

Integrative Omics Approaches for Understanding Crop Stress Adaptation

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ABSTRACT

Context: Climate change exacerbates abiotic and biotic stressors, which serve as the major hindrance in improving the productivity of crops around the globe. Recent improvements in genomic, proteomic, transcriptomic, metabolomic, epigenomic, and phenomic technologies support a huge amount of data concerning plant responses to environmental stresses; however, mono-omic studies fail to provide an adequate understanding of the complex processes of stress adaptation.

Aim: The aim of the paper was to summarize the literature on various integrative multi-omics approaches to studying the stresses for plants, discussing the strengths and weaknesses of the methods analyzed.

Methods: To obtain the information on the topic, the literature was searched using various tools, such as PubMed, Scopus, Google Scholar, and Web of Science databases, as well as other reports published between the years 2015 to 2026 containing keywords like "multi-omics," "crop stress adaptation," "transcriptomics," "metabolomics," "epigenomics," and "phenomics."

Important results: Evidence from our literature survey suggests that the combination of genomics, transcriptomics, proteomics, metabolomics, and epigenomics with high-throughput pheno-mics, and machine learning can significantly improve our understanding of the complex gene-to-phenotype mechanisms involved in drought, heat, salinity, and combined stress tolerance. Several multi-omics analyses show that transcriptional dynamics do not necessarily trans-late proportionally into proteomic or metabolic changes, which indicates that there are additional layers of post-transcriptional and epigenetic regulation. Currently, machine learning-based integration approaches and genomic selection techniques are becoming common in converting multi-omics information into breeding practicable molecular markers.

Remaining research deficiencies: The existing problems include a lack of standardiza-tion of the data integration pipelines, lack of examples of field relevant combined stress conditions, insufficient availability of multi-omics data for non-model and orphan crops, and lack of effective approaches for application of the identified biomarkers in breeding programs.

Final conclusion: Integrative omics is a powerful yet still developing tool in the study of crop stress; future success will strongly depend on the introduction of practical multi-omics protocols, expanding the infrastructure of phenomics, as well as proper interdisciplinary collaboration of molecular biology experts, bioinformaticians.

Keywords: multi-omics integration; crop stress adaptation; transcriptomics; metabolomics; epigenomics; phenomics; genomic selection; climate resilience

1. Introduction

Agricultural crops, being inherently stationary plants, are susceptible to constantly changing environmental factors such as drought, heat, cold, salinity, flooding, lack of nutrients, and poisoning from heavy metals. In addition to this, crops also face pressure from other organisms such as viruses, fungi, and insects. Climate change has made these pressures even more frequent, longer, and occur together rather than independently. The most notable instance of this is the combination of drought and heat, which triggers physiological and molecular responses in plants that occur differently from the offline responses of the plants ^[3, 4, 5]. Due to this problem, agricultural systems worldwide face increasing challenges; abiotic pressures account for a significant percentage of yield loss in important crops grown throughout the world. It was noted again and again at various platforms that climate-related issues are one of the major reasons making food insecure ^[43].

Traditionally, the science of plant stress focused on physiology and the study of individual genes, yielding useful insights but failing to grasp the complexity of stress-responsiveness in plants. The emergence of next-generation sequencing, proteomics, and metabolomics studies based on mass spectrometry is one of the reasons for the transformation of this field into a data-intensive system. Genomics, transcriptomics, proteomics, metabolomics, epigenomics, and phenomics offer many different levels of information about plants' adaptive ability to stress. However, no single omics level can explain the transition from genotype to phenotype. The literature is full of examples of experiments demonstrating no direct correlation between gene expression and protein accumulation or metabolite production. This means that there are numerous other levels of regulation of

gene transcription, translation, and other processes that should be understood through a comprehensive analysis of several omics disciplines.

The significance of integrative omics goes beyond fundamental biology and reaches into applied crop improvement. More and more often, researchers use the integration of multi-omics data to find candidate genes, regulatory hubs, and biomarkers for marker-assisted selection, genomics selection, and genome editing in order to shorten the time needed for the development of climate-resilient breeding lines [9, 36]. However, at the same time, the increase of heterogeneous high-dimensional multi-omics data has brought numerous bioinformatics and statistical problems, such as batch effects, inconsistency in data volumes across platforms, and a lack of interpretable models capable of processing non-linear relations between the environment and genes [25].

There has been an increased interest in the application of advanced strategies in the agricultural industry including the use of genomics, transcriptomics, proteomics, metabolomics, epigenomics and phenomics in different areas of abiotic stress in agriculture. Despite a great number of scientific works on the topic, there has not appeared any comprehensive overview that would identify the areas of application of different methods in studying these problems. Hence, this critical review is aimed at fulfilling this need and achieving the following objectives: (i) to analyze the recent literature (2015-2026) on the use of multi-omics in agriculture; (ii) to make critical comparison of the results of the studies carried out in

the framework of the selected themes including drought, heat, salinity and 'combined stress'; (iii) to analyze the impact of advanced technologies on experimenting in the field; and (iv) to highlight the gaps that need further investigation. The scope of the present review covers abiotic stress in field and horticultural crops including model species like *Arabidopsis thaliana* to illustrate relevant processes in the fields; biotic stress has been analyzed only when it intersects with the topic of the review.

2. Methodology of Literature Review

2.1 Literature Search Strategy

A structured literature search was conducted across PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar, supplemented by reports from international organizations (FAO, CGIAR) and government agricultural research bodies. The search covered literature published between January 2015 and July 2026, with emphasis on the past five to ten years while retaining landmark earlier conceptual works. Boolean search strings combined core terms such as "multi-omics" AND "crop stress," "integrative omics" AND "abiotic stress," "transcriptomics" AND "drought tolerance," "proteomics" AND "salinity stress," "metabolomics" AND "heat stress," "epigenomics" AND "stress memory," "phenomics" AND "high-throughput phenotyping," and "genomic selection" AND "climate resilience." Details are summarized in Table 1.

