

Innovations in the Molecular Mechanisms in Plants and Different Biological Applications

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Abstract

For their protection during the very adverse conditions produce different types of primary and the secondary metabolic compounds. As these stresses progressed in plants, a multi - gene response is triggered which caused changes in many of the proteins, signaling molecules, primary and secondary metabolites, amino acids and so on. The metabolism in plants is disrupted which leads to metabolic enzymes inhibition, substrates shortage, an increased demand of some particular compounds or all these factors combination. In this review, we showcase various kind of abiotic stresses which harms the plant. We also describe how the time scale variable stresses impact profile of secondary metabolites which could be used to identify different stresses. This paper has ability to attract researchers' attention operating on the quantitative trait locus mapping with metabolites and also metabolomics genome wide linkage.

Keywords: Environmental stress, Signaling pathways, Secondary metabolites, Transcription factors, Networks.

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1. INTRODUCTION

As plants are sessile in nature, bears to several types of environmental stresses. The undesirable environmental conditions include biotic stress such as herbivores invasion and pathogenic infections [1, 2]. Abiotic stress includes salinity, cold, drought, heat stress [2, 3], toxicants [4, 5], and the deficiency of nutrients. The main stressors that affect the productivity of plant and food production are salt, temperature and drought [5]. Thus, improving plant stress resistance is essential for better production from agriculture as well as the environment stability, because the crops having less tolerance to stresses intake more fertilizer and water, putting a pressure on environment [6]. Plants make a variety of natural products in response to environmental stimulus. These organic products which are produced in the plants through metabolic-pathways that are an important component of plant growth for the abiotic and biotic stresses [7]. The abiotic and biotic stress products can be primary or secondary metabolic

byproducts that are generated via epigenetic and genetic controlled processes [8]. Furthermore, their transportation necessarily involves an extra regulation [9]. Plants respond differently to abiotic and biotic stresses. Biotic signals are induced by receptors, whereas abiotic signals are sensed by perturbing the plasma membrane [1, 9]. Abiotic stresses have received more attention than biotic stresses due to the ease with which it can be studied in terms of secondary metabolites and plant physiology [10]. According to the most recent literature, grapevine accumulates metabolites such as trehalose, betaine, and glycine as an osmoprotectant against the salt stress [2, 8]. The researchers also examined the ROS detoxifying enzymes activity, which become highly activated in response to lipid peroxidation induced by O₂ and H₂O₂. The miRNA and transcriptomic approaches based on the next generation sequencing help in regulatory genes identification involved in resistance to abiotic stresses in legume crops of diverse range [2].

Research on the peach plants revealed differences in biochemical, gene expression and physiology during the drought stress versus normal conditions. Furthermore, under stress, plants gathered proline and sorbitol contents in contrast to sucrose, fructose, and glucose [33]. Systems biology strategies are being used to learn about the roles of regulators, gene regulatory systems, transcriptional factors and pathways in the biosynthesis of different plant metabolites under various environmental and physiological conditions [10]. The phenolic compounds are plant's most distributed natural substance [11]. Many of the phenolic compounds, like esters, glycosides, flavonoids, amides, and some others, can be found in the leaf extract of vascular plants [12]. Furthermore, polymeric-phenolics like suberin, melanin and lignin are commonly found in these plants [13]. Plant metabolites, as opposed to proteins and mRNA transcripts, are a composite of expression of genes, protein-interaction, and different regulatory processes that are closer to phenotype. As a result, plant metabolites are used to investigate the molecular phenotypes of plants as a response to oxidative conditions in order to explore unique patterns associated with stress tolerance [6].

2. Environmental Stresses in Plants Metabolism

Biotic-stress is the main cause of crop yield declines globally. Crop productivity is reduced due to the abiotic stresses like drought, high temperature and salinity [11]. As a result, crop loss is determined by the severity, duration, and the developmental status of plant that is subjected to environmental stress. Drought high levels of stress that inhibits the growth and development of plant. Drought stress reduces the carbon dioxide assimilation capacity of plant and also lowered the photosynthetic efficiency. Drought inhibits CO₂ diffusion into the sub-stomatal chamber, causing closure of stomata and reduction in the rate of photosynthesis. PSII is lowered by reducing Carbon diffusion by inducing production of H₂O₂ and photorespiration [12]. Excessive production of anti-oxidant compounds like phenols, glutathione and ascorbic acid causes oxidative stress in the plants [12]. Drought stress can alter the ratio of carotenoids and chlorophyll a and b content. Catharanthus roseus and Cotton both showed a decrease in chlorophyll concentration during the drought [13]. Flavonoids and anthocyanins formed during the drought can assist plants in resisting to drought stress. The purple color chilly is more resistant to drought stress as compared to green cultivar [8].

