Review Article

ISAH Indian Journal of Arid Horticulture
Year 2024, Volume-6, Issue-1 (January - June)

Role of metabolome in enhancing crop resilience to abiotic stress in horticultural crops-A review

Abdullah Zaid[1], Anand Singh[2], Akhilesh Kumar Srivastava[2], Vishvajeet Singh[1] and Paramanand Prajapati[1]

[1]Ph.D. Scholar, [2]Professor, Department of Fruit Science, College of Horticulture, Banda University of Agriculture and Technology, Banda

ARTICLE INFO

Received: 05 February 2025
Accepted: 20 February 2025

Keyword: Abiotic stress, metabolomics, phytohormones, proteomics, stress tolerance

doi:10.48165/ijah.2024.6.1.2

ABSTRACT

Abiotic stresses, including drought, salinity, extreme temperatures, and nutrient deficiencies, pose significant challenges to global agriculture, threatening food security and crop productivity. The metabolome, encompassing the complete set of metabolites within an organism, plays a pivotal role in plant responses to such stresses. Metabolomics, the large-scale study of metabolites, provides insights into the biochemical pathways and mechanisms underlying stress tolerance. Plants deploy complex metabolic reprogramming to mitigate stress effects, involving osmoprotectants, antioxidants, phytohormones, and secondary metabolites. For instance, compounds like proline, glycine betaine, and sugars act as osmolytes to maintain cellular homeostasis, while antioxidants such as ascorbate and glutathione mitigate oxidative damage. Stress-responsive phytohormones like abscisic acid (ABA) regulate stomatal closure and activate downstream signaling pathways. Furthermore, secondary metabolites, including flavonoids and alkaloids, contribute to stress resistance by modulating growth and defense. Advancements in metabolomics technologies, such as mass spectrometry and nuclear magnetic resonance, enable comprehensive profiling of stress-induced metabolites, offering opportunities to identify key biomarkers and pathways. These insights facilitate targeted breeding and biotechnological interventions to develop stress-resilient crops. Integrating metabolomics with genomics, transcriptomics, and proteomics can provide a holistic understanding of stress tolerance mechanisms, paving the way for sustainable agricultural practices. This study underscores the critical role of the metabolome in enhancing crop resilience to abiotic stress and highlights the potential of metabolomics in addressing global agricultural challenges through precision breeding and metabolic engineering.

Introduction

The most advanced "omics" study to describe the metabolic profile of living things is metabolomics (Dubery *et al.*, 2013). The metabolome, is a last downstream output of the genome, that is made up of many tiny molecules with

---

Corresponding author: srivastavahort@yahoo.com (Dr. A.K. Srivastava)

molecular masses under 2000 Da that vary greatly in terms of their structure and chemical makeup. Detection followed by identification, and measurement of every molecule (or subset) in biological samples is known as metabolomics (Kumar *et al*., 2016). According to Kosmides *et al.* (2013) metabolomics investigations can identify metabolites from exogenous sources including medications and diets in addition to endogenous metabolites. Accordingly, metabolomics includes a wide range of small molecules or metabolic intermediates, including organic acids, ketones, aldehydes, amines, steroids, amino acids, peptides, lipids, nucleic acids, carbohydrate, vitamins, hormones, signaling molecules, and secondary metabolites like flavonoids and polyphenols (Collino *et al*., 2013).

Metabolomics is a broad word that refers to the comprehensive qualitative and quantitative investigation of the metabolites found in living things under specific environmental conditions (Freund and Hegeman, 2017). Metabolomics reproduces more detailed information on the biological regulatory mechanisms than transcriptomics and proteomics (Dos Santos *et al*., 2017). The study of metabolic profiling of higher plants for the clarification of their stress tolerance mechanisms has benefited greatly from the development of several metabolomics techniques, such as nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry (MS). Over the past fifteen years, various metabolomics techniques have been applied to the study of plants and how they interact with their surroundings. In order to reduce agricultural losses brought on by imposed stresses, metabolic reactions of plants to different stresses are becoming more and more significant. Numerous reports about focused studies looking at metabolites at the level of a specific metabolic pathway have been published. These investigations laid the groundwork for more extensive study conducted over the past 20 years. In plant science, metabolomics is becoming more and more significant for improving plant quality, finding essential natural compounds, and above all evaluating how different abiotic stresses affect a plant's physiology and growth (Genga *et al*., 2011). The rapidly developing field of metabolomics aids in plant phenotyping, which may help to improve the crop plants' nutritional value (Alla *et al*., 2012).

Plant metabolomics is a powerful tool that can be applied in a variety of fields, including fingerprinting of genotypes and ecotypes, comparing mutants with their wild types, determining the activity of bioactive compounds of medicinal plants, and the effects of the environment on plant physiology. This is because plants contain a remarkably diverse range of metabolites when compared to animals (Wolfender *et al*., 2013). A variety of metabolites are produced by plants, some of which are necessary for normal metabolic functions including respiration and photosynthesis (primary metabolites) or for environmental survival (secondary metabolites). Although secondary metabolites are not necessary for plant growth, development, or reproduction, they are critical for plant survival and fecundity, particularly for defense and signaling (Wolfender *et al*., 2013). The number of metabolites in plants is so high that it is estimated that there are 2,00,000 metabolites in total, of which 7000–15,000 are found in each species and approximately 3000–5000 are found in leaves (Kim *et al*., 2010). Over the past 20 years, plant metabolomics has advanced to a promising concept and been cleverly applied in the fields of plant biotechnology and physiology (Cusido *et al*., 2014).

Plant science has effectively used metabolomics techniques like NMR, capillary electrophoresis-mass spectrometry (CE-MS), direct injection mass spectrometry (DIMS), high-performance liquid chromatography (HPLC) with photodiode array detection, thin layer chromatography with ultraviolet (UV) detection, and mass spectrometry (MS) in conjunction with gas chromatography (GC) or liquid chromatography (LC) (Wolfender *et al*., 2013). Plant metabolomics is commonly studied using GC-MS, LC-MS, DIMS, and NMR, among other techniques. The great sensitivity and resolution of MS make it superior to NMR. Prior to being passed via the mass analyzers, the analytes in MS are first ionized. Numerous ionization methods exist, including matrix-assisted laser desorption/ionization (MALDI), rapid atom bombardment, electrospray ionization (ESI), atmospheric pressure chemical ionization, and electron impact ionization (EI). Targeted and nontargeted metabolomics are two types of metabolic techniques that can be used to research the many metabolites found in plants.

