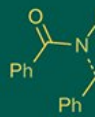


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Genomics-assisted breeding and multi-omics approaches for accelerating crop improvement: From genetic diversity to climate-resilient varieties

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Abstract

Global agriculture faces challenges due to climate change, extreme weather, resource degradation and population growth. Conventional crop breeding alone cannot achieve the genetic gains required to sustain global food security. Genomics-assisted breeding and multi-omics approaches have emerged as transformative paradigms for crop improvement. The integration of high-throughput genomics, transcriptomics, proteomics, metabolomics and phenomics enables comprehensive dissection of complex traits, facilitating characterization of landraces, wild germplasm and elite cultivars. Genomics-assisted breeding strategies, including marker-assisted selection, marker-assisted backcrossing, genomic selection and pan-genome allele mining, accelerate breeding cycles by increasing selection accuracy. Advanced omics layers provide mechanistic insights into stress perception, signal transduction, metabolic reprogramming and physiological adaptation under environmental stressors. CRISPR paired with Cas proteins further empowers precision gene editing, enabling targeted allele replacement and multiplex genome modification. This review synthesizes technological innovations in crop genomics and multi-omics integration, highlighting applications in major cereal, legume and oilseed crops. We discuss computational frameworks, systems biology platforms and machine learning models that decipher biological data into actionable breeding decisions. Finally, we address technological bottlenecks, regulatory landscapes and strategic roadmaps necessary to translate genomic discoveries into climate-resilient crop varieties.

Keywords: Genomics-assisted breeding, multi-omics, climate resilience, genomic selection, crispr-cas editing, germplasm diversity

Introduction

Agriculture must guarantee food security for a population exceeding nine billion by 2050 ^[41]. This task is complicated by climate change, manifesting in rising temperatures, altered precipitation, droughts and extreme weather ^[33]. Ecosystems encounter stresses, including salinization, freshwater depletion, land loss and pathogen outbreaks ^[4]. Staple crops such as rice, wheat, maize, soybean and sorghum suffer yield declines under stress, threatening food security.

Traditional plant breeding, relying on phenotypic selection, drove yield gains during the Green Revolution ^[16]. However, conventional selection presents limitations when targeting complex traits like drought tolerance, nitrogen use efficiency, heat resilience and yield stability. Polygenic traits are controlled by quantitative trait loci with minor individual effects and display genotype-by-environment interactions ^[5]. Consequently, traditional breeding requires extended timelines, taking eight to fifteen years to register a cultivar.

To bridge the gap between genetic gain requirements and field progress, agricultural science has transitioned toward genomics-driven breeding ^[52]. Next-generation sequencing and molecular genotyping platforms enable breeders to dissect genetic variation at nucleotide resolution ^[22]. Genomics-assisted breeding integrates molecular tools, computational genetics, statistical modelling and phenotyping to accelerate selection intensity and parental choices ^[6].

Biological systems operate as networks where genomic DNA serves as the blueprint, transcribed into RNA, translated into proteins and transformed into metabolic networks dictating phenotypes ^[25]. Single-omics analyses capture isolated biological layers. Multi-

omics approaches combining genomics, transcriptomics, proteomics, metabolomics and phenomics allow holistic characterization of stress response pathways [32]. Complemented by CRISPR-Cas genome editing, multi-omics frameworks enable candidate gene identification, facilitating targeted modification of germplasm. This review examines the shift from traditional breeding to genomics-assisted breeding and multi-omics integration for engineering climate-resilient crops. Furthermore, recent breakthroughs in AI and deep learning are transforming how multi-omics data is parsed in breeding pipelines. Deep neural networks decode high-dimensional epigenomic, transcriptomic and metabolic interactions under fluctuating climates. By bridging the genotype-to-phenotype gap, genomics-assisted breeding shifts from empirical phenotypic selection to multi-omics predictive design, enabling breeders to proactively engineer climate-resilient crop varieties tailored to future agro-ecological niches.

Harnessing genetic diversity and germplasm resources

Genetic diversity provides raw material for plant breeding and crop adaptation [35]. Domestication and selection for yield traits created genetic bottlenecks, narrowing the genetic base of modern cultivars [49]. Monocultures lack the genetic variation necessary to withstand climate extremes and biotic threats. Re-establishing resilience requires systematic exploration of landraces, wild relatives and genebank accessions [30].

