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Research Paper

Artificial Intelligence-Based Multi-Omics in Biotic and Abiotic resistance

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Abstract: Recent advances in biotechnology have catalyzed the rapid emergence of high-throughput omics. This has enabled access to multi-layer information from the genome, epigenome, transcriptome, proteome, metabolome, and collectively as "panomics". Panomics represents an integrative framework that unifies multiple layers of 'omics' information— generated across diverse individuals and natural genetic variation. Panomics has highlighted in the promoter region of stress tolerance–related genes in plants. By placing artificial intelligence AI at the core of analytical pipelines, panomics transforms high-dimensional raw data into biologically meaningful and experimentally testable hypotheses. Recently integration of image-based phenotyping and advanced computational modeling have enhanced the transformative potential and panomics presents substantial analytical, computational, and interpretative challenges, especially in the integration, standardization, and biological contextualization of heterogeneous datasets. The convergence of panomics and AI has profoundly expanded our understanding of genome plasticity, highlighting the functional importance of dispensable and variable genes. These genes are increasingly recognized for their critical roles in agronomic performance, disease resistance, abiotic stress tolerance, and adaptive phenotypic plasticity. Besides this in recent years artificial intelligence (AI) has demonstrated considerable potential for modeling nonlinear relationships and integrating complementary multimodal information to study biotic and abiotic stress resistance. Collectively, these developments underscore a paradigm shift toward AI-enabled panomics-driven gene discovery. Great progress has been made with AI-based multi-omics analysis and its application in plant stress tolerance will be presented.

Keywords: Panomics, Biotic and Abiotic, Stress tolerance

Introduction:

The present day's ongoing global warming and climate change adversely affect plants through imposing environmental (abiotic) stresses and disease pressure (Gao et al. 2022; Roychowdhury et al. 2023; Liu et al. 2024). Major abiotic stresses, including drought, heat, salinity, cold, and adversely affect plant growth and development, leading to significant reductions in yield and quality. Some of the strategies adopted by plants immune system to tackle these crises is by molecular rearrangements and activation of stress-responsive genes. Omics approaches have identified candidate genes and pathways, although the understanding of post-transcriptional regulation is a relatively new domain (Hua et al. 2023). Multi-omics approaches, integrating genomics, transcriptomics, proteomics, and metabolomics, provide comprehensive data for stress response understanding (Martin et al. 2024). Combining data from different layers promises enhanced crop improvement by identifying molecular players in stress tolerance. It facilitates unraveling regulatory networks and identifying biomarkers for crop enhancement. This knowledge ultimately pushes in developing stress-tolerant crop varieties through breeding or genetic engineering (Naincy and Kumar 2026). This review summarizes and integrates the omics approach towards tolerance for various biotic and abiotic stress. The panomics framework—encompassing genomics, transcriptomics, proteomics, metabolomics, epigenomics, proteogenomics, interactomics, ionomics, and phenomics—has emerged as a powerful and versatile toolbox for elucidating complex stress-adaptive networks in plants (Roychowdhury et al. 2023). A brief review shall be presented

Artificial intelligence-based multi-omics:

He et al. (2022) reported that with biotechnological advancements, innovative omics technologies are constantly emerging. Artificial intelligence has demonstrated the ability to analyze complementary multi-modal data streams within the oncology realm. The collateral development of multi-omics technologies and artificial intelligence algorithms has promoted the development of cancer precision medicine (He et al. 2022). Li et al. (2025) provided an in-depth analysis of integrated uses of omics technologies, genome editing, protein design and high-throughput phenotyping, in crop improvement, supported by artificial intelligence-enabled tools. Bradbury et al. (2025) reviewed strategies for the integration of genome editing with omics, artificial intelligence, robotics, and advanced farming technologies to improve crop performance.

Abiotic stress:

Plants have evolved various strategies to adapt and thrive in rapidly changing environments. The abiotic stress conditions that most adversely affect the plant growth and crop yield are linked with water deficiency, ion imbalance, and temperature extreme (Zhang et al. 2020). Through the application of integrated *omics* approaches it has been possible to analyze the plant traits associated with abiotic stress responses and tolerance mechanisms (Rai et al. 2017). These adaptive mechanisms involve molecular-level rearrangements, spanning gene expression from transcriptional regulation to mRNA processing, translation, protein modification, or turnover (Hu et al. 2023). Gao et al. (2022) studied metabolic and physiological changes in the roots of two Oat cultivars in response to complex saline-alkali stress. The analyses of different metabolites of roots of tolerant and sensitive cultivars provided an important theoretical basis for understanding the mechanisms of saline-alkali tolerance and increased our knowledge of plant metabolism regulation under stress. Meanwhile, some related metabolites, such as proline, betaine, and p-coumaryl alcohol, can also be used as candidates for screening saline-alkali tolerant oat cultivars (Gao et al. 2022).

