

# Role of DREB genes in the regulation of salt stress-mediated defense responses in plants

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## ABSTRACT

Abiotic stress plays a major role in plant growth and its development, multiple stress elements such as drought, cold, elevated temperature, and heavy metal contamination may influence them. However, salinity is still a universal abiotic stressor that stunts plant development worldwide. During such adverse conditions, certain stress-resistant genes are upregulated, wherein dehydration responsive element binding (DREB) genes are one such class of apetala 2/ethylene responsive element binding protein which binds to dehydration responsive element (DRE)/C-repeat that can be activated by the action of abscisic acid-dependent or independent pathway. DREB genes influence the stress tolerance of various plants, the cis-element DRE present adjacent to the foremost promoter area of stress-receptive genes is where the DREB transcription factors fix osmotic stress in plants, and their subclasses DREB1 and DREB 2 also involved in cold and dehydration stress, respectively. As per Central Soil Salinity Research Institute, salinity affects nearly 67,44,968 ha of land in India. This review focuses on salinity stress, its influence on the activation of the DREB genes, and its effect on eliciting structural and functional changes in plant development and transgenic research.

## ARTICLE HIGHLIGHTS

- Role of DREB genes in stress tolerance.
- Challenges associated with the control of stress-tolerant plants.
- DREB genes offer promising results in salt-affected areas when introduced in transgenic plants.

## 1. INTRODUCTION

Salinity is still one of the threatening abiotic stress problems that influence plant development worldwide, alongside excessive temperature, drought, heavy metal contamination, and cold. According to the “food and agriculture organization of the united nations,” sodicity or salinity affects more than 6% of the earth’s terrain [1]. Saline soils occur through a process of “Salinization” mainly due to the weathering

of minerals, whereas sodic soils have high sodium concentrations in their cation exchange complex. About 67,44,968 ha in India is affected due to salinity, and about 3,68,015 ha in Tamil Nadu is affected due to salinity or sodicity (<https://cssri.res.in/extent-and-distribution-of-salt-affected-soils-in-india/>). In the peninsular plain, salt-affected areas cover 18% of sodic soils and are distributed in Andhra Pradesh, Tamil Nadu, and Karnataka states [Figure 1] [2]. Salinity affects plants invariably, it may cause delayed, shunted plant growth, sustain transpiration fetches large volumes of salt into the shoot, specifically into the long-standing leaves. Thus wearing them, finally, limits of the stream of nutrients are the main leading cause that determines the yield effect [3]. Depending on the salinity concentration, it will affect the physiological and metabolic processes, whereas higher accumulation of NaCl ions in the plant tissues increases osmotic potential (OP), reactive oxygen species (ROS) accumulation to their level of osmolytes Na<sup>+</sup> toxicity. It is known that there are several genes and transcription factors (TFs) that come into play when plants are under stress conditions, initiate transcription of salt responsive genes, and develop tolerance to withstand unfavorable conditions, and they help us understand their mechanisms [4]. Under abiotic stress tolerance,

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it has been reported that TFs such as MYB, MYC, bZIP, WRKY, DELLA, NAC, and dehydration responsive element binding (DREB) play a significant role. The genes that encode late embryogenesis abundant (LEA) protein, proline synthetase, or betaine synthetase that helps in generating drought or salinity-tolerant plants are mainly involved in signal transduction and gene expression [5].

This review summarizes the function of DREB TFs under abiotic stress and their adaptation. Under Environmental stress, the TF binds to the dehydration responsive (DRE)/C-repeat (CRT) in the promoter region. The plant-specific TF DREB regulates gene expression (rd29A, kin1, and erd10) in response to stress conditions [5]. The promoter of these Liu *et al.*, 1998 genes contains the cis-acting element of both abscisic acid-responsive element (ABRE) and a DRE/CRT that functions in both ABA gene expressions, respectively. Abiotic stress-inducing genes, including DREB TFs, were cloned and described in many plants. For instance, overexpression of DREB/CBF genes in *Oryza sativa*, *Triticum, Paspalum notatum*, and *Nicotiana tabacum* improves stress tolerance. However, the stress-regulating promoters were activated by their specific TFs [6,7]. Overall this review will give the diversity of DREB genes and its role in stress tolerance in plants. This information may be adopted to develop stress-tolerant plant varieties in the future.