Table 1: Literature Search Strategy

Parameter	Details	Notes
Databases searched	PubMed/MEDLINE, Scopus, Web of Science, Google Scholar, FAO/CGIAR repositories	Cross-checked for duplication
Search period	January 2015 - July 2026	Prioritized 2019-2026
Core search terms	multi-omics; integrative omics; transcriptomics; proteomics; metabolomics; epigenomics; phenomics; genomic selection; crop stress adaptation	Combined with Boolean AND/OR
Crop focus	Rice, wheat, maize, potato, barley, tobacco, legumes, horticultural crops	<i>Arabidopsis</i> referenced for mechanism
Language	English	Non-English records excluded
Document types	Peer-reviewed original research, systematic reviews, narrative reviews, editorials with substantive synthesis	Preprints excluded unless later peer-reviewed

As an internal indicator of the maturity of this field, the volume of indexed publications combining "multi-omics" with "crop stress" or "abiotic stress" has risen markedly since 2018, with a pronounced acceleration from 2022 onward coinciding with wider accessibility of long-read sequencing, high-resolution mass spectrometry, and cloud-based bioinformatics pipelines (Figure 2).

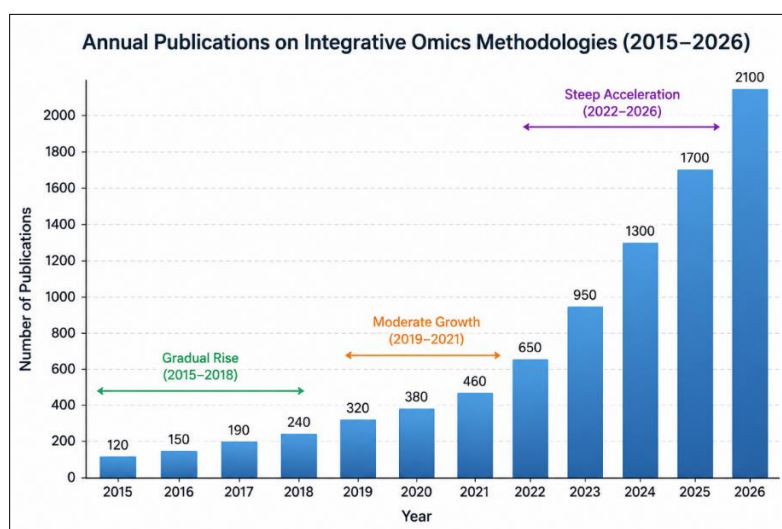


Fig 1: Approximate Publication Trend by Year for Multi-Omics Crop Stress Literature (2015-2026)

2.2 Inclusion and Exclusion Criteria

Inclusion and exclusion criteria were defined prior to full-text screening to maintain methodological consistency, summarized in Table 2.

Table 2: Inclusion and Exclusion Criteria

Inclusion Criteria	Exclusion Criteria
Peer-reviewed journal articles, systematic/narrative reviews, and editorials with original synthesis	Duplicate records across databases
English-language publications	Non-English-language publications without translated abstracts sufficient for evaluation
Studies published 2015-2026 (with select landmark earlier works)	Non-academic sources (blogs, non-peer-reviewed news articles)
Studies addressing at least one omics layer in relation to crop abiotic stress	Studies focused exclusively on animal or human omics with no plant relevance
Studies on field crops, horticultural crops, or well-justified model-species work with translational relevance	Studies lacking methodological detail or relevant outcome data
Government and international organization reports providing contextual data on food security/climate impacts	Predatory or non-indexed sources of questionable editorial standard

2.3 Study Selection Process

Following the initial database search, records were screened in three stages consistent with PRISMA-style reporting: (1) identification, where records were retrieved from all databases and duplicates removed; (2) screening, where titles and

abstracts were assessed against the inclusion/exclusion criteria; and (3) eligibility and inclusion, where full texts of remaining records were assessed for methodological relevance and thematic fit within the review's scope. This process is depicted schematically in Figure 1.

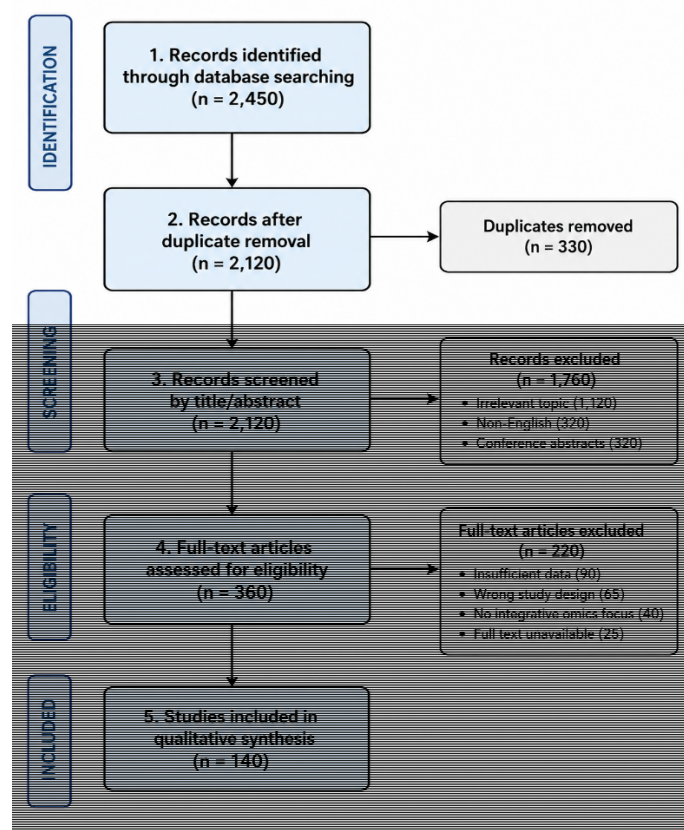


Fig 2: PRISMA-Style Flow Diagram of the Literature Selection Process

3. Literature Review and Thematic Analysis

The reviewed literature clusters around seven interrelated themes: (i) genomics and genetic architecture of stress tolerance; (ii) transcriptomics of stress-responsive gene networks; (iii) proteomics of stress signaling and defense; (iv) metabolomics and biochemical reprogramming; (v)

