Transcription Factors involved in Abiotic stress responses in Maize (*Zea mays* L.) and their roles in Enhanced Productivity in the Post Genomics Era.

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Background: Maize (*Zea mays* L.) is a principal cereal crop cultivated worldwide for human food, animal feed, and more recently as a source of biofuel. However, as a direct consequence of water insufficiency and climate change, frequent occurrences of both biotic and abiotic stresses have been reported in various regions around the world, and recently, this has become a constant threat in increasing global maize yields. Plants respond to abiotic stresses by utilizing the activities of transcription factors, which are families of genes coding for specific transcription factor proteins. Transcription factor target genes form a regulon that is involved in the repression/activation of genes associated with abiotic stress responses. Therefore, it is of uttermost importance to have a systematic study on each transcription factor family, the downstream target genes they regulate, and the specific transcription factor genes involved in multiple abiotic stress responses in maize and other staple crops.

Method: In this review, the main transcription factor families, the specific transcription factor genes and their regulons that are involved in abiotic stress regulation will be briefly discussed. Great emphasis will be given on maize abiotic stress improvement throughout this review, although other examples from different plants like rice, Arabidopsis, wheat, and barley will be used.

Results: We have described in detail the main transcription factor families in maize that take part in abiotic stress responses together with their regulons. Furthermore, we have also briefly described the utilization of high-efficiency technologies in the study and characterization of TFs involved in the abiotic stress regulatory networks in plants with an emphasis on increasing maize production. Examples of these technologies include next-generation sequencing, microarray analysis, machine learning and RNA-Seq.

Conclusion: In conclusion, it is expected that all the information provided in this review will in time contribute to the use of TF genes in the research, breeding, and development of new abiotic stress tolerant maize cultivars.

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Abstract

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Introduction

Abiotic stresses for instance drought, salinity, cold, high temperatures and mineral toxicity are the main cause of major crop yield reductions worldwide, reducing expected average yields of the major crops by more than 50% (Prasad et al., 2011; Mahalingam, 2015). Plants are sessile beings that are continuously exposed to various changes in the environmental conditions. Variations in the environment involving both biotic and abiotic stresses have negative effects on economically important crops like maize (Ramegowda and Senthil-Kumar, 2015). Evolutionary changes have helped many plants adapt to different adverse conditions. Some species show a marked increase in tolerance to various abiotic stresses compared to others (Phukan et al., 2014). Due to global warming and the climatic abnormalities accompanying it, the frequencies of combined biotic and abiotic stresses have significantly increased, leading to reduced growth and yield of the major crops worldwide (Mittler., 2006; Pandy et al., 2015; Ramegowda and Senthil-Kumar, 2015). Moreover, continuous manifestations of abiotic stresses such as heat and drought together, has led to severe reductions in crop yields as opposed to when these stresses occur separately during the different growth stages (Mittler., 2006; Prasad et al., 2011).

Maize (*Zea mays* ssp. Mays L) is one of the most important cereal crops cultivated worldwide (particularly in Africa and South America). Global maize production increased from 255 million tonnes in 1968 to 1,134 million tonnes in 2017 representing an average annual growth of 3.46%.

(https://knoema.com/atlas/World/topics/Agriculture/Crops-Production-Quantity-tonnes/Maize-production). Maize production has significantly enlarged in both the developing countries and the developed countries (Wang et al., 2013).

Maize is a staple food in many parts of the world; it is consumed directly by humans, used for animal feed, and in other maize products such as corn syrup and corn starch. In the last century, maize has been utilized as a model system in the study of various biological events and systems including paramutation, transposition, allelic diversity, and heterosis (Bennetzen and Hake., 2009). Recently, maize has been identified as a potential sustainable feedstock, as well as a model system for research in the bioenergy and biofuel industries (Perlack et al., 2005). Continuous study in maize genetics has led to further understanding of other related C4 grasses such as Elephant grass (*Miscanthus gigantus*) and switchgrass (*Panicum virgatum*) as scientists aim to develop and domesticate these plants (Perlack et al., 2005). However, maize belts around the world which range from the latitude 40^{o} South to the latitude 58^{o} North are exposed to continuous effects of both biotic and abiotic stresses (Gong et al., 2014). Abiotic stresses, like salinity, drought, nutrient deficiency, and high and low temperatures are the major environmental factors that negatively influence maize production. In particular, intense waterlogging, extreme temperatures, and drought have significantly affected maize yields (Ahuja et al., 2010).

Plants must cope with a variety of abiotic stresses including extreme temperatures, heavy metals, osmotic stresses, and high light intensity. Under stress, accumulation of some metabolites positively regulates plants response to both abiotic and biotic stresses thus protecting plants from multiple stresses (Rasmussen et al., 2013). Changes in ions fluxes, callose accumulation, phytohormones, and ROS are the first responses induced to tackle the stresses, leading to metabolic reprogramming in the plants defenses (Bartoli et al., 2013).

Reactive oxygen species such as hydrogen peroxide (H_2O_2) and superoxide ($\bullet O^{-}_{2}$) which are produced due to oxidative stresses, inhibit photosynthesis and cause vast cellular destruction

(Allan and Fluhr, 2007). ROS are normally removed rapidly by antioxidative mechanisms, although this removal can be hindered by the stresses leading to an increase in ROS concentration inside the cells, and further increasing the damage caused (Allan and Fluhr, 2007).

Another pathway involved in abiotic stress responses in plants is the Mitogen-Activated Protein Kinase (MAPK) cascades. MAPK cascades are activated following the recognition and perception of stress stimuli and control the stress response pathways (Wurzinger et al., 2011). They are highly conserved in eukaryotes and are responsible for signal transduction in various cellular processes under different biotic and abiotic stress responses. Because MAPKs are involved in various stress responses, they play a main role in the combination of biotic and abiotic stresses (Amajová et al., 2013).

Additionally, hormone signaling in plants is another important pathway involved in biotic and abiotic stress responses and the primary hormone involved is ABA. An increase in ABA concentration in plants under abiotic stress modulates the abiotic stress-regulation network (Xiong et al., 2002), while biotic stress is mediated by antagonism in other stress hormones such as JA/ET and SA (Liu et al., 2008). The role of ABA in abiotic stress responses has been widely described throughout this review.

Plants do not respond to multiple stresses by way of a linear pathway. The responses are complex circuits involving various pathways in tissues, cellular specific compartments and the interactions of signaling molecules in controlling a particular response to a stimulus (Dombrowski, 2003). Due to abiotic stresses, numerous proteins and gene transcripts are altered through the regulation of protein turnover and gene expression (Jiang et al., 2007; Wong et al., 2006).

In this review, we will briefly describe the main TF families and the interactions of these TFs with the *cis*-acting elements (CREs) which are present in the promoter regions of stress responsive genes. Even though TF regulons have been described recently by (Gahlaut et al 2016; Joshi et al., 2016), this review will focus on TFs involved in abiotic stress tolerance with a specific focus on maize. We will also focus on new ways of increasing production of maize by utilizing currently available genomic information, tools and data.

Survey methodology

All published manuscripts cited in this review were obtained from different databases including Pubmed, Web of Science, EBSCO, Google Scholar, research gate, Science Direct, SCOPUS, JSTOR, SciELO, and Semantic Scholar. Key words such as “maize stress tolerance”, “transcription factors involved in abiotic stress responses”, “abiotic stress”, “transcription factor downstream genes”, and “regulons involved in abiotic stress” were searched between 10 January to 25 October 2018. We have critically analyzed articles to provide an in-depth and comprehensive research trend focusing on the TFs involved in abiotic stress tolerance in maize. Furthermore, we have provided perspectives on the latest research as well as previous findings with focus on TF families involved in abiotic stress responses in maize.

151

152 **Functions of Transcription Factors**

153 Abiotic stress-induced genes are generally classified into two main groups based on their protein
154 products. One type includes the genes coding for products which directly allow cells to resist
155 environmental stresses for instance osmotic regulatory protein, late embryogenesis abundant
156 (LEA) protein, enzymes synthesizing proline, betamine, malondialdehyde (MDA) and other
157 osmotic regulators and anti-freezing proteins (Loredana et al., 2011). The second type of genes
158 are regulatory proteins which operate in the signal transduction networks, for example, molecular
159 chaperones, functional proteins, and transcription factors (TFs) or kinases (Song et al., 2013;
160 Loredana et al., 2011).

