



Role of Plant Transcription Factors in Abiotic Stress Tolerance

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Abstract

The plants are constantly facing different environments of abiotic stress, which harm growth and crop productivity. Plants have other mechanisms to avoid and adapt under diverse circumstances of abiotic stress, which differ from one species to another. Transcriptional factors are a master regulator of various abiotic stresses, including DREB, MYB, WRKY, NAC, bZIP belonging to families. Transcription factors interfering with promoter regions cis-elements uncontrolled other stress-responsive genes. Expression of different transcription stress response mechanisms under abiotic stress environment and protein level has avoided crop yield losses. By using other promoters to enhance outcomes under stress circumstances, these abiotic stress-resistant TFs may be genetically engineered to generate transgenic plants that are salt, drought, heat, and cold resistant. The role of the transcription factor in transgenic plant tolerance to abiotic stress is the focus of this review.

Keywords: Transcription Factor; Stress Tolerance; Abiotic Stress

Introduction

Plants are exposed to harsh external environments throughout their lives due to their sessile nature, which hinders their growth and development. The economic decline in the global productivity of crops results from increased climate change-induced abiotic stress, resulting in food security and availability challenges for the rapidly rising populations [1]. Precipitation was the most crucial aspect of strong defence programming against abiotic and biotic stress [84]. Including transcriptional reprogramming of genes, involving various transcriptional factors and multi-level work influencing many signals during the evolution from several methods to avoid adverse effects of abiotic stress, including high temperature, salinity, drought and biotic stress [85]. In addition, to cope with abiotic stress, many biochemical and physiological modifications are observed to acclimate under specified stress conditions. They have been reported to be controlled at the molecular level by raising modulation and control of stress-responsive genes [2].

AREB/ABF, WRKY, NAC, bHLH, ZFP, DREB1/CBF, DREB2, and MYB/MYC regulators have been implicated in increasing plant-specific stress response. A study of these stress-inducible genes involved found the existence of complex regulatory mechanisms between the detection of abiotic stress signals and the expression of stress-response genes. Overexpression of genes that regulate the transcription from several downstream stress-responsive genes appears to be a potential mechanism [3].

Role of Plant Transcription factor

Plants have built a complex acclimatization strategy to cope with different environmental stress conditions. They have physiological, biochemical, cellular levels through the production of various phytohormones, antioxidant synthesis, osmolyte formation, stomata closure, waxy cuticle and adaptive responses against abiotic stress response. Plants have a stress response signalling at the molecular level. Sensing pathways adapt through main steps: signal process-

ing, signal transduction, and production of stress-responsive genes under abiotic stress conditions [4,5].

Abiotic stress reactions increase the cumulative ROS level, leading to cell death and increased cell oxidative damage. Many tiny secondary messengers serve as signalling molecules that are found in the cell cytoplasm, such as reactive oxygen species (ROS), calcium ions (Ca^{2+}), inositol phosphate, phosphatidylinositol [6]. Auxin, cytokinin, gibberellic acid, abscisic acid, ethylene, and salicylic acid are phytohormones that act as secondary messengers and signal transduction pathways during the stress response [6,7]. ABA is a key regulator of abiotic stress responses in plants, particularly drought survival, and is linked to the gene regulatory network that allows plants to survive with water scarcity [8].

Secondary messengers that play a significant part in signal transduction pathways. Under abiotic stress conditions, some phosphatase and protein kinases levels enhance intracellular space. Plants activate several signal transduction pathways, including mitogen-activated protein kinase (MAPK) and calcium-dependent protein kinases (CDPKs), in response to abiotic and biotic stress [8]. Due to the strict modulation involved in the accurate identification and binding of TFs to the Promoter Region, plant TFs may also be regulated by various post-transcript modification activities, such as sumoylation ubiquitination of a highly regulated network to govern stress-responsive gene expression. In this review, we have summarized role of various transcription factors such as MYB, DREB, NAC and WRKY TFs.