Biotic stress:

Biotic stress refers to the adverse effects on plants caused by living organisms, including pathogens (such as fungi, bacteria, viruses, and nematodes), insects, herbivores, and competing plants (weeds) (Mittler 2022). To fight these attackers, plants develop different metabolic and genetic responses whose final outcome is the production of either toxic compounds that kill the pathogen or deter its growth, and/or semiotic molecules that alert other individuals from the same plant species. Plants respond to biotic stress through complex defense mechanisms involving pathogen recognition, signal transduction, activation of defense-related genes, and the production of protective metabolites and proteins (Kumar et al. 2026). A sophisticated defense network is activated to orchestrate transcriptional reprogramming using a two-tiered defense approach (Dodds and Rathjen 2010; Tsuda and Katagiri 2010). Pathogen/microbe associated molecular patterns (PAMP/MAPM) triggered immunity. PAMP-elicited compounds are highly diverse and specific of every plant species and can be divided into preformed metabolites or phytoanticipins that are converted into toxic molecules upon pathogen perception, and toxic metabolites or phytoalexins that are produced only upon pathogen attack. PTI constitutes the inducible defense through an array of early cellular responses comprising of ion flux across the membrane, production of reactive oxygen species (ROS) and mitogen-activated protein kinase (MAPK) cascades phosphorylation and long-term later responses that induce callose deposition (Mittler et al. 2022). Omics techniques also allow us to learn more about the biological cycle of the pathogens in addition to the identification of novel virulence factors in pathogens and their host targets. Both approaches become important to decipher the mechanism underlying pathogen attacks and to develop strategies for improving disease-resistant plants. Moreover, plant volatile emissions are also modified in response to pathogen attack to alert neighboring individuals or to make plants less attractive to pathogen vector arthropods.

Crosstalk Between Responses to Biotic and Abiotic Stresses:

Recent evidence underscores the complexity of interactions between biotic and abiotic stress response pathways, revealing extensive aberrant signaling crosstalk under combined stress conditions (Nejat and Mantri 2017; Hussain et al. 2022). .According to Nejat and Mantri (2017) the global climate change is predicted to have a negative impact on biotic stress resistance in plants. Therefore, comprehensive plant transcriptome analyses under combined stress conditions are essential to identify both general stress-responsive and pathogen-specific genes that collectively contribute to multi-stress tolerance, thereby enabling plants to better adapt to the challenges imposed by climate change.

Genomics:

The genome comprises the complete complement of genetic material within an organism, encompassing the entire DNA sequence, including both protein-coding genes and non-coding regions. Genomics involves the comprehensive analysis of an organism's genome to elucidate gene structure, function, evolution, and interactions. Such genomic insights have significantly advanced our understanding of the molecular mechanisms underlying organismal responses to environmental stressors (Fig. 1). Among these, abiotic stresses—including drought, salinity, extreme temperatures, and nutrient deficiencies—constitute major constraints on crop growth, development, and productivity.

Targeted manipulation of genes with well-defined functions has become feasible through advanced genome-editing technologies, particularly the clustered regularly interspaced short palindromic repeat (CRISPR)-Cas system. This system has demonstrated high efficiency in functional characterization of plant stress-responsive genes associated with drought tolerance (Ha et al. 2013; Salvi and Tuberosa 2015), salinity stress (Sheoran et al. 2022; Tanin et al. 2022), heat stress (Selamat and Nadarajah 2021), and cold stress (Prakash 2022).

The CRISPR-Cas system has proven highly efficient in characterizing the functionality of plant-responsive genes related to drought (Ha et al. 2013; Salvi and Tuberosa 2015), salinity (Sheoran et al. 2022; Tanin et al. 2022), heat (Selamat and Nadarajah 2021), and cold stress (Prakash 2022).