161 Networks of transcription factors together with transcription factor binding sites (TFBS) directly
162 control transcriptional regulation of plant genes (Chaves and Oliveira, 2004). Transcription
163 factors are proteins usually consisting of two domains, namely (1) the DNA binding domain
164 (DB) and (2) an activation domain (AD). A TF binds to the *cis*-acting element (TF binding site)
165 located in the promoter region of a stress-induced gene with the support of a DB domain
166 (Yamasaki et al., 2013). This event brings the AD close to the target gene leading to repression
167 or activation of this gene. A large percentage of genes in the plant genome (nearly 10%)
168 essentially encode for transcription factors (Franco-Zorrilla et al., 2014). TFs activate or repress
169 the activity of RNA polymerase, leading to gene regulation. TFs can be categorized into various
170 families based on their DNA binding domains (Riechmann et al., 2000). Since abiotic stresses
171 are quantitative traits that might require regulation of several genes including the TF genes, and
172 since a single transcription factor may regulate several genes that are involved in abiotic stress
173 tolerance. A detailed study of all TFs associated with abiotic stress regulatory mechanisms in
174 maize will be significantly rewarding. For example, Xu et al. (2006) successfully converted flood
175 sensitive rice genotypes into flood-tolerant varieties by introgression of the *sub1* locus which
176 encodes an (ethylene response factor) TF, leading to the induction of about 900 stress-responsive
177 genes.

178 TF DNA-binding domains are strongly conserved between species, to the extent of using these
179 characteristics to classify the TFs into various families (Fig. 1). These families differ among
180 plant species in that different plant systems have between 26 to 83 TFs families (Jin et al., 2014).
181 In *Arabidopsis*, for instance, approximately 34 families consisting of 1533 TFs have so far been
182 classified (Riechmann et al., 2000). Additionally, in *Arabidopsis* and many other plants,
183 transcriptome data revealed a number of pathways which respond to abiotic stresses
184 independently, pointing to the possibility that susceptibility or tolerance of both biotic and
185 abiotic stresses are controlled by a sophisticated gene regulatory network at the transcriptome
186 level (Umezawa et al., 2006).

187 Abscisic acid (ABA) is the principal hormone involved in the coordination of abiotic stress in
188 plants (Fig. 1). This hormone regulates a complex gene regulatory system that enables plants to
189 handle decreased moisture availability (Cutler et al., 2010). ABA-dependent gene activation
190 pathways were identified as pathways which determine stress tolerance by the induction of at
191 least two separate regulons: the first one is the myeloblastosis oncogene (MYB)/
192 myelocytomatosis oncogene (MYC) regulon and the second one, is the ABA-responsive element
193 binding protein/ ABA-binding factor (AREB/ ABF) (Abe et al., 1997; Saibo et al., 2009) (Fig.

1). ABA- independent regulons include; the NAC (CUC, NAM and ATAF) and the zinc-finger homeodomain (ZF-HD) regulon (Nakashima et al., 2009; Saibo et al., 2009) (Fig. 1).

The different stress tolerance responsive TFs normally function independently, although there is a possibility that some level of cross-link occurs between these TFs (Fig. 2). Many studies have shown that ABA-independent and ABA-dependent pathways might converge at several unexpected points. This points of convergence represent transcriptional repressors and enhancers interacting indirectly or directly with DRE/C repeat and ABRE and hence initiate synergistic interactions between ABA response and osmotic stress (Fig. 2).

The above mentioned TF families have been studied in detail in a number of important food crops and also in model plant systems including; *Arabidopsis thaliana*, *Oryza sativa*, *Triticum aestivum*, *Sorghum bicolor*, *Vitis vinifera*, *Hordeum vulgare*, *Solanum tuberosum,* and *Brassica napus*. Recent studies have shown the functions of abiotic stress-responsive TFs, and their potential roles to be used in future for purposes of molecular breeding and improvement of different crop varieties.

Much progress has been achieved in our understanding of transcriptional regulation, signal transduction, and gene expression in plant responses to abiotic stresses (Zhu et al., 2010). In rice for example, overexpression of a NAC TF encoding gene, *SNAC1* resulted in increased yields and increased tolerance to drought in transgenic plants (Hu et al., 2006). Overexpression of a *Glycine soja* NAC TF designated as *GsNAC019* in transgenic Arabidopsis resulted in plants that were tolerant to alkaline stress at both the seedling and mature stages although the transgenic plants had reduced sensitivity to Abscisic acid (ABA) (Cao et al., 2017). Similarly, functional analysis of a *Pyrus betulifolia* NAC TF gene designated as *PbeNAC1*, revealed that this gene is involved in the regulation of cold and drought stress tolerance (Jin et al., 2017). Additionally, a chickpea (*Cicer arietinum*) stress associated TF, *CarNAC4* was linked with reduced MDA content and water stress rates in response to salinity and drought stress respectively (Yu et al., 2016).

Ramakrishna et al. (2018) showed that overexpression of a finger millet bZIP TF gene *EcbZIP17* in tobacco plants resulted in higher germination rate, increased biomass, and increased survival rate in the transgenic plants. Furthermore, the transgenic tobacco plants also showed increased seed yields compared to the control plants. Likewise, Xu et al. (2016) showed that transgenic Arabidopsis and soybean seedlings overexpressing a soybean bZIP TF designated as *GmbZIP110* had improved salt tolerance, suggesting that *GmbZIP110* functions as a positive regulator involved in salt stress tolerance. Functional analysis of *GmbZIP110* in transgenic Arabidopsis revealed that this gene could bind to the ACGT motif and regulate many downstream target genes (Cao et al., 2017). Elsewhere, overexpression of an Arabidopsis bZIP TF designated as *ABF3* in transgenic alfalfa (*Medicago sativa*) under the command of a sweet potato oxidative stress-inducible promoter *SWPA2,* resulted in improved growth under drought stress (Wang et al., 2016c). In hot pepper (*Capsicum annuum*), overexpression of a bZIP encoding gene *CaBZ1* in transgenic potato significantly improved dehydration stress tolerance without any detrimental effects on plant growth or yield (Moon et al., 2015).

Overexpression of *OsMYB55,* a rice MYB encoding gene in transgenic maize resulted in improved plant growth as well as decreased negative effects of drought and high temperature (Casaretto et al., 2016). Wei et al. (2017) demonstrated that *CiMYB3* and *CiMYB5* cloned from *Cichorium intybus* were both involved in the fructan pathway degradation in response to various

abiotic stresses. In banana (*Musa paradisiaca*), overexpression of an MYB TF gene designated as *MpMYBS3* significantly improved tolerance to cold stress in transgenic plants (Dou et al., 2015). Elswhere, a MYB TF gene designated as *MtMYBS* from *Medicago truncatula* was able to enhance salt and drought tolerance in transgenic Arabidopsis by improving the primary root growth (Dong et al., 2017). Likewise, overexpression of *GaMYB62L* from cotton (*Gossypium arboreum*) in transgenic *Arabidopsis* resulted in enhanced drought tolerance (Butt et al., 2017).

The exogenous expression of *AtDREB1A* (Dehydration responsive element binding proteins) gene from *Arabidopsis* in transgenic *Salvia miltiorrhiza* resulted in plants with higher antioxidant activities and photosynthetic rates under drought stress (Wei et al., 2016). Elsewhere, overexpression of *SbDREB2A* from *Salicornia brachita* in transgenic tobacco resulted in improved growth and seed germination under hyperionic and hyperosmotic stresses (Gupta et al., 2014). Zhang et al. (2015) cloned SsDREB protein from *Suaeda salsa* and showed that this protein enhances the photosynthesis rate in transgenic tobacco plants under drought and salt stresses.

In the WYKY TF gene family, *OsWRKY71* from rice was found to act as a positive regulator to cold stress tolerance by regulating several downstream genes like *WSI76* and *OsTGFR* (Kim et al., 2016). VIGS (Virus-induced gene silencing) of *GhWRKY6* gene from cotton (*Gossypium hirsutum*) led to increased sensitivity to various abiotic stresses in the silenced plants (Ullah et al., 2017). Elsewhere, *SIDRW1* and *SLWRKY39* which are WRKY TFs were found to confer both abiotic and biotic stress tolerance in tomato (*Solanum lycopersicum*) by activating both abiotic stress and pathogenesis-related downstream genes (Liu et al., 2014a; Sun et al., 2015).