DREB Transcription factor

Abiotic stress tolerance AP2/ERF TFs are dehydration sensitive element-binding proteins (DREBs) that activate several abiotic stress-related genes and induce stress tolerance in plants. They play a crucial role in ABA-independent processes by triggering stress-responsive genes. By using yeast one-hybrid screening, the first DRE binding proteins found in *Arabidopsis* were DREB1A and DREB2A and CBF1 [9,10]. In *Arabidopsis thaliana*, DREB1 and DREB2 are two subgroups of the DREB subfamily that directly bind and trigger stress-responsive gene expression. These sequences bind and start the DRE sequence and are first recorded in the *rd29A* promoter. In millet crops, various other DREB2 proteins have been identified, such as DREB2A and DREB2, activating stress tolerance genes and increasing salinity survival, drought, and freezing stress [11,12].

The 60-amino-acid AP2/ERF domain is a highly conserved DNA-binding motif in DREB. The amino acid sequences of valine 14 and glutamic acid 19 are highly conserved and play a vital role in recognizing and adequately binding DRE cis-elements. In the N-terminal region, the first YRG of 20 amino acids is highly basic, hydrophobic, and has a high DNA binding affinity due to its essential nature [12].

There are 18 acidic amino domains in the C-terminal region responsible for the amphipathic alpha-helix responsible for protein-protein interaction. The LWSY motif is found at the C-terminal end of the protein, while the DSAW motif is located at the ERF/AP2 domain's terminus. With the essential amino acid-rich sequence PKRPAGRTKFRERHP as NLS, DREB protein has one or two nuclear localizations for entrance into the nucleus. The transcriptional activator found in the C-terminal region is an acidic amino acid [12,13].

DREB under the abiotic stress response

The overexpression of rice gene *OsDREB2A* improves immunity under the influence of salinity and osmotic stress. Overexpression of the rice gene *OsDREB2A* in soybeans improves salt tolerance [13]. Transgenic tobacco harbours the *EsDREB2B* *E. songoricum* gene, enhancing abiotic and biotic stress [15]. Lettuce *LsDREB2A* gene over-expression in transgenic *Arabidopsis* enhances drought tolerance [16]. Sugarcane genome analysis had established several SsDREB genes (100,102,105) that play a vital role in response to cold stress [17]. Similarly, the overexpression of *DcDREB1A* in *Arabidopsis* increases lignin content, minimizes stomata apertures, and enhances SOD and POD levels under drought stress response [18]. In addition, studying the expression of *Ammopiptanthus nanus* helps find that EVM0023336.1 and EVM0013392.1 are responsible for osmotic and cold stress responses [66]. Common bean DREB genes with variable nucleotide sequences such as *PvDREB5A* and *PvDREB1F* have resistance capability under cold, salt, drought and ABA stress [21]. *Arabidopsis* genes *AtDREB1A* and *AtDREB2C* overexpression in transgenic soybean improve resistance to drought [22]. Similarly, *Caragana korshinskii* *CkDREB1* overexpression in *Arabidopsis* increases low temperature and drought stress tolerance [23]. Exogenous melatonin treatment to strawberries improves cold stress tolerance by lowering hydrogen peroxide MDA levels and raising various enzymatic antioxidants levels by increasing DREB/CBF-COR pathways expression levels [24].

bZIP Transcription factor

The bZIP is one of the most prominent TF families, a name derived from the highly conserved bZIP domain. The ZIP domain is made up of two functional regions, a conserved essential area and a highly variable leucine zipper region, each of which is 60-80 amino acids long. The bZIP TF is a leucine zipper dimerization motif with a primary part that binds DNA. The variable N-x7-R/K motif of roughly 16 hydrophobic amino acids is responsible for DNA binding and nuclear localization signals in the bZIP domain, which is positioned at the N-terminus. It comprises heptads that repeat leucines or other hydrophobic amino acids at the C terminus end, which are precisely nine amino acids responsible for particular recognition and dimerization. The bZIP protein binds to DNA and produces a coil-coil structure on top of it (zipper) [26]. In general, bZIP recognizes a cis-acting DNA element with an ACGT core motif in plants. In the case of a plant, bZIP binds like C-box (GACGTC) and G-box (CACGTG), A-box (TACGTA). However, specific bZIP proteins recognize and bind non-palindrome sequences. In *Arabidopsis*, there are 78 members of the bZIP gene family, 89 or 92 in rice (*Oryza sativa*), 125 in maize (*Zea Maize*), 160 in soybean (*Glycine max*) and 247 in *Brassica napus* [26]. Based on sequencing similarities of their particular domains, plant transcription factor bZIP is divided into thirteen classes (designated A, B, C, D, E, F, G, H, I, J, K, L, and S) [26,27].