## 2. ACTIVATION OF DREB BY ABA

ABA helps to maintain physiological responses and coordinating in stress-responsive gene activation during different signal transduction pathways. Due to the environmental crisis, there are many changes in the hormone level. The plant hormone ABA acts as an indicator of salinity and drought stress plants in their physiological signals [8]. During OP, the ABA not only adapts to the triggered environmental stress but can also upregulate the stress-responsive gene involved in gene expression [9].

In the ABA signaling pathway, the gene cluster is controlled by certain TF and has two different regulons to activate their stress adaption: (i) The ABA-responsive element-binding protein/ABA-binding factor (AREB/ABF) regulon and (ii) the MYB/MYC regulon [10,11]. Further ABA-independent regulons are: (i) The cold-binding factor/dehydration responsive element binding (CBF/DREB) regulon and (ii)

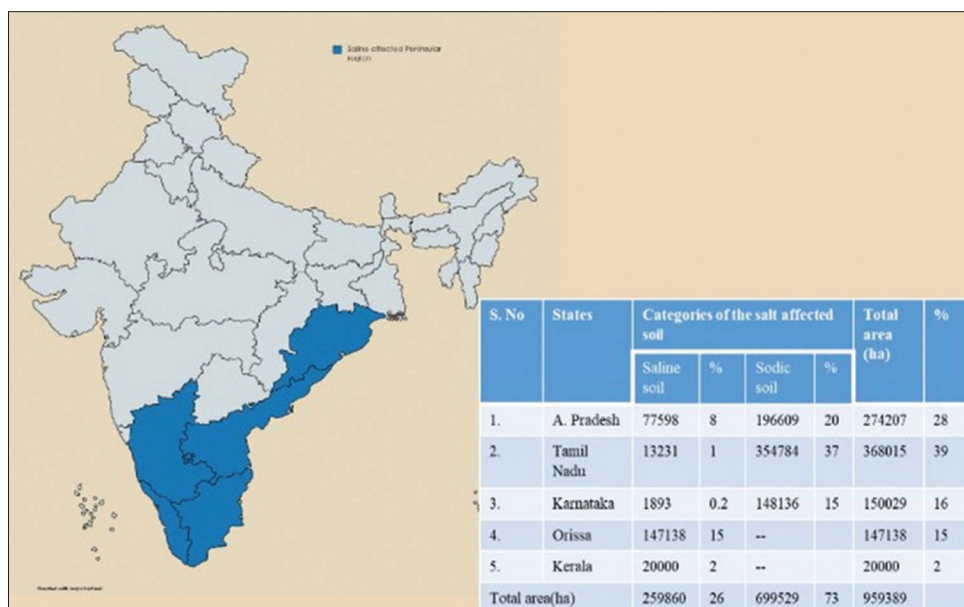
the NAC and zinc-finger homeodomain regulon [12]. The APETALA 2 (AP2)/ethylene responsive element binding protein (EREBP) (ERF) family of TFs functions by both ABA-independent and ABA-dependent pathways [13].

The study of ABA-responsive genes helps us to understand the characterization of ABA-responsive cis-elements, cloning, and characterization of Tfs, ABA-induced signal pathway to ABA-induced transcription, protein interactions, and post-translational modifications [11].