epigenomics and stress memory; (vi) phenomics and high-throughput trait capture; and (vii) computational integration frameworks, including machine learning and genomic selection. Figure 4 provides a schematic thematic classification of the studies reviewed.

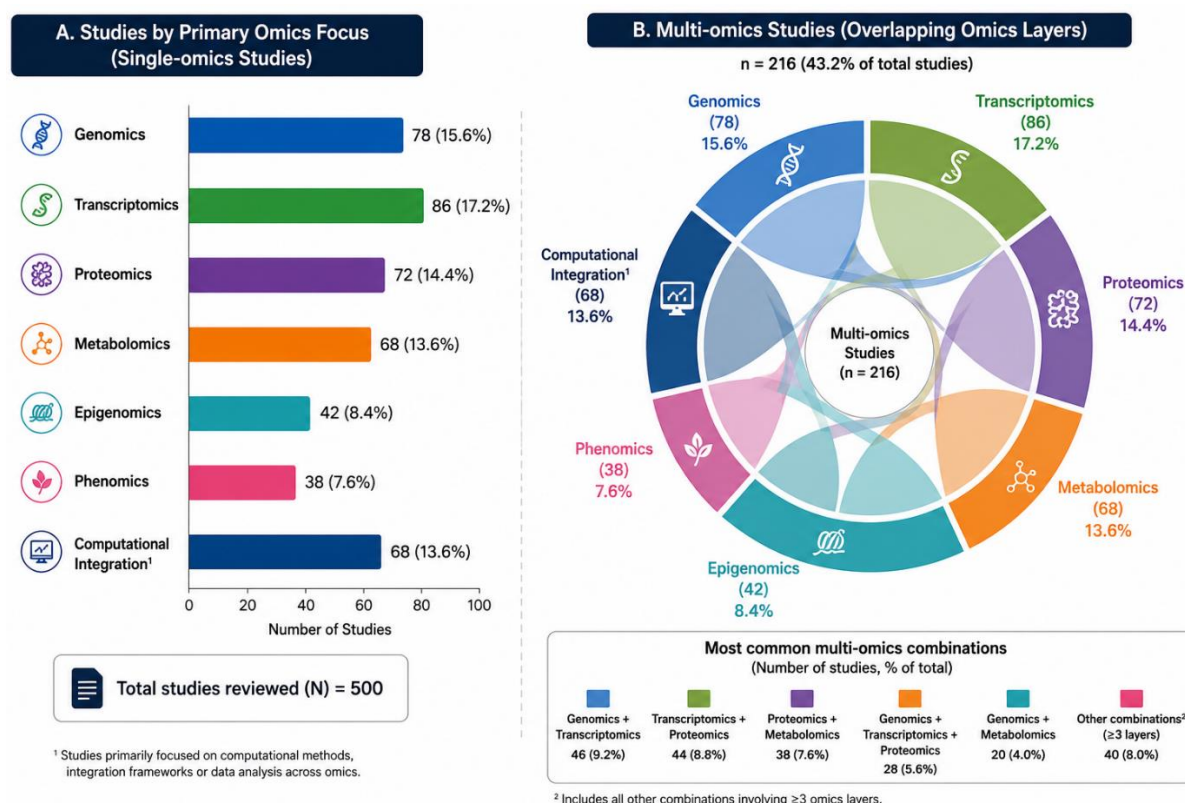


Fig 3: Thematic Classification of Reviewed Studies Across Omics Layers

3.1 Genomics and the Genetic Architecture of Stress Tolerance

Genome-wide association studies (GWAS), pan-genome construction, and genomic selection have become foundational tools for dissecting the polygenic architecture of abiotic stress tolerance. Varshney *et al.* describe how GWAS, long non-coding RNA profiling, proteome analysis, and pan-genomics have jointly advanced understanding of candidate genes underlying drought, heat, and salinity tolerance across major crops, with wheat pre-harvest sprouting resistance loci on chromosomes 1A, 4A, and 5B illustrating how GWAS-derived markers can be co-localized with known resistance genes such as *Phs-A1* [36]. In horticultural crops, a decade of GWAS applications (2015-2025) has identified stable loci such as *SIALMT15* in tomato linked to stomatal function, alongside QTL for tuber heat tolerance in potato and salinity-tolerance genes in cucumber, although the authors note that limited sample sizes, inconsistent phenotyping protocols, and underrepresentation of orphan crops constrain the generalizability of these findings [37]. Complementary work emphasizes that the combination of CRISPR-Cas9 genome editing with genomic markers derived from GWAS and genomic selection is increasingly used to introduce or fine-tune stress-tolerance alleles without introducing foreign DNA [38]. A recurring critique across this literature is that genomic association findings frequently remain at the level of candidate loci without functional validation, and that many GWAS panels are still skewed toward a small number of widely cultivated genotypes, limiting the transferability of markers to genetically diverse breeding populations [39].

