barriers and limits the global use of climate-resistant crops that are critically needed to fight climate change and ensure food security. Ethical issues to consider during biosafety evaluation include off-target effects, market control, and intellectual property. An international, risk-based regulatory approach is crucial to safely and efficiently adopt these beneficial technologies and secure food supply amid climate change (Movahedi et al. 2023). A comprehensive overview of CRISPR/Cas systems in various crops and their applications is illustrated in Table 2.

Integrative breeding technologies towards rapid crop resilience

Rapid generation advancements (RGA) through speed breeding

Speed breeding is emerging as a pivotal discipline that accelerates breeding generations by manipulating environmental conditions, including regulating temperature, humidity, soil moisture, carbon dioxide levels, and photoperiod. This induces early flowering, rapid seed maturation, and enhances plant growth through targeted applications of phytohormones and nutrients (Wanga et al. 2021). Standardized protocols have been developed for major crops like wheat, barley, chickpea, oat pea, and other Brassica species plants, providing deeper insights into executing speed breeding experiments using the single seed descent method under the LED lights of the photosynthetically active region (PAR) facility in a bench-top cabinet (Ghosh et al. 2018). In finger millet, *Rapid Ragi* protocol was developed implementing specific modifications on photoperiod of 9 h, optimum temperature of 29 °C, 70% humidity and dense planting supplemented with 0.17% Hoagland solution and restricted irrigation confirming 4–5 generation advancement per year with reduced maturing days and enhanced yield, paving a way for its integrating approach with MAS, GS, gene pyramiding, and rapid trait introgression (Sajja et al. 2025). The application of speed breeding with GS yields a significant increase in genetic gain and a reduction in generation intervals for Fusarium head blight resistance in wheat, outperforming traditional phenotypic selection (Nannuru et al. 2025). Researchers also combine genotypic and environmental data with observed phenotypes to screen for superior genotypes under various abiotic stress conditions. AI-based speed-breeding approaches further aid in interpreting biochemical data to explore the mechanisms of plant stress biology in maize by identifying regions with high mutation rates. GWAS and MAS can be effectively integrated with SB protocols to identify QTLs underlying biotic and abiotic stress tolerance, nutritional qualities, and high yield (Rai 2022). Moreover, Speed breeding using a combined CRISPR/Cas approach can accelerate the development of GABA-enriched tomato cultivars, heralding a new generation of functional foods in which regular consumption supports improved cognitive health (Sakthivel et al. 2025). Key advancements in this area include Chem-RGA (chemical-mediated rapid generation advancement), SpeedScan (high-throughput precision phenotyping under speed breeding), SpeedWild (protocols for harnessing wild genetic diversity for trait improvement), and SpeedAgri-tech (innovations in space and indoor farming). A schematic overview of the timeline integrating speed breeding with modern breeding tools, highlighting their impact on reducing generation time and enhancing crop improvement, is depicted in Fig. 2.

Multi-omics integration for precise crop improvement

The integration of multi-omics data with cutting-edge gene editing and modulation technologies marks a transformative era in plant breeding, shifting the focus from singular gene modifications to the precise manipulation of complex, polygenic traits (Fan et al. 2025). Such a synergistic methodology offers a holistic view of the complex biological networks that underpin critical characteristics, including yield, nutritional value, and responses to different strains (Sharma et al. 2025). Using the discoveries of multi-omics, scientists can identify key regulatory genes, map metabolic pathways, and de-escalate the interactions between genes and the environment, leading to desired phenotypes (Chachar et al. 2024). Sequencing technologies have also advanced and become more affordable, leading to a significant increase in multi-omics exploration of Annona species, with a focus on genomics and transcriptomics. The integration of complementary layers, such as proteomics, metabolomics, and phenomics, to the overall dissection of complex traits in Annona (Prasad et al. 2025). Based on transcriptomic and metabolomic profiling, genes and related products that correlate with enhanced nutrient uptake efficiency or stress

