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Omics-assisted crop improvement under abiotic stress conditions☆

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ABSTRACT

Climate change-driven diverse abiotic stresses continue to negatively affect plant growth and development, ultimately altering sustainable agricultural production and food security. Multi-omics approaches have revolutionized how plant biologists explore stress-responsive, adaptation, and tolerance mechanisms and pathways, driven by improvements in scientific practices. Therefore, this special issue was designed to feature the latest advancements in omics studies to understand and improve the stress acclimation and tolerance mechanisms in diverse plant species.

1. Introduction: Power of omics-assisted crop improvement

With the escalating impacts of climate change, diverse abiotic stresses such as drought, salinity, extreme temperatures, waterlogging, hypoxia/anoxia, metals/metalloids toxicity, nutrient imbalance, etc., continue to negatively affect plant growth and development. These stresses ultimately alter sustainable agricultural production and food security (Yang et al. 2024; Zandalinas et al. 2024). Due to their sessile nature, plants cannot escape stressful environments by relocating to a stress-free environment. Consequently, plants have evolved numerous complex mechanisms to cope with stressed conditions by adjusting their developmental, physiological, biochemical, and molecular processes in response to environmental changes (Zhu 2016; Yang et al. 2024; Zandalinas et al. 2024).

Over the past decade, omics approaches—including genomics, transcriptomics, proteomics, metabolomics, ionomics, miRNAomics, and phenomics—have revolutionized how plant biologists explore stress-responsive, adaptation, and tolerance mechanisms and pathways, driven by improvements in scientific practices (Fig. 1) (Shen et al. 2022; Raza et al. 2024a; Raza et al. 2024b). These advancements in multi-omics science have transformed stress biology into a multidisciplinary research field, opening the way for fast-tracking future crop improvement under stress conditions (Fig. 1) (Shen et al. 2022). However, more research is needed to discover several unexplored aspects of plant stress responses to achieve a more insightful and comprehensive understanding of stress signaling pathways.

This special issue was designed to feature the latest advancements in omics studies to understand and improve the stress acclimation and tolerance mechanisms in diverse plant species. This special issue published a total of 61 articles (including 50 research and 11 reviews; https://www.sciencedirect.com/special-issue/10DH2FV6RMH) from diverse groups of authors globally. These contributions offer new insights into plant stress responses and provide a more comprehensive understanding of stress tolerance mechanisms at the muti-omics level. This editorial article aims to deliver a clear overview of the recent advances in the omics field while presenting readers with up-to-date breakthroughs—-where introductory scientific discoveries meet with front-line applications for designing stress-smart crop plants and achieving sustainable agriculture. Based on scientific contents published in this special issue, this editorial discussed the publications in different sections to improve our knowledge on how omics approaches can be harnessed for designing stress-smart future crop plants.

2. Genomics interventions for crop improvement

Recent advances in genome sequencing make it possible to utilize diverse genomics tools and techniques to discover novel genes/gene families in diverse plant species (for genome sequencing, readers can explore Phytozome 'https://phytozome-next.jgi.doe.gov/', and NCBI 'https://www.ncbi.nlm.nih.gov/genome/browse#!/overview/' databases). With the help of these tools, several researchers have identified and carried out their characterization, genomic evolution, gene structure, conserved motifs, *cis*-regulatory elements, putative miRNA and transcription factors, functional annotations (i.e., GO and KEGG), 3D protein structures, protein-protein interaction networks, and expression analysis in different tissues and under diverse stress conditions, to get insights into the novel roles of newly identified genes. Here, we will briefly highlight the key insights from each gene family-related article published in this special issue. For instance, Wang et al. (2023b) identified 11 *ZmLACS* genes, and functional characterization of one of the