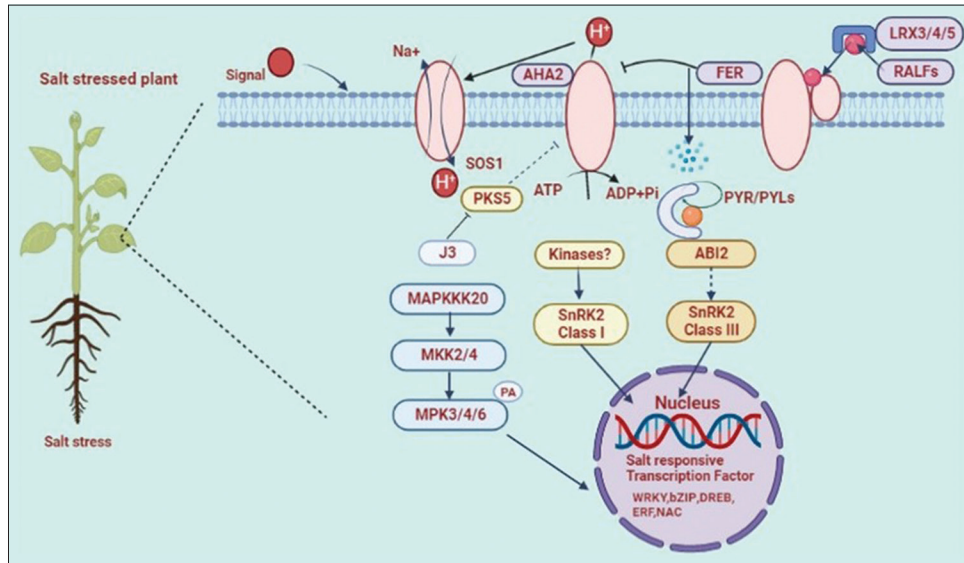
## 3. THE DRE

The activation of distinct genes in response to diverse environmental pressures has been linked to the existence of specific cis-elements, as revealed by extensive molecular investigations. C-repeat binding factors (CBFs) and DREB bind with DRE cis-acting elements and CRT that has a consensus sequence in their promoter region influences the expression [15]. Under drought, rd29A responsive gene in the promoter was first identified with a 9bp conserved core sequence (5'-TACCGACAT-3') DRE [16]. The rd29A, narrowly positioned on the genome of *Arabidopsis thaliana*, is activated by dehydration, low temperature, higher salt concentration, or dealing with the external use of abscisic acid (ABA). DRE binding factor-1, or DRBF-1, is a protein factor isolated from nuclear extracts of stressed and unstressed *Arabidopsis* plants. It particularly binds to the DRE sequence in gel-shift assays, resulting in the identification of the DREB TFs [16,17]. Hence, DREs have been involved in various abiotic stress responses through both ABA pathways [18]. The DREB1A isoform from *Arabidopsis* and *O. sativa* displayed a higher efficiency in the competitive binding assay than their DREB2A isoforms. The over-expression of OsDREB1A in transgenic *Arabidopsis* results in generating higher tolerance to drought, freezing, and salt transgenic crops [18].

Subsequently, in the promoter region, core sequence CRT (5'-CCGAC-3') was recognized under low temperatures from cold-regulated genes of *Arabidopsis* such as *Kin1*, *Kin2*, and *rab18* and was found related to the DRF motif [7,8,19]. In response to osmotic stress, the DRE 2 in rab17 promoter response is involved in an ABA-dependent pathway with a motif of 5'-ACCGAC-3' in the embryos and leaves and DRE 1 cis element 5'-ACCGAG-3' in rab17 promoter



**Figure 1:** The map represents the distribution of salt-affected peninsular region in India.



**Figure 2:** Mechanism of salinity stress tolerance in plants: Mitogen-activated protein kinase cascades, including MAPKKK20, MKK2, MKK4, MPK3, MPK4, and MPK6, are involved in the relay of salt stress signals. Salt stress induces the accumulation of ABA which activates subclass III SNF1-related protein kinase 2s (SnRK2s) through the PYR/PYLs-PP2Cs mediated regulatory module. Subclass I SnRK2 is activated through an ABA-independent pathway under osmotic stress. Activated MPKs and SnRK2s transduce signals to downstream transcription factors including dehydration-responsive element binding, modified from Zhao *et al.*, 2020 [14].

mediates ABA-dependent only in embryos, not in leaves that are drought responsive stress in maize [11]. The findings of a recent study seem to indicate that the DREB transcript is expressed in a tissue or organ-specific manner. This is due to the fact that the *Arabidopsis* plant, when exposed to salt, exhibited higher levels of expression in its roots than in its leaves [20].