Table 2 CRISPR technology applications in crop improvement through gene editing

Editing tool	Crop	Target gene	Target trait	Target modification	Phenotype achieved	Reference
CRISPR/Cas9	Rice	*OsDST*	Drought & salt stress	Knockout	↑ Drought and salt tolerance	(Kumar et al. 2020)
		OsCS511	Cold stress	Knockout	↑ Cold tolerance	(Park et al. 2024)
		OsRbohB	Heat stress	Knockout	↑ Heat stress tolerance and grain yield	(Liu et al.2025b)
		OsDSG1	Salt stress	Knockout	↑Salt stress resistance	(Ly et al. 2024)
	Wheat	*TaSal1*	Drought stress	Knockout	↑ Drought tolerance	(Abdallah et al. 2025)
		TaMKP1	Fungal stress	Knockdown	↑ Resistance to rust and mildew↑ yield	(Liu et al. 2024)
		CLE	Yield trait	Knockout	↑ Grain yield	(Liu et al. 2021a)
		ZmPL1	Drought stress	Knockout	↑Drought tolerance	(Wang et al. 2025b)
	Tomato	*SlGT30*	Drought stress	Knockout	↑ Drought tolerance	(Lv et al. 2025)
		SlAGL6	Heat stress	Knockout	↑ Yield under heat stress	(Nagamine et al. 2023)
		SlABIG1	Salt stress	Knockout	↑ Salt tolerance	(Ding et al. 2022)
		SlGATA22	Cold stress	Knockout	↑ Cold resistances	(Wu et al. 2025)
		SlPelo, *SlMlo1*	Biotic stress	Knockout	↑Resistance to YLCV & powdery mildew	(Pramanik et al. 2021)
		XSP10, *SAMT*	Biotic stress	Knockout	↑ Tolerance to Fusarium wilt	(Debbarma et al. 2023)
CRISPR/Cpf1	Tomato	*SlHKT1; SlHKT2*	Salt stress	Targeted replacement	↑ Salinity tolerance	(Vu et al. 2020)
	Rice	*OsEPFL9*	Abiotic stress	Knockout	↑ Abiotic stress tolerance	(Bandyopadhyay et al. 2020)
		OsXLG	Yield trait	Knockout	↑ Yield	(Cantos and Assmann 2024)
CRISPR/Cpfb1	Rice	*EPFL9*	Drought stress	Downregulation	↑ Drought tolerance	(Moosa et al. 2022)
Cas13a	Rice	*RSMV*	Viral stress	RNA knockdown	↑ RSMV resistance	(Zhang et al. 2019a)
	Tomato	*ToBRFV*	Viral stress	RNA knockdown	↑ Resistance to ToBRFV	(Karimi et al. 2025)
	Potato	*PI*, *HC-Pro*, *P3*, *Cl1*, *Cl2*, *VPg*	Viral stress	RNA knockdown	↑Resistance to PVY	(Noureen et al. 2022)
Base editing	Rice (dCas12i3)	*OsACCase*	Herbicide stress	ABE	↑Resistance to sethoxydim	(Lv et al. 2024)
	Rice (nCas9)	*SWEET14*	Bacterial stress	ABE/CBE	↑Resistance to *Xanthomonas oryzae pv oryzae*	(Li et al. 2025)
	Wheat (nCas9)	*TaALS*	Herbicide stress	Point mutation	↑Resistance to sulfonylurea	(Zhang et al. 2019b)
	Maize (dCas9)	*ZmALS*	Herbicide stress	CBE	↑Resistance to sulfonylurea	(Li et al. 2020)
Prime editing	Rice, Tomato	*CWINs*	Heat stress	Promoter insertion	↑Heat tolerance, yield boost	(Lou et al. 2025)
	Rice	*Xa23*	Bacterial stress	Promoter knock-in	↑Resistance to *Xanthomonas oryzae pv oryzae*	(Gupta et al. 2023)
	Wheat	*TaWTK3*, *TaACC-T2*, etc.	Agronomic traits	V223A substitution	↑Agronomic improvement	(Ni et al. 2023)
	Tomato	*CYC-B*	Agronomic trait	Downstream Start codon substitution	↑Lycopene accumulation	(Gao et al. 2025)
CRISPRa	Tomato	*SlPR-1*	Viral stress	Transcriptional activation	↑Resistance to stem canker	(García-Murillo et al. 2023)