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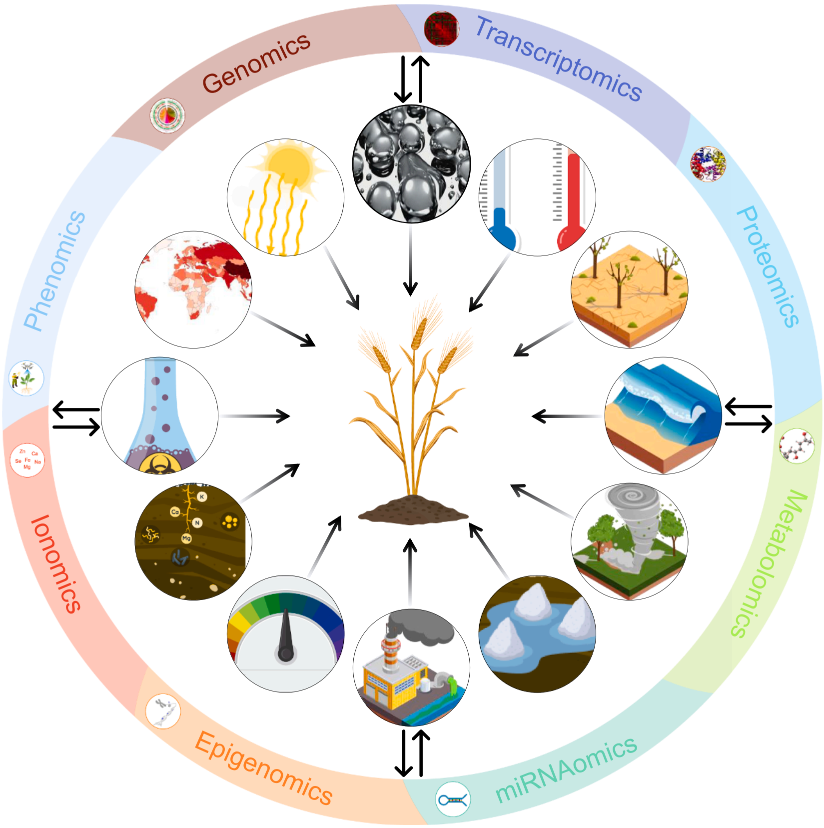

Fig. 1. Multi-omics integration for crop improvement under abiotic stress conditions. The inner circle shows a range of abiotic stresses—such as extreme temperatures, heavy metals, drought, waterlogging, salinity, wind, ozone, pH, UV light, and organic pollutants—that severely impact plant growth and development, and ultimately lead to significant yield losses. The outer circle illustrates various omics approaches, each coupled with abiotic stresses (denoted by cross-talk arrows), demonstrating their role in discovering critical mechanisms that improve stress tolerance at multiple levels. This integrative exploration of two or more omics approaches in a single study, under either the same or multiple abiotic stress conditions (known as multifactorial stress combinations), creates a strong multi-omics dataset across several plant tissues/cells. We believe that such comprehensive datasets are influential for future breeding programs targeted at designing stress-smart crops and safeguarding sustainable agriculture and food security in the face of global climate change.

candidate genes, "*ZmLACS9*" confirmed its role in heat stress tolerance in maize (*Zea mays* L.). Another maize study by Nawaz et al. (2023) reported 81 *ZmGS* genes and confirmed their role in drought stress tolerance. Rafique et al. (2023) identified seven *RcSOD* genes in China rose (*Rosa chinensis*) and suggested their role in salinity stress tolerance. In another study on China rose, Shafique et al. (2023) discovered 32 genes (including 21 for K^+ channels and 11 for transporters), and their expression was induced by salinity, drought, and heat stresses. Yang et al. (2023) identified 43 *AhUbiA* genes in peanut (*Arachis hypogea* L.) and examined their expression under cold stress and phytohormones treatment. Ahmad et al. (2023b) identified four *CsCHS* genes in cucumber (*Cucumis sativus* L.) and evaluated their expression in response to aphid infestation, cold, heat, waterlogging, and gibberellic acid treatments. In wheat (*Triticum aestivum* L.), 12 *TaIGT* genes were discovered, and their role was suggested in root architecture under drought stress (Rasool et al. 2023). In sunflower (*Helianthus annuus* L.), 73 *HabZIPs* genes were reported, and their role in salinity stress tolerance was highlighted (Rahman et al. 2023). Singh et al. (2023) identified eight *SiGSK* genes in foxtail millet (*Setaria italica* L.), and their expression was examined against salinity, oxidative and dehydration stresses. Bokolia et al. (2023) identified 101 *AsNAC* genes in oats (*Avena sativa* L.), and expression analysis confirmed their role in salinity tolerance. Rehman et al. (2023) reported nine *PtAL* genes in Poplar (*Populus trichocarpa*), and most of the genes significantly responded to cold, heat, drought, and salinity stresses. Parveen et al. (2023) reported eight *CaNHX* genes in chickpea (*Cicer arietinum* L.), and their expression was induced by salinity stress. Pahal et al. (2023) characterized 112 *CcGDSL* genes in pigeonpea (*Cajanus cajan* L.), and their expression was induced by drought stress.

