Abiotic stress signaling in plants and transgenic technology as a triumph: A review

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ABSTRACT

The plants are exposed seasonally and continuously to various environmental and biodiversity stresses that inhibit and affect their life processes from seedling to harvest stage. Several irregularities are seen in light intensity, temperature, mineral and water availability, etc. These changes keep on challenges the plant to grow and reproduce itself and produce several environmental signals. To receive these signals, the plants themselves develop a signaling network with several receptors such as phytohormones, G-protein-coupled receptors, kinases, and hormone receptors. Signal transduction produces a cellular response in plants which initiates the physiological and developmental responses. This article reveals a keen and in-depth analysis of several mechanisms and perceptions of signal transduction during exposure to several kinds of abiotic stresses in plants, along with a generic pathway of signaling in plants. Plant abiotic stress often plays a pivotal role in causing losses through salinity, heat, cold, drought, etc. To understand and overcome these problems through conventional breeding, which was mainly dependent on genetic variations, several studies are going on model plants such as *Arabidopsis*, rice, and *Brachypodium*; the accessibility of sources for these genomes is in the processing stage in wheat. On the other hand, the advancements in genome editing opened the doors for scientists to incorporate the desired trait in a particular plant species. The emerging developments in the second-generation genome editing technologies like CRISPR/cas9 paved the path for plant biologists to develop a trait more efficiently and rapidly, unlike conventional breeding methods. This review plots the importance of signaling during abiotic stress and transgene technology to prevail over abiotic stress in plants by ingesting desired traits in a plant.

1. INTRODUCTION

Plants are living entities exposed to continuous variable conditions that challenge their life from seedling to harvesting stage, leading to lower yield and creating major complications biotically and abiotically to researchers and scientists working all over the globe. This includes pathogens, insect-pests, nematodes as biotic agents, and abiotic factors such as heat, cold, nutrient deficiencies, heavy metal toxicities, drought, and salinity [1,2]. A fundamental question arises that "how plants overcome these adverse conditions and maintain their balance is the primary question of concern." When a plant is exposed to a certain kind of stress, it triggers a broad spectrum of responses that alter gene expression, cellular metabolism, variations in growth rate, and a sharp decline in yields. Regularly increasing in environmental pollution, it's evident that the future is exposed to rapid abiotic changes and leads to develop an atmosphere which is unfavorable to plant growth and development, and hence, there is an urgency to improve varieties that are resilient to abiotic stresses to promise food security and safety in preceding years. The probability of survival during stressful conditions will be high if the plants grown in biologically diverse soil and agroclimatic situations. Signaling in plants usually involves three basic steps those includes reception, transduction, and response. Growth and productivity of crops are hampered largely due to the abiotic stresses and under the present context of climate change, there is the requirement for the adaptation of suitable measures. For this, there is a need to understand the molecular mechanism for the development of suitable varieties combatting ill effect of abiotic stresses [3].

The activation of a single and different signal transduction network permits plants to acknowledge these particular stimuli. Furthermore, those signaling networks are the reason for average growth and development and communication with the external environment under specific growth conditions. These complex signaling mechanisms also allow plants to develop memory "intelligence" and "behavior" although there is a lack of a nervous system [4]. The research evidences of the past decade clearly indicated that the biochemical and genetic approaches supported the prominence of various signaling pathways in *Arabidopsis*. Along with these, stimulation of a linear and compound