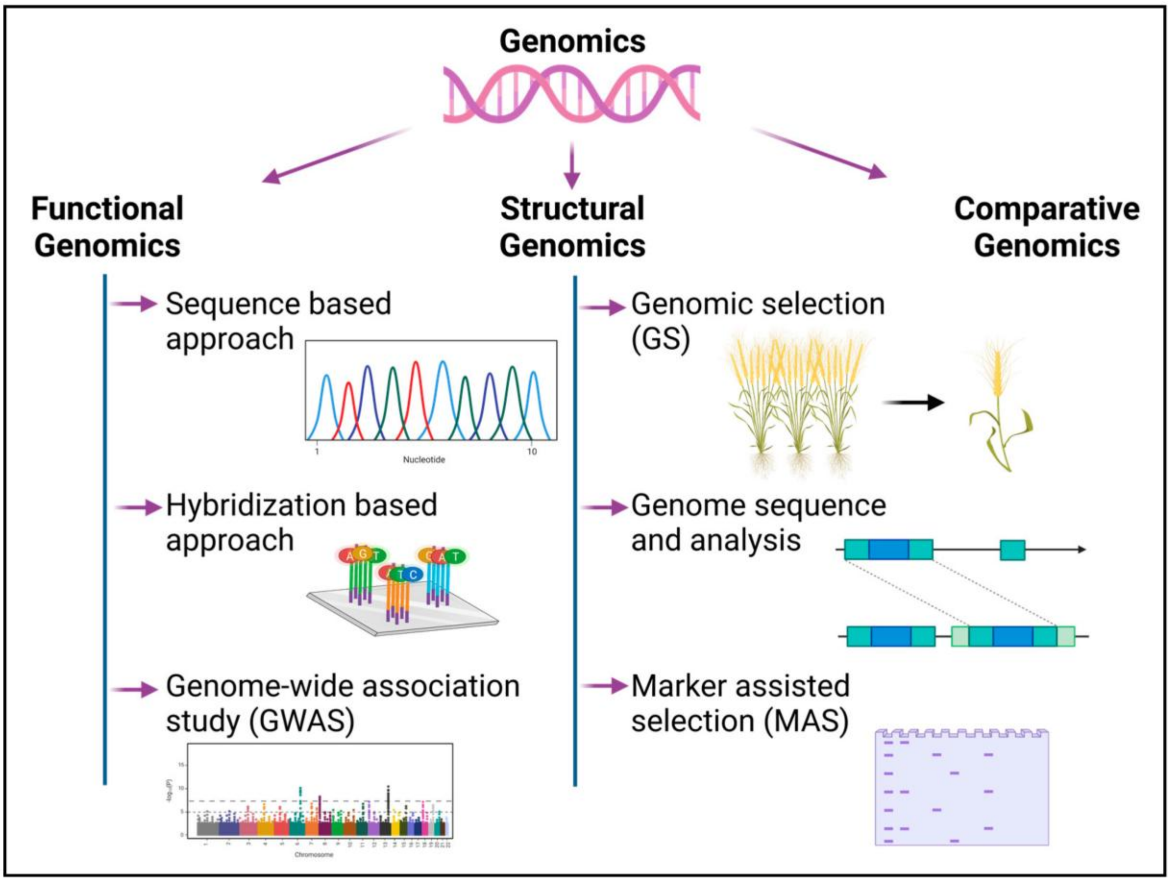

Fig.1. Different cohorts of genomics for crop assessment and improvement in relation to abiotic-stress tolerance response. The diagram was created using BioRender (https://biorender.com/) premium version. © 2023 by the authors. Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/4.0/).

Metabolomics:

Metabolites are building blocks of cellular function. Metabolomics provides deep insights into plant metabolomes and the complex biochemical networks underlying physiological processes, stress responses, and plant–environment interactions. Metabolomic analyses are broadly classified into targeted and untargeted approaches. Untargeted versus Targeted Metabolomics Studies. Untargeted, or discovery-based, metabolomics focuses on global detection and relative quantitation of small molecules in a sample (Schrimpe-Rutledge et al. 2016). In contrast, targeted, or validation-based, metabolomics focuses on measuring well-defined groups of metabolites, with opportunities for absolute quantitation.