The arrows used in the table represent the direction of trait modification: an upward arrow (↑) indicates an increase or improvement (such as enhanced resistance, yield, or tolerance). *YLCV* Yellow leaf curl virus; *PVY* Potato virus, *RSMV* Rice stripe mosaic virus, *ToBRFV* Tomato brown rugose fruit virus

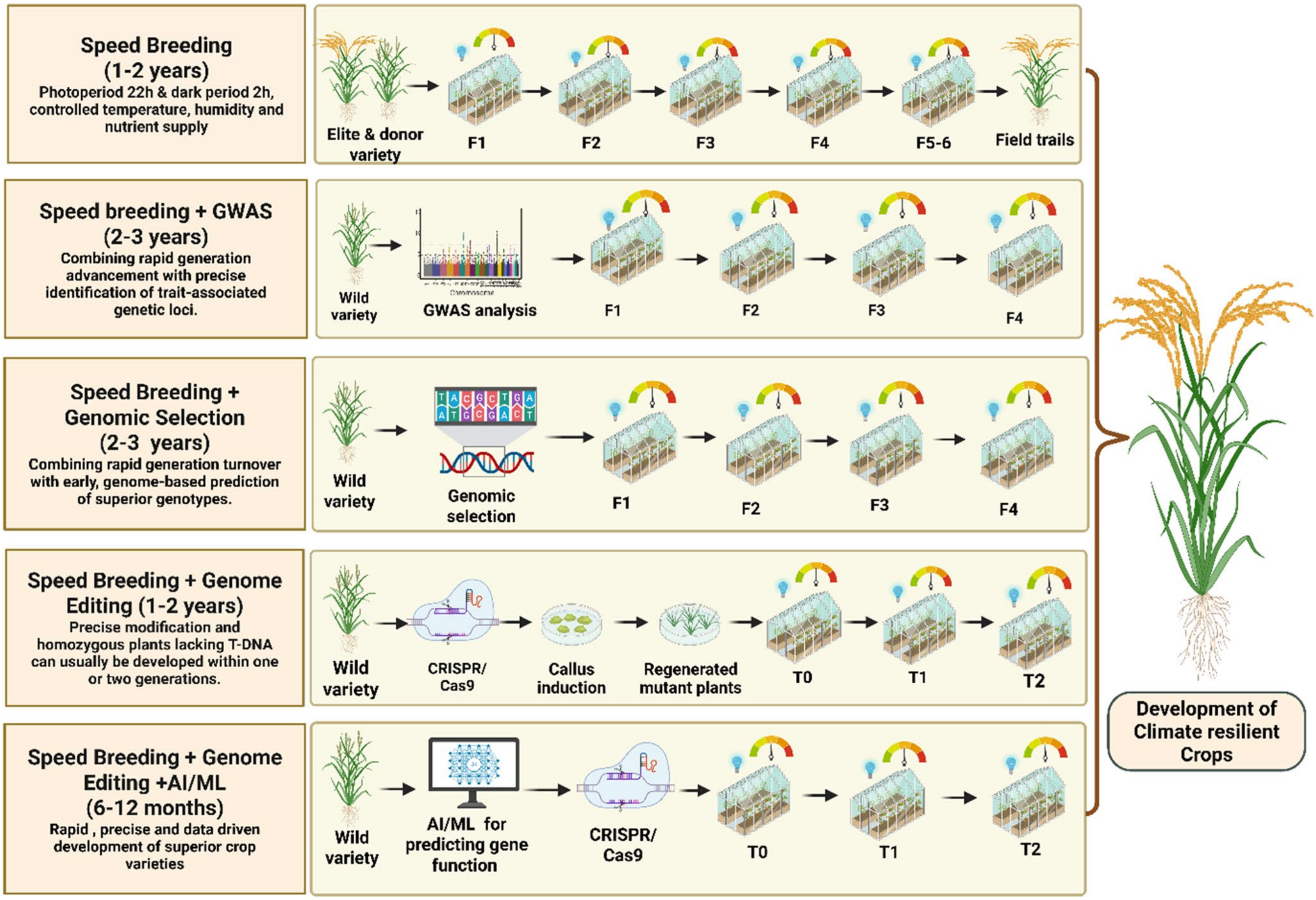

Fig. 2 Integrated speed breeding with modern breeding approaches for accelerated development of climate-resilient crops. This figure provides a comparative overview of various modern breeding approaches that integrate speed breeding with genomic tools, including GWAS, genomic selection, genome editing, and AI/ML-based analytics, to rapidly develop climate-resilient crop varieties. Each method accelerates generation turnover while enhancing selection accuracy or trait targeting. Depending on the integration level, elite crop varieties can be produced within 6 months to 3 years, a significant reduction from traditional breeding timelines. This figure was created using BioRender (https://www.biorender.com/) and some elements were adapted from BioRender templates

tolerance can be accurately identified and readily modified using complex tools, such as CRISPR/Cas systems or base editing. A synthesis of these methods has enormous potential to create high-end varieties of crops that are more precise and come to their fruition sooner, leading to the creation of crops with tailored nutritional profiles (e.g., higher vitamin or mineral content), higher resistance to more biotic and abiotic stress, and more efficient use of resources, which will eventually make agricultural technologies more sustainable (Fan 2024). A better understanding of the complex interactions among genes that confer drought tolerance, as revealed by multi-omics, can be used to target gene editing to enhance water use efficiency without affecting yield (You et al. 2019). The ability to tune gene expression through epigenetic editing or RNA-guided systems provides more detailed regulation of trait expression that can adaptively respond to changing environmental conditions. (Singh et al. 2021). Plants demonstrate a dynamic coordination of genes, proteins, and metabolites, particularly in response to abiotic stress. Although the instructions for adaptation are encoded in the genome, the actual physiological responses are predominantly reflected at the proteomic and metabolomic levels. In this context, proteomics and metabolomics play a crucial role in uncovering the molecular regulators and pathways involved in stress-induced adaptations (Sun et al. 2022). Integrating genetic markers with transcriptomic and metabolic data within multi-omics genomic selection frameworks provides extensive insights, leading to more accurate predictions of