



Identification of Different Stress Responsive Genes induced in Crops for Climate Changes: A Review

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ABSTRACT: Numerous environmental stresses affect plants, lowering and restricting the productivity of crops used in agriculture. Plants are subject to two ecological stresses: biotic and abiotic stress. Major crop plants are lost due to abiotic stress, which includes radiation, salinity, floods, droughts, temperature extremes and heavy metals. Biotic stress can result in attacks by various pathogens, including bacteria, fungi, oomycetes, nematodes and herbivores. Due to their sessile nature, plants cannot avoid these environmental cues. Plants have evolved various defense mechanisms to deal with these dangers from biotic and abiotic stresses. Ecological stresses have a disastrous effect on the growth and yield of plants in the field. Recent research has shown that plants' responses to combinations of two or more stress conditions are unique and cannot be directly extrapolated from the responses of plants to each of the different stresses applied individually. The field environment differs significantly from the controlled conditions used in laboratory studies and frequently involves the simultaneous exposure of plants to multiple abiotic and biotic stresses conditions.

Keywords: Environmental stresses, temperature, fungi, drought, radiation, bacteria, nematodes and salinity.

INTRODUCTION

The increasing risks that global warming to crop growth and yield due to biotic and abiotic stresses make it a cause for concern worldwide (Ramegowda and Senthil Kumar 2015). Abiotic stresses that adversely affect productivity in agriculture include salinity, drought and heat and cold waves. Currently, abiotic stresses like heat, cold, drought and salinity account for more than 60% of yield losses in all major crops (Reis *et al.*, 2012). The beneficial goal of "food for all," set by nations worldwide is made more difficult by the growing global population. By 2050, the estimated 60% increase in cereal production is undoubtedly insufficient to feed the world's population of approximately 9.7 billion people. Achieving sustainable growth in food production for the growing population necessitates making the best use of the resources at hand. Expanding the productivity of the world's harsher environments and raising agricultural productivity is critical given the exponential growth in global population. Regrettably, the most of land with potential for agriculture is located in arid regions. Several studies have revealed that India's agriculture, food security and water availability have all been negatively impacted by climate change (Burney *et al.*, 2014). One of the main consequences of climate change is an increase in air temperature, which causes yields to drop sharply and may lead to

significant changes in cropping patterns. It is well known that high temperatures cause plants to respire more quickly, which may lessen the benefits of higher photosynthetic rates brought on by higher CO₂ concentrations (Bagley *et al.*, 2015). According to Hof *et al.*, (2015), an increase in the average temperature is foreseen to increase the frequency of illnesses and pest damage as well as evaporation. This could lead to a need for irrigation water, a resource that is already running out globally (Fader *et al.*, 2016). Consequently, plants have been observed to experience an increase in drought or low moisture stress as a result of rising air temperatures, which poses a significant challenge to crop productivity globally. The average yields of major crops are declining due to the rapid increase in desertification worldwide (Bray, 1997). Reduced moisture stress lowers crop yields in arid and semi-arid areas. Plants under drought stress undergo various physiological, biochemical and molecular changes. Both soil and plant water potential declines under drought stress. Drought stress results in decreased water potential and reduced turgor pressure, stomata closure, leaf growth and rate of photosynthesis (Monte, 1986; Ozturk, 1998). Low water stress is also known as drought stress, it occurs when a plant experiences a more water loss through transpiration than it takes up through its roots, leaving the plant in a state of water deficit. Drought tolerance in agriculture refers to a crop

plant's capacity to endure and maintain productivity under prolonged environmental conditions of water deficit with loss (Mitra, 2001). Various morphological, physiological and biochemical characteristics results in drought tolerance. According to Ingram *et al.* (1996); Zandalinas *et al.* (2017), Plants alterations may relate to gene expression, metabolic pathways, osmotic adjustments, repair systems, etc. The mechanisms underlying plants' ability to withstand drought have been the subject of numerous attempts in the fields of molecular biology and genomics. Numerous transcriptionally-responsive genes to drought stress have been found and confirmed (Growth *et al.*, 2010; Joshi *et al.*, 2016). Plants respond differently to drought stress, these changes are essential in determining a plant's survival, distribution throughout its range and yield. While most crops are sensitive to water shortages, especially in the flowering to seed development stage, some crops grown in semi-arid and arid regions, like pigeon pea, pearl millet and sorghum can tolerate drought. This suggests that these crops have developed numerous interconnected strategies and a tolerance mechanism to survive in drought-prone environments. It is challenging to characterize the phenotypic and physiological parameters required for choosing the improved crop under drought stress due to the wide variation in the duration and severity of drought stress and the lack of knowledge regarding the complexity of drought stress. Genomics techniques such as genome sequencing have partially addressed this challenge, which is crucial for identifying genes linked to drought tolerance in many crops and creating markers connected to drought stress. These days, many significant crop genomes have already been sequenced, providing a wealth of opportunities to comprehend the molecular mechanism underlying the crops' ability to withstand abiotic stress. On the other hand, not much genomic research has been done on orphan crops like pearl millet. The current emphasis is on characterizing these orphan plant species transcriptomes to understand the composition and function of various genes involved in the response to drought stress. The most practical way to investigate the differential expression of genes is to create cDNA-based EST (Expressed Sequence Tags) libraries. The EST sequence data constitutes a valuable resource that may be applied to various genomic research projects. Furthermore, according to Mishra *et al.* (2007), it serves as a platform for comprehending the mechanisms underlying plant adaptation to multiple stresses. Given the growing drought conditions, we must create food crop genotypes resistant to abiotic stress conditions. The naturally occurring variations of our major crops are becoming a limited gene pool, which is restricting breeding strategies for crop improvement. For this reason, we must search the varied natural habitat for genetic resources to find novel genes or allelic variations of already-known genes. Recombinant DNA technology can be useful for transfer genes from such tolerant crops to cereal crops, creating transgenics that are resistant to drought. As a member of the Poaceae family, pearl millet may be a more suitable substitute than genes from other dicots or