High-throughput genotyping of genebank accessions

Repositories hold millions of accessions, yet much of this resource remains underutilized due to insufficient characterization [37]. Genomics initiatives have initiated resequencing of global germplasm collections. Genotyping-by-sequencing and whole-genome resequencing of rice, wheat, chickpea and barley accessions have revealed single nucleotide polymorphisms, insertions, deletions and structural variants [55]. Digitizing genebank collections enables construction of core collections capturing genetic diversity with minimal redundancy, facilitating evaluation under stress. Low-pass whole-genome sequencing combined with high-density SNP imputation has accelerated the digitization of massive germplasm collections at reduced cost [55]. This enables cataloging of rare alleles across global genebanks, unlocking previously inaccessible genetic variation for stress resilience [30].

genome-wide association studies and pan-genomics

Genome-wide association studies leverage historical recombination events across populations to identify genetic variants linked to target traits [24]. High-density SNP coverage combined with field phenotyping has pinpointed loci governing root architecture, stomatal conductance, osmotic adjustment and canopy temperature under stress [51]. Reliance on a single reference genome is inadequate for capturing structural variation. Pan-genomes incorporating core genes present in all individuals and dispensable genes unique to specific accessions have unveiled stress-tolerance genes absent in reference lines [50]. Pan-genomic analyses in soybean and rice have identified copy number variations associated with salt tolerance, disease resistance and aluminum toxicity adaptation. Graph-based pan-genomes have emerged as a superior paradigm, replacing single linear references with graph structures that represent complex

structural variations and presence-absence variations across accessions. Multi-locus GWAS algorithms deployed on graph genomes significantly enhance statistical power for complex agronomic traits [24].

Allele mining and pre-breeding strategies

Wild crop relatives and landraces harbor ancestral alleles offering superior stress tolerance, yet hybridization with elite cultivars introduces wild traits through linkage drag [60]. Genomics-assisted allele mining combined with pre-breeding overcomes this constraint. High-throughput sequencing identifies superior allele haplotypes at target loci, which are introgressed into elite backgrounds via marker-assisted backcrossing [46]. Advanced backcross QTL analysis and nested association mapping populations enable transfer and evaluation of novel wild alleles, broadening the genetic foundation of breeding programs. Haplotype-led pre-breeding systematically isolates target beneficial wild alleles into elite genetic backgrounds while suppressing linkage drag [64]. Marker-assisted backcrossing combined with genomic selection allows breeders to quickly purge non-target wild genomic fragments, accelerating elite germplasm enhancement.

Genomics-assisted breeding and marker-assisted selection

Genomics-assisted breeding replaces indirect phenotypic selection with direct selection based on DNA markers linked to target genes [10]. DNA markers, including simple sequence repeats and single nucleotide polymorphisms, are non-destructive, developmentally neutral and unaffected by environment, allowing rapid screening of breeding lines at seedling stage.

Marker-assisted selection and marker-assisted backcrossing

Marker-assisted selection (MAS) is effective for traits governed by major genes or large-effect quantitative trait loci [42]. Marker-assisted backcrossing (MABC) transfers major stress-tolerance loci into elite cultivars while minimizing linkage drag. In MABC, foreground selection tracks the target locus, while background selection uses genome-wide markers to recover the recurrent parent genome within two to three backcross generations [23]. A landmark MABC application is the introgression of the Submergence 1 (Sub1A) locus into Asian rice cultivars like Swarna and IR64, generating flood-tolerant varieties surviving two weeks of underwater submergence without yield loss [45]. High-throughput single nucleotide polymorphism (SNP) platforms, such as KASP and targeted sequencing (AmpSeq), have reduced marker cost and turnaround times to under 48 hours, enabling real-time selection within early segregating generations.

marker-assisted gene pyramiding

Climate change causes compound stresses in agricultural fields, demanding multi-stress resistance. Marker-assisted gene pyramiding permits simultaneous accumulation of multiple major genes conferring resistance to distinct stresses within a single genotype [40]. In rice, gene pyramiding has combined bacterial blight resistance genes (xa5, xa13, Xa21), blast resistance genes (Pi2, Piz-5) and submergence tolerance (Sub1A), resulting in durable multi-stress resilient varieties [13]. Similar strategies have been

implemented in wheat for rust resistance and in maize for drought tolerance. Haploblock-assisted pyramiding strategies utilize dense SNP marker panels to track specific chromosome segments harboring multiple co-located resilience alleles, preventing recombination breakdown during backcrossing and ensuring durable multi-gene defense integration.