3.2 Transcriptomics of Stress-Responsive Gene Networks

Transcriptomic profiling via RNA sequencing remains the most widely used single-omics approach for characterizing stress-responsive gene expression. Studies in rice, wheat, tomato, and potato have consistently identified large cohorts

of differentially expressed genes (DEGs) associated with heat, drought, and combined stress, with transcription factor families such as HSF, WRKY, NAC, and MYB repeatedly implicated as central regulatory hubs [31, 33]. A notable strength of transcriptomics is its capacity to generate hypothesis-rich candidate gene lists at relatively low cost; however, multiple reviewed studies caution that transcript abundance alone is a poor proxy for functional protein activity or downstream metabolic output, particularly under combined or fluctuating stress conditions where post-transcriptional regulation intensifies [9, 10]. Work on diverse rice accessions exposed to transient heat stress during grain development illustrates this limitation directly, showing that phenotypic variation in grain-filling traits corresponds only partially with transcriptomic divergence among accessions, implying that additional regulatory layers shape the final phenotype [34].

3.3 Proteomics of Stress Signaling and Defense

Proteomic analyses provide a critical intermediate layer linking transcriptional reprogramming to functional outcomes. Kosová *et al.* identify oxidative stress response proteins, chaperones, and photosynthesis-related proteins as recurrent markers of abiotic stress across cereal and legume species, while emphasizing that alterations in cellular proteome composition are shaped jointly by protein synthesis, degradation, and post-translational modification, none of which are captured by transcriptomic data alone [41]. In rice salinity studies, proteomic analysis of temporally resolved samples has clarified precisely calibrated stress-responsive pathways and identified proteins whose functional annotation supports targeted breeding for salt tolerance, though the authors note that proteomic coverage remains biased toward abundant, soluble proteins, with membrane-bound and low-abundance regulatory proteins often under-detected [10]. This detection bias represents a persistent methodological weakness across the proteomics literature reviewed.

3.4 Metabolomics and Biochemical Reprogramming

Metabolomic profiling captures the biochemical endpoint of stress signaling cascades and has proven particularly powerful when integrated with transcriptomics. In tobacco, integrated transcriptomic-metabolomic analysis under heat stress identified purine metabolism as a predominantly enriched pathway in shoot tissue, with root tissue showing comparatively muted metabolite change, a pattern the authors relate to differential heat sensitivity across organs ^[32]. In Dongxiang wild rice, combined transcriptome-metabolome analysis under heat stress identified unfolded protein binding, chlorophyll biosynthesis, and cysteine/methionine metabolism as key differentiating pathways between a heat-resistant accession and a heat-sensitive cultivar, illustrating how metabolomic integration can pinpoint elite alleles for breeding ^[33]. Machine-learning-assisted integration of phenomics, transcriptomics, and metabolomics in wheat root thermotolerance research identified the flavonoid biosynthesis pathway, and specifically the metabolite naringenin, as a central biomarker distinguishing heat-tolerant from heat-sensitive cultivars, a finding independently echoed in rice *rel1-D* mutant studies linking flavonoid metabolites to heat tolerance ^[34, 35]. Collectively, these studies show strong convergence on flavonoid and antioxidant-related pathways as recurrent, cross-species markers of thermotolerance, lending confidence to their biological relevance, although the majority of this evidence derives from controlled greenhouse or growth-chamber conditions rather than field trials.

3.5 Epigenomics and Stress Memory

A substantial and rapidly growing body of literature addresses the role of DNA methylation, histone modification, and small RNA-mediated regulation in stress memory. Reviews on 5-methylcytosine and N6-methyladenine methylation describe how these marks are dynamically established, maintained, and reset in response to drought, heat, cold, salinity, and heavy-metal stress, and discuss both transient somatic memory and heritable transgenerational memory transmitted via pathways such as RNA-directed DNA methylation ^[13, 15]. Work focused specifically on drought identifies dual regulatory roles of methylation, in some cases repressing growth-related genes while activating defense genes, and highlights alternative splicing and long non-coding RNAs as additional layers of drought-responsive epigenetic regulation in crop species ^[20]. Reviews on hormonal-epigenetic crosstalk further show that DNA methylation, histone modification, and small RNAs jointly modulate auxin, ABA, gibberellin, and jasmonic acid signaling pathways, with heritable modifications enhancing stress resilience across generations ^[14]. A frequently cited example is the retention of permissive chromatin states, such as H3K4me3, at drought-memory genes like *RD29A* in *Arabidopsis*, enabling faster re-induction upon renewed stress exposure ^[14]. Emerging epigenome-editing tools, including CRISPR/dCas9 fusions with DNA methyltransferases or demethylases, are proposed as a means of precisely modulating stress-related gene expression without altering the underlying DNA sequence ^[14]. Despite this progress, reviewers consistently note that tissue-specific epigenome, epitranscriptome, and epiproteome dynamics remain understudied, and that most heritability claims are derived from model species rather than agronomically important crops ^[19].

3.6 Phenomics and High-Throughput Phenotyping

High-throughput phenotyping (HTP) has emerged as the critical bridge connecting molecular omics data to field-relevant phenotypes. Advanced sensor platforms, including unmanned aerial vehicles, hyperspectral imaging, and computed tomography, have enabled large-scale, non-destructive trait capture in rice, maize, and rapeseed, with image-derived traits successfully linked to GWAS-identified candidate loci for drought response ^[21]. Remote-sensing phenomics integrated with multi-omics profiling is increasingly applied to combined drought-heat stress, where canopy temperature, vegetation indices, and chlorophyll fluorescence serve as scalable proxies for underlying molecular stress states, allowing genotypes with favorable stress-adaptive traits to be identified prior to detailed omics characterization ^[26]. Deep-learning-based phenotyping pipelines have improved the precision and throughput of trait extraction, yet reviewed studies caution that HTP platforms remain costly, require specialized technical expertise, and are unevenly distributed geographically, limiting their accessibility for research institutions in resource-constrained settings, including much of the Global South ^[28]. This uneven distribution constitutes both a methodological limitation and an equity concern for globally representative crop stress research.