According to Li *et al.* (2014), targeted metabolomics is thought to be the most promising method for measuring a subset of metabolites that have been chemically described and interpreted. Because various isomeric forms of the same metabolite exist and cannot be distinguished based alone on their m/z ratio, it is challenging to identify the hundreds of metabolites that are found in untargeted metabolomics. Stress encounters greatly increase the quantity and concentration of metabolites that are typically generated in plants. Understanding the up and down regulation of metabolites is crucial for understanding how plants react to stress. Nonetheless, researches has put forward how the plants' metabolism responded to particular abiotic stressors, such as salinity (Chandna *et al*., 2013), heat (Bokszczanin and Fragkostefanakis, 2013), drought (Seki *et al*., 2007), or heavy metal stress (Sytar *et al*., 2013).

Metabolomics profiling of drought stress

One of the most harmful stresses to plants is drought, especially in areas where plants are irrigated by rain, which causes significant alterations in metabolism. When there is a shortage of water, physiological changes tend to increase water intake and decrease water loss, which has an impact on metabolism. As a result, among biological reactions, osmoregulators which include sugars, polyamines, alcohols, and amino acids, particularly proline accumulate to maintain cell turgor (Chaves *et al.*, 2003). Therefore, a number of metabolomics investigations into drought stress and proline buildup in dehydrated leaves have been conducted in leaf tissues, frequent proline buildup has been documented in a wide range of plants under conditions such as high salinity, heavy metals, and cold temperatures that might result in poor water availability (Hochberg *et al.*, 2013). Most of the metabolomics investigations were conducted on aerial components or primarily leaves. The metabolomics level of dehydration in *Arabidopsis thaliana* L. has been thoroughly investigated. ABA is formed during dehydration, and the species' aerial portion collected polyamines and amino acids in an ABA-dependent way. Raffinose was also produced without the help of this hormone (Urano *et al.*, 2009). Reactive oxygen species (ROS) are induced by drought stress and comprise free radicals (superoxide radicals, alkoxy radicals, and hydroxyl radicals) as well as non-radicals (singlet oxygen and peroxide of hydrogen) (Anjum *et al.*, 2017). These are extremely reactive and poisonous substances that harm proteins, carbohydrates, lipids, and DNA, disrupting cellular equilibrium. According to Davis *et al.* (2014) it has an impact on the plant's height, canopy, root development, and leaf area index. Terpenes, other cyanogenic glucosides, and other volatile components are essential for preventing adverse environmental effects in certain crop plants. Seasonal variations and drought specifically cause these chemicals to release (Griesser *et al.*, 2015). In salvia plants, diterpene provides drought tolerance by inducing the ROS scavenging system (Munn´e-Bosch *et al.*, 2001).

A. *thaliana* aerial portions also acquired flavonols and anthocyanins during water shortage, which may suggest that these chemicals help mitigate drought stress in addition to those biomarkers of drought stress. Drought stress has a greater effect on leaves than on other plant parts (Kang *et al.*, 2019). Analysis of the effects of relative humidity in apple plants revealed that terpenes including α-pinene, camphene, β-pinene, limonene, β-caryophyllene, and (E, E)-α-farnesene are released when relative humidity is low (Vallat *et al.*, 2005). Two MYB transcription factors, MdMYB88 and MdMYB124, control lignin deposition in apple xylem during drought by influencing MdMYB46, another regulator (Geng *et al.*, 2018).

It was discovered that the phytoalexin content of drought-tolerant grapes rose during drought, which further promotes resistance to biotic stress (Hatmi *et al.*, 2015). The impact of water stress on the metabolome depends on the genotype, while several metabolite contents in the leaves of the two wine cultivars (Shiraz and Cabernet Sauvignon) showed similar changes, the cv. Shiraz had more metabolites and less altered stomatal regulation than the other cultivar. In both cultivars, glycerate and galactonate dropped whereas nicotinate was the only organic acid to increase. Additionally, the phenylpropanoid pathway was altered in both genotypes, and specific amino acids (the drought stress-associated proline, as well as threonine, tryptophan, valine, leucine, and phenylalanine) were markedly elevated. Glutamate, however, rose in Shiraz and fell in Cabernet Sauvignon (Hochberg *et al.*, 2013).

Particularly drought-susceptible (DS) and drought-tolerant (DT) cultivars' responses to stress have been characterized thanks to metabolomics methods, which have also made it possible to find possible biomarkers associated with this kind of stress (Guo *et al.*, 2020). Asparagine, methionine, and γ-aminobutyric acid (GABA) all markedly elevated in DT but not in DS. Glycolic, malonic, glucoheptonic, and galactonic acids were among the organic acids that dramatically rose in DT. In DT, there was a notable accumulation of unsaturated fatty acids, such as linolenic and linoleic acids. Furthermore, there was a notable accumulation of secondary antioxidant metabolites in DT, such as fluorine and 5-methoxytryptamine. Additionally, DT showed a considerable rise in phenolic chemicals (ferulic acid, salicylic acid, and 4-hydroxycinnamic acid) and aromatic amino acids (phenylalanine). Both DT and DS cultivars showed a considerable rise in other metabolites, such as glucose-1-phosphate, D-fructose 1, 6-bisphosphate, pyruvic acid, D-glyceric acid, oxalic acid, and 2-methylfumarate. Similarly, amino acids, including proline, glycine, serine, valine, beta-alanine, threonine and isoleucine, accumulated considerably in both DT and DS.

Metabolomics methods have also been used to study the temporal dynamics of metabolite reprograming of DT and DS cultivars under drought stress. The degree of osmotic adjustment and the type of organic solutes that accumulate may also be impacted by the type of drought (acute vs. cyclic), as well as its frequency and intensity. Furthermore, it was discovered that the phytoalexin deficient4 (PAD4) gene, which is associated to phytoalexin production, plays a role in both drought tolerance and biotic interactions (Szechynska-Hebda *et al.*, 2016). While the levels of TCA-cycle metabolites (malate, succinate, alpha-ketoglutarate, and citrate) were greatly reduced, those of glycolysis intermediates (pyruvate, glucose, and dihydroxyacetone phosphate) were drastically lowered as well.

The production of phenylalanine, tryptophan, tyrosine, isoleucine, and alanine may be impacted by a decrease in pyruvate. However, the TCA cycle metabolite oxaloacetate and its amino-acidic byproducts lysine and methionine also dropped. Likewise, temperature stress led to a decrease in sugar alcohols including galactitol and mannitol. Drought reduces the output of monoterpenes in spearmint and rosemary (Delfine *et al.*, 2005).