TFs and regulons involved in abiotic stress regulation from other TF families have also been identified and described. For instance in *Populus euphratica*, exogenous expression of *PeHLH35* belonging to the bHLH TF family resulted in significant improvement in water deficit tolerance through changes in several physiological processes such as stomatal density and transcription rate (Dong et al., 2014). In tomato, overexpression of a cycling Dof factor (CDF) TF designated as *CDF3* resulted in increased biomass production and higher yields in transgenic tomato plants under salt stress (Renau-Morata et al., 2017).

TFs and the specific target genes involved in abiotic stress tolerance in maize

MYC/ MYB regulon

The MYC (myelocytomatosis)/ MYB (myeloblastosis) families of TF proteins have diverse functions and are found in both animals and plants (Abe et al., 2003). Both MYB/ MYC TFs participate in the ABA-dependent pathway involved in abiotic stress signaling (Fig. 1). The first MYB TF gene in plants was identified in Maize and was designated as *C1,* it codes for a c-MYB like TF that is involved in the biosynthesis of anthocyanin (Paz-Ares et al., 1987). In the MYB family, each TF consists of an MYB domain containing 1 to 3 imperfect repeats and is made up of around 52 amino acid residues with a helix-turn-helix (HTH) conformation which interposes inside the major grooves of DNA (Yanhui et al., 2006). Both MYB and MYC TFs are usually involved in making up the common regulons known as the MYB/ MYC regulons (Gahlaut et al., 2016).

In the maize genome, Du et al. (2013) reported 72 MYB related proteins. Chen et al. (2017) analyzed the expression profiles of 46 MYB genes from maize, in response to various abiotic stresses and found 22 genes that responded to the different stress conditions. Additionally, 16 of these genes were induced in response to a minimum of two stresses. These results suggesting that these genes could take part in signal transduction pathways involved in abiotic stress responses. Additionally, the function of *ZmMYB30* which was significantly up-regulated under drought, salt, and ABA stresses was further analyzed (Table. 1). Exogenous expression of *ZmMYB30* in *Arabidopsis* stimulated tolerance to salt and elevated the expression of eight abiotic stress corresponding genes (*ABF3*, *ATGolS2, AB15, DREB2A, RD20, RD29B, RD29A,* and *MYB2*) enabling transgenic plants to be more tolerant to adverse environmental conditions (Table. 1). Moreover, another six genes (*RD22*, *RbohD*, *P5CS1, RAB18, RbohF,* and *LEA14*) were either unchanged or slightly elevated in the transgenic *Arabidopsis* plants.

Another maize MYB TF, *ZmMYB31* was found to repress the biosynthesis of sinopoylmalate leading to increased sensitivity to UV irradiation and dwarfism in transgenic plants (Fornale et al., 2010). Furthermore, *ZmMYB31* activated a number of stress-responsive genes (*ZmF5H*, *C3H*, *ZmActin* and *ZmCOMT*) in vivo in maize, and *4CL1* and *COMT* genes in transgenic *Arabidopsis*. The roles of maize MYB related genes in response to drought stress were examined based on microarray data (Dash et al., 2012; Du et al., 2013). On the maize 18k GeneChip, 26 probe sets were shown to correspond to 32 MYB-related genes (whereby five probes represented one gene). Further analysis of this highly similar sequence data revealed that the majority of the MYB-related genes were expressed at low levels, although their expression was in response to a specific stress. Elsewhere, gene expression analysis between two maize varieties, a drought sensitive (Ye478) variety, and a drought tolerant (Han21) variety was found to be very similar (Du et al., 2013). For instance, four CCA1-like/ R-R genes (*ZmMYBR49*, *ZmMYBR19, ZmMYBR56,* and *ZmMYBR28*), six TBP-like genes (*ZmMYBR55, ZmMYBR45, ZmMYBR47, ZmMYBR31, ZmMYBR26,* and *ZmMYBR07*) and a single TRF-like gene (*ZmMYBR41*) were all elevated in response to drought stress. Expression analysis of *ZmMYBR37* an I-box-like gene, and five CCA1-like/ R-R genes (*ZmMYBR63, ZmMYBR44, ZmMYBR27, ZmMYBR18,* and *ZmMYBR03*), showed that these genes were highly down-regulated in response to drought stress. Although recovery of all these genes above was observed after re-watering (Table. 1). Similarly, a maize R1-type TF that is encoded by *ZmMYB-R1* gene was activated by cold, exogenous ABA, drought, heat and high salinity (Liu et al. 2012). Functional analysis of *ZmMYB-R1* in different tissues revealed it first reached its maximum levels in the leaves and later it was detected in the roots and stems.

In the model plant *Arabidopsis,* MYB and MYC TFs were found to accumulate in plant tissues following the accumulation of ABA (Lata et al., 2007). Seven *Arabidopsis* MYB TF genes namely *AtMYBCDC5, AtMYB77, AtMYB73, AtMYB44, AtMYB6, AtMYB7,* and *AtMYB4* were all strongly expressed in all organs, in response to several abiotic stresses (Yanhui et al., 2006). Functional analysis of two MYB/ MYC genes, (*AtMYC2* and *AtMYB2*) in transgenic *Arabidopsis* revealed that the TF proteins encoded by these two genes can bind to the promoter regions of several ABA or jasmonic-acid (JA) inducible genes. For example, *AtADH1* and *RD22* thus making the transgenic *Arabidopsis* plants ABA-responsive and more tolerant to both drought and osmotic stress *(*Abe et al., 2003).

Taken together, all the above findings suggest that *MYB* genes could be engineered in crops leading to activation of general pathways involved in abiotic stress responses in plants. For

instance, overexpression of *OsMYB55,* a rice R2R3-MYB TF significantly improved rice plants tolerance to extreme temperatures, and this was directly linked with improved amino acid metabolism (El-kereamy et al., 2012). Additionally, these findings will facilitate our understanding of gene regulation by MYB TFs, thus leading to the development of new abiotic stress tolerant crop varieties. Finally, Phylogenetic, functional and structural analyses revealed that most homologous MYB proteins that possess conserved domains have similar activities and functions in divergent plant species. Although a lot of information is available on the molecular functioning of MYB TFs in abiotic stress responses, deciphering the downstream and upstream events in MYB TFs in abiotic stress responses remains an immense undertaking.

The AP2/EREBP regulons

The AP2/EREBP (ethylene-responsive element binding protein) family is made up of a large group of plant specific TFs that are characterized by the presence of a highly conserved AP2/ethylene-responsive element binding factor (ERF). The ERF interacts directly with GCC box and/or DRE/C-repeat element (CRT) at the promoter site of downstream target genes (Reichmann and Meyerowitz, 1998). AP2/EREBP TFs play vital roles in stress responses and developmental processes such as cell proliferation, plant hormone responses, and biotic and abiotic stress responses (Sharoni et al., 2011). Based on the similarity and number of AP2/ERF domains, AP2/EREBP TFs are grouped into four main subfamilies: ERF, RAV (related to AB13/VP1), DREB and AP2 (Apetala 2) (Sharoni et al., 2011). Among these four, the DREB subfamily has been extensively studied due to the roles its TFs play in plant biotic and abiotic stress responses.

Dehydration responsive element binding proteins (DREBs) play a significant role in the ABA-independent pathways that are responsible for the activation of abiotic stress-regulatory genes (Lata et al., 2007). DREB TFs are made up of one AP2/ERF DNA binding region, which binds to the *cis*-acting element DRE composed of TACGACAT (a 9bp core sequence) and is present in the promoters of Abiotic stress-responsive genes (Gahlaut et al., 2016). The existence of this *cis*-acting element (CRE) has been recorded in several abiotic stress-responsive genes for example *RD29B* and *RD29A* in *Arabidopsis* (Yamaguchi-Shinozaki and Shinozaki, 1994). C-repeat (CRT) *cis*- acting elements consisting of the A/GCCGAC motif and which are similar to DREBs, have been identified in the promoter regions of cold-responsive genes in *Arabidopsis*, whereby the CRT elements bind to the TF CBF (CRT binding factor) in response to cold stress (Saleh et al., 2005). In *Arabidopsis* for example, exogenous overexpression of *AtDREB1/CBF* led to cold, drought, and high salinity tolerance in transgenic plants. These findings clearly suggest that DREBs/CBFs TFs have the potential to target multiple stress-responsive candidate genes in the plant genomes (jaglo-Ottosen et al., 1998; Kasuga et al., 1999).