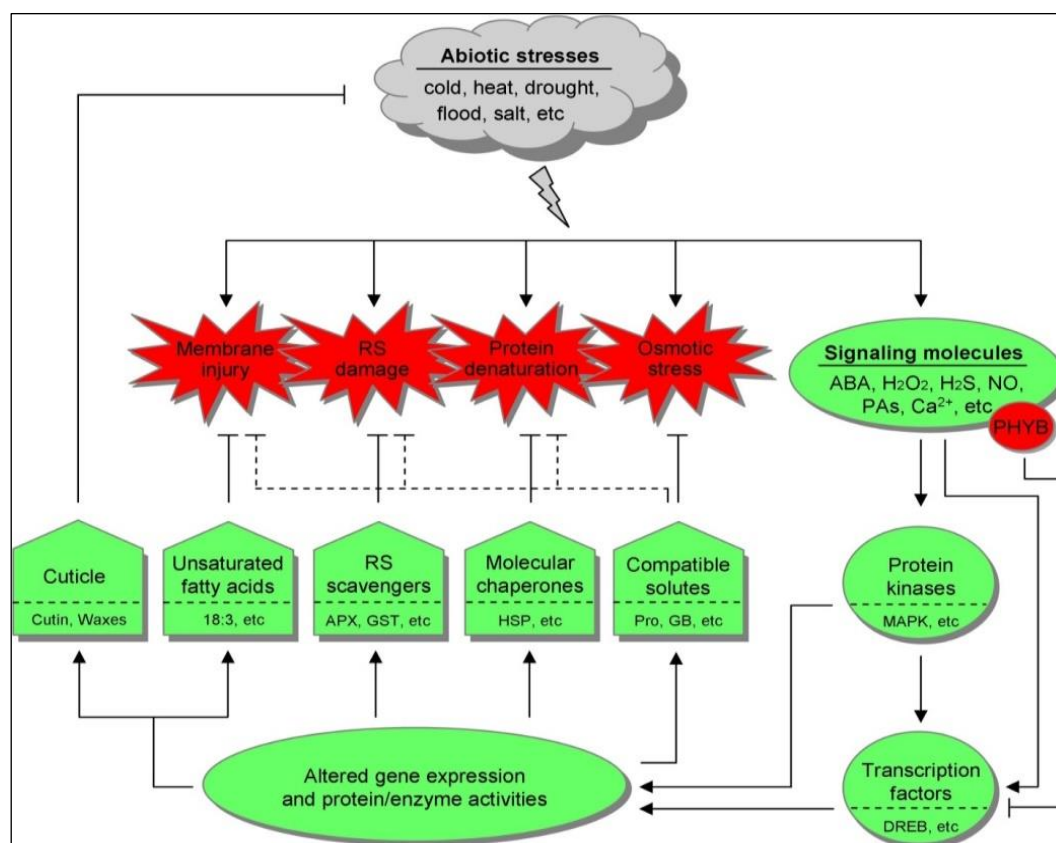


Fig. 1: Effect of environmental stresses in the metabolism of plants

Drought stress causes several amino acids accumulation such as isoleucine, leucine, and valine which work as precursor for the polyamines.

Carbohydrates and their alcohols are formed in short terms as a response to drought that is not governed by ABA-signaling, whereas amino acids are noticed

in long-term as a response to ABA-signaling [10]. Long term drought causes a metabolic-shift in the glycolysis and cycle of tri-carboxylic acid as well as a decrease in aminobutyric acid [28]. One other abiotic stress that reduces the development and growth of plant is salt stress. It causes the accumulation of salt near root zones of the plants that also causes the plant toxicity and osmotic effects due to the accumulation of saline ions in meristematic tissues of plants. Anthocyanin, polyphenolic compounds and Jasmonic acid accumulate as the result of salinity stress [14-16]. The levels of anthocyanin in the salinity sensitive plants are reduced by salinity stress [17]. Metabolism of plant is affected by the temperature stress. The temperature stress has an impact on the stability of nucleic acid, stability of protein, efficiency of enzyme and can lead to early leaf fall [18].

Heat stress causes plasma membrane damage, which can function as a temperature sensor. Heat stress also causes the PSII, ETC, and the ATP generating system damage [19]. Heat stress reduces the β -carotene in the Brassicaceae family [20], while in *Panax quinquefolius* increases the secondary root metabolites and leaf senescence [17]. Crop productivity is also reduced by heat stress, and temperatures above the freezing (0 to 15 °C) are a significant constraint in the production of crop. Cold stress causes reduction of photosynthesis and ROS formation in crops [16].