extremophiles for creating transgenic cereal crops resistant to drought stress.

Biotic stresses. Stress commonly referred to as "biotic stress" is the result of an organism being harmed by other living things, including weeds, native or cultivated plants, bacteria, viruses, fungi, parasites and both beneficial and harmful insects. An organism's ability to withstand specific stresses and the climate in which it lives determine the kinds of biotic stresses that it faces. The term "biotic stress" is still widely used and researchers dealing with it encounter numerous obstacles. For example, regulating biotic stress in an experimental setting is more complex than controlling abiotic stress (Flynn, 2003). Agricultural research has made biotic stresses a primary focus because of the substantial losses caused by cash crops deteriorates. Plant yield and biotic stress influences both practical development and economic decisions. Plant-stressor convolution, population dynamics and ecosystem nutrient cycling are all impacted by the effects of biotic injury on crop yield (Peterson *et al.*, 2001).

Inducible defense responses to insect herbivores

A plant must be distinguished between abiotic and biotic stress to protect itself against it plant reacts to a herbivore by recognizing specific chemicals prevalent in the herbivore's saliva. Herbivore-associated molecular patterns (HAMPs) or elicitors are the substances that cause a reaction in plants. By triggering signaling pathways throughout the plant, these HAMPs enable the plant to minimize damage to other regions and initiate its defense mechanism. By leading to signaling pathways throughout the plant, these HAMPs enable the plant to minimize damage to other regions and initiate its defense mechanism. Similar to aphids, phloem feeders do not inflict significant mechanical harm on plants; however, they are nonetheless considered pests and have the potential reduce crop yields significantly. To defend themselves against phloem feeders, plants have evolved a defense mechanism using the salicylic acid pathway, which is also used in infection stress. Plants target an insect's digestive system more directly. Plants use inhibitors of proteinase to achieve these. While these proteinase inhibitors enter an insect's digestive system, they attach firmly and precisely to the active site of enzymes that hydrolyze proteins, like trypsin and chymotrypsin, preventing the digestion of proteins (Taiz *et al.*, 2015).

Inducible defense responses to pathogens. Despite lacking an immune system or circulatory system like those found in animals, plants can recognize non-self-signals and use them to detect invaders. Identifying microorganism-associated molecular patterns, or MAMPs, is frequently a plant's first line of defense against microorganisms at the cell surface (Spol *et al.*, 2012). MAMPs consist of endotoxins on bacterial cell membranes and nucleic acids shared by viruses that specific pattern-recognition receptors recognize. Utilizing plant immune receptors to identify effector molecules that infections release into plant cells is another technique for detection. Effector-triggered immunity (ETI), a subset of the innate immune response, is activated upon detecting these signals in infected cells (Tsuda *et al.*, 2010). It is known that

pathogenic infection causes an increase in the synthesis of salicylic acid (SA). Plant resistance to biotrophic and hemibiotrophic pathogens is ultimately increased by producing of pathogenesis related (PR) genes, in response to elevated SA levels. According to Bari *et al.*, (2009), the ubiquitination of jasmonate ZIM domains (JAZ) proteins, which block JA signaling, is a physiological reaction to increased JA production. This leads to the degradation of the JAZ proteins and an increase in JA-activated defense genes.