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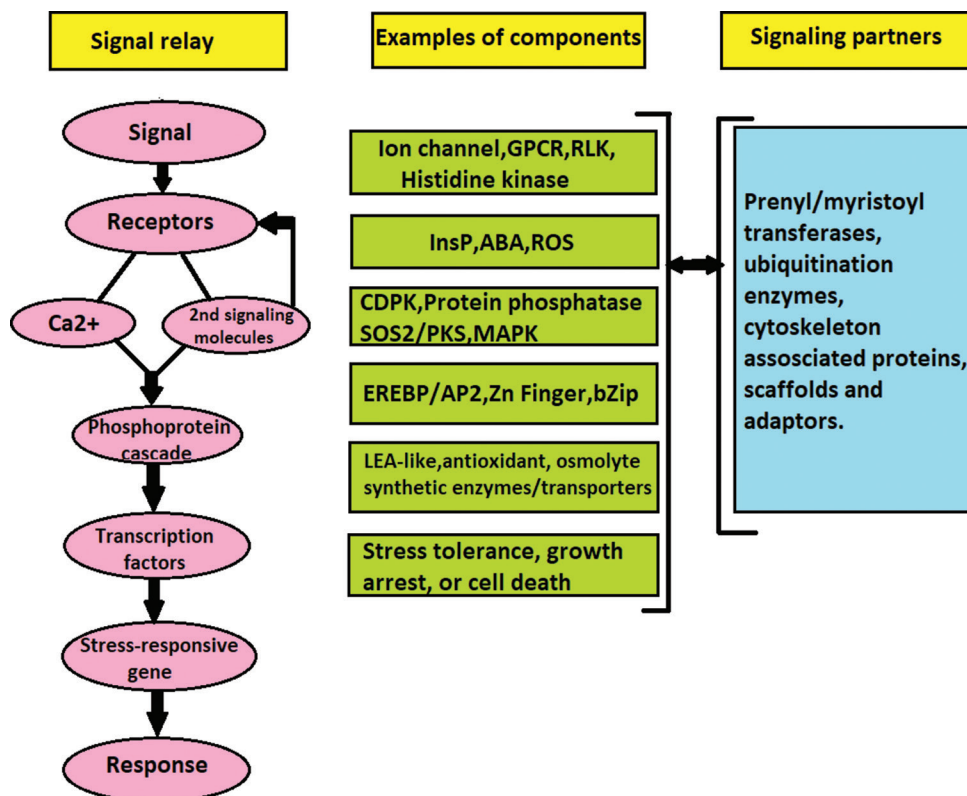*E-mail: dinkargaikwad02 @ gmail.com*

Figure 1: A generic pathway revealing signaling route in plants along with examples of components and the cascade of steps that a plant undergoes to produce a response when the plant experienced particular stress; this pathway varies according to the availability of components and kind of abiotic stress in which a plant is exposed.

Table 1: Transgenes that have been shown to confer resistance to one or more abiotic stresses.

S. No.	Transgene	Source	Transferred to	Function	Purpose
1.	Hva1	Barley	Rice	A Class-3 Lea protein	Salt stress
2.	Cor47	-	Rice	A low-temperature responsive gene product	Salt stress
3.	ADC*	Oat	Rice	Arginine decarboxylase	Salt stress
4.	P5CS	Moth bean	Tobacco	Proline-5-cabosylate synthetase	Salt stress
5.	betA	*E. coli*	Tobacco	Choline dehydrogenase+	Salt stress
6.	hsf	-	Tobacco	Heat shock factor (transcription factor)	Heat stress
7.	betB	*E. coli*	Tobacco	Betaine aldehyde dehydrogenase++	Osmotic stress
8.	SacB	*Bacillus subtilis*	Tobacco	Fructan accumulation	Drought stress
9.	codA	*Arthrobacter globiformis*	*Arabidopsis*	Choline oxidase**	Salt stress
10.	ACD1*	*Arabidopsis*	*Arabidopsis*	Arginine decarboxylase1	Freezing stress
11.	ACD2*	*Arabidopsis*	*Arabidopsis*	Arginine decarboxylase2	Drought stress

*Genes of polyamine (PA) biosynthesis, **converts choline into glycine betaine, +converts choline into betaine aldehyde, ++converts betaine aldehyde into glycine betaine transcriptional repression.

signaling response has been generated after going through particular external stress stimuli. The compound response leads to crosstalk with critical plant signaling pathways and is also linked to the plant's specific capability to overcome different environmental abiotic stress conditions [Figure 1].

After plants are exposed to stress, it stimulates various chemicals, hormonal, and secondary messengers that change their response to stress. In this regard, calcium and ABA play prime roles in plant signaling during stress [5]. Various abiotic factors following create an impact during plant stress that may be perceived by the plant's same or diverse parts [6]. In addition, different abiotic stresses perceived by the plant would induce simultaneous signaling in relation to specific abiotic stress and counteracting responses inclusive of the stimulation of high stress-responsive cascade of hormones, metabolites, and single grouped canopy-wide stomatal responses [7,8]. The activating of stress responsible signals in plants raises a new question of concern by Kollist *et al.* [9] "Are the plants capable enough of integrating different systemic signals that simultaneously originate at the same or different parts of the plant during stress combination?" They further addressed this question through systematic and local studies on *Arabidopsis thaliana* using two leaves of the same plant.

However, during these days, with the rapid advancements of novel generation sequencing technologies and nanopore sequencing [10] and the QTLs mapping identification [11], a dependable holistic approach is required for improvement of crops. In the future, genome editing technologies will act as a highly approachable elucidation for accurately recognizing exact loci and contrasting plant breeding tool that allows the incorporation of a particular gene of interest at an unambiguous location, which prompts the change to a nucleotide succession of qualities. It may help reshaping the current alleles with various analogs [12].