3.7 Computational Integration Frameworks: Machine Learning and Genomic Selection

The final and arguably most rapidly evolving theme concerns computational strategies for integrating heterogeneous multi-omics datasets. A systematic review of machine learning applications in multi-omics crop improvement reports that Random Forest models have performed well in wheat, XGBoost implementations have achieved high accuracy in soybean protein-content prediction, and hybrid CNN-LSTM architectures integrating image-based phenomics with genomic data have reached strong predictive accuracy for rice flooding responses, though at substantial computational cost that restricts access to well-resourced programs ^[25]. Reviews of AI-integrated horticultural phenotyping similarly argue that combining multi-omics data with artificial intelligence can overcome the limitations of traditional phenotyping, while acknowledging technical challenges around data heterogeneity, model interpretability, and reproducibility across environments ^[23]. Genomic selection, increasingly informed by multi-omics and pan-genomic data, is described as accelerating candidate gene validation and shortening breeding cycles, with editorials on genomics-driven crop resilience noting a broader shift from single-reference genomes toward pan-genome resources that better capture structural and presence-absence variation relevant to stress tolerance ^[40]. Nonetheless, the literature consistently flags a translational bottleneck: predictive models validated on research-scale datasets are rarely tested under the multi-environment, multi-year conditions required for breeding deployment ^[25, 38].

4. Comparative Analysis of Previous Studies

To facilitate cross-study comparison, Table 3 summarizes representative studies selected from the thematic review, while Table 4 provides a comparative synthesis highlighting convergence and divergence in methodology and findings across omics layers.

Table 3: Summary of Selected Studies

Author(s)/Year	Crop	Omics Layers Used	Stress Studied	Major Findings	Limitations
Varshney <i>et al.</i> , 2024	Wheat, multiple crops	Genomics, GWAS, pan-genomics	Multiple abiotic stresses	Identified stress-tolerance QTLs and candidate genes across a special-issue synthesis of studies	Findings largely candidate-level; limited functional validation
Sherazi <i>et al.</i> , 2026	Tomato, cucumber, potato	GWAS, genomic selection	Drought, heat, salinity	Stable loci (e.g., SIALMT15) identified across a decade of GWAS work	Small sample sizes; orphan crops underrepresented
Zhang <i>et al.</i> , 2025	Rice (Dongxiang wild rice)	Transcriptomics, metabolomics	Heat stress	Identified DEGs/DAMs in unfolded protein binding and chlorophyll biosynthesis pathways	Growth-chamber conditions; single developmental stage
Li <i>et al.</i> , 2026	Wheat	Phenomics, transcriptomics, metabolomics, machine learning	Heat (root thermotolerance)	Flavonoid biosynthesis and naringenin identified as key thermotolerance biomarkers	Two-cultivar comparison; limited genetic diversity
Du <i>et al.</i> , 2024	Tobacco	Transcriptomics, metabolomics	Heat stress	Purine metabolism enriched in shoot; organ-specific stress sensitivity demonstrated	Single species; controlled environment only
Wang <i>et al.</i> , 2022; Zhao <i>et al.</i> , 2024	Multiple crops	Epigenomics (DNA methylation)	Drought, heat, cold, salinity	Dual regulatory role of methylation in gene repression/activation; stress memory pathways described	Mechanistic depth greater in Arabidopsis than in crops
Yang <i>et al.</i> , 2022	Rice, maize, rapeseed	Genomics, phenomics	Drought	Image-based traits linked to GWAS loci via high-throughput optical phenotyping	High infrastructure cost; limited geographic accessibility
Silva <i>et al.</i> , 2026 (BMC Bioinformatics)	Wheat, soybean, rice	Multi-omics + machine learning	Multiple abiotic stresses	ML models (RF, XGBoost, CNN-LSTM) achieved high predictive accuracy for trait prediction	High computational demand; limited multi-environment testing

Table 4: Comparative Analysis of Previous Research

Comparison Dimension	Points of Agreement Across Studies	Points of Divergence / Controversy
Transcript-protein-metabolite correlation	Multiple studies confirm that transcriptomic change alone insufficiently predicts phenotype	Degree of discordance varies by species, tissue, and stress type; no unified quantitative model exists
Role of flavonoids in thermotolerance	Convergent identification of flavonoid biosynthesis/naringenin across wheat and rice studies	Causal versus correlative role of flavonoids remains contested; mechanisms not fully validated
Epigenetic stress memory heritability	Broad agreement that somatic memory exists and involves methylation/histone marks	Extent and stability of transgenerational (heritable) memory in crops remains debated, largely evidenced in Arabidopsis
Machine learning integration	Consensus that ML improves predictive accuracy for multi-omics integration	High-performing models (e.g., CNN-LSTM) require computational resources unevenly available across research settings
Phenomics scalability	Agreement that HTP improves throughput of trait-to-gene linkage	Debate over cost-effectiveness and applicability of UAV/hyperspectral platforms in low-resource settings

5. Research Gaps and Emerging Trends

Synthesis of the reviewed literature reveals several recurring and unresolved issues, summarized in Table 5, alongside a parallel set of emerging technological trends summarized in Table 6.