Abiotic Stresses. During their growth period, crop plants are subjected to various abiotic stresses, including but not limited to drought, salinity, extreme temperatures, submergence and water logging, all of which have a negative impact on their overall growth and development (Zhang *et al.*, 2010). These stresses can cause the average yields of most crops to drop by more than half. According to estimates, the global population could reach nine billion people by 2050, necessitating a rise in crop yields (Pennisi, 2008; Nakashima *et al.*, 2014). To adapt to these environmental stresses, plants change the morphological and biochemical phenotypes that affect their physiological responses and ultimately aiding their survival. Under various ecological circumstances, these stresses force plants to adapt in multiple ways, which serve as the foundation for speciation. According to the Intergovernmental Panel on Climate Change (IPCC), abiotic stresses will rise shortly due to global climate change. Abiotic stresses come in many forms and they can be applied to plants simultaneously or at different stages of their development (Tester and Bacic 2005; Hirayama and Shinozaki 2010). Plant cells absorb these stress signals at the membrane or cytoplasmic level. Plant cells absorb these stress signals through a wide range of sensors and receptors at the membrane or cytoplasmic level. They then convert these signals into a variety of signal transduction cascades that induce both primary and secondary stress responsive genes (heat shock proteins (HSPs), protective proteins, ROS scavenging enzymes, antioxidants, compatible osmolytes, etc.), which result in stress adaptation (Shinozaki and Yamaguchi-Shinozaki, 2000). In response to these stresses, plants exhibit dynamic responses involving intricate cross-talk at multiple regulatory levels (Krasensky and Jonak 2012). Changes in the transcriptome, proteome and metabolome levels are associated with plant responses. These reactions are unique to multiple stressors as opposed to single ones and every type of stress triggers a distinct gene repertoire associated with the particular environmental circumstances experienced. The agricultural sector has emphasized developing stress-resistant crops modified to grow in variable environmental conditions and provide higher plant productivity to make up for productivity losses in crops caused by stress conditions. Stress-responsive genes are the best options to giving crops stress tolerance. Identifying QTLs related to abiotic stress and their application in marker-assisted breeding and transgenic developments are underway in various crop varieties. Functional genomics has been instrumental in analyzing the genes linked to different

environmental stressors, enabling the selection of more resilient and robust crops in the future.

Drought Stress. Plants under drought stress due to a lack of water. The average metabolic process of crop plants is hampered and yield is decreases when water is unavailable to them for extended periods of time. Plants attempt to survive in these circumstances by sustaining the barest minimum of physiological activity, which entails controlling thousands of genes and different metabolic pathways (Passioura, 1997; Mitra, 2001; Luo, 2010).

Drought stress responses in crop plants. Plants undergo various physio-biochemical changes in response to drought (Table 1). The physiological changes in plants include decreased leaf area, rolling, drying and increased root growth. The biochemical changes include producing reactive oxygen species (ROS) that disrupt cellular homeostasis, accumulation of free radicals and electrolytic leakage (EL). The buildup of reactive oxygen species (ROS) leads to the breakdown of different biomolecules found in cells, including proteins, lipids, nucleic acids and pigments. This membrane damage ultimately compromises the cell's viability (Bartels and Sunkar 2005). Additionally, hormones are crucial in a variety of abiotic stress situations. Among other hormones, ABA is recognized to be important in responding to a variety of abiotic stressors, including salinity, cold and drought (Zhu, 2002). According to Seki *et al.* (2002), ABA treatment can also induce many genes in response to abiotic stresses, offering direct evidence of its role in these environmental stresses. Drought stress is directly related to ABA; it causes stomata to close to prevent water loss through transpiration and lowers the rate of photosynthesis in order to raise plants' water-use efficiency (WUE). In addition to these reactions, there are molecular reactions, which comprise signal transduction, perception and modification of gene expression and metabolic alterations that are communicated. In addition to producing vital metabolic proteins that shield cells from stress, the changed gene expressions brought on by drought stress also control the downstream signal transduction pathways.

Drought stress negatively impacts vegetative growth (Tripathy *et al.*, 2000). It has been reported that soybeans matured eight days earlier than usual due to a reduced vegetative growth. Extended drought stress further restricted its capacity to form seeds (Twidwell, 2002). Under stressful situations, there was a significant decrease in relative water content (RWC) and an increase in free proline content. One of the most often produced compatible osmolytes in response to water stress conditions is proline. Under stressful situations, the genotype showed elevated activity of peroxidase (POD) and superoxide dismutase (SOD) and decreased accumulation of catalase (CAT). According to the data, proline content and the antioxidant defense mechanism activated during water stress are related. PEG 6000-induced drought stress reduced pearl millet germination percentage and shoot growth while slightly lengthening the roots. Plants' adaptive response to drought stress was reflected in an increase in root length (Leila Rad, 2007). Several ROS-scavenging enzymes are also

activated during drought stress. Ascorbate peroxidase (APX) activity was higher in mildly stressed plants than in control plants (Sharma and Ghildiyal 2005).

However, at higher levels of drought stress, APX activity declined in the initial set of plants.

Table 1: Higher plants 'Physiological, biochemical and molecular responses under moisture deficit stress conditions (source: Reddy *et al.*, 2004).