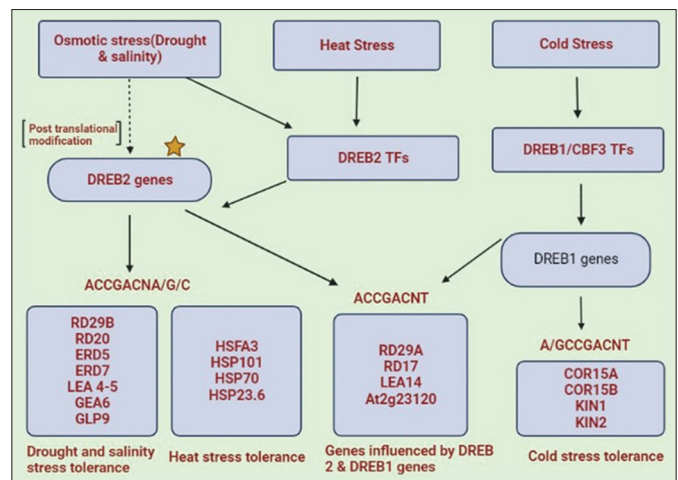
### 3.1. DREB-a Potential TF

DREB protein dichotomized such as DREB1- low temperature and involved dehydration involved in signal-transduction pathways to be associated with AP2/EREBP TF based on their plants [Figure 4] [21]. The ERF domain (58–59 amino acid) connects to cis-elements such as CRT/DRE motif and GCC box [22]. In the *Arabidopsis* family, 145 members were divided into five subfamilies, namely, AP2, ERF, RAV, DREB, and others. From *A. thaliana*, DREB 1A and DREB 2A (yeast one-hybrid screening method) identified in the first cDNAs encode DRE, CBF1 [6]. By binding with the DRE sequence, the genes are activated and expressed.

DREB1A/CBF3, DREB1B/CBF1, and DREB1C/CBF2 genes all lie one beside the other on chromosome no. 4 has been studied in *A. thaliana* [23]. Mainly, high salinity and drought are responsible for the activation of DREB2B and DREB2A TFs in *A. thaliana* [24]. Based on *Arabidopsis-DREB* (AtDREB), several other DREB genes have been isolated from different grass families. A novel gene DREB2 like SiDREB2 from foxtail millet (*Setaria italica*) has been isolated under stress tolerance [8]. Highly successive expression of DREB1A (CBF3) and DREB1B (CBF1) TFs enhances cold and dehydration tolerance in modified plants and comes under AP2/EREBP TF [25,26]. Under high salinity, dehydration, and high-temperature DREB 2 genes are influenced [Figure 3] [8].

## 4. THE STRUCTURAL CHARACTERISTICS OF DREB

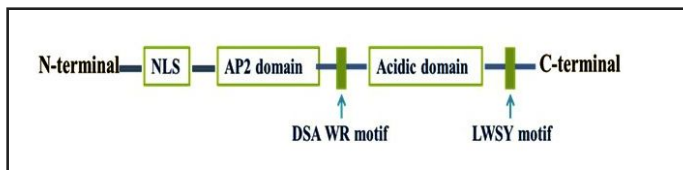
DREB protein has a conserved DNA binding motif/domain called AP2 domain which is unique to plants and contains ~60 amino acids [27].



**Figure 3:** The dehydration responsive element binding (DREB) transcription factors are influenced by abiotic stresses which are responsible for the regulation of DREB genes which activate further downstream genes that elicit stress tolerance in plants.

DREB genes with AP2 domain reported in diverse monocot and dicot plant species [28-30]. Three-dimensional analysis of the AP2 domain revealed that three-stranded  $\beta$ -sheets are connected anti-parallel by  $\alpha$ -helix structure. Furthermore, valine and glutamic acid present at positions 14 and 19, respectively, play an important role in DREB specificity [31]. AP2 domain consists of two regions: YRG region and RAYD element. YRG region consists of 20 hydrophobic and basic amino acids in N-terminal, which plays a key role in DNA binding [32]. The second region is the RAYD element which contains 40 amino acids among these 18 amino acids in the c-terminal region and was predicted to mediate protein-protein interactions [32]. Next to the N-terminal region, the basic amino acid-rich stretch has a consent sequence PKRPAGRTK-FRETRHP called as nuclear localization signal (NLS) region.