2. STRESS SIGNALING IN PLANTS: A CATARACT OF CELLULAR AND MOLECULAR CELL EVENTS

In nature, survival of plants and tolerance to different stresses were acquired to make their responses suitable to the environment. Plant responses to stress appropriateness are controlled by signaling pathways at the molecular and cellular levels. The knowledge of environmental stress begins the signals activating the downstream signaling and transcriptional processes alerting the parallel pathways. The signal transduction pathway is the beginning step; the role of the signaling during transduction is performed by receptors/sensors, phytochromes, kinases (histidine in nature), and G-protein-coupled receptors (receptor-like kinases, hormones, etc.). Further, the accumulation of secondary signaling molecules such as reactive oxygen species (ROS), ABA, and inositol phosphatase is activated. In due course, the secondary molecule-mediated modification cellular Ca^{2+} levels take place, which leads to the start of protein phosphorylation cascade, mitogen-activated protein kinase (MAPK), calcium-dependent protein kinase (CDPK), protein phosphatase, (SOS_3/protein kinase), transcription factors, and stress-responsive genes. To incorporate genetically controlled stress tolerance characters in crops, a keen consideration both the endpoints and the specificity of the essential signaling pathways are required [13]. Plant sensors can be categorized into primary and secondary messengers, which signify the overall signal transduction in plants. Primary sensors include hormones, neurotransmitters, and autocrine agents. Whereas, secondary sensors are complex and include inositol phosphatases, ROS, and ABA enter into the cell to trigger a response and act as anchors for producing intracellular signal transduction.

3. CALCIUM SIGNALING

Ca^{2+} is an essential, ubiquitous secondary sensor triggered immediately when a plant underwent specific abiotic stress signaling. Specific Ca^{2+} signatures or waves are responsible for these signaling events. These Ca^{2+} signatures are transduced through an extensive network of sensors and relay proteins, channels, exchangers, and pumps [14]. CDPKs and the SOS_3 family of Ca^{2+} sensors play a prominent role in blending this calcium signal to protein-specific phosphorylation cascades. In addition to this, reduction in Ca^{2+} mobility, localization, and higher spatial concentration levels are eased by the richness of buffering Ca^{2+} sensors [15]. The Ca^{2+}/CaM-binding protein kinases and Ca^{2+}-dependent protein kinases in plants perform transcriptional activity of heat-shock proteins [16]. CDPKs involve in gene expression and transcriptional activities, whereas SOS_3 helps in implicating ion synthesis. A straightforward experiment demonstrated by Sheen [17] who revealed that CDPK in stress signal transduction has an outcome from experiments. An active At-CDPK1 enhanced the stress-responsive HVA1 promoter operated reporter gene in maise protoplasts, especially in leaf. Plants themselves possess various presumed Ca^{2+} sensors, including a vast family of calmodulin-like proteins. The Ca^{2+}-mediated

signaling contains different proteins bonded and controlled by CaM and called CaMBP [18]. The examples of CaMBP, that may stimulate the CaM, include "small nuclear NTPases, glutamate decarboxylase, NAD-kinases, Ca^{2+} ATPases (ER and tonoplast located), kinesin-like CaMBP, heat-shock proteins and few transcription factors" of essential primary loop family.

4. ROS

ROS play a prominent role as a secondary messenger during signal transduction. Although limited information was evident on ROS controlled promotion of the redox-sensing mechanisms and the correlated signaling pathways [19], the functioning contribution of ROS-promoted signaling in the triggering of defense genes and afterward tolerance to stress or specific salutation responses has been discovered. The ROS production in plants is greatly triggered with mtΔψ. Increase in mtΔψ was accelerated by extracellular ATP. Usually, the H_2O_2 molecule is a kind of ROS as a by-product of oxidative stress H_2O_2 performs as a signaling molecule due to its high stability and longer half-life [20]. The H_2O_2 secreting from apoplastic polyamine oxidase has played a balancing role in the plant response between cell death and stress tolerance [21]. ROS may accelerate downstream signal cascades through Ca^{2+} [22]. The H_2O_2 plays an important role in signal transduction response as a by-product of proline [23]. The H_2O_2 plays a crucial role in the transduction of ABA signals in *Arabidopsis* through controlled of phosphatase activity: Protein phosphatase 2C (PP2C) enzymes ABI_1 and ABI_2. Both ABI_1 and ABI_2 act as repressive agent regulators of ABA signaling. In the rouse of H_2O_2 and glutathione, both ABI_1 and ABI_2 are repressed [24].