Physiological responses	Biochemical responses	Molecular responses
<ul style="list-style-type: none"> - Recognition of root signal - Loss of turgor and osmotic adjustment - Reduced leaf Ψ_w - Decrease in stomatal conductance to CO_2 - Reduced internal CO_2 concentration - Decline in net photosynthesis - Reduced growth rates. 	<ul style="list-style-type: none"> - Transient decrease in Photochemical efficiency - Decreased efficiency of Rubisco - Accumulation of stress metabolites like MDHA, Glutathione, Proline, Glycine betaine - Polyamines and α-tocopherol - Increased in antioxidants - Reduced ROS accumulation 	<ul style="list-style-type: none"> - Stress responsive gene expression - Increased expression in ABA biosynthetic genes - Expression of ABA responsive genes, - Synthesis of specific proteins like Late embryogenesis abundant, - Desiccation stress protein, dehydrins, etc. - Drought stresses tolerance

Mechanism of drought tolerance in plants. Plant drought resistance is stage-specific and linked to several physiological, molecular and phenological processes. As a result, it is difficult to thoroughly and accurately analyze a particular plant species' entire drought resistance mechanism. A complex trait, drought resistance is linked to multiple physiological characteristics, Plants develop variety of various defense mechanisms, to combat drought stress, such tolerance avoidance and escape (Levitt, 1972). Plants can finish their life cycle during a drought before experiencing extreme stress (Mooney *et al.*, 1987). To avoid having the growing season coincide with a localized seasonal or environmental drought, it refers to the readjustment of the life cycle or growth and developmental timings (Mitra, 2001; Manavalan *et al.*, 2009). Conversely, drought avoidance minimizes water loss and maximizes water uptake to avoid drought conditions (Chaves *et al.*, 2003). The ability of a plant to generate a commercial product under drought stress with the least amount of loss is known as drought tolerance. It is a multifaceted characteristic that involves adaptations on many levels, ranging from physiological and biochemical processes to plant morphology and anatomical structures (Blum, 2002). Numerous genes undergo transcriptional reprogramming in conjunction with drought tolerance. According to Joshi *et al.*, (2016), transcription factors are significant in controlling the expression of genes that respond to stress and act downstream during stressful situations. The three components of drought resistance in plants, drought avoidance and drought tolerance are the two main mechanisms for drought resistance (Yue *et al.*, 2006). Deciphering the genetic basis of drought tolerance in plants remains challenging

due to its quantitative nature and multiple governing genes (Price *et al.*, 2002).

Approaches for the development of stress tolerant crops

Conventional breeding approach. Drought-tolerant crops have been developed through conventional and molecular breeding techniques and some commercially viable hybrid cultivars and inbred lines with drought tolerance have been developed and released (Scott *et al.*, 1986). However, the main limitations of this approach, are the complex nature of the trait, the absence of desired genetic variations in the available germplasm pool and the need for adequate screening facilities for genotyping a large breeding population.

Transgenic approaches. Using the concepts of genetic engineering, the transgenic approach transfers genes from genotypes resistant to drought to genotypes susceptible to it. However, it requires thorough knowledge of the genes' roles concerning to drought stress. One of the main drawbacks of this approach is the selection of the major candidate gene for the desired trait, since drought tolerance involves multiple genes. Drought-tolerant crops have recently been developed in various plant species through genes coding for stress-responsive transcription factors and stress-resistant proteins (Table 2). Furthermore, current research focuses on clarifying and characterizing these critical factors and their mechanisms of action because the factors that confer enhanced drought tolerance in higher plants still need to be better understood. A more profound comprehension of the genes involved in the drought tolerance mechanism is required to genetically modify plants. The process of mapping QTLs that confer drought tolerance will make it easier to use marker-assisted breeding to develop drought-tolerant varieties.

Table 2: Major abiotic stress tolerant genes characterized in various crop species.