In maize, the role of DREB TFs has been investigated by adopting both molecular and genetic analyses. For example, *ZmDREB1A* was activated by cold stress and moderately elevated by high-salinity stress in maize seedlings (Qin et al., 2004) (Table. 1). Over-expression of *ZmDREB1A* in transgenic *Arabidopsis* led to induced over-expression of abiotic stress-activated genes giving rise to plants with enhanced tolerance to extreme drought and freezing stresses (Table. 2). Investigations were done to ascertain whether *ZmDREB1A* could induce other genes in the dehydration and/or cold pathways of wild-type plants. The results revealed that expression levels of *KIN1, KIN2*, and *COR15A* were all highly up-regulated in the 35S:ZmDREB1Aa

transgenic line under normal conditions when compared to the wild-type plants. Expression analysis of *RD17, ERD10* and *RD29A* showed that these genes were slightly up-regulated in the 35S:ZmDREB1Aa transgenic line. The above results showed that *ZmDREB1A* induces both ABA-independent genes like (*COR15A, KIN1,* and *KIN2*) and ABA-dependent genes like (*RD17, ERD10,* and *RD29A*). Therefore, it was concluded that this gene might affect the expression of dehydration and cold-responsive genes in both the ABA-independent and ABA-dependent pathways. Likewise, another DREB TF gene *ZmDBP3* was highly induced by cold and moderately induced by salinity stress (Wang and Dong, 2009) (Table. 1). Over-expression of this gene in transgenic *Arabidopsis* led to improved tolerance to both cold and drought stresses (Table. 2).

Natural variations present in the promoter region of another maize DREB TF gene *ZmDREB2,* lead to drought tolerance in maize (Liu et al., 2013) (Table. 1). In transgenic *Arabidopsis,* over-expression of *ZmDREB2* resulted in plants with enhanced tolerance to drought. Elsewhere, qRT-PCR analysis of maize leaves revealed that expression of *ZmDREB2A* was induced by dehydration, heat and cold stress (Qin et al., 2007). Overexpression of *ZmDREB2A* in transgenic *Arabidopsis* resulted in dwarf plants with enhanced tolerance to drought and heat stresses. Microarray analysis of these transgenic *Arabidopsis* plants identified a number of genes associated with detoxification and heat shock for example *RD29B* and *At5G03720*. Moreover, five genes coding for late embryogenesis abundant (LEA) proteins (*LEA14, At1g52690, At3G53040, At3G15670,* and *At2G36640*) in addition to a metabolism associated gene *AtGoIS3*, were all up-regulated under different stress treatments in the transgenic lines (Table. 1). Elsewhere, functional analysis of *ZmDBF3* showed that this TF gene was activated by drought, high temperature, salt, cold and abscisic acid (ABA). However, no significant difference was noted under methyl jasmonate (MeJA) and salicylic acid (SA) (Zhou et al., 2016). Ectopic expression of *ZmDBF3* in yeast (*Saccharomyces cerevisiae*) resulted in a higher survival rate during exposure to KCI, Na_2CO_3, $NaHCO_3$, NaCl, PEG 6000, sorbitol, and freezing temperatures. Moreover, exogenous expression of *ZmDBF3* in transgenic *Arabidopsis* considerably improved tolerance to drought, freezing and salt stresses (Table. 2). These findings, suggest that *ZmDBF3*, a novel maize DREB TF may have similar functions to a regulatory factor taking part in abiotic stress response pathways. Similarly, overexpression of *ZmDBP4* in *Arabidopsis* resulted in transgenic plants with improved cold and drought stress tolerance (Wang et al., 2011) (Table. 2). Analysis of the promoter region of *ZmDBP4* identified *cis*-acting elements which responded to abiotic stresses, suggesting that *ZmDBP4* encodes a functional factor that plays an important role in the control of multiple abiotic stress responses in maize. Elsewhere, mRNA accumulation analysis profiles of two DRE-binding proteins (*DBF1* and *DBF2*) in maize seedlings revealed that *DBF1* was induced during embryogenesis and in response to drought, ABA, and NaCl treatments (Kizis and Investigacio, 2002).

DREB TFs are versatile when it comes to abiotic stress regulation. Recently, numerous studies have been done to understand the roles DREB TFs play in abiotic stress responses and to reveal the mechanisms involved in their transcription and post transcriptional regulation. Collectively, these studies suggest that DREB TFs can be potential candidates for abiotic stress tolerance, although these studies have not addressed the vital question of whether DREB TFs can improve the yield of engineered crops under stress. Many DREB homologues have been identified and isolated from different plant species, especially from plant species with exceptional tolerance to different abiotic stresses. Thus, the focus now is to evaluate the existing methods of yield

analyses under different stress conditions and to assess transgenic plants in actual field conditions.

NAC TFs and regulons

The TF members in the NAC family, (ATAF, CUC, and NAM) represent one of the largest plant-specific TFs (Ooka et al., 2003). In the main crop species, a large number of NAC TFs have been analyzed and sequenced at the genome-wide level. These include 151 members in rice and 117 in *Arabidopsis* (Nuruzzaman et al., 2010), 204 members in the Chinese cabbage (Liu T.K et al., 2014b) and 152 members in maize (Shiriga et al., 2014). The TFs belonging to the NAC family share a greatly conserved N-terminus made up of 150-160 amino acid residues, constituting a DNA-binding domain that carries five sub-domains (A-E) and a varying C-terminal (Hu et al., 2008; Ooka et al., 2003). The NAC genes and their constituent *cis*-acting elements (NARCs) make up the NAC regulons, which further provide vital examples of finely characterized collaboration between a single TF and one or more *cis*-acting elements that associate in response to multiple stresses (Christianson et al., 2010). The roles of NAC TFs in plants have been extensively studied in rice and *Arabidopsis*. In *Arabidopsis* for example, an *ERD1* (early dehydration stress 1) gene was activated by a number of NAC TFs including *ANAC055*, *ANAC019,* and *ANAC072* (Tran et al., 2007). A rice NAC TF designated as OsNAM*,* was found to regulate the activation of five genes (*OsAH*, *OsCESA*, *OsMtN3*, *OsGdpD,* and *OsGDP*) in response to drought (Dixit et al., 2015). Several NAC TFs utilize the NACRS motif in plants, for instance *SNAC2* and *ENAC1* found in rice (Sun et al., 2012) and *ANAC055*, *ANAC072* and *ANAC019* found in *Arabidopsis* (Tran et al., 2004).

In maize, several NAC TFs involved in abiotic stress regulatory pathways have been isolated, cloned and characterized. Recently, expression analysis of *ZmSNAC1* in maize seedlings revealed that this TF gene was strongly induced by high salinity, drought, ABA treatment, and low temperature, although it was down-regulated in response to salicylic acid (SA) treatment (Lu et al.,2012). Over-expression of *ZmSNAC1* in transgenic *Arabidopsis* led to increased hypersensitivity to osmotic stress and ABA as well as enhanced tolerance to dehydration stress at the germination phase (Table. 2). These results suggest that *ZmSNAC1* acts as a multiple stress responsive TF, positively modulating abiotic stress tolerance in maize. Elsewhere, Shiriga et al. (2014) identified 11 NAC TF genes in maize that were induced by various abiotic stresses. This prediction was confirmed when these genes were differentially expressed in response to drought stress. Four genes, *ZmNAC45, ZmNAC72, ZmNAC18,* and *ZmNAC51* were all up regulated in the drought-tolerant maize genotypes and down-regulated in the drought susceptible genotypes. Recently, seven ZmNTL, NAC TFs genes (*ZmNTL1, ZmNTL2, ZmNTL3, ZmNTL4, ZmNTL5*, *ZmNTL6*, and *ZmNTL7*) were analyzed in maize seedlings and all seven genes were found to be strongly expressed in the stem and roots and down-regulated in the leaves when the plants were exposed to hydrogen peroxide and/or ABA treatments. Exogenous expression of *ZmNTL1, ZmNTL2,* and *ZmNTL5* in transgenic *Arabidopsis* led to increased tolerance to hydrogen peroxide in transgenic plants (Wang et al., 2016a). Overexpression of *ZmNAC55* in transgenic *Arabidopsis* resulted in plants which were hypersensitive to ABA at the seedling stage but showed enhanced resistance to drought when compared to the wild-type control seedlings (Mao et al., 2016). Additionally, twelve stress-responsive genes (*RD20, NCED3, ZAT10, ANAC019, LEA14, RD29B, RD29A, DREB2A, RD17, RD26, RAB18,* and *PP2CA*) were all up regulated in

response to drought stress in the transgenic lines (Table. 1). Expression profiles of *ZmNAC55* in maize revealed that this gene was induced by high salinity, drought, ABA and cold stress.