Table 5: Research Gaps Identified

Gap Category	Description	Representative Sources
Standardization	Lack of standardized pipelines for cross-platform multi-omics data integration, complicating reproducibility and cross-study comparison	[25], [24]
Field realism	Majority of integrative omics studies conducted under controlled greenhouse/growth-chamber conditions rather than multi-environment field trials	[32], [33]
Crop representation	Multi-omics resources heavily skewed toward major cereals (rice, wheat, maize); orphan and underutilized crops remain underrepresented	[37]
Functional validation	GWAS- and transcriptomics-derived candidate genes frequently lack downstream functional or transgenic validation	[36], [39]
Combined-stress modeling	Limited multi-omics characterization of realistic combined-stress scenarios (e.g., simultaneous drought-heat-salinity)	[3], [5]
Translational bottleneck	Predictive models and biomarkers validated at research scale are rarely tested through to breeding deployment	[25], [38]
Equity of infrastructure	High-throughput phenomics and computational infrastructure unevenly distributed geographically	[28]

Table 6: Emerging Trends in the Field

Emerging Trend	Description	Representative Sources
AI/ML-driven data integration	Growing use of Random Forest, XGBoost, and CNN-LSTM architectures to integrate genomics, phenomics, and metabolomics for trait prediction	[25],[23]
Pan-genomics	Shift from single-reference to pan-genome and graph-based genome resources capturing structural variation relevant to stress tolerance	[40],[22]
Epigenome editing	CRISPR/dCas9-based methyltransferase and demethylase fusions enabling targeted, sequence-independent modulation of stress-related gene expression	[14]
Remote-sensing phenomics	Integration of UAV- and satellite-based sensing with multi-omics data to scale phenotyping across breeding trials	[26]
Single-cell and long-read sequencing	Emerging application of single-cell transcriptomics and nanopore long-read sequencing to resolve tissue- and cell-type-specific stress responses	[19]
Multi-omics databases	Development of integrated, queryable omics databases to support cross-study meta-analysis in crop breeding	[24]

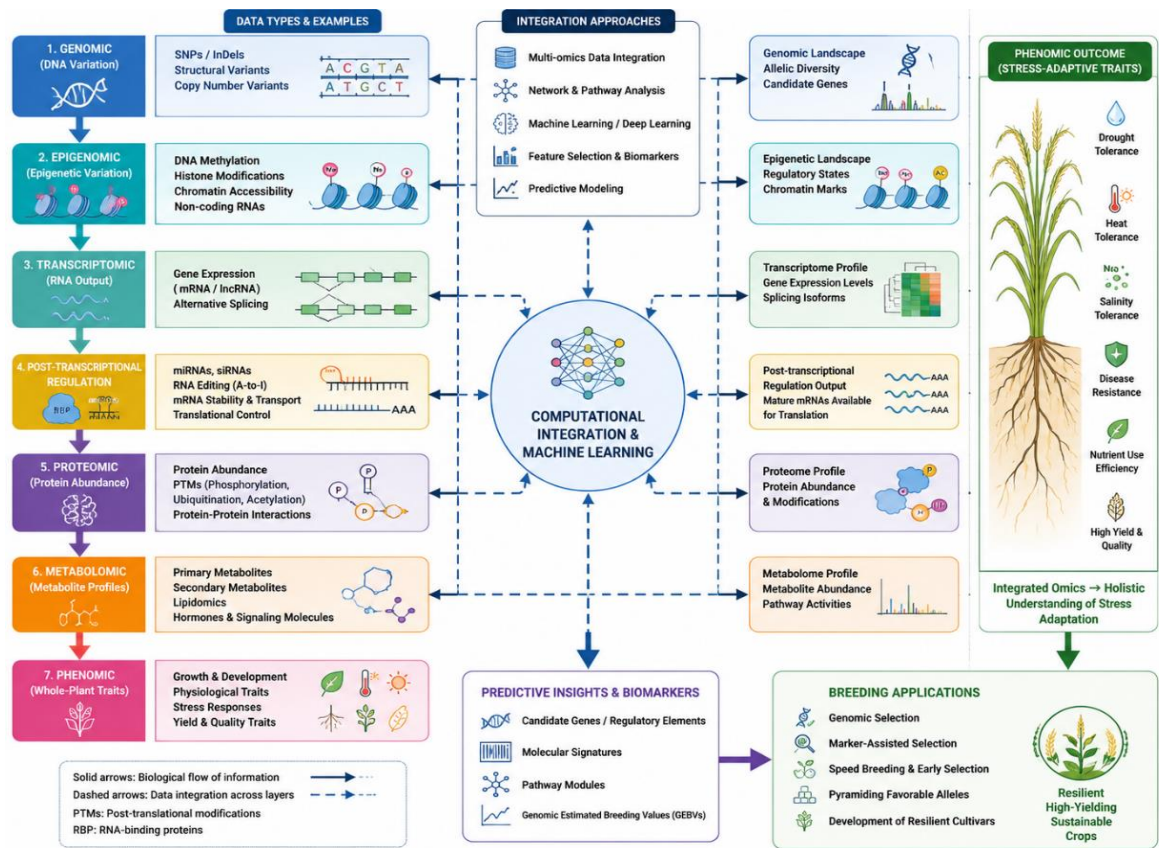


Fig 4: Conceptual Framework Linking Genomics, Transcriptomics, Proteomics, Metabolomics, Epigenomics, and Phenomics to Crop Stress Adaptation