Zhang *et al.* (2014) found that drought in potatoes caused transcriptional alterations linked to the manufacture of terpene and flavonoids. By changing their metabolic pathways, arbuscular mycorrhization (AM) gives plants the ability to withstand abiotic stress and produce protective SMs. When tomato plants experience drought stress brought on by AM, terpenes and other non-volatile isoprenoids including ABA, chlorophylls, and carotenoids are essential (Asensio *et al*., 2012; Shrivastava *et al*., 2015). Drought causes biochemical alterations in terpinene in cumin. Additionally, phenyl-1,2-ethanediol is converted to cumin aldehyde by water constraint, which may have defensive effects (Rebey *et al*., 2012). Monoterpenes, glucosides, terpenoids, carotenoids, and other volatile organic compounds (VOCs) released during drought in grapes and rosemary were linked to the prevention of drought damage (Liu *et al*., 2014).

Genes such as flavonone-3-hydroxylase, flavonol synthase, and β-carotene hydroxylase-1, which are crucial for the manufacture of flavonoids, carotenoids, and other phenolic compounds, were stimulated at the transcript level in potatoes under drought stress. Drought resistance in potato cultivars is influenced by the expression level of these genes (Fan *et al*., 2008; Andr´e *et al*., 2009). Remarkably, it was discovered that tea cultivars that could withstand drought had higher levels of the metabolites glycine, asparagine, valine, isoleucine, proline, and leucine than cultivars that could not withstand drought. Additionally, it is known that a number of amino acids function as osmolytes in cultivars that can withstand drought (Shi and Chan, 2014).

Metabolomics profiling of heavy metals stress

Heavy metals are defined as those with densities more than 5 gcm^{-3}. Fifty-three of the elements found in nature are classified as heavy metals. Because they are soluble under physiological conditions, 17 of the discovered heavy metals are accessible to living cells and are vital to both the environment and living things. Because they are toxic to living organisms at higher concentrations, several metals, such as Cu, Ni, Zn, Co, Cr, V, and W, are classified as trace elements. Other metals, such as Hg, Ag, Sb, As, Cd, and Pb, seem to be fatal to plants even though they have no direct role in plant physiology or metabolism (Nazar *et al*., 2012). The form in which heavy metals are found in soil is one of the important variables that contributes to their toxicity.

The growth and physiology of various plant species are more adversely affected by metals that are present in soluble and bio exchangeable forms, which also have higher bioavailability. Because they play a major role in vital biological processes, metals like iron, manganese, and copper are necessary for plants in one way or another. In both plants and animals, Fe, Mn, Cu, Mn, and Ni serve as cofactors for the enzymes. Heavy metals are created by the pedogenic and decaying processes of rocks and are classified based on their content in soil. In addition to natural processes, industrialization, fast population growth, the generation of anthropogenic biosolids, and agrochemical wastes raise the risk of heavy metal contamination of soil (Kashem *et al*., 2009). Because heavy metals interfere with the soil's ability to absorb vital mineral nutrients, they negatively impact a plant's metabolism, development, and reproduction.

Cadmium is the most significant heavy metal in terms of its catastrophic effects since it is more soluble and mobile in soil than other heavy metals. Plants require complex physiological and biochemical coordination, protein structure alterations, and metabolite profile variations for proper signaling and stress tolerance in order to withstand the stress caused by heavy metals. Changes in the accumulation of carbohydrates in leaf tissues can be used to measure the impacts of heavy metals (Manivasagaperumal *et al*., 2011).

Additionally, Pb poisoning reduces the mobilization of stored meals, which results in suppression of germination and seedling development due to a decrease in radical production, deterioration of proteolytic activities, and disturbance of cellular osmoregulation (Cokkizgin and Cokkizgin, 2015). Furthermore Because of its detrimental effects on chlorophyll production, transpiration, root growth, and cell division, lead not only slows down seed germination but is also associated with poor seedling growth (Jiang and Liu, 2010). In a study by Nouri *et al.* (2013), tomato plants were exposed to different concentrations of lead in contaminated soil. The results showed several negative impacts on plant growth and development such as reduced germination rate, stunted growth, chlorosis and leaf damage, altered nutrient uptake.

Proline builds up significantly under heavy metal stress and may play a significant part in osmotic adjustment, enzyme structure and function stability, organelle and cellular biomolecule stabilization (Ahmad *et al*., 2011). Nonetheless, a reduction in proline concentration has been noted in hydrophytes such as Ceratophyllum, Wolffia, and Hydrilla in response to Cd exposures (Dhir *et al*., 2004). Because they may neutralize ROS by giving electrons to hydrogen atoms, phenolic substances found in plants, such as flavonoids and lignin, are crucial in the fight against metal stress tolerance.

The phytophenolics have the ability to detoxify H_2O_2 produced in reaction to heavy metal stress by acting as antioxidants. Furthermore, under specific stressors, phytophenolics also function as pro-oxidants. According to reports, many plants treated with high amounts of Cd have higher phenolic acid contents (Sytar *et al*., 2013). Phytochelatins are cysteine-rich polypeptides that aid in metal chelation and are both heavy metal-inducible and heavy metal-binding. Heavy metal accumulation and phytochelatin synthesis have been found to positively correlate in a number of investigations. The phytochelatins are thiolic peptides that are produced primarily from glutamate, cysteine, and glycine by the heavy metal-activated enzyme phytochelatin synthase. These peptides then form complexes with the harmful metal ions and are then carried to the vacuole (Komal *et al.*, 2014). phytohormones such as auxin, cytokinin, and gibberellin can reduce the symptoms of stress By lowering heavy metal absorption and reestablishing growth and primary metabolite levels (Piotrowska-Niczyporuk *et al.*, 2012).

The antioxidant capacity of plants developing under heavy metal stress is increased by phytohormones, which also increase the levels of nonenzymatic antioxidants like glutathione and ascorbate and the activities of antioxidative enzymes. An essential component of the signal transduction cascade that starts the plant stress response are phytohormones.

Metabolomics profiling of salinity stress

Worldwide, salinity is a common abiotic stressor that has a negative impact on crop plant yield (Negrao *et al.*, 2017). Excessive salinity results in ion toxicity and reduced nutrient uptake, osmotic imbalance, and metabolic disorders that disrupt a variety of physiological processes and slow down the plants' overall growth (Meng *et al.*, 2016). Plants react to these negative impacts by altering the metabolite pool, hormone balance, and gene expression at the cellular level.