Marker-assisted recurrent selection and fine mapping

While MAS and MABC excel for major genes, marker-assisted recurrent selection (MARS) targets complex traits controlled by multiple minor loci [27]. MARS evaluates intermediate populations from multi-parent crosses, using marker datasets to select and intermate promising individuals across cycles, accumulating favorable alleles. Fine mapping of mapped loci isolates causative genes and functional polymorphisms, enabling diagnostic markers that eliminate false positives during selection [44]. Fine-mapping utilizing large recombinant inbred line (RIL) populations and high-density maps narrows QTL intervals to sub-centimorgan levels, identifying causal nucleotides and resolving tightly linked deleterious alleles prior to commercial breeding deployment.

Genomic selection and high-throughput genotyping

Although marker-assisted selection works efficiently for major quantitative trait loci, it encounters limitations with polygenic traits like drought tolerance controlled by minor loci [20]. Genomic selection (GS), introduced by Meuwissen and colleagues, overcomes these limitations by utilizing high-density genome-wide markers to predict genetic values of unphenotyped lines [36].

Principles and workflows of genomic selection

Genomic selection relies on a two-step workflow involving a training population and a candidate evaluation population [26]. The training population consists of individuals genotyped with genome-wide markers and phenotyped across representative environments. Statistical models capture marker effects simultaneously, estimating genomic estimated breeding values (GEBVs) for each line. In the candidate population, offspring are genotyped only and GEBVs are calculated using trained model parameters, bypassing field phenotyping [12]. Optimizing training population composition using genomic relationship matrices (GRM) and core collection algorithms ensures maximum genetic connectedness between training and candidate sets, maximizing predictive accuracy while minimizing field phenotyping overhead across target environments [62].

Statistical models and machine learning in genomic selection

Accurate GEBV estimation requires parametric or machine learning models capable of handling high-dimensional data where marker predictors outnumber phenotyped observations [21]. Parametric models include Genomic Best Linear Unbiased Prediction (GBLUP), Ridge Regression BLUP (RR-BLUP) and Bayesian regression methods (BayesA, BayesB, Bayesian LASSO). Bayesian models accommodate marker effect heterogeneity, allowing large-effect and minor loci to contribute proportionally [14]. Machine learning architectures, such as Random Forests, Support Vector Machines and Convolutional Neural Networks, capture epistatic interactions and genotype-by-

environment effects [38]. Recent advancements in deep learning architectures, including Convolutional Neural Networks (CNNs) and Graph Neural Networks (GNNs), excel in capturing non-linear epistatic interactions and GxE dynamics [38]. Multi-Trait Multi-Environment (MTME) models incorporate longitudinal phenomics covariates to boost yield prediction under climate stress [62].

High-throughput genotyping and speed breeding integration

Routine adoption of genomic selection requires cost-effective genotyping platforms. SNP microarrays, target sequencing panels and reduced-representation tools such as DArTseq and genotyping-by-sequencing provide dense genome coverage at low cost [15]. Furthermore, coupling genomic selection with speed breeding protocols shortens generation turnaround times [57]. Speed breeding utilizes extended photoperiods and controlled temperatures to achieve up to six generations per year in wheat, barley, chickpea and canola. Combining genomic selection predictions with speed breeding allows unprecedented rates of annual genetic gain. Speed Breeding 2.0 protocols, utilizing optimized LED spectrums, extended photoperiods (up to 22 hours) and controlled thermal regimes, allow up to six generations per year in major crops [57]. Integrating Speed Breeding with genomic prediction enables rapid selection cycles within single calendar years.

Multi-omics integration for mechanistic insights

While genomics identifies structural genetic variations, it provides a static view of biological potential. Understanding how plants sense environmental changes, transduce signals and execute physiological adaptations requires functional omics profiling across biological organization layers [48]. Multi-omics integration provides holistic systems biology perspectives, unraveling regulatory cascades governing climate resilience.