Source of gene	Name of gene	Transformed receptor	Characteristics	Reference
<i>A. thaliana</i>	<i>DREB2A</i>	<i>Saccharum</i> sp.	Drought tolerant	Reis <i>et al.</i> (2014)
	<i>MYB96</i>	<i>Camelina sativa</i>	Heat tolerance	Lee <i>et al.</i> (2014)
	<i>Rab7</i>	<i>A. thaliana</i>	Drought and salt tolerant	Mazel <i>et al.</i> (2004)
	<i>SAP5</i>	<i>Gossypium hirsutum</i>	Drought tolerant	Hozain <i>et al.</i> (2012)
	<i>HARDY</i>	<i>O. sativa</i>	Drought tolerant	Karaba <i>et al.</i> (2007)
	<i>Hsp17.6A</i>	<i>A. thaliana</i>	Drought and salt tolerant	Sun <i>et al.</i> (2001)
<i>T. aestivum</i>	<i>NAC2a</i>	<i>Nicotiana tabacum</i>	Drought tolerant	Tang <i>et al.</i> (2012)
	<i>PIMP1</i>	<i>T. aestivum</i>	Drought tolerant	Zhang <i>et al.</i> (2012)
	<i>WRKY1 and WRKY33</i>	<i>A. thaliana</i>	Drought and heat tolerance	He <i>et al.</i> (2016)
	<i>ASR1</i>	<i>N. tabacum</i>	Drought tolerance	Hu <i>et al.</i> (2013)
	<i>ASR5</i>	<i>A. thaliana</i>	Drought tolerant	Li <i>et al.</i> (2017)
	<i>AREB1 and ABF3</i>	<i>A. thaliana</i>	Drought tolerant	Yoshida <i>et al.</i> (2010)
	<i>DREB1A</i>	<i>O. sativa</i>	Drought tolerant	Datta <i>et al.</i> (2012)
<i>O. sativa</i>	<i>ABF3</i>	<i>A. thaliana</i>	Drought tolerant	Oh <i>et al.</i> (2005)
	<i>bZIP46</i>	<i>O. sativa</i>	Drought and salt tolerant	Tang <i>et al.</i> (2012)
	<i>MYB3R-2</i>	<i>A. thaliana</i>	Drought and salt tolerant	Dai <i>et al.</i> (2007)
<i>G. max</i>	<i>BiP</i>	<i>A. thaliana</i>	Drought tolerant	Valente <i>et al.</i> (2009)
	<i>P5CR</i>	<i>A. thaliana</i>	Drought, salt and Heat tolerant	De Ronde <i>et al.</i> (2004)
<i>Z. mays</i>	<i>NF-YB2</i>	<i>A. thaliana</i>	Drought tolerant	Nelson <i>et al.</i> (2007)
	<i>NPK1</i>	<i>A. thaliana</i>	Drought tolerant	Shou <i>et al.</i> (2004)
	<i>NHX3</i>	<i>T. aestivum</i>	Drought tolerant	Zörb <i>et al.</i> (2004)
	<i>SacB</i>	<i>A. thaliana</i>	Drought tolerant	Pilon-Smits <i>et al.</i> (1995)
<i>N. tabacum</i>	<i>APX</i>	<i>A. thaliana</i>	Drought and salt tolerant	Badawi <i>et al.</i> (2004)
	<i>HVA1</i>	<i>Morusindica</i>	Drought and salt tolerant	Checker <i>et al.</i> (2012)
<i>Hordeum vulgare</i>	<i>WRKY5</i>	<i>A. thaliana</i>	Drought tolerant	Ma <i>et al.</i> (2014)
<i>Leymus chinensis</i>	<i>LAS</i>	<i>A. thaliana</i>	Drought and salt tolerant	Yang <i>et al.</i> (2011)
<i>Brassica napus</i>	<i>ASR4</i>	<i>A. thaliana</i>	Drought tolerant	Li <i>et al.</i> (2017)
<i>Setaria italica</i>	<i>IF4A</i>	<i>Arachis hypogaea</i>	Drought and salt tolerant	Rao <i>et al.</i> (2017)
<i>Pennisetum glaucum</i>	<i>ASR1</i>	<i>E. coli</i>	Drought tolerant	Padaria <i>et al.</i> (2016)

Methods to identify stress tolerant genes. To ascertain the differential expression analysis of genes under various conditions and periods, a number of molecular techniques are available. Among these methods are microarrays, serial analysis of gene expression (SAGE), subtractive hybridization, suppression subtractive hybridization (SSH), differential display reverse transcription PCR (DDRT-PCR), etc. In order to identify *P. glaucum* stress-related genes, James *et al.* (2015); Choudhary *et al.* (2015) employed the SSH technique under two distinct stress conditions heat and drought. ASR protein, APX, glyoxalase, Rab7 and aspartic proteinase were among the genes that Choudhary *et al.* (2015) found to be differentially expressed when they used PEG 30% for varying lengths of time to impose drought stress. These findings were then confirmed by qRT-PCR.

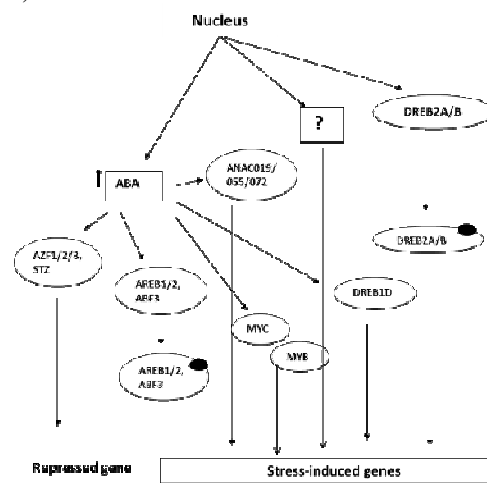
Genes induced during drought stress. It's crucial to comprehend the molecular subtleties of drought response in order to impart drought tolerance in crops. Using different approaches to gene mining, remarkable information about the types of drought responsive genes induced in other crop species has been obtained. Numerous details regarding the important genes driving the drought stress response have been made available by differential analysis at the transcriptome, proteome and metabolome levels. The synthesis of novel metabolic proteins, including osmoprotectants, heat