Targeted metabolomics focuses on the accurate identification and quantification of predefined metabolites, offering high sensitivity, specificity, and robust quantitative data. In contrast, untargeted metabolomics aims to capture a wide spectrum of metabolites by measuring mass spectrometric features without prior bias toward known compounds, thereby enhancing the likelihood of detecting novel metabolites, pathway perturbations, and unintended metabolic effects. (Fig.2). According to Tian et al. (2022) mass spectrometry-based metabolomics has emerged as a powerful technique for biomedical research, although technical issues with its analytical precision and structural characterization remain. By mining metabolomes more deeply, researchers are now primed to uncover key metabolites and their associations with diseases. The employment of untargeted metabolomics has led to new biomarker discoveries and a better mechanistic understanding of diseases with applications in precision medicine (Cui et al. 2018). Coene et al. (2018) reported that next-generation targeted and untargeted metabolic screening can be used for diagnosis of inborn errors of metabolism in individual patients. Biological interpretation of metabolomics data hinges on the ability to accurately identify metabolites. The range of confidence associated with identifications that is often overlooked is reviewed, and opportunities for advancing the metabolomics field are described (Schrimpe-Rutledge et al. 2016). While untargeted, hypothesis generating workflows exhibit many valuable attributes, challenges inherent to the approach remain. This Critical Insight comments on these challenges, focusing on the identification process of LC-MS-based untargeted metabolomics studies-specifically in mammalian systems. Metabolomics will involve temporal transcriptome, proteome, metabolome, lipidome, phosphoproteome, acetylproteome, ubiquitylproteome, epigenome and immunome.

Proteomics:

Proteomics has emerged as a preferred approach, alongside genomics and other molecular methodologies, because proteins represent the ultimate effector molecules driving phenotypic variation in living systems and play a central role in enabling plants to perceive, respond to, and tolerate diverse environmental stresses. (Yadav et al. 2023). Factors like development, cellular differentiation, and the cell cycle, as well as various environmental conditions such as abiotic stressors, can lead to diverse expressions of the same genes (Tiwari et al. 2020). Consequently, cells produce distinct sets of proteins depending on their environment, making some proteins potential biomarkers for specific environmental factors, such as abiotic stressors (Conde and Kirst 2022). Yadav et al. (2023) reviewed different proteomic studies undertaken in *Brassica* crops for cytoplasmic male sterility, oil content, and proteomics of floral organs and seeds, under different biotic and abiotic stresses including post-translational modifications of proteins. This has helped in understanding the role of different proteins in controlling plant phenotypes, and provides information for initiating future studies on *Brassica* breeding and improvement programs.

Transcriptomics:

Transcriptomic methodologies have significantly advanced our understanding of plant responses to abiotic stresses. Recently, the application of next-generation sequencing (NGS) for transcriptome analysis, particularly RNA-seq for small RNAs, has substantially enhanced plant genomic resources in genomics research (Naincy and Kumar 2026) . Li et al. 2025) utilized switch grass Affymetrix gene chips to identify 5365 differentially expressed probe sets (with a 2-fold cutoff) in the Alamo switch grass cultivar under heat stress. Through comparative transcriptome analysis across four monocots—switch grass, rice, wheat, and maize—16 common genes associated with protein refolding processes were identified as valuable biomarkers for discerning heat-sensitive plant germplasm (Li et al. 2013). Spitz et al. (2012) reported that views of how transcription factors regulate gene expression are changing owing to recent genome-wide studies of transcription factor binding and RNA expression.

Epigenomics:

The inheritance of stress memories through subsequent generations is regulated epigenetically as proved by the studies conducted by Friedrich et al., 2019 ; Nguyen et al., 2022; and Sharma et al., 2022. Cell type-specific gene expression patterns and dynamics during development or in disease are controlled by cis-regulatory elements (CREs), such as promoters and enhancers. Distinct classes of CREs can be characterized by their epigenomic features, including DNA methylation, chromatin accessibility, combinations of histone modifications and conformation of local chromatin (Preissl et al. 2023).

DNA and RNA sequencing enables the quantification of information-bearing molecules that encode and execute cellular biological identity. The relative abundance of RNA molecules constitutes the transcriptome, whereas chemical modifications of DNA and histone proteins, together with the three-dimensional organization of DNA within the nucleus, define the epigenome (Zhang et al., 2023). The dynamic regulation of epigenomic marks across specific chromatin states governs gene expression programs, biological functions, and phenotypic variation across diverse biological processes. Importantly, the epigenome can preserve stable chromatin states over extended periods, spanning multiple cell generations, thereby enabling the durable storage of gene expression information. The increasing availability of high-throughput epigenomic datasets generated through next-generation sequencing technologies facilitates data-driven analyses to systematically compare epigenomic landscapes across distinct tissues and cell types. According to Liu and Conesa (2025) reported the advent of single-molecule, long-read sequencing (LRS) technologies by Oxford Nanopore Technologies and Pacific Biosciences has revolutionized genomics, transcriptomics and, more recently, epigenomics research.