**Figure 4:** Schematic structure and domains of dehydration responsive element binding transcription factor.

Based on their structural characteristics, DREB proteins are classified into six subgroups from A1-A6 [31]. In several plant varieties, AP2/ERF sequence similarities have been identified in the DREB protein analysis. The lower level of sequence similarity has been identified in C- and N-terminal domains, whereas the acidic C-terminal is predicted to be functional in trans-activation, and the alkaline N-terminal acts as NLS activity. In the middle region, a rich Ser/Thr region was observed in DREB TF responsible for phosphorylation. The specific joining to CRT/DRE elements is 4Arg (R), 2Trp (W), and 1Val (V) [33] (Allen *et al.*, 1998). DRE cis binding elements, namely, E19 and V14 play an important role, while three stranded  $\beta$ -sheets and one  $\alpha$ -helix run parallelly [21]. DREB1 (CBF) regulates the cold-responsive (COR) gene, which belongs to AP2/ERF TF. From *A. thaliana*, DREB 1 subgroup consists of six genes, and DRE1B/CBF1, DRE1C/CBF2, and DRE1A/CBF3, genes are responsive in low temperatures [31]. OsDREB1A-OsDREB1D isolated from rice. DREB 1 recognizes the conserved domain of the 5-bps core sequence (CCGAC) CRT/DRE domain for low temperature in response to many COR genes. Common metabolites such as sucrose, galactinol, Myo-inositol, and raffinose play an important role in the cold response pathway. At 4°C, the CBF and COR genes expressed very early in cold and not in normal temperature [21].

Drought and high salinity stress induce DREB 2, which plays a major role in stress-responsive gene expression. DREB2B and DREB2A are major transcriptional factors among eight DREB2 type proteins, under osmotic stresses, and DREB 2C is induced by salt stress but gets affected by mannitol, ABA, and cold. OsDREB2A induced salt stress and dehydration, but low responsiveness against cold and ABA [18]. In high temperatures, the ZmDREB2A transcript level increased [34]. Mainly high salinity and drought are responsible for the activation of the DREB2A TF in *A. thaliana* [24]. These genes show slight increases in gene expression during high temperatures and there are no changes in low temperatures. Despite all research focusing primarily on DREB2 due to its relevance to environmental stresses such as drought and high salinity, it is crucial to understand that DREB1, the cold stress-responsive subclass, plays a significant role in improving plant tolerance to low-temperature conditions [8].

## 5. STRESS TOLERANCE AND OVEREXPRESSION BY THE DREB GENE

Abiotic stress responses are regulated by DREB genes, which confer stress resistance to plants. The genes that are involved in the CBF COR pathway of *A. thaliana* are identified and analyzed, TF that functions directly: FIERY2 (FRY2), low expression of osmotically responsive genes 2, a positive regulator in the pathway, and high expression of osmotically responsive genes 1, a transcriptional repressor, a negative regulator of CBFs, and [35]. CBF1/DREB1B, CBF2/DREB1C, and CBF3/DREB1A activate MYC ICE1 [36]. Protein substrate conjugated with small ubiquitin-related modifier (SUMO) is a sumoylation mechanism. SIZ1 (a SUMO E3 ligase)-dependent sumoylation can also prevent the ubiquitination of proteins [37]. This change activates/stabilizes the ICE1 protein and allows

CBF3/DREB1A gene to control the expression. CBF2/DREB1C and MYB15 act as negative regulators of CBF1/DREB1B [5,38]. OsDREB2A and AtDREB2A do not induce stress-inducible genes, even if they are highly expressed [6,18].

The conserved serine/threonine-rich region close to the AP2/ERF domain could act as a possible phosphorylation site. Under normal conditions, the AtDREB2A protein possesses a negative regulatory domain that helps plants to regulate under stress [39]. PEST acts as a signal peptide, and protein degradation is done by phosphorylation of PEST [40]. DRIPs degrade DREB2A. Overexpression of DREB2A is more stable in drip1 than wild type. Overexpression of DREBs/CBFs will lead to the formation of LEA including dehydrin and COR. LEA gene is associated with cold and water stress. Rice plants carrying a Group 3 LEA gene, barley hordeum vulgare aleurone 1 (HVA1), shown to be more resistant to salt and water stress. High levels of RWC were able to maintain in transgenics, implying that during the osmotic stress, the HVA1 protein protected the damage from cell membranes [41,42]. Inducing the expression of CBF3/DREB1A (or) CBF1/DREB1B in transgenic *Arabidopsis thaliana* under constitutive conditions has been shown to induce transcription of target COR (cold-regulated) genes and improve freezing tolerance in non-acclimated plants [25]. High expression of rd29A-GmDREB (or) Ubi-GmDREB and OsDREB1A was found to up-regulate the stress genes [43,44].