5. ABA SIGNALLING: A CENTRALIZED AND REGULATORY PATHWAY

ABA is anchored as a key secondary messenger in plants, especially during signal transduction, and plays an inevitable role during different reactions. One of the most muddled advances in stress ABA signaling recently has been the identification of ABA receptors, for example, pyrabactin resistance (PYR)/PYR1 kind of components (PYL)/RCAR [25]. The prime role of ABA is to control stress tolerance (especially during osmotic stress) through cellular dehydration tolerance genes and control plant water balance through guard cells. The genes for dehydration response are RD22 and RD29B, and systemic studies have been carried under these genes. ABA promotes the RD22 gene during drought and salt stress and often requires protein synthesis for mRNA synthesis. Fourteen different members of the protein family are called regulatory components of ABA receptor, which includes from RCAR1–RCAR14, or PYR1 and PYR1-like 1–13 proteins [26]. The discovery of PYLs initiated the basis for the ABA signaling mechanism in detail. ABA is accountable by the PYR1 and PYR1-like membrane proteins. On binding of ABA, PYR1 binds and inhibits ABI_1. When SnRK2s are revived from inhibition, they activate several transcription factors from the ABA responsive element-binding factor (ABF). ABFs lead to changes in a significant kind of gene expression. Around 10% of plant genes are found to be controlled by ABA [27]. Further, studies reviled that in the presence of ABA, ABI_1/PP2C function is repressed by ABA, which promotes RCARs at higher levels of H_2O_2. The alteration of ABA signals into suitable cell reactions where SnRKs (2/3/6/7/8)/CDPK phosphorylate the downstream spots [28].

The plants use ABA to control the stress effect, it may constantly change ABA signaling phases founded on physiological and environmental to

hold the growth processes. The bZIP subfamily members (AREB2/ABF4, AREB1/ABF2, and ABF3) are promoted by ABA, dehydration, and high salinity; likewise, Fujita *et al*. [29] mentioned that the overexpression of these factors led to the building up of drought tolerance in plants. To incorporate the role of AREB/ABF TFs in stress-related responses in vegetative tissues, a tripe mutant (areb1/areb2/abf3) is discovered. This tripe mutant is more resistant than single and double mutant in terms of primary root growth and reduced drought tolerance [30]. Microarray analysis found an altered responsive gene expression. The discovery of the LOS-5 and LOS-6 mutants outlined a prominent role of ABA in controlling osmotic stress regulation of gene expression. Although lower levels of ABA did not appear to be highly effective for the expression of DREB2A (coding for a drought stress-specific transcription factor). ABA signaling might be necessary for controlling the activity of DREB2A or its related factors in the activation of the DRE class of genes [31]. ABA signaling in plants is categorized into two types: ABA-dependent signaling [Figure 2] and ABA-independent signaling [Figure 3]. ABA has different gene families activated after exposure to other stresses, including bZIP,

NAC, MYB, and bHLH/CBF/DREB kind of gene families that contain several stress-responsive genes.