shock proteins (HSPs), Late Embryogenesis Abundant (LEA) proteins, detoxifying enzymes, antioxidants, water channels like aquaporins, ion pumps and regulatory proteins, which primarily consist of TFs (AREB, AP2/ERF, NAC, bZIP, MYC, and MYB), is either facilitated by these important genes. Protein phosphatases and kinases participate in the synchronizing of signal transduction pathways (Wani *et al.*, 2013). Important genes for the production of metabolic proteins, Sugars (fructose, fructan), sugar alcohols (mannitol, sorbitol) and zwitterionic substances (proline, glycine, betaine) are examples of compatible osmolytes. Due to their high water solubility, these build up in cells at higher concentrations under various water deficit conditions. Higher concentrations of these metabolites within the cell aid plants in coping with water deficit stress in two ways: they increase water retention or osmotic adjustment, which keeps cells hydrated and they stabilize cellular molecules by acting as osmoprotectants, which protect them from the damaging effects of ionic stress. According to Delauney and Verma (1993), proline is the most widely distributed compatible solute—small hydrophilic organic molecules that build up to high concentrations—in water-stressed plants and numerous other organisms. Proline's enhanced biosynthesis in dehydrated plants and the inhibition of its degradation

both contribute to its higher accumulation. In rice under water stress, the enzyme Δ 1-pyrroline-5-carboxylate synthase (P5CS) was induced (Zhu *et al.*, 1998). While the suppression of P5CR resulted in increased sensitivity to various abiotic stresses, higher proline content encouraged better growth under conditions of water scarcity (De Ronde *et al.*, 2000). According to additional data, Proline may help the DREB1 pathway facilitate drought adaptation. As an illustration, it has been demonstrated that transgenic rice plants that overexpress OsDREB1 or AtDREB1 (Ito *et al.*, 2006) accumulate more proline than wild-type plants under both normal and water-deficit conditions, and they also exhibit superior adaptation to water stress conditions.

Glycine Betaine (GB): Several plant families, including the Composite, Chenopodiaceae, and Gramineae, have reported on the function of glycine betaine in response to drought and salinity stress. In these and many other halotolerant plants, GB builds up in the plastids and chloroplasts (Chen and Murata, 2008). Higher levels of GB accumulation were observed in transgenic maize plants transformed with the choline dehydrogenase coding bet A gene, which regulates drought stress in the field, according to Quan *et al.* (2004). After three weeks of drought stress, transgenic plants produced 10–23% more grain per plant than untransformed plants, while control plants' reproductive development was significantly hindered. Under drought stress, BetA-transgenic cotton outperformed the wild-type controls in several physiological parameters (Lv *et al.*, 2007). Trehalose is a disaccharide that does not reduce and is crucial in the abiotic stress. It prevents denaturation of the protein and other biomolecules. Two essential enzymes, trehalose-6-phosphate synthase (TPS) and trehalose-6-phosphate phosphatase (TPP), catalyze trehalose biosynthesis in plants. However, the majority of higher plant species only accumulate trace amounts of trehalose, except highly desiccation-tolerant resurrection plants. When various abiotic stresses, such as dehydration, cold and salinity occur LEA proteins are protective and accumulate at higher concentrations. These proteins are often produced in developing embryos during the desiccation of seeds and they are also induced in stressed vegetative tissues. The hydrophilic LEA proteins are primarily responsible for protecting the membrane and protein structures, binding water, securing ions and acting as molecular chaperones (Bray, 1997). Group 3 LEA protein from barley, ABA-inducible HVA1, has been reported by Hong *et al.* (1988) to sequester ions (e.g., Na^+) during cellular dehydration. It has been investigated whether overexpressing LEA genes can improve drought tolerance. Higher growth rates and quicker recovery from the stresses demonstrated the enhanced tolerance of the HVA1-transgenic rice and the LEA-transgenic Chinese cabbage to salt stress in potted soil and water deficit conditions during the vegetative stage. By preserving their membrane structure, LEA proteins help stressed cells remain in a suitable cellular environment. Low membrane electrolyte leakage during dehydration stress indicated that transgenic plants had higher cell membrane protection than control plants (Rohila *et al.*, 2002; Babu *et al.*, 2004). The crucial regulatory

proteins that are activated during the stress response are known as transcription factors. Besides polymerases, TFs are proteins attaching target gene promoters to control gene expression. According to Joshi *et al.* (2016), transcription factors are essential for both triggering and regulating the expression of various stress-responsive genes. Different stress responses share certain transcription factors. To fully comprehend abiotic stress tolerance, a thorough examination of transcriptional regulatory systems is necessary. A "Regulon" is a collection of multiple genes activated or inactive by the same transcription factor in response to the same signal. There are two categories for the four main "Regulons" are involved in abiotic stressors, such as drought stress. 1. An ABA-dependent pathway controlled by the AREB/ABF, NAC, and MYB families; 2. An ABA-independent pathway run by DREB TFs carrying the APETALA2 (Flower patterning protein) DNA binding motif (Saibo *et al.*, 2008).