OsDREB1F, a novel rice DREB TF, was successfully cloned and characterized using subtractive suppression hybridization and further expression analysis showed that OsDREB1F was induced by abiotic stress instead of biotic stress. Both *Arabidopsis* and rice transgenic plants showed high tolerance to salt and drought stress, mainly due to the presence of the OsDREB1F gene [45]. Using agrobacterium-mediated transformation, GmDREB6 was successfully transformed and overexpressed in soybean plants, which further resulted in increased salt tolerance by proline accumulation. This study concluded that the GmDREB6 gene acts as a potential candidate to improve salt stress tolerance in genetically modified plants [46]. OsDREB1A and AtDREB1A genes, when expressed together retarded the growth and induced stress tolerance. In OsDREB1A growth retardation and stress, tolerance is low as compared to AtDREB1A in *A. thaliana* due to the induced target gene [5]. ZmDREB in *A. thaliana* TaDREB3 AND TaDREB2 in barley and wheat induced stress tolerance [47,48]. The longevity of the sunflower is not increased when the HaDREB2 is overexpressed in the sunflower [49,50].

## 6. REGULATION OF DREB TRANSCRIPTION BY SALINITY STRESS

Although DREB1/CBF genes respond more to cold and high-temperature stress, there are some DREB1/CBF genes such as MbDREB1 from *Malus domestica*, Br CBF from Chinese cabbage, VviDREB1 from *Vaccinium vitis-idaea* and OsDREB1F from rice, these genes, which are mainly responsive to cold stress also acts on dehydration and other *ex vivo* ABA treatment which are also regulated by high salt concentrations, but they may not necessarily provide tolerance to plants against high salinity [48]. Along with AREB, DREB1-type proteins such as CBF/DREB1 homologs, DREB1F, and CBF4/DREB1D may function under high-salt conditions in the expression of the rd29A gene [51]. It was shown that DREB2 genes were activated by high salt concentrations and dehydration but there was no activation in low-temperature stresses [52]. However, there are many DREB2-type genes that are also controlled by low-temperature responses [53-55]. There is some sort of cross-talk between DREB2 and DREB1 modes wherein DREB1/CBF and DREB1D are stimulated

by osmotic stress [51]. The genes that are regulated under high salinity stress are *cor6.6/kin2*, *kin1*, *rd29A/ltr78/cor78*, and *cor47/rd17* which follow a non-ABA based signal transduction pathway [51,56-58]. The promoter region of these genes contains both ABRE and DRE.

In rice, DREB, AREB/ABF, and NAC (NAM, ATAF1/2, and CUC2) have been identified and characterized as major TF families regulating salt tolerance [59]. In *Arabidopsis*, gene expression in response to osmotic and cold stress was regulated by major cis-acting elements such as ABRE and DREB along with DRE/CRT [60]. Eighty-three AP2 predicted proteins were documented from *Bryum argenteum* transcriptomic analysis and further reported that genes, namely, TR29644|c0\_g1\_i1 (DREB-Ba-unique), TR54730|c0\_g1\_i1 (ERF), TR119737|c13\_g1\_i1 (DREB), and TR27842|c0\_g1\_i1 (DREB) were correlated with enhanced salt and osmotic stress tolerance in transgenic yeast [28]. Transgenic *Arabidopsis* overexpressing *Camelia sinensis* DREB gene showed increased salt and drought tolerance, further resulting in up-regulated expression of ABA-dependent and independent stress-induced genes [61]. Overexpression of the GmDREB1 gene in transgenic wheat improves salt tolerance by up-regulating the expression of osmotic stress-related proteins with a reduction in the occurrence of cell injury [62].