Elsewhere, seven NAC TF genes analyzed in maize seedlings (*Zma001259*, *Zma000584*, *Zma029150*, *ZmSNAC052*, *Zma003086*, *Zma054594,* and *Zma0064*93) were all found to be up regulated in response to salt stress in all tissues (Lu et al., 2015). In response to PEG treatment, three of the above-mentioned genes, namely *Zma0064*93, *Zma003086* and *Zma000584* were significantly up regulated in the roots only, while *Zma001259*, *Zma029150, Zma000584,* and *Zma054594* were all strongly expressed in both the roots and shoots. Five genes, *Zma054594*, *Zma000584, Zma001259, Zma003086,* and *ZmSNAC052* were activated by cold stress although in varying degrees. In conclusion, due to the strong expression in response to ABA treatments, these seven genes could play a vital role in the ABA-dependent signaling network in maize.

Numerous advancements in NAC TFs functional studies have been achieved over the past few years. However, most of these studies are related to the involvement of NAC TFs in biotic stress responses. To achieve a deeper understanding of NAC TFs in abiotic stress responses, it is of vital importance to identify the main components of signal transduction pathways that interact with these TFs. Utilizing data obtained from microarray analyses could help in the direct determination of specific NAC DNA- binding sites on a global scale under different abiotic stress conditions.

Finally, numerous studies have demonstrated the use of stress-responsive NAC TFs in the improvement of abiotic stress tolerance in crops by genetic engineering. In view of the specificity of NAC TF in multiple stress responses, NAC TFs that are induced by multiple abiotic stresses are promising candidates in the engineering of plant varieties with improved multiple stress tolerance (Shao et al., 2015). Moreover, field evaluation of engineered crops containing NAC TF genes and efficient promoters, for reducing detrimental effects triggered by overexpression of some NAC genes must be considered (Rushton et al., 2008).

bZIP TFs: AREB/ABF regulon

The ABA-responsive element (ABRE; PyACGTGG/TC), is a conserved *cis*-acting element bound by the basic Leucine Zipper Domain (bZIP) TFs (Loredana et al., 2011). The ABRE was first established on the promoter region of ABA-activated genes by (Giraudat et al., 1994). The bZIP TFs, belong to one of the largest and diversified TF families in plants. They are categorized into ten subfamilies based on the presence of extra conserved motifs and the basic region sequence similarities (Perez-Rodrigues et al., 2010). AREB/ABF TFs are characterized by a strongly conserved bZIP domain made up of two structural components [a leucine (Leu) zipper and a basic region], the leucine (Leu) zipper is composed of heptad repeats of Leu and/ or other heavy hydrophobic amino acid residues and controls hetero- and or homodimerization of the bZIP proteins. The basic region is composed of 16 amino acids with the indistinguishable N-x7-R/K-x9 motif and is responsible for DNA binding and nuclear localization (Jakoby et al., 2002). The bZIP TFs, which are part of the AREB/ABF regulons, give an excellent example of interactions involving stress-responsive genes and TFs carrying the *cis*-acting element (ABRE). In maize, a bZIP TF gene *ABP9* that has the ability to bind to the AREB2 motif located in the *Cat1* promoter region was activated by drought, salt, H_2O_2, and ABA (Zhang et al., 2011). Exogenous expression of *ABP9* in *Arabidopsis* led to significant tolerance to freezing, salt,

oxidative stress and drought in transgenic plants. Transgenic *Arabidopsis* plants also showed enhanced sensitivity to exogenously supplied ABA during stomatal closure, seed germination, and root growth. Furthermore, transgenic plants expressing *ABP9* showed reduced levels of oxidative cellular damage, reduced cell death and reduced levels of ROS.

More recently, Wang et al. (2017) demonstrated that *ABP9* enhanced salt and osmotic stress tolerance in transgenic cotton plants. Overexpression of *ABP9* resulted in elevated transcripts of several stress responsive-genes (*GhNCED2*, *GhDBP2*, *GhZFP1*, *GhHB1*, *GhSAP1,* and *GhERF1*) in the transgenic cotton plants in response to salt stress (Table. 2). Additionally, transgenic plants were shown to have higher germination rates, and improved root systems in a greenhouse setting and reduced stomatal density and stomatal aperture in a growth room. Finally, the relative water content (RWC) and survival rate of the transgenic plants was significantly higher compared to the control plants in response to drought. Wang et al. (2012) demonstrated that expression of *ZmbZIP60* was highly activated by a wide range of stresses including ABA, high salinity, tunicamycin treatment and dehydration (Table. 1). In the wild-type *Arabidopsis*, over-expression of *ZmbZIP60* resulted in plants with enhanced tolerance to dithiothreitol (DDT) stress. Furthermore, Li et al. (2018) discovered a major QTL governing heat-induced *ZmbZIP60* expression and deduced that the upstream region of *ZmbZIP60* plays a vital role in regulating responses to heat stress in maize.

Similarly, Ying et al. (2011) cloned and characterized a maize bZIP TF gene designated as *ZmbZIP72,* which was induced by drought, ABA and high salinity stress (Table. 1). *ZmbZIP72* was differentially expressed in various organs in maize. Overexpression of *ZmbZIP72* in transgenic *Arabidopsis* led to enhanced tolerance to drought, partial tolerance to salinity and hypersensitivity to osmotic stress and ABA treatment. Furthermore, the transgenic *Arabidopsis* plants also showed enhanced expression of several ABA-inducible genes including (*RAB18*, *HIS1-3,* and *RD29B*). Elsewhere, microarray analysis of two specific maize inbred lines, a drought-sensitive Ye478 line, and a drought tolerant Han21 line revealed that 22 ZmbZIP genes might play a critical role in drought tolerance (Wei et al., 2012a). In the same report, *ZmbZIP37* an orthologous gene of two rice genes *OsbZIP72* and *OsbZIP23* that both play vital roles in drought tolerance and ABA response in rice, was found to be up-regulated in response to drought stress in maize. Similarly, cloning and characterization of a bZIP TF gene *ZmbZIP17* from the Han21 maize inbred line revealed that this gene was up regulated in response to drought (Jia et al., 2009). Real-time PCR analysis revealed that *ZmbZIP17* was highly up regulated in response to heat, salinity, drought, and ABA stresses immediately, suggesting that this gene represents an early responsive gene that reacts to various abiotic stresses. Elsewhere, expression analysis of two maize bZIP TF genes *ZmbZIP107* and *ZmbZIP54* revealed that these two genes were highly elevated in a lead tolerant maize line when compared to a lead sensitive line in response to different treatments of lead (Zhang et al., 2017) (Table. 1). Recently, Ma et al. (2018) demonstrated that *ZmbZIP4* was induced by drought, cold, high salinity, ABA, and heat in maize seedlings. Overexpression of *ZmbZIP4* led to an improved root system, increase in the number of lateral roots, and longer primary roots in transgenic maize. Additionally, genome-wide analysis of *ZmbZIP4* target genes by immunoprecipitation sequencing, unearthed a number of downstream stress response genes that were positively regulated by *ZmbZIP4*. These downstream target genes included *ZmRD21, ZmLEA2, ZmRD20, ZmGEA6, ZmNHX3,* and *ZmRAB18.* Collectively, these results suggested that *ZmbZIP4* is a positive regulator of abiotic stress response that takes part in root development in maize.