breeding values (Wörheide et al. 2021). An integrative analysis was conducted to examine the interactions among genetic variations, gene expression, protein levels, and metabolic responses to salt stress in Arabidopsis, and a set of new transcription factors regulating salt tolerance was identified (Satrio et al. 2024; Thingujam et al. 2025). The results of a multi-omics analysis of *Allium mongolicum* under drought stress demonstrated coordinated gene and pathway expression, suggesting the effectiveness of integrative omics in breeding climate-tolerant plants (Ma et al. 2024). These hypotheses of multi-omics derived will also be proved with the help of high-throughput functional genomics in addition to faster phenotyping to accelerate the breeding of plants to be more predictive and prescriptive and make it a much faster process to create the kind of climate-resilient and nutrient-dense crops necessary to support global food security (Abdullah-Zawawi et al. 2022).

Systems biology tools for stress response modelling

Systems biology methods are revolutionizing current knowledge of plant stress responses by offering holistic, multi-omics models that integrate data with computational models. This paradigm enables researchers to unravel the complex regulatory networks, feedback, and crosstalk among molecular layers, such as genomics, transcriptomics, proteomics, metabolomics, and phenomics, which determine a plant's adaptive responses to biotic and abiotic stresses (Mosa et al. 2017). These models help determine major hubs and bottlenecks, as well as alternative pathways controlled or silenced by stress, providing predictive information about plant behavior. Using transcriptomic and proteomic analyses as examples, the coordination of the expression of stress-responsive genes and proteins can be studied by considering drought or salinity events (Waseem and Aslam 2024). In addition, the repositioning of metabolism to nutrient deficiency or pathogen attack is also revealed by the metabolically flux analysis based on the measurement of metabolomics, integrated into models of metabolism, and which reflects changes in primary and secondary production of metabolites, which is a key component of the stress response (Gao and Zhao 2024). The latest developments in ML and AI enable the analysis of large multi-omics datasets to identify predictive biomarkers and predict plant responses to novel stressors, which is especially essential given the unpredictability of climate change (Morabito et al. 2025). Overall, these systems biology models, by providing a dynamic, integrated view of stress responses, are essential for developing targeted breeding strategies and climate-resilient crops with enhanced, durable tolerance to multiple environmental challenges.