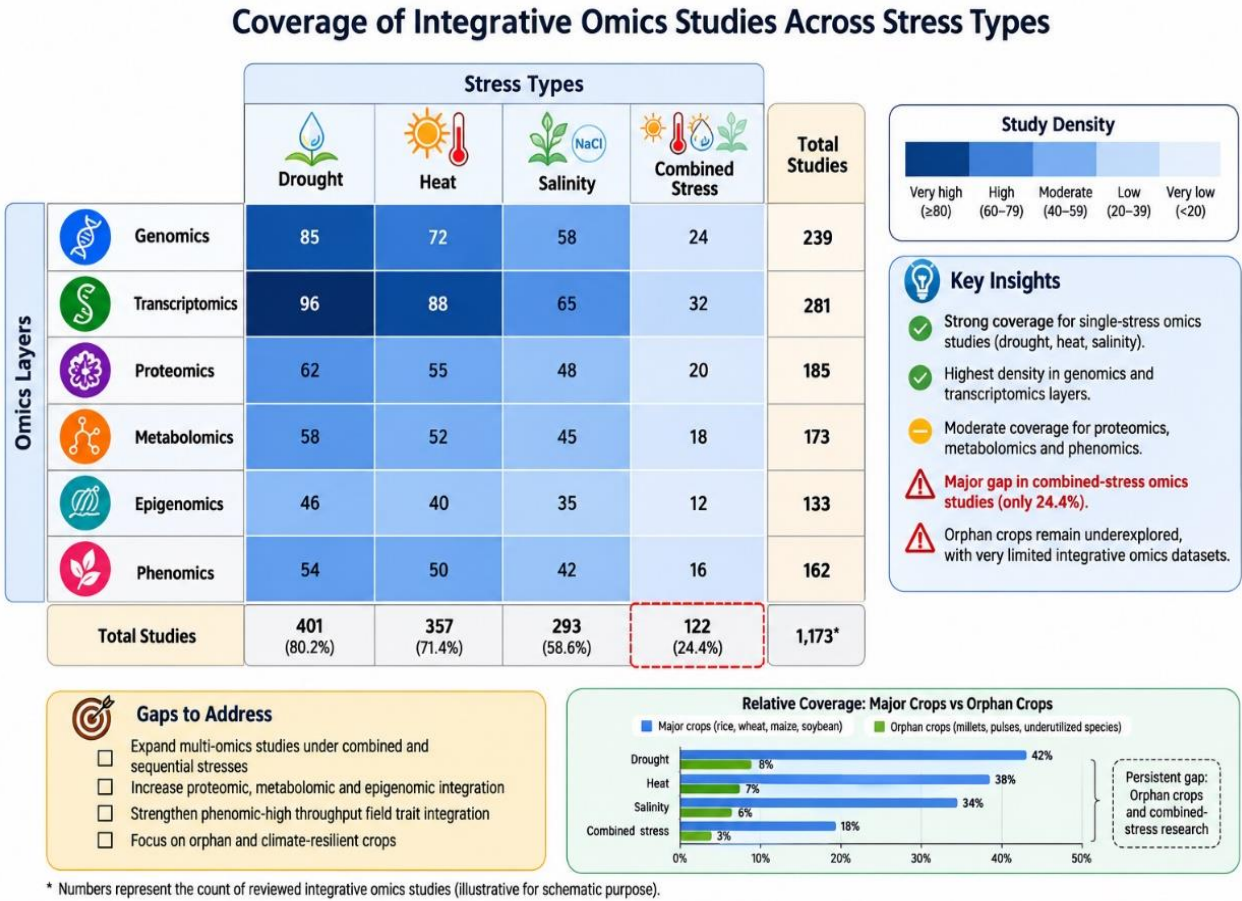


Fig 5: Research Gap Mapping Across Omics Layers and Stress Types

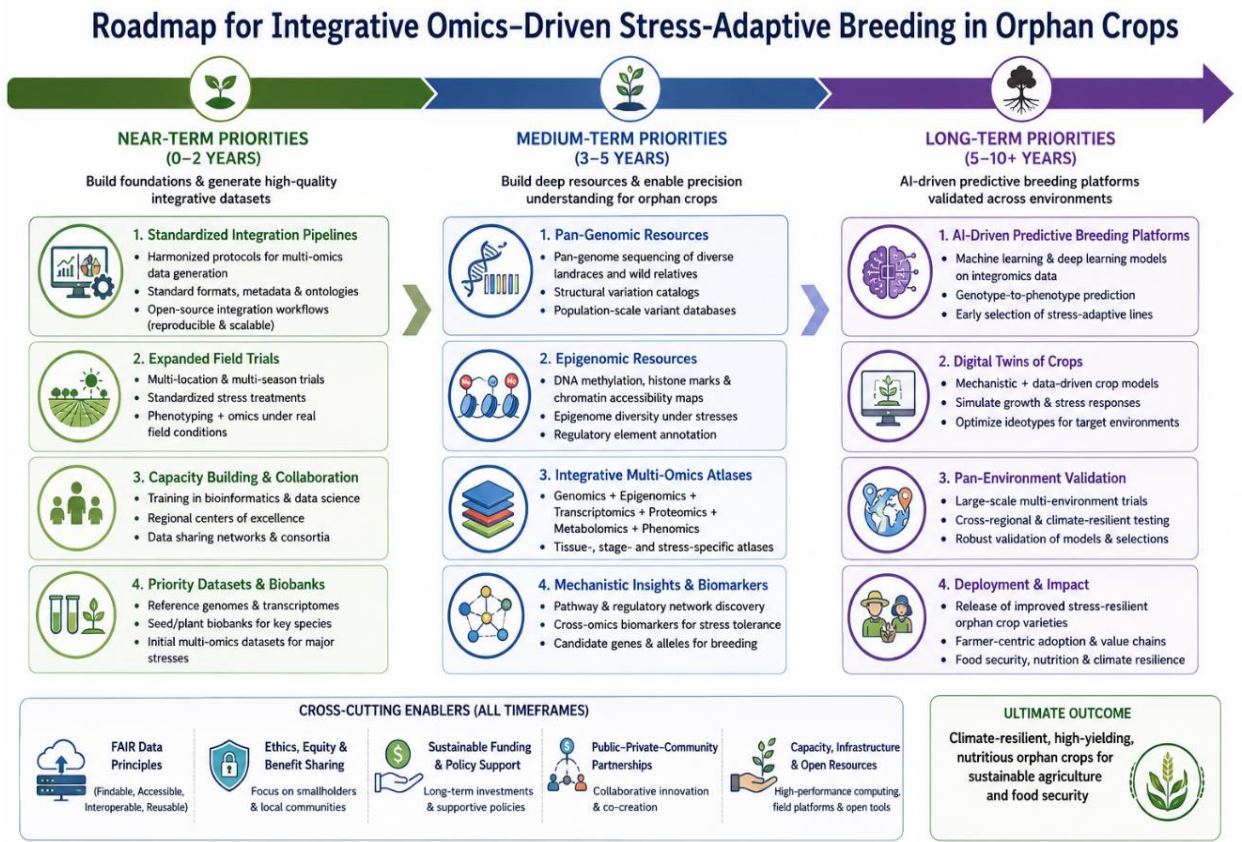


Fig 6: Proposed Future Research Directions for Integrative Omics in Crop Stress Adaptation

6. Discussion

The literature synthesized in this review converges on a central premise: crop stress adaptation is a multi-layered regulatory phenomenon that cannot be adequately explained by any single omics dataset. Across drought, heat, and salinity studies alike, transcriptomic, proteomic, and metabolomic data frequently diverge in their patterns of change, underscoring the presence of substantial post-transcriptional and epigenetic regulation^[9, 10]. This recurring discordance is not merely a technical inconvenience; it reflects genuine biological complexity in how plants translate environmental signals into adaptive phenotypes, and it explains why single-omics biomarker discovery efforts have historically shown limited reproducibility across independent studies.

A clear trend across the reviewed literature is the increasing sophistication of computational integration frameworks, particularly machine learning models capable of handling non-linear, high-dimensional relationships among omics layers^[25]. These tools have demonstrably improved predictive accuracy for traits such as protein content, flooding response, and thermotolerance. However, a critical evaluation of this trend reveals an important caveat: high predictive performance in controlled research settings does not automatically translate into deployable breeding tools, since most models have not been validated across the multi-environment, multi-season conditions that determine real-world cultivar performance^[25, 38]. This gap between algorithmic sophistication and field-level applicability represents one of the more consequential unresolved tensions in the field.

The convergent identification of flavonoid biosynthesis pathways as thermotolerance biomarkers across independently conducted wheat and rice studies is a notable point of agreement that strengthens confidence in the biological relevance of this pathway^[34, 35]. Yet even here, the evidence base derives predominantly from controlled environmental conditions and a small number of contrasting genotypes, raising legitimate questions about generalizability across the broader genetic diversity present in global crop germplasm. Similarly, while epigenomic research has firmly established the existence of stress-responsive DNA methylation and stress memory, the extent to which these mechanisms are heritable and agronomically exploitable in crops, as opposed to model species such as *Arabidopsis*, remains only partially resolved^[13, 19].

Phenomics occupies a particularly important structural position within the integrative omics paradigm, functioning as the interface between molecular data and field-relevant, breeding-actionable traits. The growing use of remote-sensing and AI-assisted phenotyping platforms represents a genuine methodological advance^[26, 28], yet the uneven global distribution of this infrastructure raises an equity concern that is rarely addressed explicitly in the literature: research institutions in resource-limited settings, including many regions most vulnerable to climate-driven crop stress, have comparatively limited access to these tools. This has practical implications for whose crops, and whose farming systems, ultimately benefit from integrative omics research.