In conclusion, the promoter region of each abiotic stress responsive gene might carry a single or several proximal or distal coupling elements (CE) for instance, CE 3 and CE1 which activate the expression of abiotic stress-responsive genes. In addition, Shen et al. (1996) identified CEs in *Hordeum vulgare* that form an abscisic acid response complex (ABRC), which could be a necessary component in triggering ABA-mediated gene expression. Collectively, the above reports confirmed the participation of bZIP TFs in the ABA signaling pathway. These findings could be useful in the future development of better genotypes with improved tolerance to various abiotic stresses (Todaka et al., 2015). An accurate understanding of the functions of bZIP TFs in crops will require an accurate mapping of the location of bZIP genes in the different plant organs.

WRKY TFs and WRKY regulons

WRKY proteins represent the largest superfamily of TFs, which are specific to plants. WRKY TFs control plant growth and development and spur tolerance against both abiotic and biotic stresses (Tripathi et al., 2014). WRKY TFs are usually identified by a WRKY domain made up of 60 amino acid residues, and contains a highly conserved WRKYGQK sequence followed up by a zinc- finger motif. The WRKY domain shows a strong binding affinity for a *cis*-acting element known as W-box (TTGACC/T), which is present in a number of abiotic stress responsive genes (Rushton et al., 2010; Ulker and Somssich, 2004).

Several WRKY TFs involved in abiotic stress tolerance have recently been reported in maize. For example, functional analysis of *ZmWRKY33* under different abiotic stresses, revealed that this gene was activated by cold, dehydration, ABA and salt treatments (Li et al., 2013). Over-expression of *ZmWRKY33* in transgenic *Arabidopsis* led to the activation of two stress-activated genes (*RD29A* and *DREB1B*), which were both up-regulated resulting in enhanced salt tolerance in the transgenic plants (Table.1). The above-mentioned results strongly suggest that this maize WRKY TF plays a vital role in abiotic stress regulation in maize. Elsewhere, Wang (2013) demonstrated that exogenous over-expression of *ZmWRKY44* in transgenic *Arabidopsis* resulted in plants that were moderately sensitive to NaCl stress. In maize seedlings, ZmWRKY44 was induced by high temperature, salt stress, ABA, and hydrogen peroxide treatments. Recently, *ZmWRKY17* was cloned, characterized and its expression was analyzed in maize seedlings (Cai et al., 2017) (Table. 1). The results showed *ZmWRKY17* was induced by ABA, salt and drought stresses. Additionally, constitutive expression of this gene in transgenic *Arabidopsis* led to a striking reduction in tolerance to salt stress, as confirmed by the physiological assays performed on relative electrical leakage, malondialdehyde (MDA) content, cotyledons greening rate and root growth. Still in the same study, RNA-Seq analysis showed that eight stress-related genes (*DREB1F, KIN1, bHLH92*, *RD29A, RD29B, NAC019, RD22,* and *MYB101*) were significantly up-regulated in the wild-type plants when compared to the transgenic plant lines in response to salt stress. However, expression of *NCED5* was higher in transgenic plants under the same stress. Together, these results give a strong indication that *ZmWRKY17* may function as a negative regulator in response to drought stress in maize. This could be due to elevated levels of ABA ensuing as a direct response to salt stress through the ABA signaling system. Wei et al. (2012b) compared the expression profiles of 31 WRKY genes in two maize lines, a drought-sensitive Ye478 line and a drought tolerant Han21 line. The results showed that the expression of the WRKY genes in the drought-tolerant Han21 line changed less, and the seedlings recovered faster

when re-watered, as opposed to the drought-sensitive Ye478 seedlings. In the same study, the expression of *ZmWRKY115* was decreased as a direct result of drought stress. Elsewhere, qRT-PCR expression analysis showed that *ZmWRKY58* was activated by salt, drought and ABA treatments (Cai et al., 2014) (Table. 1). Constitutive expression of *ZmWRKY58* in transgenic rice led to delayed germination and constrained post-germination growth and development. However, transgenic seedlings over-expressing *ZmWRKY58* reported increased tolerance to both salt and drought stresses (Table. 2). Similarly, Wang et al. (2018a) identified a WRKY TF gene named *ZmWRKY40* (Table. 1). A number of stress-related transcriptional regulatory factors were located in the promoter region of this gene. In maize, *ZmWRKY40* was induced by high salinity, drought, abscisic acid (ABA) and high temperature. Overexpression of *ZmWRKY40* in *Arabidopsis* led to enhanced drought tolerance in the transgenic plants. Additionally, overexpression of *ZmWRKY40* induced the expression of three stress-responsive genes *DREB2A*, *STZ* and *RD29A* in transgenic *Arabidopsis*. Recently, the expression of *ZmWRKY106*, a member of the WRKYII group was found to be induced by high temperature, drought, and exogenous ABA treatment, but was weakly induced by salinity (Wang et al., 2018c). Overexpression of *ZmWRKY106* in transgenic Arabidopsis led to improved tolerance to heat and drought. Additionally, *ZmWRKY106* positively regulated the expression of several stress response genes including *RD29A*, *CuZnSOD*, *DREB2A,* and *NCED6.* The above results strongly indicate *ZmWRKY106* may play an important role in the abiotic stress response pathways in maize by regulating stress-related genes.

In the model plant *Arabidopsis,* two WRKY genes WRKY 60 and WRKY 18 were found to regulate ABA signaling positively while one WRKY gene *WRKY40* negatively regulated ABA signaling. These three WRKY genes mentioned above, bind to the promoter region of several genes including some TFs genes like (*DREB1A/CBF3, ABI5,* and *DREB2A*), and several stress-regulated genes like (*COR47* and *RD29A*) in the process controlling their expression (Shang et al., 2010; Chen et al., 2010).

WRKY TFs have been identified as promising candidates for crop improvement due to the strict regulations involved in the identification and binding of these TFs to the downstream target promoter regions (Phukan et al., 2016). Taken together, all the above insights highlight the multiple stress responses and diverse regulation of WRKY TFs in maize and other crops.

Other TFs and their Regulons

Apart from the five main TF families described above, other TF families take part in diverse roles in plants including, regulating responses to both abiotic and biotic stresses, and various growth and development processes. Recently, extensive research has uncovered stress-mitigating roles of a number of TFs whose responses to abiotic stressors were previously unknown in maize. Three of these TF families are briefly described below.

Homeodomain-leucine zipper I (HD-ZIP) I

HD-Zip proteins represent a large TF family that is specific to plants. HD-Zip proteins have been cloned and characterized in several important crops and some model plants such as rice, *Arabidopsis*, tomato and sunflower (Johannesson et al., 2003; Lin et al., 2008; Agalou et al., 2008; Manavella et al., 2006). HD-Zip proteins are characterized by a DNA-binding

homeodomain (HD) and a neighboring leucine zipper (Zip) motif whose function is to mediate protein dimerization (Ariel et al., 2007). HD-Zip proteins belonging to the subfamily I are believed to take part in the majority of plant responses to abiotic stresses (Ariel et al., 2007). In *Arabidopsis* for example, analysis of four HD-Zip TFs (*ATHB6*, *ATHB7*, *ATHB5* and *ATHB12*) revealed that these genes were up-regulated or repressed by either ABA or drought stress (soderman et al., 1996; Lee et al., 2001; Soderman et al., 1999; Johannesson et al., 2003). These results suggest that these four genes may play a vital role in the regulation of abiotic stress regulatory networks in plants.