## 7. PROCESSES OF TRANSCRIPTIONAL REGULATION OF THE DREB GENE UNDER SALINITY STRESS

DREB2A transcription, in *Arabidopsis*, in action to high salinity and dehydration, is controlled by various cis-elements independently in the DREB2A promoter [63,64]. The two major elements of the DREB2A promoter are an ABRE and linking element three (ACGCGTGTCTC) type sequence, which induces dehydration-like expression [65]. DREB2A genes can be activated by two downstream genes; one is complementary to both DREB1A and DREB2A, which has promoter sequence ACCGACNT in their promoter region; the other being DREB2A specific ACCGACNA/C/G in their promoter regions. They can be activated by high salinity, drought, and cold [39]. For the DREB2A gene, to be activated, phosphorylation, methylation, and acetylation are some of the post-translational modifications required for their initiation, but this is still debatable [66]. A negative regulatory domain was found in the DREB2A gene, which, when deleted, transforms the gene into a more dynamic form. Growth impedance was observed in transgenically mutated *Arabidopsis* plants when the dynamic form of DREB2A (DREB2-CA) was over-synthesized. These plants had considerable tolerance to salinity stress but insignificant tolerance toward freezing.

## 8. PLANT REACTIONS TO SALINITY AND DROUGHT STRESS

The following is a tabulated representation of TFs that are activated during osmotic stress effects in distinct vegetal species [Table 1] [8]. These TFs help in sustaining the plant's structural integrity and prevent the formation of ROS.

## 9. CHALLENGES IN CONTROLLING STRESS TOLERANCE PLANTS

From first crossings to commercial release, it usually takes 12–15 years to show doubt about abiotic stress-tolerating sugarcanes through breeding [85]. Functional genomics and genetic markers may speed up this process by assisting in the screening of every individual employed in crosses, either as progeny or parent, reducing the amount of time and money necessary for agronomic evaluation. Despite all claims, transgenic approaches have not completely achieved abiotic stress

tolerance in crops [86], because abiotic stress tolerant bioengineering is usually aimed to find a single gene that encodes for a single protein, resulting in low-pressure resistance. Multifaceted abiotic stress-tolerating plants enhance DREBs and they may have the capability to boost crop plant water usage efficacy in drought-prone settings. Despite all of these encouraging improvements, there have been a number of problems that need to be addressed to attain true success with DREB transgenic. Transgenic plants of DREB are exposed to many environmental stresses and may react differentially. Stress

**Table 1:** Transcription factors initiated by stress responses.

Gene	Inducible by	Species	References
CBFs	Cold	<i>Brassica napus</i>	[67]
CBF1	Cold	<i>Lycopersicon esculentum</i> , <i>A. thaliana</i>	[68,69]
CBF2	Cold	<i>A. thaliana</i>	[69]
CBF3	Cold	<i>A. thaliana</i>	[25]
CBF4	Drought	<i>A. thaliana</i>	[51]
DREB2C	Salt, mannitol, cold	<i>A. thaliana</i>	[53]
OsDREB1B	Cold	<i>O. sativa</i>	[18]
OsDREB1C	Drought, cold, wound	<i>O. sativa</i>	[18]
OsDREB1D	None	<i>O. sativa</i>	[18]
OsDREB1F	Drought, salt, cold	<i>O. sativa</i>	[45]
OsDREB2C	None	<i>O. sativa</i>	[70]
OsDREB2E	None	<i>O. sativa</i>	[70]
WDDREB2	Drought, salt, cold	<i>T. aestivum</i>	[71]
HvDRF1	Drought, salt	<i>Hordeum vulgare</i>	[72]
ZmDREB2A	Drought, salt, cold, heat	<i>Zea mays</i>	[34]
PgDREB2A	Drought, salt, cold	<i>Pennisetum glaucum</i>	[73]
SbDREB2	Drought	<i>Sorghum bicolor</i>	[74]
CaDREB-LP1	Drought, salt, wounding	<i>Capsicum annum</i>	[75]
AhDREB1	Salt	<i>Artiplex hortensis</i>	[76]
GmDREBa	Drought, salt, cold	<i>G. max</i>	[77]
GmDREBb	Drought, salt	<i>G. max</i>	[77]
GmDREBc	Drought, salt	<i>G. max</i>	[77]
GmDREB2	Cold	<i>G. max</i>	[78]
DmDREBa	Cold	<i>D. moriflorium</i>	[79]
OsDREB 1F	Drought, salt, cold	<i>O. sativa</i>	[45]
OsDREBL	Cold	<i>O. sativa</i>	[80]
WCBF2	Cold, drought	<i>T. aestivum</i>	[81]
GmDREB	Drought, cold	<i>G. max</i>	[82]
PpDBF1	Cold, drought	<i>G. max</i>	[78]
PNDREB1	Drought, cold	<i>Arachis hypogea</i>	[83]
DvDREB2A	Drought, heat, cold	<i>Dendrothema</i>	[54]
DmDREB b	Cold	<i>D. moriflorium</i>	[79]
PeDREB2	Drought, salt, cold	<i>Populus euphratica</i>	[84]
SbDREB2A	Drought, salt, heat	<i>Salicornia brachiata</i>	[50]