In reaction to cold stress, plants make cryoprotectants, which include low - molecular - weight nitrogenous compounds such as sugar alcohols, glycine, and proline [21]. To acclimate to extreme cold, the plants also generate suberin and lignin deposits [22-26]. Ultra violet light is also an environmental factor that limits growth and development of plant. Plants produce numerous metabolites in the protection of UV, for instance, Ultra violet light (280 to 320 nm) induces

the production of anthocyanin in apples when coupled with the red light [27]. When compared to a culture retained in complete darkness for ten days, the culture subjected to constant intensity of light (300 to 600 lx) accumulates more pigments. Light irradiation rises the accumulation of anthocyanin in strawberry and *Daucus carota* cell cultures [28]. Ultra violet (300 to 400 nm) can cause the accumulation of flavonoids in pea plants root [29].

2.1. Abiotic Stresses Influence Primary Metabolites

It is critical to produce a wide range of crops tolerant to stress in order to better know the processes of response of plants to multiple concurrent abiotic stresses. This procedure also illustrates the various metabolites production that aid in plant survival under unfavorable situations. In response to various difficult weather conditions, the plant initiates a physiological reaction at transcriptional level that initiates post-translational protein changes that further affect accumulation and alteration of metabolites, resulting in a specific physiological-response in contradiction of abiotic stresses [29]. Metabolism of plant can be disrupted due to lack of substrate or enzymes; these can also be disrupted due to the high demand for a specific compound and the gathering of such factors. The metabolic pathways are affected by the rise and decline of secondary metabolites as a result of the plant's growth conditions and the other units such as proteome and transcriptome. These are in charge of the linked metabolites synthesis. The several intermediate signaling streams have been isolated as abiotic stress progresses [7]. Without quantitative measurement, these secondary metabolites can be used as metabolic-fingerprinting to recognize the metabolic signatures linked to a particular stress response. The information is then subjected to a pattern detection study to detect features unique to a fingerprint, as each stress has distinct metabolites [30].

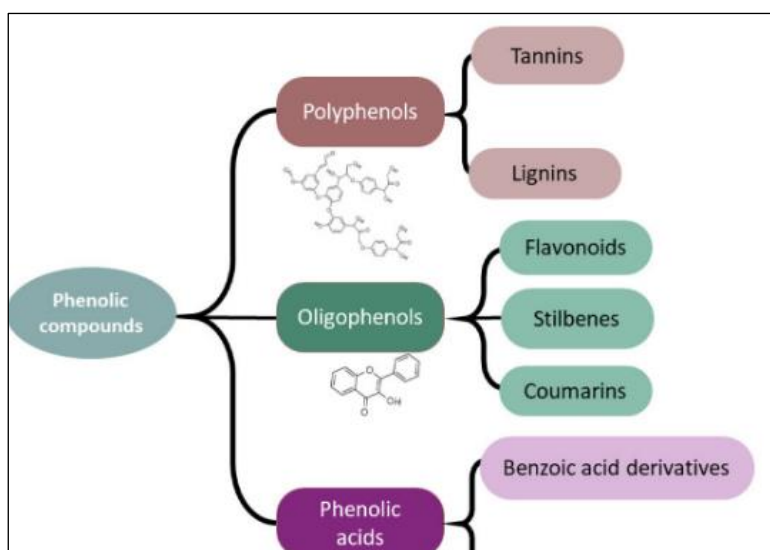


Fig. 2: Shows the nature of different bioactive compounds

2.2. Abiotic Stress Signaling and Impacts in Plants

Biotic stress, such as salinity, cold, osmotic stress, heavy metals, oxidative stress, and heat stress raises free calcium levels in the plants, which can be observed using a sensor known as reduced hyperosmolality induced calcium increase 1 referred to simply as OSCA1. In comparison to wild type plants, mutants with the compromised OSCA1 demonstrate very little calcium when blended with mannitol and sorbitol -osmotic stress material [31]. MSL-8 is an another osmotic-stress-sensor that is important for pollens, need to protect pollens from hypo-osmotic-shock. Furthermore, COLD-1 is also a cold-stress-sensor needed for rice chilling sensitivity [32]. Essential channels found in the plants include glutamate-receptor-like channels and cyclin-nucleotide-gated channels. These are the cells that play a critical role in the Ca^{2+} signals production during the stress [33, 34]. The phospholipid membranes fluidity can be affected by the cold and heat stress that is identified by the receptor like kinases, membrane proteins and channels [34]. Heat stress is also detected by the molecular chaperones, which discharge heat stress transcriptional factors which initiate heat responsive genes [22, 27]. H2A variant is another tremendous heat stress sensor, which folds DNA more firmly than H2A when stressed. Heat shock proteins and some other genes decompose the H2A.Z-nucleosome to form the DNA more accessible to pol-II transcription [25].