In rice (*Oryza sativa* L.), Ninkuu et al. (2023) reported 43 *OsBXs* genes, and their expression levels were induced by phytohormones (i.e., auxin and gibberellin) and nutrient (i.e., nitrogen, potassium, and phosphorus) treatments. Gull et al. (2023) reported 21 *OsTCP* genes and uncovered their contribution to drought and salinity stress tolerance. Ahmad et al. (2023a) discovered 31 *OsOFP* genes and expression analysis suggests their potential role in different biotic (brown planthopper_striped rice stemborer, and rice leaf folder), abiotic (salinity and drought) stresses, and phytohormones signaling pathways. Ahmad et al. (2023c) identified 27 *OsCHS* genes, and their expression was regulated by salinity, drought, and phytohormone treatments. Hussain et al. (2023a) discovered 82 *OsbZIP* genes and examined their expression levels under salinity and cold stress conditions. Kesawat et al. (2024) characterized 109 *OsPSY* genes and suggested their role in phytohormones signaling and cold, drought, osmotic, and flooding stress tolerance. Aluko et al. (2024) characterized nine *OsEIN3/EIL* genes and highlighted their potential role in mannitol, phytohormone signaling pathways, and drought stress tolerance. Kumar et al. (2024b) reported three *OsAco* genes, and their expression was induced by salinity, drought, cold, heat, and ABA treatments.

In dragon fruit (*Selenicereus undatus* L.), 17 *HuSBP* genes (Khokhar et al. 2023), 35 *HuMATE* genes (Khan et al. 2024), and 67 *HuMADS-box* genes (Hui et al. 2024) were characterized and their expression levels were regulated in response to different abiotic stresses (e.g., drought, salinity, cadmium, melatonin, and their combinations) which suggested the key role of some candidates in developing stress-smart dragon fruits.

In soybean (*Glycine max* L.), Hussain et al. (2023b) identified 20

GmMACPF genes, and the functional validation of the *GmmiR-NA169o-GmMACPF-9* module suggested its role in cold stress tolerance. Rizwan et al. (2024) discovered 37 *GmIFR* genes and examined their role against spermidine and ultrasonication treatments. Joshi et al. (2024) identified 13 *GlymaSWEET*, six *GlymaMST*, and five *GlymaSUT* genes and suggested their role in salinity stress tolerance.

In common bean (*Phaseolus vulgaris* L.), 59 *PvGST* genes were identified, and their expression patterns were examined in response to drought and salinity stresses (Anik et al. 2024). Xue et al. (2024) characterized 57 *BnLhc* genes in rapeseed (*Brassica napus* L.), and most of the genes were found to be associated with salinity stress tolerance. Narwal et al. (2024) discovered 34 *MaCIPK* genes in banana (*Musa acuminata* subsp. *burmannicoides*, var. *Calcutta 4*), and examined their expression patterns in cold and drought conditions. Zheng et al. (2024) identified 12 *JrTLP* genes in walnuts (*Juglans regia* L.) and examined their expression against pathogen infection, phytohormones treatment (auxin, ABA, MeJA, and GA), and abiotic stress (cold, heat, and salinity) conditions. In safflower (*Carthamus tinctorius* L.), 187 *AP2/ERF* genes were identified, and the functional analysis of *CtDREB52* was found to regulate flavonoid biosynthesis under UV-B treatment by interacting with *CtDFR* and *CtMYB* genes (Yufei et al. 2024). All of the above-discussed examples have discovered the role of many new genes in stress tolerance and laid the foundation for their genetic manipulation (e.g., overexpression or editing via CRISPR/Cas system) to design stress-smart future crop plants.