Transcriptomics and functional gene discovery

Transcriptomics profiles genome-wide gene expression patterns across tissues, stages and stress treatments [56]. RNA sequencing (RNA-seq) and single-cell RNA sequencing (scRNA-seq) identify differentially expressed genes, novel isoforms, alternative splicing and long non-coding RNAs under stress [47]. Comparative transcriptomic analyses between tolerant and susceptible genotypes under stress reveal regulatory transcription factor families, including WRKY, MYB, NAC, bZIP and AP2/ERF. Single-cell transcriptomics provides cell-type-specific gene expression resolution, uncovering vascular, epidermal and root cell responses to environmental cues. Single-cell RNA sequencing (scRNA-seq) and spatial transcriptomics have recently uncovered cell-type-specific transcriptional responses during drought, salinity and heat stress, resolving cell-layer heterogeneity in root endodermis and stomatal guard cells that bulk RNA-seq fails to detect.

Proteomics and post-translational regulatory networks

Proteins represent functional executors of cellular activities, but mRNA transcript abundance does not always correlate directly with protein concentration due to post-transcriptional regulation, translation efficiency and protein degradation [31]. Proteomics platforms employing LC-MS/MS and isobaric tags quantify global changes in protein

abundance under stress ^[34]. Phosphoproteomics, ubiquitinomics and redox-proteomics capture post-translational modifications activating or deactivating enzymes, signal transducers and ion channels during stress perception. Reversible protein phosphorylation mediated by SnRK2 kinases regulates ABA signaling cascades, stomatal closure and osmotic adjustment under drought. Post-translational modifications (PTMs), including phosphorylation and ubiquitination, act as critical molecular switches in plant stress signaling ^[31]. Modern LC-MS/MS phosphoproteomics identifies key kinase-substrate networks governing rapid osmotic and oxidative stress responses in crop roots and leaves.

Metabolomics and physiological biomarker identification

Metabolomics delivers a functional readout of cellular physiological status, measuring low-molecular-weight compounds produced through enzymatic pathways ^[17]. GC-MS, LC-MS and NMR spectroscopy enable untargeted and targeted metabolic profiling under stress. Stress induces metabolic reprogramming, characterized by accumulation of osmoprotectants (proline, glycine betaine, trehalose), antioxidant secondary metabolites (flavonoids, anthocyanins) and signaling lipids ^[29]. Identifying metabolic biomarkers and rate-limiting metabolic enzymes provides functional targets for molecular breeding and metabolic engineering. Untargeted mass spectrometry combined with metabolic flux analysis (fluxomics) reveals metabolic re-routing under severe heat and water deficits. Protective osmoprotectants, specialized flavonoids and phytohormone conjugates serve as biochemical biomarkers for high-throughput early screening of climate resilience.

Phenomics and high-throughput field phenotyping

Phenotyping represents an operational bottleneck in translating genomic discoveries into field varieties ^[18]. High-throughput phenomics platforms equipped with multispectral, hyperspectral, thermal and LiDAR sensors mounted on UAVs or field gantries facilitate real-time trait measurement ^[3]. Remote sensing of vegetation indices, canopy temperature depression, chlorophyll fluorescence and 3D canopy architecture captures physiological stress responses across thousands of plots rapidly. Integrating phenomic data into genomic prediction models improves GEBV accuracy across environments. Unmanned Aerial Vehicle (UAV) platforms equipped with multispectral, hyperspectral and thermal sensors enable non-destructive longitudinal monitoring of canopy temperature, NDVI and photosynthetic efficiency across thousands of breeding plots simultaneously, converting qualitative traits into quantitative digital signatures.

Systems biology and multi-omics data fusion

Integrating heterogeneous datasets across genomics, transcriptomics, proteomics, metabolomics and phenomics requires bioinformatic workflows ^[39]. Systems biology models, co-expression network analysis (WGCNA), multi-block partial least squares and deep learning autoencoders synthesize multi-layer biological information. Data fusion identifies hub genes, regulatory nodes and master metabolic switches governing multi-stress resilience, converting big data into biological knowledge for targeted crop improvement. Multi-modal machine learning algorithms and

graph embedding techniques construct integrated multi-layer regulatory networks, pinpointing master regulator hubs and metabolic nodes. Systems-level data fusion provides causal physiological models predicting plant responses to multi-factorial stress regimes.