These technologies offer distinct advantages, including the direct detection of DNA methylation and the simultaneous interrogation of long DNA fragments—often spanning multiple kilobases—together with their associated epigenetic modifications at single-molecule resolution. Such capabilities have enabled the development of novel assays for chromatin state analysis and have facilitated the integrative profiling of DNA methylation, chromatin accessibility, transcription factor binding, and histone modifications, thereby supporting a more comprehensive and high-resolution characterization of epigenomic landscapes.

Chromosomal processes such as transcription are regulated by a diverse array of post-translational histone modifications, including acetylation, phosphorylation, methylation, and ubiquitination. These modifications can function independently or synergistically in a context-dependent manner to either promote or repress chromatin-mediated processes (Berger, 2007). While certain histone modifications are believed to affect nucleosome stability, an increasingly recognized concept is that histone marks can influence one another. In this crosstalk, a specific modification may recruit or activate chromatin-modifying complexes that catalyze additional histone modifications, thereby establishing complex and dynamic regulatory chromatin states. The processes such as transcription are influenced by a variety of posttranslational modifications to histones, including acetylation, phosphorylation, methylation, and ubiquitination. These modifications may act alone or in concert in a context dependent manner to facilitate or repress chromatin mediated processes (Berger, 2007). Some histone modifications are thought to influence nucleosome stability, but an exciting emerging theme is that histone modifications can influence one another such that one modification recruits or activates chromatin modifying complexes to generate a different histone modification. Sculpting the epigenome with a combination of histone modifications and transcription factor occupancy determines gene transcription and cell fate specification (Suganuma and Workman 2008).

Discussion:

By integrating multi-omics datasets, panomics enables a more holistic and in-depth analysis of abiotic stress tolerance through comprehensive data integration, systems biology–based analytics, functional annotation, and pathway analysis, coupled with data mining and machine-learning approaches for precise genomic prediction of crop germplasm. Dynamic homeostasis is a fundamental characteristic of all living systems, referring to the capacity of biological organisms to undergo continuous temporal changes in response to various exogenous stimuli, including pharmacological interventions, dietary inputs, and environmental factors. This multidisciplinary approach empowers us to delve into the genetic and biochemical intricacies of this remarkable plant. Health care In a world marked by an increasing focus on the convergence of agriculture, nutrition, and herbal medicine, lesser-known crops have garnered fresh interest due to their capacity to tackle contemporary healthcare issues. According to Derbyshire et al. (2022) Plants' responses to stress conditions involve a highly coordinated sequence of events. Stress perception by plant cells initiates specific signal transduction pathways, leading to the generation of secondary messengers such as calcium ions, reactive oxygen species, and phytohormones. These signaling cascades activate downstream protein kinases and transcription factors, which in turn regulate the expression of stress-responsive genes. The induced genes and their gene products function at both transcriptional and translational levels to mitigate the adverse effects of the imposed abiotic stress and to re-establish cellular and physiological homeostasis. Panomics pipeline including genomics, transcriptomics, proteomics, metabolomics, epigenomics, proteogenomics, interactomics, ionomics, phenomics, etc., have become very handy nowadays.

Conclusion:

Consequently, integrated multi-omics pipelines enable the comprehensive deciphering of molecular processes, identification of stress-responsive biomarkers, discovery of targets for genetic engineering, and reconstruction of regulatory networks, thereby supporting precision agriculture strategies aimed at enhancing crop-specific abiotic stress tolerance and ensuring food security under changing environmental conditions.