Zaffar et al. (2024) studied 110 cowpea (*Vigna unguiculata* L.) genotypes and determined significant variation in root traits, with root volume, dry root weight, and tap root diameter showing promise. GWAS discovered 52 SNPs associated with root-shoot traits, with chromosome 5 being a hotspot for significant SNPs, assisting future cowpea breeding for developing drought-tolerant cultivars. Bhanbhro et al. (2023) explored the molecular and genetic mechanisms underlying drought tolerance in wheat. By summarizing the morphological, physiological, and genetic adaptation strategies for drought stress tolerance, this review highlights the complexity of the allotriploid wheat genome. A meta-analysis of QTL identified 75 meta-QTLs associated with drought tolerance. Furthermore, key genes and signaling networks crucial for drought tolerance have also been debated, which offers insights for designing drought-smart future wheat cultivars.

Rabeh et al. (2024) systematically reviewed and performed a genome-wide analysis of the aquaporin (*AQP*) gene family and highlighted their crucial role in abiotic stress responses. By investigating 82 studies and discovering over 5200 *AQP* isoforms in various plant species, this review provided insights into the functional and structural diversity of *AQP* subfamilies, including *PIPs, TIPs, NIPs, SIPs*, and *XIPs*. This meta-analysis improves our understanding of the roles of *AQP* genes in improving multiple abiotic stress tolerance in crops. The DEHYDRATION-RESPONSIVE ELEMENT BINDING (DREB) transcription factors are stress-responsive and modulate the expression patterns of downstream stress-inducible genes, which aid in multiple abiotic stress tolerance. Therefore, Sadau et al. (2024) reviewed the role of DREB transcription factors in improving multiple abiotic stress tolerance in cotton (*Gossypium* spp.). This review examines the evolutionary relationships, conserved motifs, and gene structures of *DREB* gene family in *G. hirsutum, G. raimondii*, and *Arabidopsis*. Lastly, they highlighted key *DREB* genes that help understand molecular mechanisms underlying stress responses and tolerance in cotton. This review also highlighted the scope of finding key genes for genetic engineering-guided enhanced abiotic stress tolerance in cotton and other important crops.

Qureshi et al. (2023) examined how whole genome duplication (WGD) influenced the evolution of *NLR* genes in the Vicioid clade, including legumes, e.g., chickpea, clover, alfalfa, and pea. The authors found that WGD, higher substitution rates, and post-speciation activities like gene conversion and recombination guide the NLRome expansion and subgroup diversification. Sindhu et al. (2024) found that optimal nitrogen application (80 kg ha^{-1}) in maize fields increased soil fungal diversity, with *Ascomycota, Chaetomium, Fusarium*, and *Mortierella* being the most abundant. It was noticed that this nitrogen level also increased nitrogen/carbon cycling and led to the highest maize yield (3.14 t ha^{-1}), emphasizing the role of fungal genomic interactions in improving crop productivity and sustainability.