A plant that is under stress uses less energy than it would otherwise. Alongside the shifts in the concentrations of Alteration of metabolites, including transcriptome and proteome, is also thought to be an adaptation mechanism used by plants. The rise in the cellular accumulation of suitable solutes, which comprises a variety of soluble and neutral organic molecules, is the metabolic reaction that can be best explained. In order to balance the buildup of Na+ in the vacuoles and extracellular spaces, the accumulation of suitable solutes can help lower the cytoplasm's water potential. Three interconnected factors are crucial to establishing tolerance: (1) prevention of damage, (2) restoration of homeostatic conditions under stress, and (3) potential slower growth (Sobhanian *et al.*, 2010).

Osmoprotectants, ROS scavengers, and/or metabolites involved in energy metabolism are among the metabolites whose levels are changed by salinity. Salinity exposure affects the synthesis, storage, and transportation of a variety of primary and secondary metabolites (Fraire-Velazquez and Emmanuel, 2013). While the alterations in the metabolome as a whole in reaction to abiotic stressors have not yet been fully understood, the metabolic changes in response to salt are well characterized (Widodo *et al.*, 2009). Because these metabolic and regulatory pathways are more negatively impacted by salinity, metabolites that serve as a foundation for plants to develop stress tolerance can be categorized as the metabolites of various metabolic and regulatory pathways, such as photosynthesis, amino acid biosynthesis, ROS scavengers, and the tricarboxylic acid cycle (TCA cycle). Upon exposure to stress conditions like salinity, photosynthesis is the most affected physiological process.

The plants' capacity to photosynthesize is reduced in high-salinity environments because there are fewer raw materials available as a result of the roots' diminished ability to absorb minerals and water (Grewal, 2010). Furthermore, the closing of stomata may be the cause of the decrease in photosynthesis since it lowers stomatal conductance, which in turn lowers the rate at which CO_2 diffuses. A decrease in transpiration rate may also be interpreted as a plant adaptation to lessen the amount of salt that is mobilized to the leaf tissues (Wu *et al.*, 2013). Significant accumulation of 3-PGA signifies enhanced Calvin cycle under high salinity (Wu *et al.*, 2013) The two most crucial Calvin cycle enzymes, phosphoribulokinase and sedoheptulose-1, 7-bisphosphatase, are in charge of controlling the cycle throughout the dark/light transition. The metabolites produced by the activities of these enzymes accumulate when they are upregulated in saline environments.

Salinity stress in sugar beet led to a rise in the amount of sugars and sugar derivatives, including trehalose, xylose, mannose, arabinose, inositol, and sucrose (Hossain *et al.*, 2017).Trehalose, which may play a significant role in shielding photosynthetic proteins from this stressor combination, was particularly accumulated by tomato plants exposed to a combination of heat and salinity (Rivero *et al.*, 2014). High salinity also negatively impacts energy metabolism processes like respiration and carbohydrate metabolism in addition to photosynthesis. In order to combat osmotic stress brought on by salt, plants have been shown to accumulate a variety of soluble carbohydrates, including sucrose, hexoses, raffinose, trehalose, mannobiose, and sugar alcohols. As sources of carbon and energy for the cells, soluble carbohydrates are essential to plant metabolism. Salt stress changes the amounts of soluble carbohydrates since the carbohydrate content is linked to several vital physiological functions, including respiration and photosynthesis. In addition to helping with turgor preservation, cell membrane stabilization against ROS effects, and protein breakdown prevention under stress, soluble sugars also function as osmoprotectants under osmotic stress (Lu *et al.*, 2013).

The most crucial metabolites needed by plants exposed to saline environments are amino acids, which balance their cellular osmotic concentration and scavenge reactive oxygen species. According to reports, high salinity conditions raise the amounts of certain amino acids (Zhao *et al.*, 2014). Plants' ability to withstand salt is measured by amino acids such valine, leucine, and threonine (Sanchez *et al.*, 2008). Many plants exposed to high salinity exhibit a decrease in the quantity of arginine, methionine, and cysteine the main components of total free amino acids. Following the commencement of salinity stress, plants accumulate proline as an adaptation mechanism (Kumari *et al.*, 2015). As an osmolyte and a scavenger of ROS, proline is an essential amino acid that builds up during salinity stress and shields cells from harm caused by the salt. Additionally, proline serves as a molecular chaperone to preserve the stability and integrity of enzymes. In addition to altering the GABA shunt and causing the accumulation of different osmolytes like proline, prolonged salinity with high salt dosage also caused shikimate-mediated secondary metabolisms with elevated levels of aromatic amino acids like tyrosine, tryptophan, and phenylalanine (Zhang *et al.*, 2011).

When plants are under stress, ABA serves as a vital transmitter to keep their water status stable. ABA is carried throughout the plants and accumulates in the tissues of the roots and leaves as a result of salinity stress. However, the pH of the xylem/apoplast affects ABA compartmentation, which in turn controls how much ABA the stomata receive. Thus, in stressful situations, ABA affects stomatal opening and shutting, regulating transpirational water loss. The generation of H_2O_2, an intermediary signal for stomatal closure, and the amount of Ca^{2+} in the guard cell's cytoplasm are linked to ABA-induced stomatal closure under salinity (Kim and Wang, 2010).

Metabolomics profiling of cold stress

Cold stress is one of the main elements that determines how plants are organized and how they turn out. It includes both high and low temperature shocks and is thought to be the main abiotic stressor for seedlings (Awasthi *et al.*, 2015). Plant scientists are interested in temperature stress because of climate change, which has a negative impact on agricultural output globally. (Hasanuzzaman *et al.*, 2013). Important physiological processes, such as the equilibrium between primary and secondary metabolites and hormones, or the link between water and membrane consistency, respiration, and photosynthesis, can be harmed by temperature increases Hemantaranjan, 2014). There is ultimately minimal economic gain as a result of the created disruptions, which hinder metabolic development and reduce plant growth and development.

For instance, amino acids are crucial for the production of various proteins, polyamines, phenylpropanoids, glucosinolates, auxins, and indole alkaloids during cold stress, as well as for N fixation into glutamine (Hildebrandt, 2018). Polyamines play a key role in protecting plants under cold stress. They are involved in stabilizing membrane structures and mitigating oxidative damage, especially in the case of freezing temperatures (Székvári, 2011). This amino acid accumulates in plants during stress, including cold stress. It acts as an osmoprotectant by stabilizing proteins and cellular structures, preventing cellular dehydration and oxidative damage. Proline accumulation is commonly observed in many horticultural crops like tomatoes and peppers (Naylor and Morgan, 1974).