Genome editing and precision breeding strategies

Targeted genome editing technologies have revolutionized functional genomics and precision breeding, allowing researchers to introduce sequence modifications directly into elite genetic backgrounds without disturbing surrounding genomic regions ^[9].

CRISPR-Cas Systems for Crop Improvement

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) paired with Cas proteins system has emerged as the premier genome editing tool due to simplicity, versatility and efficiency ^[28]. Class 2 CRISPR systems, particularly Cas9 and Cas12a (Cpf1), use single-guide RNAs to generate double-strand breaks at target loci. Repair via non-homologous end joining induces insertion or deletion mutations, resulting in targeted gene knockouts ^[19]. Knocking out negative regulators of yield or susceptibility genes (S-genes) has proven effective. In rice, knocking out OsSWEET14 and OsSWEET11 susceptibility genes confers bacterial blight resistance, while knocking out OsERF922 enhances blast resistance. Novel Cas orthologs (such as Cas12a/Cpf1, Cas13 and compact Cas14 variants) expand targetable genomic regions by recognizing diverse protospacer adjacent motif (PAM) sequences ^[9]. Furthermore, high-fidelity Cas variants significantly reduce off-target cleavage events, ensuring high precision in commercial agronomic gene editing pipelines.

Base editing and prime editing

While standard CRISPR-Cas tools generate random insertions or deletions via double-strand breaks, base editing and prime editing permit precise nucleotide substitutions without requiring double-strand breaks or donor templates ^[1]. Cytosine base editors convert C:G to T:A, while adenine base editors convert A:T to G:C. Prime editing uses an engineered reverse transcriptase fused to a Cas9 nickase and a guide RNA to write genetic information directly into target sites, enabling substitutions, insertions and deletions ^[2]. These tools allow modification of enzymatic active sites, conferring herbicide tolerance or altering starch composition. Engineered dual-deaminase base editors allow simultaneous C-to-T and A-to-G conversions, creating codon variations for directed evolution of crop proteins. Meanwhile, engineered pegRNA architectures and dual-prime editing systems enable precise gene insertions and structural deletions with high efficiency in elite crop calli ^[63].

Multiplex genome editing and promoter engineering

Complex agronomic traits require simultaneous modification of multiple genes within pathway networks. Multiplex CRISPR vectors expressing arrays of guide RNAs facilitate editing of multiple target genes ^[59]. Furthermore, editing non-coding cis-regulatory promoter regions generates continuous quantitative variation in target gene expression levels, fine-tuning physiological responses ^[43]. De-novo domestication of wild relatives by multiplex CRISPR editing of domestication genes rapidly yields

climate-resilient crops retaining native stress resistance while possessing commercial architectural traits. Targeted editing of upstream open reading frames (uORFs) and cis-regulatory elements fine-tunes mRNA translation rates and spatio-temporal gene expression, achieving fine-grained phenotypic optimization. De-novo domestication of wild progenitors retains native abiotic stress tolerance while introducing key agronomic traits rapidly.

Case studies in developing climate-resilient crop varieties

Practical deployment of genomics-assisted breeding and multi-omics strategies has led to the release of several climate-resilient crop varieties worldwide [53].

Rice (*Oryza sativa* L.)

Rice breeding programs have deployed genomics tools to combat climate stresses [58]. Introgression of the Sub1A locus via MABC generated flood-tolerant cultivars widely adopted across South Asia. For drought-prone rainfed ecosystems, major quantitative trait loci governing yield under drought (qDTY1.1, qDTY2.1, qDTY3.1, qDTY12.1) have been pyramided into elite cultivars such as Vandana and IR64, maintaining stable grain yield under severe water deficits. Combining Sub1A, qDTY loci and salt tolerance loci (Saltol) has produced multi-stress tolerant rice lines suitable for coastal deltas. Integrated MAS and MABC strategies have successfully produced climate-smart elite rice lines (such as Swarna-Sub1 and Samba Mahsuri-Sub1) that endure up to two weeks of complete submergence without yield loss, securing food security across flood-prone Asian deltas.

Wheat (*Triticum aestivum* L.)