3. Transcriptomics helps understand molecular mechanisms underlying stress tolerance

With the help of recent innovations in sequencing technologies, transcriptomics studies help understand the known and unknown mechanisms (in terms of key genes and pathways) underlying stress tolerance in diverse plant species (Ghasemi et al. 2023; Raza et al. 2024b). For instance, desiccation tolerance is a key factor for crop improvement; however, its application in rice remains limited. In a study, Ilias et al. (2024) show that desiccation tolerance in vegetative tissues shares gene pathways originally evolved for seed desiccation. The drought-tolerant rice variety (MR303) can survive desiccation for short periods, but its capacity to recover after dehydration is hampered by cell wall irreversibility. Transcriptomic analysis shows the up-regulation of genes involved in secondary cell wall formation and the down-regulation of non-cellulosic cell wall-related genes, leading to the accumulation of lignin and cellulose. Collectively, these factors contribute to cell wall rigidity and prevent full recovery upon rehydration (Ilias et al. 2024). Gene expression in leaf and root tissues of two wild barley accessions under salinity and drought stress identified 641 differentially expressed genes (DEGs). Minimal overlap in stress-responsive genes between leaves and roots recommends distinct adaptation mechanisms. Hierarchical clustering and GO enrichment analysis emphasized genes involved in metabolic processes, oxidation-reduction, and organic substance metabolisms. These outcomes discover candidate genes and mechanisms for stress tolerance in wild barley, guiding future research on drought and salinity tolerance mechanisms (Bakır et al. 2024). In another study, Ren et al. (2024) reported that soybean displays varying degrees of salt-alkali tolerance within different germplasms. Transcriptome analysis using salt-tolerant (Heinong531) and the salt-sensitive (20_1846) varieties detected a total of 200 DEGs (93 up-regulated and 107 down-regulated) linked to salt-alkali tolerance. Functional GO analysis discovered that 29 key DEGs were involved in 14 GO terms vital for salinity tolerance mechanisms in soybeans. Furthermore, the association analysis between physiological factors and DEGs under salt-alkali stress showed that different soybean cultivars displayed unique gene expression patterns, leading to changes in physiological indices in response to stress (Ren et al. 2024).

A transcriptome analysis compared the nodule transcriptomes of soybean (Williams 82) inoculated with two *Bradyrhizobium diazoefficiens* strains (USDA110 vs. CB1809) under phosphate (Pi) deficiency. This study identified low-Pi-responsive genes and significant transcriptional differences between USDA110 and CB1809 nodules. Lower symbiotic efficiency in USDA110 nodules was due to down-regulation of an *F1-ATPase* gene, reducing ATP production. USDA110 nodules up-regulated genes in energy-demanding pathways, leading to higher metabolic costs and redox imbalance. CB1809 nodules managed energy more effectively by regulating fewer genes and improving proteins in non-phosphorylating bypasses. Notably, up-regulation of malate dehydrogenase in CB1809 nodules maintained their Pi stress response. These outcomes improve our understanding of soybean adaptation to Pi deficiency (Sulieman et al. 2024). Another study by Li et al. (2024) performed genome-wide transcriptome profiling to survey the molecular mechanisms of biotic and abiotic stress responses in two rice cultivars (RH-resistant and TN1-susceptible to brown planthopper, BPH) cultivars at 6 h after BPH infestation and needle puncturing. Key findings showed distinct stress response pathways in both cultivars. Significant changes in gene expression related to phytohormones were noticed, including JAZ-related genes in the JA pathway and IAA pathway-related genes in

TN1. Overall, these results help discover BPH-resistance genes in RH and improve our understanding of rice responses to BPH (Li et al. 2024). Cannabis fructus (*Cannabis sativa* L.) is an ancient crop that has industrial, agricultural, and medicinal uses. Effects of 60 Gy carbon ion beam irradiation on its physiological and biochemical pathways using multi-omics analysis identified new DEGs and proteins. Between radiated and unirradiated cannabis fructus stem, 2,891 DEGs, 1,145 differentially expressed proteins (DEPs), and 954 altered ubiquitination modification sites were identified. The irradiation enhanced pathways such as carbon fixation, fatty acid synthesis, JA synthesis, and glutathione metabolism, and activated the MAPK signaling pathway, highlighted their key role in irradiation tolerance (Wang et al. 2023a).

4. Proteomics-driven insights into stress tolerance mechanisms

Proteomics is another omics vital omics for understanding stress tolerance, which helps discover changes in protein expression and pathways related to plant responses and tolerance to abiotic stresses (Yan et al. 2022; Jan et al. 2023; Raza et al. 2024b). Plants under salinity stress often face ionic homeostasis disorders. Therefore, a study by Damaris et al. (2024) investigated the transcription factor *OsMYBc* that regulates *OsHKT1;1* to control Na^+ accumulation in rice shoots. Analyzing root tissues from a T-DNA mutant of *osmybcc-1* and its wild type after 12 hours of salinity stress showed an accumulation of more K^+ in leaf tips in the wild type. Proteomics identified 8,523 differentially expressed proteins (DEPs), with 7,598 quantifiable. DEPs enriched in DNA repair pathways were found in mutants without salinity treatment, while DEPs related to reactive nitrogen species were enriched in mutants after salinity treatment. High-affinity nitrate transporter (NRT) DEPs were enriched in both groups under stress conditions, and the *NRT2.1*-overexpressing rice showed greater salinity tolerance than its knockout mutant. These findings feature root protein dynamics under salinity stress and suggest targets for MYB transcription factors in mitigating salinity stress in plants (Damaris et al. 2024).