Artificial intelligence-powered predictive modelling

AI, especially ML and deep learning, is introducing a new sort of revolution in the area of stress management and crop stress biology. The fundamental role of AI is to transform the breeding activity by giving breeders the power to monitor farms at all times, allowing them to shift their focus to more strategic tasks and freeing them from the time-consuming requirement of on-farm presence (Talaviya et al. 2020). It provides unprecedented data analysis, predictive modelling, and real-time intervention capabilities to deal with climate change, like drought, heat, and pests, through the processing of complex datasets as a result of high-throughput phenotyping, multi-omics technologies, and remote sensing (Eftekhari et al. 2024). To detect stress rapidly and with high accuracy, AI models, especially convolutional neural networks (CNNs), are used to analyze RGB, thermal, hyperspectral, and multispectral images. Protein-coding genes, cis-regulatory elements, studies of gene expression, prediction of subcellular localization and protein-protein interactions, and the comprehension of gene ontology, metabolic pathways, phenotypes, and genomic prediction are among the bioinformatics analyses where a multitude of ML tools and algorithms can be utilized (Mahood et al. 2020).

The AI-based analytical systems have also become the key aspect to connect multi-omics data to a single, understandable breeding pipeline which would allow one to understand better the interactions between the genomic, transcriptomic, proteomic, and metabolomic layers in the plant response to stress. These signatures from diverse omics can be combined to provide a system-scale view of the gene-protein-metabolite networks that dictate adaptation by AI, thereby enhancing the discovery of resilient genotypes. AI algorithms predict how plants respond and enhance management by seamlessly integrating genomic, transcriptomic, environmental, and phenomic data. This predictive ability helps select resilient plant varieties for breeding and guides farming practices, such as carefully applying low-dose stressors to boost plant health (Sharma et al. 2025). This integrative ability has been further developed recently. Graph-based deep learning models and CNNs are more frequently used to combine transcriptomic and metabolomic profiles and to reconstruct the regulatory networks underlying stress signaling pathways (Lim et al. 2025). Autoencoder-based models also contribute by compressing high-dimensional multi-omics data into biologically meaningful representations, improving the prediction of stress-resilient phenotypes (Liu et al. 2021b). AI tools pave the way for precision breeding strategies to develop climate-resilient crops. Table 3 summarizes the major AI and ML algorithms used in plant breeding, highlighting their data inputs, categories, and predictive applications, and provides a practical overview of their utility in multi-omics-driven breeding strategies.

Table 3 AI and ML algorithms in plant breeding: data inputs, categories, and predictive uses

AI/ML Algorithm	Category	Typical Input Data	Prediction/Output	Key References
Random Forest (RF)	Supervised Learning (Ensemble Method)	Genomic selection data, phenotypic traits	Predicts yield, stress tolerance, and genotype environment interactions	Wójcik-Gront et al. 2024
Support Vector Machine (SVM)	Supervised Learning (Classification/Regression)	Spectral data, morphological features	Classifies stress levels and plant health from imaging data	Sun et al. 2025
Deep Neural Networks (DNNs)	Deep Learning (Multi-layer Perceptron)	High-throughput phenotyping, omics data	Predicts yield, growth performance, and trait correlations	Saha et al. 2025
Convolutional Neural Networks (CNNs)	Deep Learning (Image Processing)	RGB/hyperspectral imaging data	Detects diseases, nutrient deficiencies, and morphological variations	Nikitha et al. 2024
Gradient Boosting Machines (XGBoost)	Supervised Learning (Ensemble Boosting)	Genomic + environmental data	Improves genomic estimated breeding values (GEBVs)	Li et al. 2018
K-means Clustering/PCA	Unsupervised Learning (Dimensionality Reduction/Clustering)	Multi-environment trial data	Groups genotypes by performance and adaptability	Bai et al. 2025
Recurrent Neural Networks (RNNs)	Deep Learning (Sequential/Temporal Modeling)	Time-series environmental and growth data	Forecasts yield trends, phenological stages, and stress responses	Ingole et al. 2024
Bayesian Neural Networks (BNN)	Probabilistic Deep Learning	Genomic, phenotypic, and environmental covariates	Provides uncertainty-aware trait predictions	Maldonado et al. 2020
Gaussian Process Regression (GPR)	Probabilistic/Kernel-based Learning	Genomic marker data	Models nonlinear genotype–phenotype relationships	Sharp et al. 2016
Ensemble Learning (Stacked/Hybrid ML)	Meta-learning (Model Integration)	Genomic + multi-omics datasets	Combines multiple models for enhanced prediction accuracy	Aqil et al. 2022
Autoencoders (AE)	Deep Learning (Unsupervised Feature Extraction)	High-dimensional omics data	Extracts latent features and reduces data dimensionality	Pardede et al. 2018