Global wheat production faces threats from rising temperatures and drought. International breeding networks led by CIMMYT have integrated genomic selection into routine breeding pipelines, accelerating genetic gain for heat and drought tolerance [11]. Genomic prediction models incorporating spectral reflectance phenotyping data have increased selection accuracy for yield stability under hot environments. Additionally, marker-assisted pyramiding of leaf rust (Lr), stripe rust (Yr) and stem rust (Sr) resistance genes safeguards wheat yields against pathogen shifts. High-throughput spectral reflectance phenotyping coupled with GS has enabled CIMMYT wheat lines to achieve continuous genetic gains under terminal heat stress. Pyramiding durable rust resistance genes (e.g., Sr2, Lr34, Yr18) ensures broad-spectrum protection against evolving fungal pathotypes.

Maize (*Zea mays* L.)

The DroughtTolerant Maize for Africa project utilized marker-assisted breeding and genomic selection to release drought-tolerant hybrid maize varieties across sub-Saharan Africa [8]. These hybrids exhibit a twenty to thirty percent yield advantage over conventional commercial hybrids under drought stress. Transcriptomic and metabolomic analyses identified key genes involved in kernel sink strength and delayed leaf senescence (stay-green trait), providing selection criteria for maintaining photosynthesis during grain filling under water scarcity. Integrating automated canopy temperature depression phenotyping into genomic selection models has accelerated the deployment of DTMA hybrids, achieving yield stability under severe

flowering-stage drought and nitrogen deficiency across varied sub-Saharan soil types.

Legumes and coarse cereals

Chickpea, pigeonpea, sorghum and pearl millet are vital for nutritional security in dryland agriculture. Whole-genome resequencing of chickpea accessions identified genomic regions governing root depth and drought tolerance, leading to marker-assisted development of high-yielding drought-tolerant varieties such as Pusa 10216 [54]. In sorghum and pearl millet, genomic selection and GWAS have accelerated breeding of stay-green, heat-tolerant and blast-resistant hybrids adapted to semi-arid tropics. Whole-genome resequencing of over 3,300 chickpea accessions identified functional loci governing seed weight, root depth and early vigor [64]. Genomic selection models trained on dryland trials are currently driving rapid breeding turnover in chickpea and pigeonpea across semi-arid regions.

Challenges, technological bottlenecks and future perspectives

Despite progress, several technological, computational and policy challenges hinder the full potential of genomics-assisted breeding and multi-omics approaches in crop improvement [7].

Phenotyping bottlenecks and data integration

While genotyping cost has dropped, field phenotyping remains a constraint. High-throughput phenomics platforms generate volumes of image and sensor data, requiring computational infrastructure and machine learning pipelines for trait extraction. Furthermore, integrating multi-layer omics datasets across spatial and temporal scales demands standardized data architectures, database interoperability and multi-view machine learning algorithms. Standardizing multi-omics metadata architectures according to FAIR data principles, alongside edge-computing AI systems for instant sensor processing, is essential to alleviate data processing bottlenecks in large-scale phenomics centers.

Genotype-by-environment interaction and epistasis

Genotype-by-environment (GxE) interaction complicates genomic prediction models, as marker effects estimated in one environment may not predict performance accurately in different climatic zones or seasons. Incorporating environmental covariates, micro-climate sensor data and crop growth physiological models into genomic prediction frameworks is essential to model GxE interactions accurately. Additionally, higher-order epistatic gene-gene interactions must be incorporated into predictive models to capture non-additive genetic variance underlying complex traits. Coupling biophysical crop growth models (e.g., APSIM, DSSAT) with machine learning GS algorithms allows explicit simulation of physiological reaction norms across future climate scenarios, significantly improving yield predictions under weather extremes.

Regulatory frameworks and public acceptance

Commercialization of genome-edited crop varieties is influenced by global regulatory landscapes. Countries like the United States, Brazil, Argentina, India and Japan have established science-based regulatory frameworks that exclude transgene-free gene-edited crops (SDN-1 and SDN-2 categories) from GMO oversight. Restrictive regulatory

policies in certain regions delay technology adoption. Establishing harmonized global regulations and transparent public engagement is crucial to ensure broad access to genome-edited climate-resilient crops. Harmonizing global trade regulations for genome-edited crops and establishing

open-access technology transfer mechanisms are imperative to ensure smallholder farmers in vulnerable developing regions gain equitable access to climate-resilient crop innovations.