Hasan et al. (2023) reviewed the proteomic mechanisms involved in salinity stress tolerance in rice, describing methods like salinity sensing, ROS scavenging, and protein folding, synthesis, and degradation. This review also features the role of proteomics in finding salinity-responsive networks, proposing insights into the breeding and designing of salinity-smart future rice cultivars through advanced molecular and proteomics approaches.

5. Metabolomics-guided discovery of metabolic biomarkers and pathways

Metabolomics is a powerful tool in stress tolerance that enables the discovery of key metabolic pathways and biomarkers associated with enhanced plant stress tolerance (Bueno and Lopes 2020; Yan et al. 2022; Raza et al. 2024b). For instance, Singh et al. (2024) used untargeted metabolite profiling and comparative biochemical and biological investigation of the high-temperature tolerant (HTT) tomato hybrid VRNTH18283 and the sensitive (HTS) VRNTH19072 to identify altered metabolic pathways and biomarker metabolites associated with enhanced antioxidant activity in HTT variety. Higher fruit weight, yield, and biochemical content (e.g., total soluble sugar, acidity, ascorbic acid, and lycopene) were observed in HTT. Moreover, greater metabolite diversity was observed in HTT (11,453 m/z features) vs. HTS (8,834 m/z features). In HTT, a total of 423 metabolites were up-regulated and 410 down-regulated. Functionally annotated metabolites were mainly enriched in diverse metabolic pathways, including linoleic and linolenic acid metabolism, monoterpenoid biosynthesis and degradation, cutin, suberin, and wax biosynthesis, and sphingolipid metabolism. This study provided insights into key biomarkers and pathways for improving heat tolerance in tomato plants.

In another study, Ghasemi et al. (2023) examined the impact of drought stress on secondary metabolite production in cumin plants and related transcriptional changes under drought stress. Drought stress increased levels of beta-carotene, lycopene, terpenes, anthocyanin, phenolic compounds, flavonoids, and alkaloids, demonstrating an adaptive shift. In addition, the key biosynthetic genes (e.g., *PAL, DAHP synthase, DXS, HMGR*, and *GPPS*) were up-regulated under drought stress. Flavonoids increased overly, advising alternative synthesis pathways. Strong correlations between gene expression and metabolite levels emphasized the role of transcriptional regulation in drought tolerance in cumin. Likewise, Singh and Roychoudhury (2023) screened four rice cultivars (Badshahbhog, Swarna, Sukumar, and Shatabdi) for fluoride tolerance via transcript levels and metabolic shifts. Shatabdi accumulated significant fluoride, hampering growth and causing oxidative stress and pigment degradation. In contrast, Badshahbhog showed higher levels of osmolyte-related metabolites (e.g., proline, amino acids, and glycine betaine) and antioxidants (e.g., SOD, CAT, APX, and GPX), maintaining expression of photosynthetic genes, which helped rice plants to overcome fluoride toxicity.

6. non-coding RNAs: Insights into small players with a big impact on crop improvement

MicroRNAs (miRNAs) are small, non-coding RNA molecules, typically 21-23 nucleotides long, that are crucial in regulating gene expression (Pagano et al. 2021; Raza et al. 2023a). In the drought-sensitive variety Swarna, sRNA-seq data discovered nine novel miRNAs and 27 differentially expressed known miRNAs at the booting stage under drought stress. Key miRNA/transcript modules affecting drought response and yield included Osa-miR169a, Osa-miR171b/f, Osa-miR172d-3p/5p, Osa-miR1876, Osa-miR397a, and Osa-miR530-3p. These findings suggest that low spikelet fertility and high grain chalkiness in Swarna are due to the modulation of specific miRNA/transcript modules. In short, this study identifies potential target genes for improving drought tolerance in rice to ensure food security (Kumar et al. 2024a).