Additionally, AI aids in understanding the intricate genetic basis of stress tolerance by identifying key genes, complex regulatory networks, and molecular markers, thereby accelerating MAS and GE efforts (Zhang et al. 2024a). AI-driven robotics automates HTP, streamlining data collection and analysis for extensive germplasm screenings (Admas et al. 2025). Orphan crops, such as finger millet, remain unexplored despite offering nutritional benefits and climate resilience. The integration of advanced breeding technologies with AI-driven analyses, along with the leveraging of existing datasets, can accelerate genetic gains and unlock the potential of finger millet. (Mane et al. 2024). The integration of AI with precise genome editing thus represents a transformative approach, enabling faster, more predictable, and sustainable crop improvement for global food security (Jiang et al. 2025). While challenges persist in data standardization, model interpretability, and the need for robust and diverse training datasets, the continuous evolution of AI promises to significantly enhance our ability to breed and manage crops for greater resilience. Figure 3 shows the coordinated use of advanced platforms, including Multi-omics, NGS, CRISPR/Cas, Speed breeding, and AI, to develop climate-resilient crops.

Future prospects and conclusion

The compiled literature clearly demonstrates that modern crop breeding is moving toward integrated, data-driven pipelines that unify genomics, multi-omics, high-throughput phenotyping, genomic selection, and advanced gene-editing technologies for developing climate-resilient cultivars. Although substantial progress has been made in dissecting complex stress-response pathways and identifying elite