Salinity of soil is the major issues limiting production of agriculture around the globe. Sodium ions toxicity, oxidative stress, and hyperosmotic stress are all caused by increased salt-meditation [34]. The sodium ions stress causes calcium binding to the EF-hand calcium binding proteins calmodulin and the B subunit of calcineurin CnB to become inflamed. SOS3 identifies calcium signaling, which is initiated by salt stress, and initiates a serine-protein-kinase SOS2. In the plasma membrane, SOS2 initiates the Na^+/H^+ antiporter SOS1 [35]. This is long distance carrier -HKT1 that unpacks Sodium ions from roots xylem to prevent Sodium ions from entering the transpiration point. Since it loads Sodium ions in the phloem for backflow to the root during salt stress [36].

During the cold stress metabolism of plant is influenced by the enzymes involved in metabolism and also by gene expression reprogramming [15]. Chilling stress increases the formation of transcription factors in the temperate region plants, and also AP2 domain protein CBFs, that activate the expression of the cold sensitive COR-genes [15]. The ICE1 bHLH transcriptional factor regulates CBF-genes through proteasomal-degradation, which is influenced by SUMO E3 ligase SIZ1 [15]. Cold stress causes plastid reversing signal tetrapyrrole to initiate diurnal oscillations in the CBF [36]. Cold stress may have an influence fluidity of membrane that is identified by

plasma membrane proteins and calcium ion channels. As a consequence, calcium ion responsive protein kinases and MAPK flows are activated to control COR-gene-expression [37].

2.3. Secondary Metabolites Synthesis as Defensive Molecules during the Abiotic Stresses in Plants

In Arabidopsis plant abiotic stress demonstrate that secondary-metabolites play no role in monotonous plant growth. Secondary-metabolites are synthesized from the primary-metabolites through processes involving hormonal signaling, transcriptional factors and amino acid metabolism [35-38].

Isoprenoids are important plant metabolites that are produced in chloroplasts to maintain abiotic stresses. Because of volatility in their nature, these are evaporable from the plant tissues. Production of isoprenoid occurs in response to drought, heat and osmotic stress with auxins signal transduction pathways regulating physiology and protecting the plants from the ROS [39]. Mevalonate, non-mevalonate units and tocopherol are main isoprenoids products. Lignin is a vital phenylpropanoids by-product produced in the abiotic stresses via MYB and C2H2Zn transcription factors via auxin and ABA signaling. During a stress condition, biosynthesis of lignin includes strengthening and acclimation the cell wall of plant. Plants wilt in cold and dry conditions, but the inclusion of lignin aids in transport of water. Formation of lignin promotes less cell expansion and the development. Because of lignin, the plant cell wall becomes watertight, limiting apoplastic transport through the use of ion selection [8]. Alkaloids are the secondary nitrogen containing compound present in vascular plants. This may be found in the gymnosperms and monocots [3, 9, 12].

The primary purpose of alkaloids is to protect the crops from the infection of microbes and the attack of herbivores by producing toxic chemicals such as pyrrolizidine-alkaloids (PAs). Melatonin is a toxic chemical which has a strong antioxidant potential when contrasted to the vitamins and is found in both plant and animal species. Melatonin is essential for the reproduction, development, growth, and seed germination of plant. During the period of stress, this substance can interact with the ROS to gives oxygen. The derivatives of melatonin include N-acetyl-5-methoxykynuramine (AMK) and 3-hydroxymelatonin (3OH-Mel). Both of these derivatives of melatonin have higher anti - oxidant properties, that safeguard the plants from the oxidative stress [35-39].

3. CONCLUSION

Plants' ability to tolerate abiotic stresses is primarily determined by their ability to maintain appropriate levels of primary metabolic activities and protection mechanism. During the adverse environmental conditions, various secondary metabolites are manufactured, that are species specific

at specific stress stimuli. Figure 1 depicts the plant's cellular level defence mechanism in response to the abiotic stresses. For the characterization and identification of secondary metabolites, the current metabolomics field relies on the mass-spectrometry and magnetic-resonance. It is critical to integrate the results of metabolomics with biological sciences in order to obtain a good knowledge of metabolomics. Nevertheless, the integration is hindered by the lack of data in the system and insufficient participatory models among omics.

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