Source: Shankar and Venkateswarlu (2011)

Fig. 1. Classes of genes induced by water-deficit stress.

According to transcriptome studies, numerous primary and secondary stress-responsive genes were found to be expressed in rice exposed to abiotic stresses. Primary stress responsive genes comprise elements of signal transduction pathways such as stress receptors, enzymes that synthesize secondary messengers, MAP kinases, transcription factors and proteins that mitigate stress such as heat shock proteins, late embryogenesis abundant (LEA) proteins, compatible osmolytes and water channels (Aquaporins) (Todaka *et al.*, 2012). In rice and Arabidopsis, both ABA dependent and independent TFs are crucial during drought response (Todaka *et al.*, 2012).

DREB1/CBF regulon: One category of transcription factor not dependent on ABA is DREB1. Three distinct DREB1-type genes—DREB1A, DREB1B and DREB1C—have been identified in Arabidopsis. The core sequence A/GCCGAC is present in the cis-acting sequence that serves as a binding site for these transcription factors. In Arabidopsis, DREB1 TFs are crucial for responding to stresses like cold, high salinity, and drought (Yamaguchi-Shinozaki and Shinozaki, 2005).

DREB2 regulon: Additionally, DREB2 TF functions independently of ABA. Like DREB1, it too has an AP2 domain and is brought on by heat, salinity, and drought. At least four DREB2 homologs have been found in rice, with OsDREB2A and OsDREB2B being induced by heat, salinity, and drought (Matsukura *et al.*, 2010).

AREB regulon: Abiotic stress is a significant time for the ABA hormone. It accumulates during drought-induced water shortages and is an essential signal molecule for stress reactions and tolerance (Fujita *et al.*, 2011).

NAC regulon: NAC transcription factors play a critical role in both biotic and abiotic stresses. They make up one of the largest plant-specific TFs. The acronym NAC denotes a set of three distinct genes that share a specific kind of domain known as the NAC domain: Numerous NAC genes have been identified by genome sequencing of crop species, including *Vitis*, *Oryza*, *Arabidopsis*, and citrus (NAM stands for no apical meristem). In rice and *Arabidopsis*, more than 100 NAC genes have been found (Nakashima *et al.*, 2014; Le *et al.*, 2011). Drought, high salinity and cold stressors activate NAC-type transcription factors, which regulate the expression of multiple stress-responsive genes in *Oryza* and *Arabidopsis*.

Calmodulin (CaM) genes induced by drought stress. Calcium binding proteins, a significant class of Ca²⁺ sensor proteins, are members of the calmodulin (CaM) gene family. These proteins regulate a wide range of target proteins, which play a crucial role in cellular signaling cascades (Reddy *et al.*, 2001; Sanders *et al.*, 2002; White *et al.*, 2003; Ranty *et al.*, 2006). CaM proteins are normally inactive, but when calcium is present, they become active. Elevated concentrations of calcium ions in the cytosol indicate most abiotic stresses. By interacting with calcium sensor proteins like calmodulin, calcium functions as a secondary messenger of the signal transduction pathways and can directly or indirectly activate downstream components. It exists in both the plant and animal kingdoms and is naturally acidic. It is believed to be the primary intracellular Ca²⁺ receptor in all eukaryotes and is this protein family's most widely distributed member. All eukaryotes share a highly conserved amino acid sequence for CaM proteins (Kawasaki, 1994). Within a single plant species, CaM proteins can exist in multiple isoforms. Four functional EF-hand Ca²⁺ binding domains are present in plant CaMs.

ASR genes induced by drought stress. ASR (abscisic acid stress ripening) proteins and various polypeptides determine a plant species' stress tolerance. ASR proteins have been repeatedly identified in response to different abiotic stresses, such as drought, salinity, cold or osmotic stress in many plant species (Amitai-Zeigerson *et al.*, 1995; Gilad *et al.*, 1997; Vaidyanathan *et al.*, 1999; Maskin *et al.*, 2008). Notably, each plant species' ability to adapt to water deficit conditions varies greatly and plays a significant role in both productivity and natural geographical distribution. Additionally, ASR is important in controlling the ripening of fruit in strawberries and tomato, where it has been shown that RNAi lines delay fruit ripening and overexpressing ASR lines promote fruit softening (Meena *et al.*,