In maize, *Zmhdz10* was the first HD-Zip TF to be isolated and characterized (Zhao et al., 2014). Expression of this gene was activated by abscisic acid (ABA) treatment and salinity stress (Table. 1). Exogenous over-expression of *Zmhdz10* in transgenic rice resulted in improved tolerance to salt and drought stress and enhanced sensitivity to ABA. Furthermore, the transgenic plants had elevated levels of proline and reduced malondialdehyde (MDA) content when compared to the wild-type plants (Table. 2). Transgenic *Arabidopsis* plants over-expressing *Zmhdz10* exhibited strong tolerance to salt and drought stresses, at the same time, expression patterns of several ABA-responsive genes namely (*ABI1, RD29B, P5CS1,* and *RD22*) were altered. The above results give a strong indication that *Zmhdz10* serves as a transcriptional regulator that can positively regulate both salt and drought stress tolerance in the ABA-dependent pathway in plants. Recently, Qing and Wei (2018) isolated and characterized a maize HD-ZIP TF designated as *Zmhdz12*. Tissue expression analysis revealed that this TF was strongly expressed in the leaves compared to other tissues. In transgenic *Arabidopsis*, *Zmhdz12* was activated by drought as observed when the drought resistant transgenic lines were compared to the wild-type lines. Similarly, expression status of 17 *Zmhdz* I genes from maize (*Zmhdz1* to *Zmhdz17*) revealed that all these genes were either repressed or up-regulated due to drought stress (Zhao et al., 2011). Additionally, many of the genes above belonging to the same subgroup in the phylogenetic tree, showed similar patterns of expressions. Elsewhere, *ZmHDZ4* was isolated and characterized in maize for its role in drought stress tolerance (Wu et al., 2016). Overexpression of *ZmHDZ4* in transgenic rice resulted in plants with enhanced tolerance to drought.

In conclusion, it is worth noting that HD-Zip proteins play crucial roles in cuticle formation, so they might be involved in abiotic stress tolerance and protection against plant pathogens (Chew et al., 2013). In addition, the roles described above make HD-Zip TFs ideal candidates for genetic engineering in maize and other major crops. Although more in-depth studies are needed in order to ascertain the function of individual HD-Zip family members in response to various abiotic stresses.

Heat Shock Proteins (HSPs)

All organisms are composed of an evolutionarily conserved, fast cellular defense system known as heat shock (HS) response, which regulates various reactions associated with heat stress and a variety of chemical stressors (Lin et al., 2011). HSPs were first discovered in the salivary glands of *Drosophila* in response to heat shock (Ashburner and Bonner, 1979). HSFs family members function by binding to the promoter of chaperones referred to as heat shock proteins. HSF TFs have a 3 N-terminal section and a C-terminal section in addition to leucine amino acid (Schuetz et al., 1991). HSPs can be categorized into six main families, (Hsp90, Hsp40, Hsp90, Hsp60,

Hsp70, and Hsp110) based on their molecular sizes (Wang et al., 2004). HSPs in plants were first characterized in tomato (Scharf et al., 1990), and since then more HSFs have been reported in other plants such as *Arabidopsis*, rice, sunflower and wheat (Hubel and Schoffl, 1994; Yamanouchi et al., 2002; Almoguera et al., 2002; Shim et al., 2009). A survey recently reported that there are at least 24 HSFs in *Brachypodium*, 21 in *Arabidopsis*, 30 in maize, 25 in rice, 52 in soybeans and 27 in tomatoes (Scharf et al., 2012). In the model plant *Arabidopsis*, a HsfA2 mutant displayed tolerance to osmotic stress, salt, and heat stresses, suggesting that this gene is involved in several abiotic stress response networks and pathways (Ogawa et al., 2007).

Few HSPs gene have been isolated and characterized in maize. Jinhui et al. (2015) isolated and characterized a Hsp70 gene named *ZmERD2* (Early Responsive to Dehydration 2) from maize (Table. 1). Expression patterns of *ZmERD2* revealed that this gene was induced by cold, high salinity, dehydration, heat stress, and PEG but was not induced by abscisic acid (ABA). Further expression analysis revealed *ZmERD2* was instantly activated at 42^{o}C and its peak was reached after 1 hour of exposure to heat stress. Elsewhere, expression patterns of 22 Hsf genes from maize showed that these genes were differentially expressed when subjected to heat stress (Lin et al., 2011). Further analyses from this study revealed that *ZmHsfA2* subclass in maize has close relations with heat shock response. This is after three HsfA2 genes (*ZmHsf-17*, *ZmHsf-01,* and *ZmHsf-04*) were strongly expressed in response to heat stress. In addition, six more genes were highly up-regulated in response to heat stress (*ZmHsf-03*, *ZmHsf-01*, *ZmHsf-23*, *ZmHsf-24*, *ZmHsf-04, and ZmHsf-25*). These results pointing to the specific roles these genes play in maize in response to heat stress. Li et al. (2015) recently cloned a maize HSF designated as *ZmHsf06* from maize and transformed it in *Arabidopsis thaliana*. Expression analysis of the transgenic plants over-expressing *ZmHsf06* revealed that this gene was induced by drought and heat stress (Table. 2). The above results were confirmed by biochemical and physiological evidence that showed that the transgenic plants displayed longer axial root length, higher seed germination rate, elevated levels of chlorophyll in leaves as well as reduced osmotic potential (OP) and malondialdehyde (MDA) content when compared to the wild-type plants. Based on the above results, it's evident *ZmHsf06* could have future potential use in molecular breeding in maize as well as other crops for improved drought and heat stress tolerance.

Collectively, it is important to mention that HSPs have been shown to have a close association with reactive oxygen species (ROS), meaning that plants have gained a stronger level of ROS regulation throughout the course of evolution (Banti et al., 2010). Therefore, understanding the roles played by HSPs in plant responses to abiotic stresses will be useful in the engineering of abiotic stress tolerant crop varieties. HSP have been studied and characterized in a number of important crop varieties as mentioned above, although their functional plasticity and genome sequence data is still limited (Echevarria-Zomeno et al., 2016).

NF-Y Transcription Factors

Nuclear factor Y also referred to as CBF (CCAAT binding factor) or heme activator protein (HAP), is a complex made up of three subunits NF-YB (CBF-A or HAP3), NF-YA (CBF-B or HAP2) and NF-YC (CBF-C or HAP5) (Nardini et al., 2013; Wang et al., 2018b). The NF-Y TF family has been comprehensively studied in animal systems, and it was found that each subunit is encoded by a single gene in yeast and mammals (Mantovani., 1999). NF-Y transcription factors interact with other factors in the regulatory network to induce or inhibit the expression of

downstream target genes (Benatti et al., 2008). Unlike mammals and yeast, plants have many NF-Y subunit genes (Wang et al., 2018b). For example, in *Arabidopsis* 13 genes encoding NF-YB, 10 genes encoding NF-YA and 13 genes encoding NF-YC have been reported (Siefers et al., 2009). Additionally, individual NF-Y subunits have been shown to play vital roles in plant abiotic stress tolerance (Sato et al., 2014; Ma et al., 2015).

Even though maize has numerous NF-Y subunits, very few studies have been done to investigate the roles these subunits play in response to abiotic stress (Wang et al., 2018b). Nelson et. (2007) demonstrated that transgenic maize with elevated levels of *ZmNF-YB2* showed improved tolerance to drought stress based on responses from various stress-related parameters which included stomatal conductance, chlorophyll content, reduced wilting and leaf temperature (Table. 2). Recently, overexpression of a NF-YB transcription factor complex member designated as *ZmNF-YB16* resulted in improved drought and dehydration resistance in transgenic inbred maize line B104 during reproductive and vegetative stages (Wang et al., 2018b) (Table 1). Analysis of gene expression in the photosynthesis system between the WT and transgenic plants revealed that several genes were up-regulated in the transgenic plants when compared to the WT plants. Examples of genes up-regulated included GRMZM2G117572 (encoding the photosystem II PsbZ protein), GRMZM2G414660 (encoding the photosystem II cytochrome b599 subunit) and GRMZM5G831399 (encoding the photosystem II PsbH protein) among others.