*A. thaliana*: *Arabidopsis thaliana*, *T. aestivum*: *Triticum aestivum*, *O. sativa*: *Oryza sativa*, *G. max*: *Glycine max*, *D. moriflorium*: *Dendrothema x moriflorium*

tolerance is induced by the DREB TF, which increases the expression of a variety of stress-related genes. It is possible that DREBs have detrimental effects on many biosynthetic pathways, resulting in unexpected effects in transgenic plants [87]. Unexpected consequences may alter the pattern of interaction between transgenic and non-target organisms, resulting in a negative impact on biodiversity. When DREB is combined with other stress-related genes, tolerance to one stress is sometimes suppressed rather than augmented to several stresses, presumably due to the silence of a gene to another, as seen in sugar cane [88]. Recombinant sugarcane shows highly tolerant to different types of pressures, indicating the typical complexity of the sugarcane genome as a whole, as well as gene interactions and being subjected to various environmental stresses at the same time.

## 10. FUTURE ASPECTS

By approaching “omics,” we can understand DREB regulation controlling the downstream signaling pathways in transgenic plants. The novel upregulated stress genes and their promoters can be helpful to improve new stress-tolerant varieties and can map the linkage groups among different transgenic plants. Eventually, DREB the gene can be used as a candidate gene in developing functional markers that help the environment to evolve various superior plant varieties in stress tolerance by genetic modification. A molecular mechanism between abiotic and biotic stress response should be in-depth, still, now few DREB transgenic plants under abiotic stress tolerance are tested to reveal their resistance to biotic stresses.

## 11. CONCLUSION

Abiotic stress plays a major role in a plant’s maturity and development, salinity is a key stress element that inhibits plant development and causes ROS, to counter these plants have multiple stress-responsive genes which are activated TFs that play a major role under abiotic conditions. Depending on both pathways, the DREB genes were expressed but it largely falls under the ABA-independent activation pathway. Plants have multiple domains and motifs which have a major function in the initiation of stress-receptive TFs. One such TF family is DREB TFs; DREBs belong to the AP2/ERF-type TF family, which has a major role in plant development and helps in the maintenance of plants during environmental stresses. The DREB TFs bind to DRE/CRT and help in the gene expression and activation of DREB genes, it is believed that DREB TFs and DRE/CRT sequence form a complex and further process the signaling of DREB genes. The DREB gene is responsible for the activation of other downstream genes which helps in equilibrating OP in stress-inflicted plants. Apart from downstream genes DREB genes are responsible for the activation of early responsive to dehydration genes, LEA genes, and sucrose phosphate synthase genes. DREB genes invariably control sugar biosynthesis and expression of LEA genes Although each DREB gene has its own individual stress-responsive motifs which help in resistance to environmental stresses, activation of other DREB and stress-receptive genes directs that there is some sort of cross-talk taking place which helps the plant in a functional form. DREB2A is the main class of stress-susceptible genes that takes part in salinity stress response. However, there are some plants that induce DREB1 genes during osmotic stresses which indicates that initially all stress responses were managed by a primary gene and over the course of time, plants evolved more sophisticated genes to maintain their cellular integrity. Saline water irrigation is the future of agriculture, plants that have high nutritional value and which can withstand salinity and waterlog are needed ever increasingly, for this to happen, DREB2A genes seem to

be the perfect answer and transgenic plants with this candidate gene show promising results in salinity affected areas.

## 12. 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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## 14. CONFLICTS OF INTEREST

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

## 15. ETHICAL APPROVALS

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

## 16. DATA AVAILABILITY

All the data is available with the authors and shall be provided upon request.

## 17. PUBLISHER’S NOTE

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