Raffinose was found to be a potential biomarker of cold tolerance in Arabidopsis (Korn *et al.*, 2010). Even though ecotypes influence the overall reaction. The majority of this species' heat shock metabolite reactions, including increases in amino acids derived from pyruvate and the TCA-cycle, were similar to those brought on by cold (Kaplan *et al.*, 2004). With global temperatures rising heat is a significant abiotic stressor that consistently affects crops in many nations. It appears that low-temperature-activated signaling triggers modifications in cold-regulated gene expression, which contribute to the active reconfiguration of the metabolome.

Metabolomics mediated crop improvement

The ongoing development of cultivars that can withstand environmental disturbances and generate higher-quality and more abundant product is required because of the growing need for food and fodder. Breeding techniques that are quicker, more accurate, and less expensive are necessary in modern agriculture to increase crop quality and yields (Khakimov *et al.*, 2014). This calls for the creation of biomarkers to assess the quality of finished goods, genetic modification, and high-throughput analytical methods such as metabolomics for crop breeding to increase crop yields under stress.There are numerous benefits of using metabolites as a primary plant phenotype. A valuable technique for examining relationships between phenotypes and QTLs, mQTLs, and Whole Genome Association Studies (GWAS) that use mQTL (mGWAS) to identify and assess changes in metabolic adaption under different stressors in metabolomics (Templer *et al.*, 2017).

Metabolite profiling's ability to identify mQTLs and mGWAS has improved metabolomics' standing in metabolic marker-assisted plant breeding. Numerous mQTLs and mGWAS have discovered a correlation between metabolic content and genomic area in a number of crop species. Phytate in mustard, secondary metabolite composition in rice, vitamin A content, starch content, lignocellulosic biomass quality, and carotenoids in tomatoes, kernel composition, and multi-traits in sugar beets are a few examples. Utilizing mQTL/mGWAS to identify tomato fruit size, flavor, color, and nutrient content has demonstrated that the metabolomics approach is a practical method or instrument for understanding how plants respond to different environmental stressors. As a result, the findings helped breeders to increase crop resistance for several environmental stressors. Therefore, the accuracy and effectiveness of plant breeding are significantly improved by metabolically assisted varietal development (Christ *et al.*, 2018; Hill *et al.*, 2015).

Finding metabolic biomarkers for particular environmental conditions or plant growth stages may result from a thorough analysis of metabolites associated with plant growth and development as well as responsiveness to various stress situations. Nonetheless, the identification of metabolic biomarkers requires the extensive application of univariate in addition to multivariate data analysis of metabolic data. To identify a group of biomarkers to distinct developmental stages and their function during pest interaction, GC-MS-based non-targeted metabolic profiling has been used in rice (Agarrwal *et al.*, 2014). Throughout all of their developmental stages, tomato flesh and seeds showed altered metabolic makeup, which was useful for breeding actions that targeted particular stages. sugars, Fatty acids, organic acids and amino acids, were the main biomarker sets identified by the salinity stress adaptive metabolites of both wild and farmed soybeans (Li *et al.*, 2019).

Finding metabolite indicators that are unique to stages and stress will aid in crop breeding efforts by providing a focused approach. Additionally, new insights on gene annotation are produced by combining data from genomics and metabolomics. Finding the genetic regions controlling the amount and quality of metabolites has been made easier with the use of the integrated omics method (Abdelrahman *et al.*, 2019).

Conclusion

The metabolome plays a pivotal role in enhancing crop resilience to abiotic stress by providing insights into the biochemical and physiological responses plants deploy to survive adverse conditions. Key metabolites, such as osmoprotectants, antioxidants, and secondary metabolites, act as defense agents, helping plants mitigate damage caused by stressors like drought, salinity, heat, and nutrient imbalances. These molecules contribute to maintaining cellular homeostasis, protecting macromolecules, and sustaining metabolic flux under stress conditions. By integrating metabolomics with advanced breeding and biotechnological approaches, researchers can identify stress-resilient crop varieties. Tools such as genome-wide association studies (GWAS) and gene editing technologies like CRISPR-Cas9 can be leveraged to enhance or engineer metabolic pathways linked to resilience. Furthermore, metabolomics aids in understanding the dynamic interactions between plants and their environment, enabling the development of more targeted and sustainable agricultural practices. In summary, the metabolome serves as both a diagnostic tool and a functional component in building crop resilience. Its study not only deepens our understanding of plant stress physiology but also opens avenues for developing climate-resilient crops, which are essential for global food security in the face of environmental challenges.

Acknowledgements

The authors would like to express their thanks and gratitude to the Authorities of Banda University of Agriculture and Technology, Banda for their assistance and support to compile and write the review article.

Conflict of Interest

The authors have no conflict of interest.

References

Abdelrahman, M., Hirata, S., Sawada, Y., Hirai, M.Y., Sato, S., Hirakawa, H., Mine, Y., Tanaka K. and Shigyo, M. 2019. Widely targeted metabolome and transcriptome landscapes of *Allium fistulosum*–A. cepa chromosome addition lines revealed a flavonoid hot spot on chromosome 5A. *Sci. Rep.,* 9(1): 1–15.

Agarrwal, R., Bentur, J.S. and Nair S. 2014. Gas chromatography mass spectrometry based metabolic profiling reveals biomarkers involved in rice-gall midge interactions. *J. Integr. Plant Biol.,* 56(9): 837–848.

Ahmad, P., Nabi, G. and Ashraf, M. 2011. Cadmium-induced oxidative damage in mustard [*Brassica juncea* (L.) Czern. &Coss.] Plants can be alleviated by salicylic acid. *S. Afr. J. Bot.*, 77: 36–44. https://doi.org/10.1016/j.sajb.2010.05.003

Alla, M.M.N., Khedr, A.H.A., Serag, M.M., Abu-Alnaga, A.Z. and Nada, R.M. 2012. Regulation of metabolomics in *Atriplex halimus* growth under salt and drought stress. *Plant Growth Regul.*, 67: 281–304. https://doi.org/10.1007/s10725-012-9687-1

Andr´e, C. M., Schafleitner, R., Legay, S., Lef`evre, I., Aliaga, C. A. A., Nomberto, G., Hoffmann, L., Hausman, J.-F., Larondelle, Y. and Evers, D. 2009. Gene expression changes related to the production of phenolic compounds in potato tubers grown under drought stress. *Phytochemistry,* 70: 1107–1116.