Table 1: Comparative overview of multi-omics platforms, technologies, key outputs and applications in crop stress resilience

Omics Layer	Primary Technical Platforms	Key Biological Outputs	Target Applications in Crop Improvement
Genomics	WGRS, GBS, SNP microarrays, PacBio, Oxford Nanopore	SNPs, InDels, CNVs, structural variants, pan-genomes	QTL mapping, GWAS, MAS, genomic selection, pan-genome allele mining
Transcriptomics	RNA-seq, scRNA-seq, Iso-Seq, microarrays	Differentially expressed genes, isoforms, lncRNAs, single-cell maps	Identification of stress-responsive transcription factors and regulatory networks
Proteomics	LC-MS/MS, TMT, iTRAQ, DIA-MS, phosphoproteomics	Protein abundance, post-translational modifications, protein complexes	Elucidation of signal transduction cascades and functional enzyme activity
Metabolomics	GC-MS, LC-MS, NMR spectroscopy, FT-ICR-MS	Primary/secondary metabolites, metabolic pathways, osmoprotectants	Biomarker discovery, metabolic pathway engineering, physiological profiling
Phenomics	UAV imagery, hyperspectral, thermal camera, LiDAR, gantries	NDVI, canopy temperature depression, 3D architecture, growth rate	High-throughput field phenotyping, GxE modeling, real-time stress monitoring

Table 2: Successful applications of genomics-assisted breeding and genome editing for developing climate-resilient crop varieties

Crop Species	Target Climate Stress	Genomics / Omics Approach	Key Target Loci / Genes	Achieved Agronomic Phenotype
Rice (<i>Oryza sativa</i>)	Flash flooding / Submergence	Marker-Assisted Backcrossing (MABC)	Sub1A locus	Complete submergence tolerance for up to 14 days without yield loss
Rice (<i>Oryza sativa</i>)	Reproductive stage drought	Marker-Assisted Gene Pyramiding	qDTY1.1, qDTY2.1, qDTY3.1	Maintained high grain yield under severe field drought conditions
Wheat (<i>Triticum aestivum</i>)	Terminal heat & drought stress	Genomic Selection & Phenomics	Genome-wide marker predictions	15-20% higher genetic gain for yield stability under hot dryland conditions
Wheat (<i>Triticum aestivum</i>)	Stem and stripe rust disease	Marker-Assisted Selection	Sr2, Sr50, Yr15	Durable multi-pathogen resistance against emerging rust races
Maize (<i>Zea mays</i>)	Severe water deficit	Genomic Selection & MARS	Complex polygenic networks	20-30% higher grain yield under drought stress in sub-Saharan Africa
Chickpea (<i>Cicer arietinum</i>)	Terminal drought stress	WGRS & MABC	Root architecture QTL (qRoots)	Enhanced root depth and yield maintenance under dryland environments
Rice (<i>Oryza sativa</i>)	Bacterial blight resistance	CRISPR-Cas9 Gene Editing	OsSWEET14, OsSWEET11	Broad-spectrum bacterial blight resistance via promoter knockouts

Conclusion

Accelerating crop improvement to achieve climate resilience and global food security requires integration of genomics-assisted breeding, multi-omics platforms, high-throughput phenomics and genome editing technologies. Genomics-assisted breeding strategies, including marker-assisted selection, gene pyramiding and genomic selection, enhance selection efficiency and shorten breeding cycles. Multi-omics approaches provide deep mechanistic understanding of stress physiology, identifying functional candidate genes and regulatory networks. CRISPR-Cas precision genome editing enables rapid modification of elite cultivars. Overcoming phenotyping bottlenecks, refining predictive GxE computational models and harmonizing regulatory frameworks will be pivotal in translating multi-omics innovations into farmers fields, rendering agriculture sustainable amidst changing climates.

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Declarations

Conflict of interest

the authors declare that they have no conflict of interest.

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Author Contributions

RKS conceptualized the review, drafted the manuscript outline and wrote the main sections. AS synthesized multi-omics and genome editing sections. VS analyzed computational models, genomic selection frameworks and constructed tables. All authors reviewed and approved the final manuscript.

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