6. ROLE OF ETHYLENE IN ABIOTIC STRESS

Ethylene use in plants is not only restricted up to the ripening of fruits but also it indulges in various developmental activities along with several responses when plants face abiotic stresses. Ethylene synthesis triggers during different environmental stresses. Enzymes such as amino cyclopropane-1-carboxylic acid, synthases, and oxidases are responsible for ethylene biosynthesis [32]. Biosynthesis of ethylene is usually a feedback mechanism which involves different signaling agents such as nitric oxide (NO) and hydrogen sulfide. The synthesis of ROS and its signaling was supported by ethylene during different abiotic stresses, namely, heavy metal, low temperature, drought, and flood. Ethylene sensory system acts as a constitutive triple response which leads plants to have short shoots and increased the lateral root growth which indirectly helps the plant to overcome different abiotic stresses. Ethylene responds positively in salt stress tolerance [33].
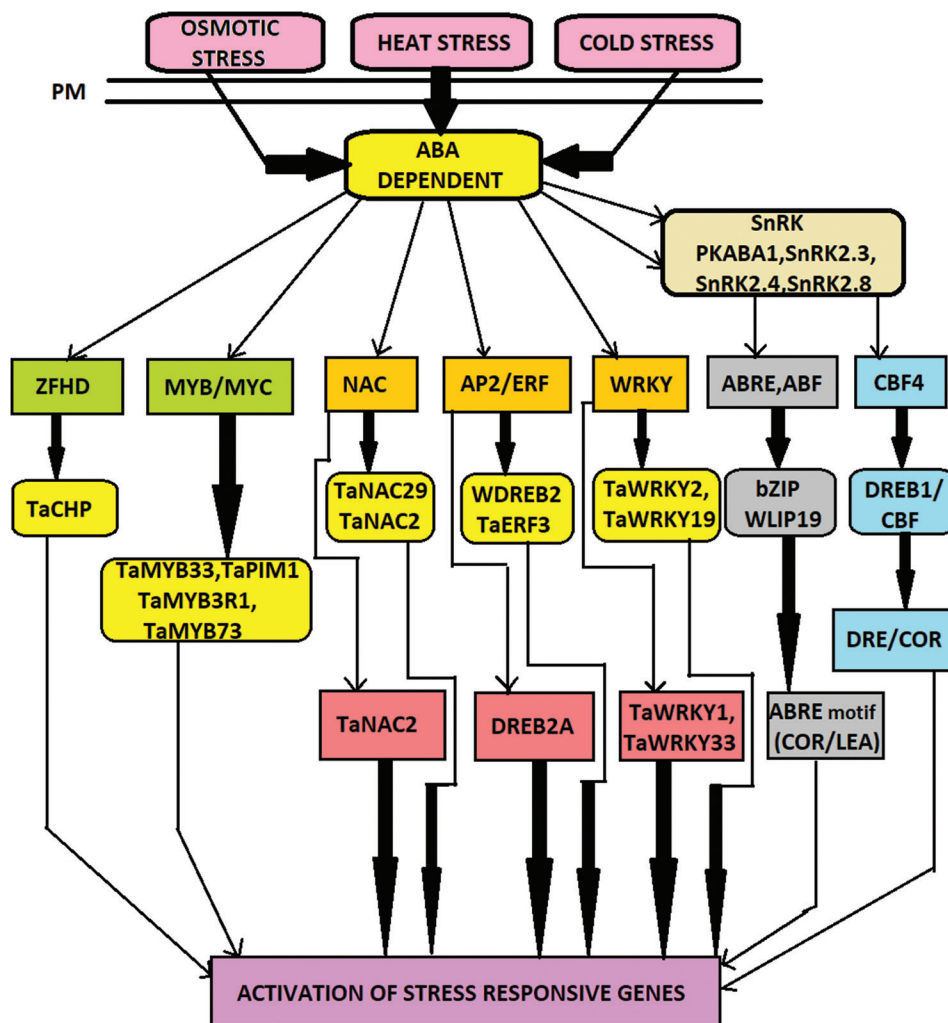