Anjum, S. A., Ashraf, U., Tanveer, M., Khan, I., Hussain, S., Shahzad, B., Zohaib, A., Abbas, F., Saleem, M. F. and Ali, I. 2017. Drought induced changes in growth, osmolyte accumulation and antioxidant metabolism of three maize hybrids. *Front. Plant Sci.*, 8.

Asensio, D., Rapparini, F. and Penuelas, J. 2012. AM fungi root colonization increases the production of essential isoprenoids vs. nonessential isoprenoids especially under drought stress conditions or after jasmonic acid application. *Phytochemistry,* 77: 149–161.

Awasthi, R., Bhandari, K. and Nayyar, H. 2015. Temperature stress and redox homeostasis in agricultural crops. *Front. Environ. Sci.,* 3: 1–24.

Bokszczanin, K.L. and Fragkostefanakis, S. 2013. Perspectives on deciphering mechanisms underlying plant heat stress response and thermo tolerance. *Front. Plant Sci.*, 4: 315. https://doi.org/10.3389/fpls.2013.00315

Chandna, R., Azooz, M.M. and Ahmad, P. 2013. Recent advances of metabolomics to reveal plant response during salt stress. In: Ahmad, P., Azooz, M.M., Prasad, M.N.V. (Eds.), Salt Stress in

Plants. *Springer*, New York, pp. 1–14.

Chaves, M.M., Maroco, J.P. and Pereira, J.S. 2003. Understanding plant responses to drought from genes to the whole plant. *Funct. Plant Biol.,* 30: 239–264.

Christ, B., Pluskal, T., Aubry, S. and Weng, J.K. 2018. Contribution of untargeted metabolomics for future assessment of biotech crops. *Trends Plant Sci.,* 23(12):1047–1056.

Collino, S., Martin, F.P. and Rezzi, S. 2013. Clinical metabolomics paves the way towards future healthcare strategies. Br. *J. Clin. Pharmacol.*, 75:619–629. https://doi.org/10.1111/j.1365-2125.2012.04216.x

Cusido, R.M., Onrubia, M., Sabater-Jara, A.B., Moyano, E., Bonfill, M. and Goossens, A. 2014. A rational approach to improving the biotechnological production of taxanes in plant cell cultures of Taxus spp. *Biotechnol. Advt*., 32: 1157–1167. https://doi.org/10.1016/j.biotechadv.2014.03.0

Davis, R., Earl, H. and Timper, P. 2014. Effect of simultaneous water deficit stress and Meloidogyne incognita infection on cotton yield and fiber quality. *J. Nematol*., 46: 108.

Delfine, S., Loreto, F., Pinelli, P., Tognetti, R. and Alvino, A. 2005. Isoprenoids content and photosynthetic limitations in rosemary and spearmint plants under water stress. *Agric. Ecosyst. Environ*., 106: 243–252.

Dhir, B., Sharmila, P. and Saradhi, P.P. 2004. Hydrophytes lack potential to exhibit cadmium stress induced enhancement in lipid peroxidation and accumulation of proline. *Aquat. Toxicol*., 66:141–147. https://doi.org/10.1016/j.aquatox.2003.08.005

Dos, Santos., V.S. Macedo., F.A. do Vale, J.S., Silva, D.B. and Carollo, C.A. 2017. Metabolomics as a tool for understanding the evolution of Tabebuiasensulato. *Metabolomics,* 13:72.

Dubery, I., Tugizimana, F., Piater, L. and Dubery, I. 2013. Plant metabolomics: a new frontier in phytochemical analysis. *S. Afr. J. Sci*., 109: 1–11. https://doi.org/10.1590/sajs.2013/20120005

Fan, M., Jin, L. P., Huang, S. W., Xie, K. Y., Liu, Q. C. and Qu, D. Y. 2008. Effects of drought on gene expressions of key enzymes in carotenoid and flavonoid biosynthesis in potato. *Acta Horticulturae Sinica,* 35: 535.

Fraire-Velazquez, S. and Emmanuel, V. 2013. Abiotic stress in plants and metabolic responses. Abiotic Stress - Plant Responses. *Appl. Agric.*, https://doi.org/10.5772/54859

Freund, D.M. and Hegeman, A.D. 2017. Recent advances in stable isotope-enabled mass spectrometry-based plant metabolomics. *Curr. Opin. Biotechnol*., 43: 41–48. https://doi.org/10.1016/j.copbio.2016.08.002

Geng, D., Chen, P., Shen, X., Zhang, Y., Li, X., Jiang, L., Xie, Y., Niu, C., Zhang, J. and Huang, X. 2018. MdMYB88 and MdMYB124 enhance drought tolerance by modulating root vessels and cell walls in apple. *Plant Physiol*., 178: 1296–1309.

Genga, A., Mattana, M. and Coraggio, I. 2011. Plant Metabolomics: a characterization of plant responses to abiotic stresses. Abiotic Stress Plants *Mech. Adapt*., 1–43. https://doi.org/10.5772/23844

Grewal, H.S. 2010. Water uptake, water use efficiency, plant growth and ionic balance of wheat, barley, canola and chickpea plants on a sodic vertosol with variable subsoil NaCl salinity. *Agric. Water Manag*., 97 (1): 148–156. https://doi.org/10.1016/j.agwat.2009.09.002

Griesser, M., Weingart, G., Schoedl-Hummel, K., Neumann, N., Becker, M., Varmuza, K., Liebner, F., Schuhmacher, R. and Forneck, A. 2015. Severe drought stress is affecting selected primary metabolites, polyphenols, and volatile metabolites in grapevine leaves (*Vitis vinifera* cv. Pinot noir). *Plant Physiol. Biochem*., 88: 17–26.

Guo, X., Xin, Z., Yang, T., Ma, X., Zhang, Y., Wang, Z., Ren, Y. and Lin, T. 2020. Metabolomics response for drought stress tolerance in Chinese wheat genotypes (*Triticum aestivum*). *Plants*, 9: 520.

Hasanuzzaman, M., Nahar, K., Alam, M., Roychowdhury, R. and Fujita, M. 2013. Physiological, Biochemical, and Molecular Mechanisms of Heat Stress Tolerance in Plants. *Int. J. Mol. Sci.,* 14: 9643–9684.

Hatmi, S., Gruau, C., Trotel-Aziz, P., Villaume, S., Rabenoelina, F., Baillieul, F., Eullaffroy, P., Cl´ement, C., Ferchichi, A. and Aziz, A. 2015. Drought stress tolerance in grapevine involves activation of polyamine oxidation contributing to improved immune response and low susceptibility to *Botrytis cinerea*. *J. Exp. Bot*., 66: 775–787.