Under the abiotic stress condition, TFs bZIP incorporate ABA-responsive element-binding proteins (AREB) or ABRE binding factors (ABF), essential ABA-dependent gene expression regulators [27]. In *Arabidopsis*, bZIP proteins such as AtZIP17, AtbZIP28 and AtbZIP28 are endoplasmic reticulum bZIP proteins under stress conditions. Group S1 bZIPs (AtbZIP1, AtbZIP2, AtbZIP11, AtZIP44, and AtbZIP53) and, in particular, heterodimers with group C bZIPs (AtbZIP9, AtbZIP10, AtbZIP25, and AtbZIP63) form metabolic programming during stress conditions. Some bZIP proteins regulate carbohydrate energy metabolism and amino acid catabolism [28]. They play a crucial part in the root-specific response. Low temperature (4°C) enhanced the expression of the OsbZIP52 gene in OsbZIP52/RIBZ5 isolated from rice panicles, while drought, salt, or ABA did not [29].

In addition, *Arabidopsis* overexpression with a C-ZIP transcription factor, TabZIP14-B, increased physiological activity, increased salt tolerance, and increased stress response. When the bZIP rice

transcription factor OsbZIP16 is overexpressed in *Arabidopsis*, it is regulated by drought stress [30]. Transgenic sweet potatoes overexpress the bZIP transcription factor IbABF4, which decreases MDA H2O2 activities under different abiotic stress to increase photosynthetic responses [31]. Furthermore, in *Arabidopsis*, overexpression of TabZIP (*Traes 7AL 25850F96F.1*) increases heat and other abiotic stress tolerance [15]. In *Arabidopsis*, overexpression of the CsbZIP18 gene suggests resilience to cold stress [33]. Increased photosynthetic efficiency, antioxidant activity, shoot and root growth, and stress tolerance increased with an HBP1b gene expression into transgenic rice seedlings [34]. Similarly, the ectopic expression of rice F-bZIP transcription factor, OsbZIP50 in *Arabidopsis* controls the supply of zinc to a plant that is very useful for biofortification [35]. TabZIP genes reported in wheat where TaABI5 physically interacts with cold-resistant transcription factor TaICE1, suitable for studying resistance for abiotic stress tolerance in plants [36].

MYB transcription factor

The MYB transcription factors are among the second biggest plant transcription factors. From the v-Myb oncogene, the first MYB gene is extracted [37]. The MYB protein DNA-binding domain is made up of one to four imperfect repeats of 51-53 amino acids that form a helix-turn-helix structure. The hydrophobic core contains three regularly spaced tryptophan residues that extend to the DNA major groove and are essential for recognizing the unique DNA sequence. Four kinds of proteins are defined based on the number and position of repetitions in the MYB domain: 1R-MYB (one repeat), 4R-MYB (four repeats), R1R2R3-MYB (three repeats), and R2R3-MYB (two repeats). Plant species generally have their R2R3-MYB class type, which is the most common [37].

Arabidopsis provides 198 MYB genes, whereas rice contributes 183, making MYB the second biggest group of plant transcription factors. R2R3-MYB is the largest subfamily of the MYB family, having evolved from the progenitor of 3R-MYB by duplication of either R1-MYB. The 2R-MYB subfamily is divided into three subgroups in plants, each one with different DNA binding specificities: a subset that is very similar to c-MYB, a subset that encodes proteins in a preserved position by genes with an intron, and a subgroup that encodes proteins at a different intron position, according to phylogenetic analysis. The 2R-MYB proteins subfamily has two parts: an N terminus that binds DNA and a C terminus that contains a

variable area. Based on domain position, the 2R-MYB subfamily is classified into 22 groups. Around 120 members of the 2R-MYB subfamily are found in *Arabidopsis*, while roughly 90 members found in rice [24,25,28].