Taken together, the evidence supports a cautiously optimistic assessment of integrative omics as a genuinely transformative approach to crop stress research, while also indicating that the field remains in a phase of methodological consolidation rather than mature, routine translational application. The theoretical contribution of this body of work lies in demonstrating that gene-to-phenotype relationships in stress

adaptation are fundamentally systems-level phenomena; the practical implication is that breeding programs seeking to exploit this knowledge will need sustained investment in standardized, interoperable multi-omics infrastructure rather than continued reliance on isolated, single-omics studies.

7. Conclusion

In this review article, the current literature on cutting-edge multi-omics strategies for crop stress coping mechanisms has been put together using information from journals active from 2015 to 2026. It was found that the integration of omics disciplines allows us to better understand the mechanisms of stress adaptation than any particular omics discipline. It was mentioned that flavonoid metabolism, the impact of transcription factors, and the epigenetic memory process are identified among the most significant findings, and innovations resulting from the use of high-throughput phenotyping and machine learning in studies of the integration of omics for crop adaptation are described. However, the review also emphasizes the pressing need for improvement in the technologies used in the multi-omics studies and the need for transferring the theoretical results into practice.

The importance of this synthesis lies in making it clear that successful study of crop stress adaptation requires not just additive single-omics methods but also systems-level integrated approaches, given the complexity of its regulation. For researchers, the authors recommend increased efforts toward the establishment of standardized interdisciplinary multi-omics databases, the use of integrative omics in orphan crops, and adequate validation of functional role of promising genes discovered through GWAS and transcriptomics. Practitioners and policymakers should seek prioritized investments in shared phenomics infrastructure, especially in environments vulnerable to climate change. Future research should emphasize the necessity of investigating crop responses to combined stresses in order to simulate field environments accurately, increased application of single-cell and long-read sequencing, and continued development of fast and interpretable machine learning techniques. Researchers aware of the ability of integrative omics to benefit agricultural science will have to engage in effective collaborations with the experts from the molecular biology, bioinformatics, and plant breeding domains.

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