Hemantaranjan, A. 2104. Heat stress responses and thermo tolerance. *Adv. Plants Agric. Res.,* 1: 1–10.

Hildebrandt, T. M. 2018. Synthesis versus degradation: directions of amino acid metabolism during Arabidopsis abiotic stress response. *Plant Molecular Biology,* 98: 121–135.

Hill, CB., Taylor, JD., Edwards, J., Mather, D., Langridge, P., Bacic, A. and Roessner, U. 2015. Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. *Plant Sci.,* 233:143–154.

Hochberg, U., Degu, A., Toubiana, D., Gendler, T., Nikoloski, Z., Rachmilevitch, S. and Fait, A. 2013. Metabolite profiling and network analysis reveal coordinated changes in grapevine water stress response. *BMC Plant Biol.,* 13: 184.

Hossain, M. S., Persicke, M., El-Sayed, A. I., Kalinowski, J. and Dietz, K. J. 2017. Metabolite profiling at the cellular and subcellular level reveals metabolites associated with salinity tolerance in sugar beet. *Journal of Experimental Botany,* 68: 5961–5976.

Jiang, W. and Liu, D. 2010. Pb-induced cellular defense system in the root meristematic cells of *Allium sativum* L. BMC *Plant Biol*., 10: 1–40.

Kang, Z., Babar, A., Khan, N., Guo, J., Khan, J., Islam, S., Shrestha, S. and Shahi, D. 2019. Comparative metabolomic profiling in the roots and leaves in contrasting genotypes reveals complex mechanisms involved in post-anthesis drought tolerance in wheat. *PLoS ONE,* 14, e0213502.

Kaplan, F., Kopka, J., Haskell, D.W., Zhao, W., Schiller, K.C., Gatzke, N. and Guy, C.L. 2004. Exploring the Temperature-Stress Metabolome of Arabidopsis. *Plant Physiol.,* 136: 4

Kashem, M.A., Kawai, S., Kikuchi, N., Takahashi, H., Sugawara, R., and Singh, B.R. 2009. Effect of Lherzolite on chemical fractions of Cd and Zn and their uptake by plants in contaminated soil. *Water. Air. Soil Pollut*., 207: 241–251. https://doi.org/10.1007/s11270-009-0132-7

Khakimov, B., Bak, S. and Engelsen, SB. 2014. High-throughput cereal metabolomics: current analytical technologies, challenges and perspectives. *J. Cereal Sci.,* 59 (3):393–418.

Kim, H.K., Choi, Y.H. and Verpoorte, R. 2010. NMR-based metabolomic analysis of plants. *Nat. Protoc*., 5: 536–549. https://doi.org/10.1038/nprot.2009.237

Kim, T.W. and Wang, Z.Y. 2010. Brassinosteroid signal transduction from receptor kinases to transcription factors. *Ann. Rev. Plant Biol.,* 61: 681–704. https://doi.org/10.1146/annurev.arplant.043008.092057

Komal, T., Mustafa, M., and Kazi, A.G. 2014. Heavy metal induced adaptation strategies and repair mechanisms in plants. *J. Endocytobiosis Cell Res*., 25, 33–41.

Kosmides, A.K., Kamisoglu, K., Calvano, S.E., Corbett, S.A. and Androulakis, I.P. 2013. Metabolomic fingerprinting: challenges and opportunities. *Crit. Rev. Biotechnol*., 205–221.

Kumar, M., Kuzhiumparambil, U., Pernice, M., Jiang, Z. and Ralph Peter, J. 2016. Metabolomics: an emerging frontier of systems biology in marine macrophytes. *Algal Res*., 16: 76–92. https://doi.org/10.1016/j.algal.2016.02.033

Kumari, A., Das, P., Parida, A.K. and Agarwal, P.K. 2015. Proteomics, metabolomics, and ionomics perspectives of salinity tolerance in halophytes. *Front. Plant Sci*., 6:1–20. https://doi.org/10.3389/fpls.2015.00537.

Li, K., Wang, X., Pidatala, V.R., Chang, C.P. and Cao, X. 2014. Novel quantitative metabolomic approach for the study of stress responses of plant root metabolism. *J. Proteome Res.,* 13:5879–5887. https://doi.org/10.1021/pr5007813

Li, X., Peng, T., Mu, L. and Hu, X. 2019. Phytotoxicity induced by engineered nanomaterials as explored by metabolomics: perspectives and challenges. *Ecotoxicol. Environ. Saf.,* 184:109602

Liu, F., Xu, G., Wu, X., Ding, Q., Zheng, J., Zhang, R. and Gao, Y. 2014. Effect of drought stress and re-watering on emissions of volatile organic compounds from *Rosmarinus officinalis*. *J. Zhejiang A&F Univ*., 31: 264–271.

Lu, Y., Lam, H., Pi, E., Zhan, Q., Tsai, S. and Wang, C. 2013. Comparative metabolomics in Glycine max and Glycine soja under salt stress to reveal the phenotypes of their offspring. *J. Agric. Food Chem.,* 61: 8711–8721. https://doi.org/10.1021/jf402043m

Manivasagaperumal, R., Balamurugan, S., Thiyagarajan, G. and Sekar, J. 2011. Effect of zinc on germination, seedling growth and biochemical content of cluster bean (*Cyamopsis tetragonoloba* (L.) Taub). *Curr. Bot*., 2:11–15.

Meng, F., Luo, Q., Wang, Q., Zhang, X., Qi, Z. and Xu, F. 2016. Physiological and proteomic responses of diploid and tetraploid black locust (*Robinia pseudoacacia* L.) subjected to salt stress. *Sci. Rep*., 14: 20299–20325. https://doi.org/10.3390

Munn´e-Bosch, S., Mueller, M., Schwarz, K. and Alegre, L. 2001. Diterpenes and antioxidative protection in drought-stressed Salvia officinalis plants. *J. Plant Physiol*., 158:1431–1437.

Naylor, A. W. and Morgan, P. W. 1974. Metabolism of proline and other amino acids during water stress. *Plant Physiology*, 53(6):929–935.

Nazar, R., Iqbal, N., Masood, A., Khan, M.I.R., Syeed, S. and Khan, N.A. 2012. Cadmium toxicity in plants and role of mineral nutrients in its alleviation. *Am. J. Plant Sci*., 3:1476–1489. https://doi.org/10.4236/ajps.2012.310178

Negrão, S., Schmöckel, S.M. and Tester, M. 2017. Evaluating physiological responses of plants to salinity stress. *Ann. Bot*., 119:1–11. https://doi.org/10.1093/aob/mcw191

Nouri, J., Khoshgoftarmanesh, A. H. and Mardani, A. 2013. Lead toxicity on tomato (*Solanum lycopersicum*) plants and its effect on growth, physiological, and biochemical parameters. *Environmental Toxicology and Chemistry*, 32(4):858-866.