Role of MYB under abiotic stress condition

The 2R-MYB subfamily plays a unique role in various abiotic stress conditions such as metabolism regulations, cell growth and hormonal control, in the sense of different stress reactions. MYB family response to abiotic stress by ABA signalling. AtMYB2 shows an ABA-mediated response to drought stress in *Arabidopsis* [37]. Rice OsMYB4 shown to react to cold and drought tolerance in transgenic *Arabidopsis*, tomatoes and apples [38]. In rice, overexpression of OsMYB1R1 improves resistance to drought stress by reducing ABA vulnerability in increased soluble sugar and free proline [39].

Glycine max transcription factor GmMYB12B2 can increase the tolerance capacity to salinity and UV radiation in transgenic *Arabidopsis* [40]. ZmMYB30, ZmNHX1, ZmHKT1 high expression of salinity tolerance gene in [41]. In transgenic tobacco plants, sugarcane tolerance SoMYB18 in salinity and dehydration [42]. Under drought stress circumstances, overexpression of GmMYB84 in *Arabidopsis* increased antioxidant activity and a longer tap root [43]. Similarly, overexpression of the soya bean gene, GmMYB12, enhances flavonoid accumulation ensures membrane probity by regulating the osmotic stress resistance of transgenic *Arabidopsis* [44]. Due to drought and salt stress, overexpression of OsMYB6 in Rice resulted in increased proline content, SOD, and CAT activity. In the presence of abiotic and biotic stresses, the expression of the soya bean transcription factor GmMYB81 promotes seed germination [45]. In contrast to overexpression of the grapevine gene VvMYB1, it increases the synthesis of flavonoid in transgenic *Arabidopsis* to survive abiotic stress. Under drought stress, anthocyanin biosynthesis can identify the new StR2R3-MYB gene [47].

Rice salt and drought stress tolerance is also mediated by the TF genes OsMYB91 and OsMYB48-1. Ectopic overexpression of SiMYB305 in *Arabidopsis* has increased plant tolerance to drought, NaCl, and mannitol [48]. LDOX1, MYB6 gene expression increased under cold stress is responsible for anthocyanins productions in purple-black carrots [49].

NAC Transcription factor

The NAC is one of the significant plant-related transcriptional factors. The NAC is derived from three genes: NAM (no apical meristem), ATAF1 and -2, CUC2 (cup-shaped cotyledon). NAC TF has a highly conserved N-terminal region and a variable C-terminal region. The domain comprises 160 amino acids and is separated into five sub-domains (A-E) [51].

Similarly, overexpressing ThNAC7 in *Arabidopsis* showed increased proline content, enriched stress-responsive genes and ROS scavenging activity under osmotic and salt stress conditions [52]. MdNAC029 overexpression causes cold tolerance in apple and *Arabidopsis* via the CBF-dependent mechanism [53]. In addition, the expression of NAC TF JUNGBRUNNEN 1 (JUB 1) in *Arabidopsis* has improved dehydration resistance by regulating the promoters of CaMV 35S and RD29A [54].

ABA hypersensitivity, root alterations, and leaf shape are improved by *Arabidopsis* expression of CmNAC1 during abiotic stress reactions [82]. Under abiotic stress regulation, OsNAC2 regulates ABA-dependent genes (OsLEA3) and OsSAPK1 and enhances crop yields [83]. AIR3, ARF2, and ABA-responsive genes ABI1 and ABI5 increase lateral root development in transgenic *Arabidopsis* plants containing the soybean NAC gene GmNAC109 [55]. GmSNAC49 expression improves drought tolerance in *Arabidopsis* by upregulating the drought and ABA signalling pathways [56]. PbNAC TFs implicated in abiotic stress response discovered in the white pear transcriptome analysis [31]. N-terminal NAC is primarily responsible for ABA sensitivity [57]. Some stress-responsive genes in *Medicago*, such as MfNAC26, MfNAC35, MfNAC79, MfNAC88, and MfNAC95, have been found and may have stress tolerances [58]. ROS production and harmful modulation of plant tolerance to abiotic stress in transgenic *Arabidopsis* with the PwNAC30 gene [59]. Gene silencing of RcNACo91 is responsible for positive controlling drought stress and mitigation of stress resistance in rose plants [60]. In *Triticum aestivum*, TaNAC5D-2 is responsible for stomatal closure under drought stress [61]. Expression of GmSNAC49 in *Arabidopsis* improves drought tolerance via upregulating the drought and ABA signalling pathways [62]. PbNAC TFs implicated in abiotic stress response was discovered in the white pear transcriptome analysis [63].