and ripening (Jia *et al.*, 2016). For the first time, the tomato's ASR protein was found to be a water/ABA stress-induced protein (Iusem *et al.*, 1993). Additionally, homologs of these proteins have been found in several plant species, such as the lily (Wang *et al.*, 1998), potato (Schneider *et al.*, 1997), melon (Hong *et al.*, 2002), rice (Vaidyanathan *et al.*, 1999), maize (Virilouvet *et al.*, 2011), apricot (Mbeguie-A-Mbeguie *et al.*, 1997), pummelo (Canel *et al.*, 1995), grape (Cakir *et al.*, 2003), strawberry (Chen *et al.*, 2011), and banana (Henry *et al.*, 2011). However, the model plant *Arabidopsis thaliana* did not recognize these proteins (Carrari *et al.*, 2004). These proteins are hydrophilic and may have a protective function in situations where there is a water deficit (Wang *et al.*, 2005; Konrad and Bar-Zvi 2008). They are members of the low molecular weight charged hydrophilin group. The ASR gene family has different documented members in different plant species, and each member's function varies depending on the host and stress levels. However, the precise function of each member is still unknown. The overexpression of ASR1 genes from wheat and tomatoes in tobacco (Kalifa *et al.*, 2004a; Hu *et al.*, 2013) and the increased tolerance to salt and drought (LLA23) in *Arabidopsis* (Yang *et al.*, 2005; Hsu *et al.*, 2011) are examples of how the interfamily transfer of these proteins improves tolerance limits. These findings confirm the role of ASR genes in stress response even in systems where they are not endogenously present. Various traits genetically control drought tolerance and is typically inherited quantitatively (Blair *et al.*, 2010). According to Carrari *et al.* (2004); Philippe *et al.* (2010), the molecular characterization and sequence comparison revealed that ASR gene members of a single plant species are more closely related than those of other plant species, suggesting that these originated from the late duplication and may have species-specific functions. The majority of ASR proteins consist of two well-conserved regions: the first region, which includes a nuclear localization signal (NLS) at the C-terminal region (Kalifa *et al.*, 2004b), has a stretch of His residues at the N-terminal and contains sequence-specific DNA binding activity (Rom *et al.*, 2006). There are various cellular levels where the ASR proteins are located. ASR proteins confine in the nucleus in various cell types (Kalifa *et al.*, 2004; Wang *et al.*, 2005) and play a regulatory role, possibly as transcription factors or as chaperones (Wang *et al.*, 2005; Frankel *et al.*, 2006; Konrad and Bar-Zvi 2008). The ASR proteins in the cytosol exhibit chaperone-like activity (Konrad and Bar-Zvi 2008). Padaria *et al.* (2016) have successfully isolated and characterized the ASR gene from *Zizypus nummularia*, a species of tree that can withstand extreme water stress. When PEG was present, ZnASR1-expressing *E. coli* demonstrated improved survival under simulated drought stress conditions. ASR4—a recently identified ASR gene from *Setaria italica* showed a significant increase in expression after treatment with ABA, NaCl and PEG. Additionally, it has been discovered that the ASR4 gene's promoter is bound by the ABA-responsive DRE-binding protein (ARDP). Additionally, *A. thaliana*'s ASR4 gene was altered, and the transgenic lines exhibited improved

drought tolerance (Li *et al.*, 2017). Similarly, the rice ASR gene, or ASR5, has also been described. After being isolated from the upland rice variety IRAT109 (*Oryza sativa* L. ssp. japonica), the ASR5 gene was overexpressed in rice, and transgenic lines with improved drought tolerance were demonstrated by Arabidopsis (Li *et al.*, 2017).

CONCLUSIONS

One of the principal abiotic stresses that have a negative impact on agricultural productivity is drought. Significant changes in the global climate in recent years have increased the frequency and severity of droughts. Drought is one of the leading natural causes of severe food shortages in developing nations and is a significant contributing factor to famine and malnutrition. It impacts food security's availability, stability, accessibility and utilization the four pillars. When plants are exposed to environments that restrict water during different developmental stages, various physiological and developmental changes are triggered. There is little understanding of the fundamental biochemical and molecular mechanisms underlying drought stress, transduction, and tolerance. Moreover, genetic engineering is a precious tool for understanding the of drought tolerance mechanism. Because, it can manipulate genes, transcription factors, signaling proteins and genetic regulatory networks that shield plant cells from water deficits. Furthermore, by expanding our understanding of the mechanisms underlying drought, plant breeders have made significant strides towards creating drought-tolerant lines or cultivars for a few key crops. Nevertheless, conventional breeding method is highly labor, time and money-intensive. Because marker-assisted breeding can quickly determine the value of thousands of a crop's genomic regions under stress, it is a more efficient breeding method. By using a technique known as transformation, certain crops with innate mechanisms for surviving droughts can be used as a source of genes for drought tolerance, which can then be used to develop desirable crops.

FUTURE SCOPE

Present review clearly suggests the significant role of different methods to mitigate the drastic changes in the global climate ecological environment to enhance resistance against both biotic (living) and abiotic (non-living) and organism challenges in the ecological atmosphere. Thus, these methods could be used for developing new resistant genotypes with characteristic properties against various types of stresses in plant system to mitigate the physical loss of produce the cultural and economic losses in the agricultural and sustainable development.

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Conflict of Interest. None.

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