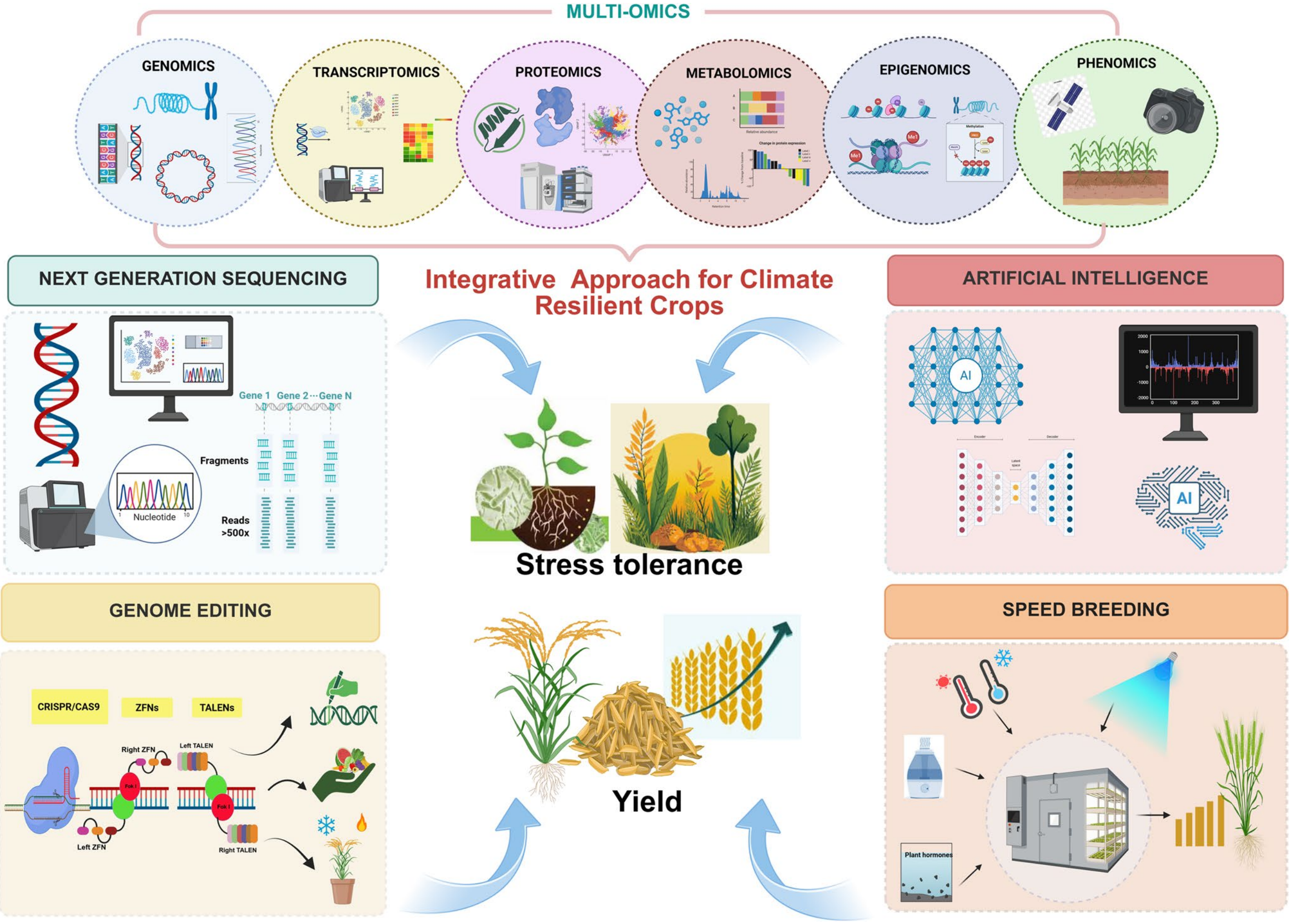

Fig. 3 Holistic crop improvement through integrated approaches: The figure presents an integrative framework for modern crop breeding and development. It highlights how the convergence of multi-omics technologies, next-generation sequencing, genome editing, artificial intelligence, and speed breeding can be leveraged to improve plant traits. Together, these advanced tools drive the development of crops that exhibit superior stress tolerance and increased yield. This figure was created using BioRender (https://www.biorender.com/) and some elements were adapted from BioRender templates

alleles for climate resilience, several limitations remain evident across the literature. Marker-based approaches, including MAS and GWAS, continue to face challenges in capturing the small-effect loci that underlie highly polygenic stress traits. GS, despite its strong predictive power, is constrained by high genotyping costs, limited diversity in the training population, and environment-specific prediction accuracy. Likewise, HTP and multi-omics technologies generate large volumes of heterogeneous data that require advanced AI-driven analytical frameworks for effective integration. Emerging tools such as epigenomics, pan-genomics, base and prime editing, and spatiotemporally regulated CRISPR platforms offer powerful avenues for precision breeding. Yet, concerns regarding off-target effects, regulatory acceptance, and the need for rigorous multi-environment validation remain major considerations for their broad deployment.

In conclusion, the future of climate-resilient crop breeding depends on integrating omics technologies, predictive AI models, precision editing, and faster selection cycles in a systems-level approach. As the existing literature shows, addressing current challenges in data integration, cost, and field validation will be crucial for turning molecular innovations into varieties ready for farmers. By following the prioritized research plan outlined above, modern breeding programs will be better equipped to develop sustainable, high-yielding, and resilient crops that support global food and nutrition security amid a rapidly changing climate.

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Data availability No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate Not applicable.

Consent for publication Not applicable.

Competing interests The authors declare no competing interests.

Clinical trial number Not applicable.

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