WRKY Transcription factor

The WRKY is one of the most significant transcriptional factors in the plant, recorded in soil living amoebae, such as *Dictyostelium discoideum* and protozoan *Giardia lamblia*. The WRKY family consists of approximately 109 rice and 74 in *Arabidopsis*, 76 in *Fagopyrum tataricum* [66], 158 *AhWRKY* in *Peanut*. By using VIGS, the two differentially expressed genes-SmWRKY26 and SmWRKY32 were confirmed in response to cold stress. 79 IbWRKY in sweet potatoes, 97 PgWRKY in Pearl millet [64], 101 OrWRKY in *O. rufipogon* [65]. The N-terminal end is a conserved WRKYGQK sequence with a Zn finger-like motif. The DNA binding domain is 60 amino acids long with a four-stranded β -sheet and zinc finger motifs. Based on the presence of the WRKY domain, further divided into three different subgroups, Group I consists of 2 WRKY domains, Group II and III, with a single DBD with Zn finger motifs. On the presence of primary amino acids sequences, Group II was further classified into IIa, IIb, IIc, IId, and IIe. Essential nuclear localization signals, serine/threonine-rich regions, leucine zippers, glutamine-rich regions, proline-rich regions, kinase domains, TIR-NBS-LRR domain and transcriptional regulation structure are only a few of the WRKY subgroups. TFs WRKY binds downstream genes, which regulate signalling through kinase or phosphorylation with W-box present at the promoter. WRKY typically binds to W-box reports that bind non-Wbox elements, such as OsWRKY13, which binds to W-box and PRE4 (TGCGCTT) elements. In the context of NtWRKY12, it binds to a SURE-like element but not to a W-box element [64-66].

Abiotic stress modulation by WRKY TFs

GhWRKY41/SpWRKY1 is responsible for salt and drought tolerance in transgenic tobacco via influencing stomatal conductivity and ROS levels [67]. Through ABA signalling and auxin stabilizing, the stress, development, and hormonal response gene AtWRKY46 in *Arabidopsis* induce the growth of lateral roots in saline stress [68]. In transgenic *Arabidopsis*, the sunflower HaWRKY76 shows drought and flood tolerance. Rice OsWRKY74 controls Pi equilibrium, Fe deficiency and cold stress [69]. Under various abiotic stress conditions, the WRKY33 C-terminal domain binds several VQ proteins such as SIB2 and SIB1 (Sigma Factor-Interacting Protein). GmWRKY12, a WRKY soybean transcription factor, is involved in salinity and drought stress. Recently identified soybean gene *Glyma.19G094100* and *Glyma.16G054400* under phosphorous deficiency and abiotic stress response [70]. According to a genome-wide study, *Glycyrrhiza glabra* genes are implicated in a variety of

stress responses, including GgWRKYs 2, 33, 28, salinity, senescence, and cold stress. [71]. The microarray of wheat research found that TaWRKY090 and TaWRKY014 were involved in drought stress response. At the same time, TaWRKY (008,45,122) was responsible for drought and heat stress response [72]. Meanwhile, buckwheat genome research revealed four FtWRKY (6, 74, 31,7) genes activated in response to heat, drought, salt, and cold stress [73].

Similarly, WRKY genes of *Juglans regia* JrWRKY2, JrGSTU23, JrVHAc4 participated in a many increase in physiological genes expression MDA, SOD, POD, GPX, APX and ABA-mediated mechanisms under drought stress responses [74]. Furthermore, the grape transcription factor VvWRKY30 demonstrated lower ROS, increased antioxidant activity, proline, osmoticum content, and glycol-metabolism in transgenic *Arabidopsis* during salt stress [75]. Additionally, a rice transcriptional factor, OsWRKY29, repressed seed dormancy by downregulating the OsVP1 and OsABF1, ABA signalling pathways [76]. Cowpea *VuWRKY18,21,75* participate in signalling pathways under drought stress conditions [77]. Furthermore, in *Arabidopsis*, overexpression of IbWRKY2 improves drought and salt stress tolerance [78]. Similarly, TaWRKY46 overexpression improves osmotic stress tolerance via ABA-independent and ABA-dependent mechanisms [81]. Again, the WRKY8 transgenic tomato showed reduced MDA H_2O_2 under biotic and abiotic stress responses [79].