Figure 2: ABA-dependent signaling pathway during different temperature stress. During heat stress, ABA signaling was controlled through NAC, AP2/ERF, and WRKY transcription factors (TFs). During osmotic stress, the signaling was controlled by ZFHD, MYB/MYC, and TFs. All these TFs ultimately lead to downstream activating of stress-responsive genes. Cold stress controls the ABA-independent pathway through CBF/DREB1 TFs. The los5 mutation alters (primarily reduces) the induction of different stress-responsive genes by cold and blocks the promotion of RD29A, COR15, COR47, RD22, and P5CS by osmotic stresses [31].
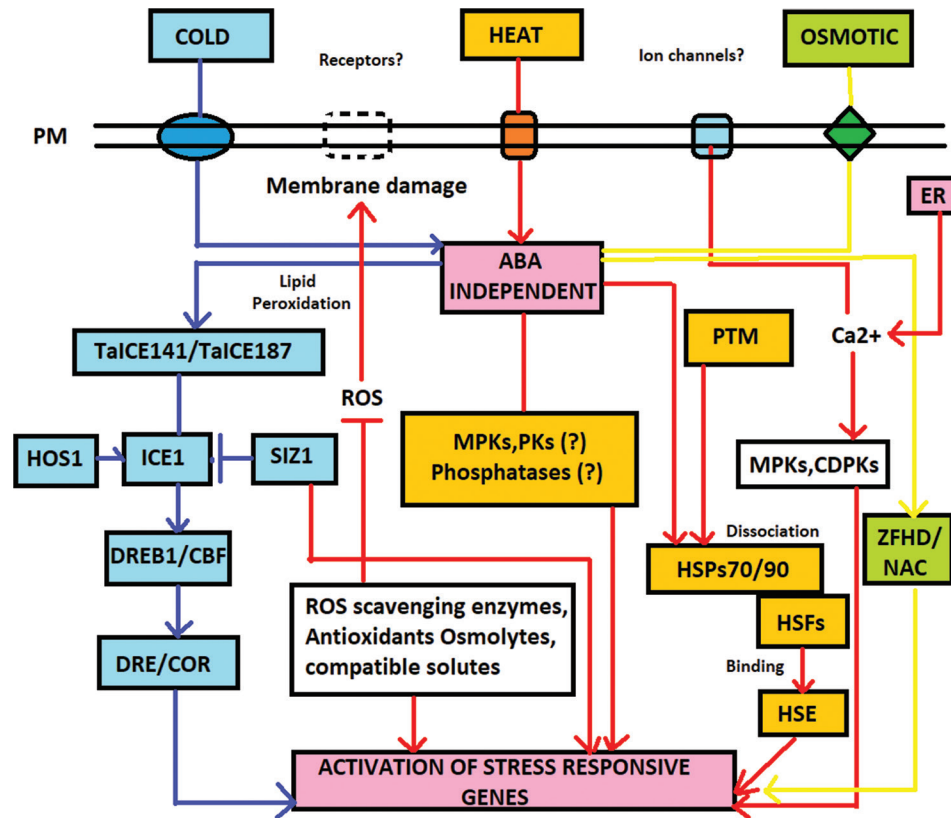
Figure 3: ABA-independent pathway in exposure to various abiotic stresses. Ion channels like OSCA1 and COLD1 control stress. Cold stress in ABA-independent signaling is controlled by ICE1 involving DREB. In contrast, osmotic stress is mediated by ZFHD/NAC TFs. In heat stress, the stress response is induced through ROS. This, in turn, activates MPKs, PKs, and other phosphatases, which can trigger HSFs. Several ABA-inducible genes include a reserved, ABA-responsive cis-acting element called ABRE (ABA-responsive element PyACGTGGC) in their promoter regions. The ABREs core motif, ACGT, is located in G-boxes of various genes alternative to different physiological and environmental conditions.
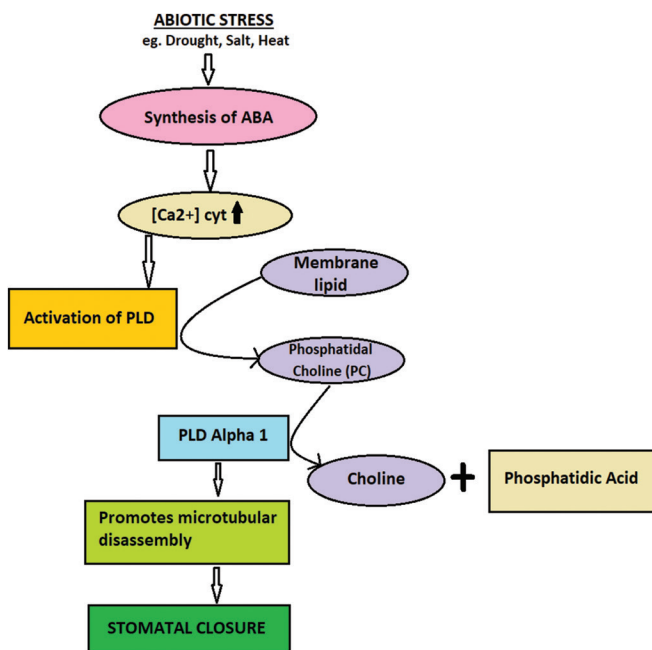

Figure 4: Crosstalk between different factors such as ABA, phosphatidic acid, and phospholipid signaling during different abiotic stresses responses through phospholipase D (PLD) by triggering different immunity responses [45].

During abiotic stresses, ethylene signaling usually depends on ROS concentration of the plants [32]. Ethylene plays the key role during the regulation of the metal stress, especially cadmium which is one of the most phytotoxic inorganic ions stimulating the biosynthesis of ethylene in plants [34]. Furthermore, ethylene directs the plants development and photosynthesis processes under both stressed and normal conditions. Ethylene is a well-known ruler of flood tolerance in plants. Ethylene accumulation increases in paddy field during water lodging conditions which shows an opposite action to ABA.

7. ROLE OF CYTOKININ SIGNALING IN ABIOTIC STRESS

Cytokinin not only helps in cell division and differentiation but also the recent discoveries reveal that cytokinin can be responsible for developing plant immunity under abiotic and biotic stresses [35]. Cytokinins are the derivatives of adenine and purines. The role of cytokinin during abiotic stresses is related with the regulation of hormonal balance and interactions with other hormones such as ethylene, ABA, salicylic acid, and jasmonic acid. Cytokinin has both positive and negative impacts in plant abiotic stresses. Isopentenyl transferase gene from *Agrobacterium tumefaciens* was inserted into the tobacco genome to control the stress inducible promoter. The similar work was done in transgenic rice and groundnut which ultimately increased the cytokinin levels and showed an enhanced drought tolerance [36].