References:

Gao, Y., Jin, Y., Guo, W., Xue, Y. and Yu, L. (2022) Metabolic and physiological changes in the roots of two oat cultivars in response to complex saline–alkali stress. Frontiers in Plant Science, 13, 835414. https://doi.org/10.3389/fpls.2022.835414

Roychowdhury, R., Das, S. P., Gupta, A., *et al.* (2023) Multi-omics pipeline and omics-integration approach to decipher plant abiotic stress tolerance responses. Genes, 14(6), 1281. https://doi.org/10.3390/genes14061281

Liu, L., Si, L., Zhang, L., Guo, R., Wang, R., Dong, H. and Guo, C. (2024) Metabolomics and transcriptomics analysis revealed the response mechanism of alfalfa to combined cold and saline–alkali stress. The Plant Journal, 119, 1900–1919. https://doi.org/10.1111/tpj.16896

Hua Z. (2023) Deciphering the protein ubiquitylation system in plants. J. Exp. Bot. 2023 Nov 21, 74(21):6487-6504. doi: 10.1093/jxb/erad354

John Martin, J. J., Song, Y., Hou, M., Zhou, L., Liu, X., Li, X., Fu, D., Li, Q., Cao, H. and Li, R. (2024) Multi-Omics Approaches in Oil Palm Research: A Comprehensive Review of Metabolomics, Proteomics, and Transcriptomics Based on Low-Temperature Stress. Int. J. Mol. Sci. Jul 13;25(14):7695. doi: 10.3390/ijms25147695.

He, X., Liu, X., Zuo, F., Shi, H. and Jing, J. Artificial intelligence-based multi-omics analysis fuels cancer precision medicine. Semin Cancer Biol. 2023 Jan; 88, 187-200. doi: 10.1016/j.semcancer.2022.12.009. Epub 2022 Dec 31. PMID: 36596352.

Li, G., An, L., Yang, W., Yang, L., Wei, T., Shi, J., Wang, J., Doonan, J. H., Xie, K., Fernie, A. R., Lagudah, E.S., Wing, R.A. and Gao, C.. Integrated biotechnological and AI innovations for crop improvement. Nature. 2025 Jul;643(8073):925-937. doi: 10.1038/s41586-025-09122

Bradbury, A., Clapp, O., Biacsi, A. S., Kuo, P., Gaju, O., Hayta, S., Zhu, J. K., Lambing, C. (2025) Integrating genome editing with omics, artificial intelligence, and advanced farming technologies to increase crop productivity. Plant Commun. 2025 Jul 14, 6(7), 101386. doi: 10.1016/j.xplc.2025.101386

Zhang, H., Zhao, Y. and Zhu, J. K. (2020). Thriving under stress: how plants balance growth and the stress response. Dev. Cell 55, 529–543. doi: 10.1016/j.devcel.2020.10.012

Rai, A., Saito, K. and Yamazaki, M. (2017) Integrated omics analysis of specialized metabolism in medicinal plants. Plant J. 2017 May;90(4), 764-787. doi: 10.1111/tpj.13485

Hu, Y., Wang, X., Xu, Y., et al. (2023) Molecular mechanisms of adaptive evolution in wild animals and plants. Sci China Life Sci. 2023 Mar;66(3):453-495. doi: 10.1007/s11427-022-2233-x

Mittler, R., Zandalinas, S.I., Fichman, Y., Van Breusegem, F. (2022) Reactive oxygen species signalling in plant stress responses. Nat. Rev. Mol. Cell Biol. 2022 Oct;23(10), 663-679. doi: 10.1038/s41580-022-00499-2

Kumar, A., Arora, S., Ogita, S., Yau, Y.-Y. and Mukherjee, K. (Eds.). (2026) *Biotechnological innovations: "Omics" and Sustainable Development Goals*. New Delhi, India: Tech Sar. 342 pp.

Nejat, N. and Mantri, N. (2017) Plant immune system: Crosstalk between responses to biotic and abiotic stresses—the missing link in understanding plant defence. Current Issues in Molecular Biology, 23, 1–16. https://doi.org/10.21775/cimb.023.001

Ha, B. K., Vuong, T. D., Velusamy, V., Nguyen, H. T., Shannon, J. G. and Lee, J. D. (2013) Genetic mapping of quantitative trait loci conditioning salt tolerance in wild soybean (*Glycine soja*) PI 483463. *Euphytica, 193,* 79–88. https://doi.org/10.1007/s10681-013-0919-1

Sheoran, S., Gupta, M., Kumari, S., Kumar, S. and Rakshit, S. (2022) Meta-QTL analysis and candidate genes identification for various abiotic stresses in maize (*Zea mays* L.) and their implications in breeding programs. *Molecular Breeding, 42*, Article 26. https://doi.org/10.1007/s11032-022-01282-5

Tanin, M. J., Saini, D. K., Sandhu, K. S., Pal, N., Gudi, S., Chaudhary, J. and Sharma, A. (2022). Consensus genomic regions associated with multiple abiotic stress tolerance in wheat and implications for wheat breeding. Scientific Reports, 12, Article 13680. https://doi.org/10.1038/s41598-022-17833-7

Selamat, N. and Nadarajah, K. K. (2021) Meta-analysis of quantitative trait loci (QTL) identified in drought response in rice (*Oryza sativa* L.). Plants, 10, Article 716.