Future prospective

Screening stress-sensitive genes and then resolving the promoter structure to check if TFs coordinate gene expression by binding across cis- and trans-acting areas is the easiest way to gather relevant TFs for genetic engineering. Transcriptome data analysis from diverse plant tissues under various abiotic stress conditions vs controlled settings can aid in the development of a shortlist of possible TF-containing genes. Moreover, subsequent expression analyses to determine candidate genes, in-plant functional of these genes, are needed for electing the most acceptable candidate for genetic engineering. Entirely identifying post-transcriptional regulation and the candidate TFs is further mandatory to collect complete information about the TF action and their interactions with other members. Production of both mutant and overexpression lines in agricultural plants is widespread to play for functional investigations of important TFs. Various *Arabidopsis* TF producing genes describe similar abiotic stress tolerance abilities introduced to agricultural plants.

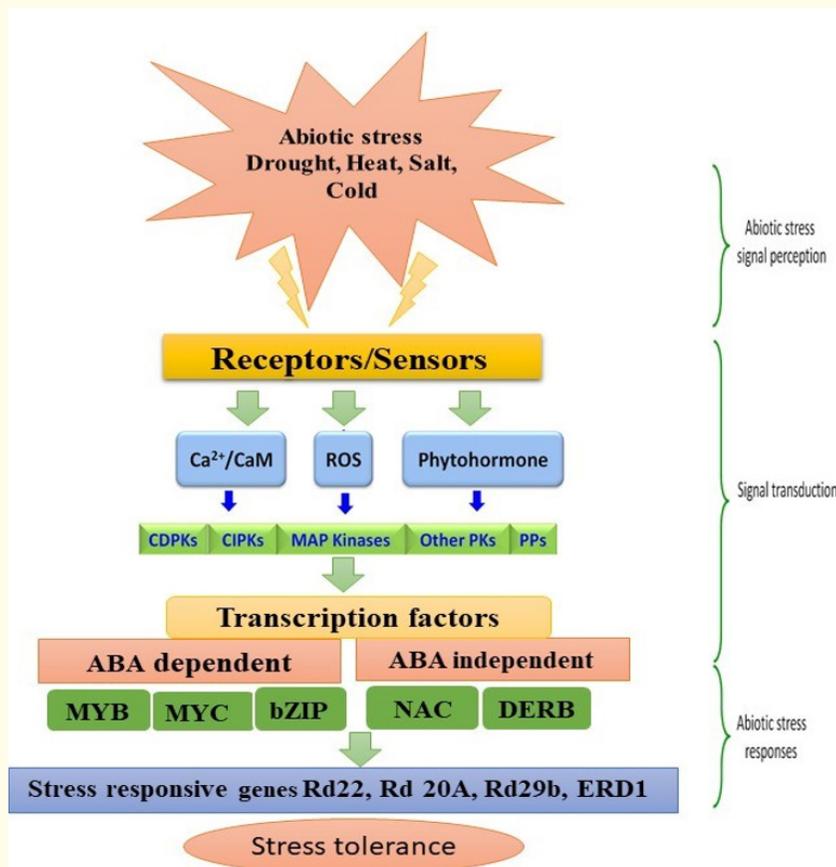


Figure 1: A schematic representation of abiotic stress tolerance in plants.

Family	Gene	Plant	Stress	Reference
DREB	<i>LsDREB2A</i>	<i>Lettuce</i>	Drought	16
	SsDREB (100,102,105)	Sugarcane	Drought	17
	DcDREB1A	<i>Daucus carota</i> L	Drought	18
	EVM0023336.1, EVM0013392.1	<i>Ammopiptanthus nanus</i>	Cold, osmotic stress	19
	GmDREB1	Wheat	Salinity	20
	PvDREB5A	<i>Phaseolus vulgaris</i>	Cold, salinity	21
	CkDREB1	<i>Caragana korshinskii</i>	Drought, low temperature	23
	DREB/CBF-COR	Strawberry	Cold	24
	<i>ZmAP2/ERF</i>	<i>Zea mays</i>	Salinity, drought	25