Long non-coding RNAs (lncRNAs) are a class of regulatory RNA molecules that do not code for proteins but play imperative roles in adjusting gene expression at various levels, shaping multiple biological mechanisms in plants (Wierzbicki et al. 2021; Das et al. 2023). In a review, Das et al. (2023) comprehensively reviewed the key role of lncRNAs in regulating plant responses to soil salinity. This review emphasizes how lncRNAs manipulate gene expression via *cis*- and *trans*--regulation, function as competing endogenous RNAs, and serve as precursors to small ncRNAs. Several salinity-associated lncRNAs have been discovered in different plant species; nevertheless, their underlying stress tolerance mechanisms remain unclear. So, Das et al. (2023) discussed the need for more investigations to better understand how lncRNAs regulate plant salinity stress responses and beyond.

7. Ionomics for crop improvement

Ionomics is a dynamic side of omics-based stress tolerance, which involves the comprehensive examination of plant elemental profiles, suggesting insights into nutrient differences and metal toxicity under stress conditions (Huang and Salt 2016). In a wheat study, Anas et al. (2023) used histological and ionomics approaches to examine the impact of nickel (Ni) contamination in Pakistan's irrigation water and soil. Two wheat cultivars, SKD-1 and Borlaug-16, were exposed to Ni stress (100 mg L^{-1}) for 21 days. Ionomics analysis discovered higher Ni translocation in SKD-1 due to lower Ni accumulation in Borlaug-16 roots. Borlaug-16 had higher root trace elements (Cr, Cu, Mn, Pb, and Zn), while SKD-1 demonstrated improved leaf nutrients (Ca, Fe, Mg, Na, and P). Borlaug-16 also exhibited thicker root cortex and stele and lower oxidative stress due to higher antioxidant enzyme activities (SOD, CAT, and APX). In contrast, SKD-1 experienced more oxidative damage. Lower Ni uptake in Borlaug-16 and stronger antioxidant response advise remarkable Ni stress tolerance, suggesting insights for sustainable crop production globally by exploring ionomics.

8. Integration of machine learning and phenotyping for designing stress-smart crops

Integrating machine learning (ML) with advanced phenotyping methods is fast-tracking crop breeding, specifically for enhancing abiotic stress tolerance. In the context of omics for crop improvement, this integration approach assists to link genotype-phenotype associations, allowing fast-forward breeding of stress-smart crops (Cravero et al. 2022; Shen et al. 2022; Yoosefzadeh Najafabadi et al. 2023; Raza et al. 2024a; Raza et al. 2024b; Shen et al. 2024). For instance, high-throughput phenotyping (HTP) using UAV-based multispectral imaging and ML models was utilized to examine 553 wheat genotypes under drought stress (including irrigated and rainfed) conditions. Traits, e.g., plant height and yield, were evaluated with high accuracy, and the deep learning model (H2O-3) projected yield with a notable R^2 of 0.80. This study determines the effectiveness of integrating multispectral data with ML for actual phenotyping and breeding of drought-smart wheat varieties (Sharma et al. 2024b). In another study, Pappula-Reddy et al. (2024) examined drought tolerance in chickpea using non-destructive, image-based techniques (including RGB, NIR, and IR imaging). The HTP program effectively captured data on key agro-physiological traits, and image-based traits demonstrated strong correlations with physically recorded data, e.g., photosynthetic rate, chlorophyll fluorescence, NIR reflectance, stomatal conductance, etc. This study highlights the power of using image-based screening for breeding drought-smart chickpea varieties, mainly in rainfed conditions where water stress is frequent. Another study by Sharma et al. (2024a) assessed heat tolerance in 184 wheat genotypes using multispectral vegetative indices, aerial images, and ML approaches. The random forest classifier accurately distinguished heat-sensitive, moderate, and tolerant genotypes. A principal component analysis condensed data dimensionality, which assisted better categorization accuracy. Overall, this study emphasizes the role of HTP-driven ML models in discovering heat-tolerant genotypes, specifically under late-sowing conditions when heat stress is most severe (Sharma et al. 2024a). Based on these studies, it can be assumed that the integration of ML models with advanced HTP platforms can be harnessed to design stress-smart future crop plants.