Okkizgin, A. and Cokkizgin, H. 2015. Effects of lead ($PbCl_2$) stress on germination of lentil (*Lens culinaris* Medic.) lines. *Afr. J. Biotechnol*., 9:8608–8612.

Piotrowska Niczyporuk, A., Bajguz, A., Zambrzycka, E. and Godlewska Zylkiewicz, B. 2012. Phytohormones as regulators of heavy metal biosorption and toxicity in green alga *Chlorella vulgaris* (Chlorophyceae). *Plant Physiol. Biochem*., 52:52–65. https://doi.org/10.1016/j.plaphy. 2011.11.009

Rebey, I. B., Jabri-Karoui, I., Hamrouni-Sellami, I., Bourgou, S., Limam, F. and Marzouk, B. 2012. Effect of drought on the biochemical composition and antioxidant activities of cumin (*Cuminum cyminum* L.) seeds. *Ind. Crop. Prod.*, 36:238–245.

Rivero, R. M., Mestre, T. C., Mittler, R., Rubio, F., Garcia-Sanchez, F. and Martinez, V. 2014. The combined effect of salinity and heat reveals a specific physiological, biochemical and molecular response in tomato plants. *Plant, Cell & Environment,* 37:1059–1073.

Sanchez, D.H., Lippold, F., Redestig, H., Hannah, M.A., Erban, A. and Krämer, U. 2008. Integrative functional genomics of salt acclimatization in the model legume Lotus japonicas. *Plant J.,* 53:973–987.

Seki, M., Umezawa, T., Urano, K. and Shinozaki, K. 2007. Regulatory metabolic networks in drought stress responses. *Curr. Opin. Plant Biol*., 10:296–302. https://doi.org/10.1016/j.pbi.2007.04.014.

Shi, H. and Chan, Z. 2014. Improvement of plant abiotic stress tolerance through modulation of the polyamine pathway. *J. Integr. Plant Biol*., 56:114–121.

Shrivastava, G., Ownley, B. H., Aug´e, R. M., Toler, H., Dee, M., Vu, A., Kollner, T. G. and Chen, F. 2015. Colonization by arbuscular mycorrhizal and endophytic fungi enhanced terpene production in tomato plants and their defense against a herbivorous insect. *Symbiosis*, 65:65–74.

Sobhanian, H., Motamed, N., Jazii, F.R., Nakamura, T. and Komatsu, S. 2010. Salt stress induced differential proteome and metabolome response in the shoots of *Aeluropus lagopoides* (Poaceae), a halophyte C4 plant. *J. Proteome Res*., 9:2882–2897. https://doi.org/10.1021/pr900974k

Sytar, O., Kumar, A., Latowski, D., Kuczynska, P., Strzałka, K. and Prasad, M.N.V. 2013. Heavy metal-induced oxidative damage, defense reactions, and detoxification mechanisms in plants. *Acta Physiol. Plant,* 35:985–999. https://doi.org/10.1007/s11738-012-1169-6

Szechynska-Hebda, M., Czarnocka, W., Hebda, M. and Karpinski, S. 2016. PAD4, LSD1 and EDS1 regulate drought tolerance, plant biomass production, and cell wall properties. *Plant Cell Rep*., 35:527–539.

Székvári, P. 2011. Polyamines and their role in cold stress tolerance of plants. *Acta Biologica Hungarica*, 62(2):179-190.

Templer, S.E., Ammon, A., Pscheidt, D., Ciobotea, O., Schuy, C., McCollum, C., Sonnewald, U., Hanemann, A., Förster, J., Ordon, F. and von Korff, M. 2017. Metabolite profiling of barley flag leaves under drought and combined heat and drought stress reveals metabolic QTLs for metabolites associated with antioxidant defense. *J. Exp. Bot.,* 68 (7):1697–1713.

Tschaplinski, T.J., Abraham, P., Jawdy, S.S., Gunter, L., Martin, M.Z., Engle, N.L., Yang, X. and Tuskan, G. 2019. The nature of the progression of drought stress drives differential metabolomic responses in *Populus deltoides*. *Ann. Bot.,* 124:617–626.

Urano, K., Maruyama, K., Ogata, Y., Morishita,Y., Takeda, M., Sakurai, N., Suzuki, H., Saito, K., Shibata, D. and Kobayashi, M. 2009. Characterization of the ABA-regulated global responses to dehydration in Arabidopsis by metabolomics. *Plant J.,* 57:1065–1078.

Vallat, A., Gu, H. and Dorn, S. 2005. How rainfall, relative humidity and temperature influence volatile emissions from apple trees in situ. *Phytochemistry,* 66:1540–1550.

Widodo, Patterson, J.H. Newbigin., E. Tester., M. Bacic, A. and Roessner, A. 2009. Metabolic responses to salt stress of barley (*Hordeum vulgare* L.) cultivars, Sahara and Clipper, which differ in salinity tolerance. *J. Exp. Bot*., 60, 4089–4103. https://doi.org/10.1093/jxb/erp243

Wolfender, J., Rudaz, S., Choi, Y.H. and Kim, H.K. 2013. Plant metabolomics: from holistic data to relevant biomarkers. *Curr. Med. Chem*., 20:1056–1090.

Wu, D., Cai S., Chen M., Ye L., Chen Z. and Zhang H. 2013. Tissue metabolic responses to salt stress in wild and cultivated barley. *PLoS One,* 8. https://doi.org/10.1371/journal.pone.0055431

Zhang, J., Zhang Y., Du Y., Chen S. and Tang H. 2011. Dynamic metabolomic responses of tobacco (*Nicotiana tabacum*) plants to salt stress. *J. Proteome Res*., 10:1904–1914. https://doi.org/10.1021/pr101140n

Zhang, N., Liu, B., Ma, C., Zhang, G., Chang, J., Si, H. and Wang, D. 2014. Transcriptome characterization and sequencing-based identification of drought-responsive genes in potato. *Mol. Biol. Rep*., 41:505–517.

Zhao, X., Wang, W., Zhang, F., Deng, J., Li, Z. and Fu, B. 2014. Comparative metabolite profiling of two rice genotypes with contrasting salt stress tolerance at the seedling stage. *PLoS One,* 9:1–7. https://doi.org/10.1371/journal.pone.0108020