Schrimpe-Rutledge, A. C., Codreanu, S. G., Sherrod, S. D. and McLean, J. A. (2016). Untargeted metabolomics strategies: Challenges and emerging directions. Journal of the American Society for Mass Spectrometry, 27(12), 1897–1905. https://doi.org/10.1007/s13361-016-1469-y

Tian, H., Ni, Z., Lam, S. M., *et al.* (2022). Precise metabolomics reveals a diversity of aging-associated metabolic features. *Small Methods, 6*(7), e2200130. https://doi.org/10.1002/smtd.202200130

Cui, L., Lu, H. and Lee, Y. H. (2018) Challenges and emergent solutions for LC–MS/MS-based untargeted metabolomics in diseases. Mass Spectrometry Reviews, 37(6), 772–792. https://doi.org/10.1002/mas.21562

Coene, K. L. M., Kluijtmans, L. A. J., van der Heeft, E., *et al.* (2018) Next-generation metabolic screening: Targeted and untargeted metabolomics for the diagnosis of inborn errors of metabolism in individual patients. Journal of Inherited Metabolic Disease, 41(3), 337–353. https://doi.org/10.1007/s10545-017-0131-6

Yadav, B. G., Aakanksha, Kumar, R., Yadava, S. K., Kumar, A. and Ramchiary, N. (2023). Understanding the proteomes of plant development and stress responses in *Brassica* crops. Journal of Proteome Research, 22(3), 660–680. https://doi.org/10.1021/acs.jproteome.2c00684

Tiwari, J. K., Buckseth, T., Zinta, R., Saraswati, A., Singh, R. K., Rawat, S., Dua, V. K. and Chakrabarti, S. K. (2020) Transcriptome analysis of potato shoots, roots and stolons under nitrogen stress. *Scientific Reports, 10*, Article 1152. https://doi.org/10.1038/s41598-020-58030-6

Conde, D. and Kirst, M. (2022) Decoding exceptional plant traits by comparative single-cell genomics. Trends in Plant Science, 27, 1095–1098. https://doi.org/10.1016/j.tplants.2022.07.002

Li, Y. F., Wang, Y., Tang, Y., Kakani, V. G. and Mahalingam, R. (2013) Transcriptome analysis of heat stress response in switchgrass (*Panicum virgatum* L.). BMC Plant Biology, 13, Article 153. https://doi.org/10.1186/1471-2229-13-153

Spitz, F. and Furlong, E. E. M. (2012) Transcription factors: From enhancer binding to developmental control. Nature Reviews Genetics, 13, 613–626. https://doi.org/10.1038/nrg3207

Friedrich, T., Faivre, L., Bäurle, I. and Schubert, D. (2019) Chromatin-based mechanisms of temperature memory in plants. Plant, Cell & Environment, 42, 762–770. https://doi.org/10.1111/pce.13373

Nguyen, N. H., Vu, N. T. and Cheong, J. J. (2022). Transcriptional stress memory and transgenerational inheritance of drought tolerance in plants. *International Journal of Molecular Sciences, 23*, 12918. https://doi.org/10.3390/ijms232112918

Sharma, M., Kumar, P., Verma, V., Sharma, R., Bhargava, B. and Irfan, M. (2022). Understanding plant stress memory response for abiotic stress resilience: Molecular insights and prospects. Plant Physiology and Biochemistry, 179, 10–24. https://doi.org/10.1016/j.plaphy.2022.03.004

Preissl, S., Gaulton, K. J. and Ren, B. (2023). Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 24(1), 21–43. https://doi.org/10.1038/s41576-022-00509-1

Zhang, D., Deng, Y., Kukanja, P., *et al*. (2023) Spatial epigenome–transcriptome co-profiling of mammalian tissues. *Nature*, *616*, 113–122. https://doi.org/10.1038/s41586-023-05795-1

Suganuma, T. and Workman, J. L. (2008) Crosstalk among histone modifications. Cell, 135(4), 604–607. https://doi.org/10.1016/j.cell.2008.10.036