9. Reviews on the integrated multi-omics for understanding stress responses and tolerance mechanisms

Integrating multi-omics approaches, such as genomics, transcriptomics, proteomics, metabolomics, etc., has been critical in progressing our understanding of abiotic stress responses and tolerance mechanisms in non-food grass species, grapes, and African crops. In plant stress biology, these approaches deliver new insights into molecular and biochemical responses to multiple abiotic stresses. For instance, Mondal et al. (2024) reviewed multi-omics to harness the stress tolerance mechanisms of non-food grass species (e.g., turf, ornamental, and forage grasses). They highlighted how multi-omics could fill research gaps and fast-track the designing of stress-smart and indicate the worth of integrating these tools for future crop improvement (Mondal et al. 2024). In grapes (*Vitis* spp.), omics approaches have harnessed smart genetic strategies to improve temperature stress tolerance, delivering valuable insights into future fast-forward breeding strategies to boost temperature tolerance in sustainable grape production (Yadav et al. 2024). Diverse abiotic stresses also significantly hamper African agriculture and food security. In this context, Mmbando (2024) reviewed the application of omics approaches that have been playing a key role in improving yield and stress tolerance in staple crops like maize, rice, sorghum, soybeans, cassava, etc., and contributing to inform breeding strategies. Modern omics, coupled with AI and ML, were investigated for breeding and designing crop plants tolerant to multifactorial abiotic stresses. This review suggested the need for a broad understanding of combined stress responses via integrated omics approaches (Joshi et al. 2023).

Raza et al. (2023b) reviewed the key role of phytohormones in managing and improving plant growth and development under cold stress conditions. They also provided insights into the cold stress tolerance mechanisms from multi-omics studies of phytohormones-encoding genetic players. Lastly, this review also presented the power of state-of-the-art genetic engineering tools (e.g., transgenic breeding or gene editing via CRISPR system) to manipulate phytohormones-related key genes for improving cold stress tolerance in different plant species. Kumar et al. (2023) reviewed the key impact of rising temperatures on seed biochemical composition in major cereal crops, e.g., wheat, rice, and maize. Heat stress, specifically during reproductive and grain-filling stages, unsettles key processes and leads to detrimental changes in seed quality, modifying carbohydrates, proteins, oils, and other nutrients. Despite the known impacts on crop yield, less attention has been given to these biochemical changes. Therefore, Kumar et al. (2023) call for more research into heat-induced variations in seed quality to inform breeding approaches for improving heat tolerance. They also presented current gaps and challenges in mitigating heat stress impacts on crop's nutritional value.

10. Remarks and recommendations

In this special issue, we have published a total of 62 articles including 50 research, 11 reviews, and this concluding editorial. These articles present comprehensive new insights into plant stress responses and tolerance mechanisms at a multi-omics level. We hope that our readers will find these both valuable and inspiring. The subject clearly shows that the field of "omics-assisted crop improvement under abiotic stresses" is not only highly dynamic but also promptly progressing, providing many openings for scientists to build their research niches. In the future, integrating omics with ML and HTP will further modernize crop improvement in the face of a rapidly changing climate. Likewise, there is a growing number of research efforts exploring single-cell omics for crop improvement. Therefore, we need to implement single-cell omics approaches to, more specifically, harness stress responses and tolerance mechanisms. Altogether, integrating multi-omics with genetic engineering, synthetic biology, and speed breeding techniques will be game changers in designing future stress-smart crops. These developments will be key for safeguarding food security, enabling us to feed the growing population despite the challenges posed by global climate change.

Declaration of competing interest

The author/guest editor (Ali Raza) is an Editorial Board Member of Plant Stress and was not involved in the editorial review or the decision to publish this article. The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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