bZIP	SibZIP01-SibZIP63	sesame	Light signalling	27
	IbABF4	Sweet potato	Drought, salinity	31
	7AL 25850F96F.1	<i>Triticum aestivum</i>	Heat, salinity	32
	<i>CsbZIP18</i>	<i>Camellia sinensis</i>	Freezing tolerance	33
	HBP1b	<i>Oryza sativa</i>	Heat, salinity	34
	<i>OsbZIP50</i>	<i>Oryza sativa</i>	Zinc deficiency	35
	TabZIP96	<i>Triticum aestivum</i>	Freezing	36
MYB	GmMYB12B2	<i>Glycine max</i>	UV radiation	40
	ZmNHX1, ZmHKT1 ZmMYB30	<i>Zea mays</i>	Salinity	41
	GmMYB84	<i>Glycine max</i>	Drought	43
	OsMYB6	<i>Oryza sativa</i>	Drought, salinity	44
	GmMYB81	<i>Glycine max</i>	Salinity, drought	45
	VvMYBF1	<i>Vitis vinifera</i> L.	Drought, salinity	46
	StR2R3-MYB	<i>Solanum tuberosum</i>	Drought	47
	MYB-6, LDOX-1	<i>Daucus carota</i> L.	Cold	49
	SiMYB305	sesame	Salinity	48
NAC	PgNAC 30,42	Pearl millet	Drought, salinity	50
	<i>MfNACsa</i>	<i>Theobroma cacao</i>	Drought	51
	JUB1	<i>solanum lycopersicum</i>	Drought	54
	GmNAC109	<i>A.thaliana</i>	Salinity, drought	55
	GhNAC	Tobacco	Salinity, drought	56
	MfNAC26, MfNAC35, MfNAC79, MfNAC88, MfNAC95	<i>Medicago falcata</i>	Drought, salinity	57
	PwNAC30	<i>Picea wilsonii</i>	Salinity, Drought	58
	ZmSNAC13	<i>A.thaliana</i>	Drought, salinity	59
	RcNAC091	<i>Rosa chinensis</i>	salinity	60
	TaNAC5D-2	<i>Triticum aestivum</i>	Drought	61
WRKY	PgWRKY	<i>Pennisetum glaucum</i>	Salinity	64
	WRKY	<i>Oryza rufipogon</i>	salinity	65
	JrWRKY2, JrGSTU23, JrVHAc4	<i>Juglans regia</i>	Drought	74
	<i>TaWRKY46</i>	<i>Triticum aestivum</i>	Osmotic stress	39
	<i>Glyma.19G094100</i> <i>Glyma.16G054400</i>	<i>Glycine max</i>	Low phosphorous	70
	GgWRKYs 2, 33, 28	<i>Glycyrrhiza glabra</i>	Salinity	71
	VvWRKY30	Grape vine	Salinity	69
	VvWRKY18,21,75	<i>Vigna unguiculata</i>	Drought	77
	<i>AtWRKY53</i>	<i>Arabidopsis</i>	Drought	
	WRKY8	<i>Solanum lycopersicum</i>	Salinity, drought	78

Table 1: Transcription factors response to abiotic stresses.

Conclusion

This chapter intensified our understanding of the mechanical system and adapted to abiotic stresses in the plant. It also provides a group of appropriate genes for overexpression studies in transgenic plants that increased abiotic stress tolerance. Other biological processes like growth and development, senescence, and yield will be required to unravel the specific stress-responsive TF genes from different families to govern abiotic stresses. To minimize the negative effects of abiotic stress, we will focus on genetic engineering, such as modifying the expression of critical TFs for stress tolerance in certain relevant and geographical patterns. The role of TF structure in abiotic stress responses in several agricultural plants is discussed in this chapter. This complex scientific topic is employed in plant study and looks for predicted necessities.

Declarations

Author Contributions

SS: Conceptualization, Methodology, Data curation, Writing-original draft, Writing- review and editing and SC: data duration, writing-review and editing. All authors read and approved the final manuscript.

Availability of Data and Materials

The datasets supporting the results of this article are included within the article.

Ethics Approval and Consent to Participate

This study does not contain any research requiring ethical consent or approval.

Consent for Publication

Not applicable.

Competing Interests

The authors declare that they have no competing interests.

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