8. NO SIGNALING

The NO has been proven as a crucial factor to overcome different abiotic stresses in plants by activating the enzymatic and non-enzymatic systems. Being a highly reactive and abundant, NO signaling plays a dynamic role in enhancing metabolic activities of plants. NO is involved in the regulation of multiple processes of plants during their growth, development, reproduction, and responses to the external environment and biotic interactions. It has become apparent that NO is formed and utilized as a signaling and defense cue by both partners in multiple forms of plant interactions with their microbial counterparts, ranging from symbiotic to pathogenic modes [37]. Testing of NO releasing nanoparticles on plants is highly relevant, as those can replace chemical NO donors both in plant research and in possible agricultural applications [38]. NO improves plant potential to cope up with the abiotic stresses by boosting plant growth, photosynthetic activity, stomatal conductance, accumulation of compatible solutes, maintains ion homeostasis, and reverse oxidative damage by stimulating antioxidant defense apparatus. It also alters the expression of defense-associated genes, and thereby, influences the phenotypic response of plant genotypes [39]. NO is both extra- and intra-cellular messenger which promotes several physiological and molecular mechanisms. These secondary messenger molecules are produced due to the reaction of L-arginine to L-citrulline by NO synthase. NO regulates its action through proteins, namely, ADP ribosyl transferase and guanylate cyclase. In plants, nitrate reductase helps in the synthesis of NO by catalyzing NADPH independent reduction of nitrate to NO. Along with NO synthesis, this pathway also involves in ABA-regulated stomatal closure.

9. CYCLIC NUCLEOTIDE SIGNALING

It is a single phosphate nucleotide with a bond arrangement between sugar and phosphate group. Usually, nucleotides are made up of three components, namely, a pentose sugar, nitrogenous base, and single phosphate group. The most prominent nucleotide includes cAMP and cGMP. They have a broad spectrum of protein ligand reactions which can be identified as secondary messengers. They act as secondary messengers through relaying the signals of primary messengers such as hormones and neurotransmitters [40]. These act as secondary messengers due to transmission of signal that activates in enzymes interiorly and known as adenylyl cyclase. Their synthesis is derived from common components such as ATP and GTP. The rise in the cAMP in cell occurs through changing the molecular activities in the cytoplasm using protein kinase A which acts as a dependent protein kinase that phosphorylates target protein. The cGMP nucleotide is synthesized by means of GTP using the enzyme guanylyl catalase cGMP and acts as a secondary messenger for NO. The effects of cGMP are mediated through protein kinase G. Along with these, nucleotides IP3 (inositol-1,4,5-triphosphate) is also plays the role of a secondary messenger which diffuses through cytosol and binds to receptors which are present in endoplasmic reticulum releasing the Ca ions in cytosol for activating the response. Cyclic nucleotides also implicate lot of functions such as stomatal closure, gene transcription, pathogen attack, seed germination, pollen tube growth, chloroplast development, and cation fluxes.

10. CROSSTALK BETWEEN MOLECULES

Crosstalk between several molecules during abiotic stress helps in the survival against the ill effects and steady development of plants. Each signaling component which is participating in different signaling pathways leads to the formation of cross-talking network which coordinates responses to different stress. The increase in Ca^{2+} ultimately increases the phospholipase (PLD) which activates biotic and abiotic stresses. The PLD is differentiated into various gene families whose functions are categorized into abiotic and biotic stresses. PLD α gene family helps in the closure of stomata and, in turn, induces the synthesis of PA and triggering of MPK6 which increases the salt stress tolerance in plants [Figure 4] [41]. PLD delta activity increases during dehydration stress [42]. ABA, which is the primary phytohormone, responds to plant abiotic stress and activates PLD that hydrolyzes the membrane lipid to phosphatidylcholine further inducing the stomatal closure [43]. The intracellular rise in Ca^+ levels mediated by ABA helps to trigger PLDs by regulating the binding of Ca^+ to PLDs [44,45]. MAPKs cascades of reactions act as a converging point for different abiotic stress signaling pathways by amplifying and integrating signals from a diverse range of stimuli and elicit an appropriate physiological response inclusive of cellular proliferation, differentiation, and development. The basic mechanism underlying in the functioning of genes is important for developing transgenic plants. Each stress is a multigenic trait, and therefore, the manipulation may result in alteration of a large number of genes as well as the products. A deeper understanding of TFs regulating these genes, the products of major stress responsive genes, and crosstalk between different signaling components should remain an area of intense research activity in future.

11. TRANSGENE TECHNOLOGY TO REPRESS ABIOTIC STRESS

With more comprehensive onset in climatic changes, achieving agricultural sustainability becomes highly complicated. Advances in genetic engineering and transgenic breeding make crop sustainability easier by incorporating resistance genes from wild and uncultivated species to cultivated species. Different approaches such as QTL mapping, miRNAs, CRISPR technology, and transgenic breeding speeded up crop breeding compared to traditional breeding approaches. Plant responses to environmental stress possess a complex signaling pathway, and identification of related genes and unraveling responses to the practical application requires a multidisciplinary tactic. Numerous researchers have anticipated that CRISPR/Cas9 technology helps many plants and could transform agriculture drastically, ensuring that food security and food security needs are met for a growing population. Transgenic technology has been considered a rapidly growing agriculture technology (ISAAA 2017) due to its rapidity and ease of transferring genes from one species to the other across the taxonomic border using some non-conventional methods. Plant miRNAs act as a critical regulator in mediating specific stress responses during biotic and abiotic stress [46]. Two new rapid breeding approaches have been used recently, IMAGE (haploid-inducer mediated genome editing) and Hi-Edit (haploid induction-edit), merge haploid induction with CRISPR/Cas9-mediated genome editing was utilized to bring beneficial characteristics in elite inbred lines within two generations, which was tedious [47]. Transgenic tomato plants that can tolerate increased temperature (40°C) using overexpression of cytosolic ascorbate peroxidase (Capx) gene; however, transgenic chilli (*Capsicum annuum*) expressing wheat Na^+/H^+ antiporter gene (TaNHX2) to overcome salinity [48,49]. Further studies showed transgenic tomato plants showing tolerance to cold injury and salinity by ingesting of cAPX gene, derived from pea [50]. Likewise, many genes have been developed to ensure resistance toward environmental stress through transgene technology [Table 1].

12. CRISPR/cas9: A PREREQUISITE FOR THE SECOND GREEN REVOLUTION

The CRISPR/cas9 system utilized site-directed nucleases to modulate the plant genome with enormous accuracy. It gasped a worldwide consideration because of its wider applications on different streams. It includes homology-directed repair, gene silencing, DNA-free CRISPR-cas9 gene editing, and transcriptional repression [51]. To modify a genome through CRISPR-cas9, the targeted genome sequence has to produce double-strand breaks with the help of sequence-specific nucleases (SSNs) to produce a variety of mutations. Usually, SSNs used are transcription activator-like effector nucleases, zinc-finger nucleases, and CRISPR/Cas9 [52,53]. CRISPR/Cas9 separates the foreign DNA through two components, Cas9 and sgRNA. Cas9 is a DNA endonuclease derived from different bacteria, such as *Staphylococcus aureus*, *Brevibacillus laterosporus*, *Streptococcus thermophilus*, and *Streptococcus pyogenes* are the most widely used for Cas9 isolation [54,55]. The significant significance of CRISPR/Cas9 involves gene knockouts in organisms for revealing the function of single or multiple gene targets through gene mutation [56]. CRISPR system not only helps in developing plants to biotic stress but it also often creates genes required for overcoming plant abiotic stresses in plants such as wheat (TaDREB2 and TaERF3) [57], maize (ARGOS8) [58], tomato (SlMAPK) [59], and rice (OsPDS, OsMPK2, and OsBADH2) [60] supports plants during exposure to different plant abiotic stress conditions.

13. CONCLUSION

Various predictions indicated that the temperature on earth would rise from 3 to 5°C over the coming 50–100 years, making the planet earth unsuitable for the development and growth of the plants. There is still a scope to reveal signaling mechanisms in plants that geneticists and plant biologists can use the information to improve the desired trait to overcome the stress environment. Signal transduction is a complex process and often requires different genetic tools and approaches to know the signaling pathways that plants underwent during various abiotic stresses. Many signaling pathways are independent, while few can crosstalk with each other pathways to perceive a specific signal. The accessibility of *Arabidopsis* genome (the *Arabidopsis* Genome Initiative, AGI, 1996) and different reverse genetic tools to create knockout mutants prompts the spotting of additional signaling components with a prominent picture of the abiotic stress signal network. Molecular screens, for example, utilization of the RD29A-LUC transgene as a reporter gene, are the beginning to expose new signaling determinants. The utilization of CRISPR/Cas9 is primarily concerned with genome editing as well as transcription regulation. In addition, DNA labeling and editing of epigenomes with CRISPR/Cas9 have been reported, yet they are not applied in plants.

14. AUTHORS' CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agreed to be accountable for all aspects of the work. All the authors are eligible to be an author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

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16. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

17. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

18. DATA AVAILABILITY

Data presented in the article based on the available literature in the open source which was duly cited.

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