Analysis of the co-expression between miR169, miRNA family and ZmNF-YA TFs in transgenic *Nicotiana bethamiana* revealed that mutations in deletion sites terminate the regulation of zma-miR169 (Luan et al., 2014). The expression levels of *zma-miR169l, zma-miR169i,* and *zma-miR169a* were all inversely correlated with *ZmNF-YA11, ZmNF-YA6,* and *ZmNF-YA7* over the short term. However, over the long term, the expression levels of all the NF-YA genes and miR169s decreased, revealing that *ZmNF-YA11, ZmNF-YA6,* and *ZmNF-YA7* could not have been regulated by zma-miR169 in response to PEG stress after 15 days. Majority of the zma-miR169s were up-regulated by external ABA and down-regulated by drought stress but showed an early increase in expression and later a decline in response to salinity stress. Recently, Su et al. (2018) identified a NF-Y TF designated as *ZmNF-YA3*. Genome-wide analysis revealed that *ZmNF-YA3* was linked to more than 6000 sites in the maize genome, 2259 of which are linked with genic sequences. Moreover, it was shown that *ZmNF-YA3* could significantly improve high temperature and drought tolerance in maize by binding to the promoter region of three downstream genes (*ZmMYC4, ZmbHLH92,* and *ZmFAMA*).

In conclusion, all of the insights obtained above suggest NF-Y TFs play an important role in abiotic stress tolerance in maize by regulating several vital downstream genes involved in important aspects of abiotic stress responses, and plant growth and development, for instance, photosynthesis and ER stress response. Therefore, NF-Y TF genes could be engineered in maize and other crops in order to improve their abiotic stress tolerance, leading to improved production.

Engineering of TFs

The recent discovery of TFs as potential tools in the manipulation and engineering of quantitative traits such as drought and salinity has ignited the development of novel technologies based on TFs and benefiting not only gene discovery but also crop improvement. Engineering of TF activity has been a major target in these efforts, a direction that offers future promises in

modulating metabolic pathways. For example, over-expression of DREB2 resulted in no stress tolerance improvement because proteins are composed of domains that limit the induction of their target genes downstream (Liu et al., 1998). Sakuma et al. (2006) obtained drought-tolerant plants by removing this repressor function through the engineering of point mutations. An undesirable effect of overexpressing stress-related TFs is that sometimes it negatively affects the growth and development of a plant leading to stunted growth or toxicity (Hussain and Amjad, 2011). Elsewhere, over-expression of *ZmDREB2A* under a stress-activated promoter in the transgenic plants led to significant improvement in drought tolerance (Qin et al., 2007).

Transcriptional down regulators that repress gene expression in response to various abiotic stresses are also important tools in manipulating drought tolerance. For example, over-expression of a yeast transcription repressor *CaZPF1* in *Arabidopsis* led to drought tolerance in transgenic plants (Kim et al., 2004). In the model plant *Arabidopsis,* systematic analysis of TF families resulted in the discovery of target genes that have the potential to enhance abiotic stress tolerance in major crops (Reichmann et al., 2000). A good example is the discovery of *AtNF-YB1* gene that belongs to the Nuclear factor Y TF family (Nelson et al., 2007). The orthologue of (*AtNF-YB1*) gene in maize, (*ZmNF-YB2*) when over-expressed in transgenic maize, resulted in drought-tolerant crops (Table. 2). These findings emphasized the significance of TFs, especially when used in the engineering of plants.

The abiotic stress response networks in plants are very complex due to the large number of gene families involved and the complicated associations between the *cis*-acting elements and the TFs. In addition, a single TF may regulate a large number of target genes with similar *cis*-elements whereas TFs from different families may regulate a single target gene with different types of *cis*-acting elements (Hussain and Amjad, 2011). Therefore, abiotic stresses regulating TFs not only function independently but also co-regulate abiotic stress responses between each other (Wang et al., 2016b) (Fig. 2). As mentioned throughout this review, genetic engineering of TF genes will be much more significant than manipulating a single functional gene. Thereafter, validation of the identified genes should be performed in model crops as well as the main crops by utilizing a stress-inducible promoter to reduce the detrimental effects brought about because of over-expression of certain TFs (Lan et al., 2017). Moving forward, all of these advances will help elucidate the detailed regulatory channels taking part in multiple abiotic stress responses in plants, leading to the acquisition of target TF genes for enhanced breeding of abiotic stress-tolerant plants with improved desirable qualities and yields.

Current and post genomics approaches

Abiotic stresses represent a combination of various distinct traits consisting of a quantitative pattern of inheritance. Therefore, in order to efficiently understand the plants response to the different abiotic stresses at the molecular level, a deeper understanding of the systems involved in transcription regulation is required. Trait mapping, functional characterization, genomic selection, rapid RNA and DNA high-throughput SNP genotyping tools, sequencing technologies, and other platforms are currently used to analyze the genetic mechanisms of different abiotic stresses including drought, salinity, and cold in an effort to speed up the breeding process in maize (Nepolean et al., 2018).

Genome editing techniques are the most recent technologies applied in gene function analyses and manipulations. RNA interference (RNAi) is a rapid and inexpensive technique utilized to analyze gene function in targeted gene knockdown analyses (Rabara et al., 2014). However, a disadvantage of this technique is that the inhibition of gene function is not complete and this could lead to unintended off-target effects leading to misinterpretation of results (Gaj et al., 2013). Of the targeted genome editing approaches currently available, clustered regulatory interspaced short palindromic repeats 'CRISPR' is the most effective system used in editing plant genomes (Cong et al., 2013). CRISPR artificial transcription factors (CRISPR-ATFs) are gaining popularity as an effective system for regulating in vivo plant gene expression (Lowder et al., 2018). For instance, two novel systems (CRISPR-Act2.0 and mTALE-Act) were developed that could be used to study gene regulatory networks and the control mechanisms involved in plants (Lowder et al., 2018).

The other systems are transcription activator-like effectors nucleases (TALENS) (Boch et al., 2009) and Zinc-finger nuclease (ZFNs) (Kim et al., 1996). Another approach with huge potentials in functional genomics in plants is targeting-induced local lesions in genomes (TILLING). For example, a TILLING approach known as ecotilling, which was used to identify variations in natural populations, was successfully used to identify TFs in rice associated with drought tolerance (Yu et al., 2012). These techniques are vital in the selection of better quality genotypes and target genes in the abiotic stress tolerance research in maize.

Another approach currently being explored is the use of machine learning in the study of TFs gene regulatory networks. Predictions of TF binding sites (TFBSs) and their corresponding transcription factor target genes (TFTGs) using machine learning approaches has made substantial contributions to the study of gene regulatory networks (Cui et al., 2014). Understanding the interplay between TFs, TFBSs and TFTGs is vital in understanding the mechanisms involved in the gene regulatory processes taking place during biotic and abiotic stress responses in plants. Various computational algorithms are available in form of software packages. Additionally, expansive use of these software packages has revealed that even though some techniques were developed for one species, the same techniques can be used to analyze the dataset from other species (Cui et al., 2014). For example, a combination of Context Likelihood of Relatedness algorithm analyzed on *Escherichia coli* (Faith et al., 2007), Double Two-way t-tests algorithms analyzed on *Escherichia coli* and Learning Module Networks algorithm tested on yeast (Joshi et al., 2009) was used to identify the presence of oxidative stress regulatory transcription factors in Arabidopsis (Vermeirssen et al., 2014). Moreover, The Algorithm for the Reconstruction of Gene Regulatory Networks (ARACNE) (Margolin et al., 2006) was established to deduce transcriptional regulations in human immune B cells, but was later used to deduce transcriptional interactions regulating root physiological and developmental processes in Arabidopsis (Chavez et al., 2014).

Gene regulatory networks (GRNs) provide insights into the relationships between TFs and their corresponding target genes (Koryachko et al., 2015). For instance, network component analysis (NCA), a computational method developed for analysis of TF-gene interactions in microbial TF-GRNs, was employed to quantitatively analyze TF-GRNs critical in floral development in Arabidopsis (Misra and Sriram, 2013). The results showed that the NCA model adequately accounted for the total gene expression analysis in a TF-GRN of seven TFs (AG, HY5, SEPALLATA3, AP3/P1, AG, AP2, and AGL15) and 55 genes. Strong interactions were present between different TF- gene pairs, such as, *LFY* and *MYB17, AG* and *CRC, AP2* and *RD20,*

AGL15 and *RAV2* and finally *HY5* and *HLH1*. In maize, a machine learning algorithm GENIE3 was used together with numerous RNA-Seq expression data to establish a four tissue (root, SAM, seed, and leaf) specific GRNs (Huang et al., 2017). The results showed that even though many TFs were expressed in multiple tissues, a multi-level examination predicted regulatory roles for many TFs. Additionally, 76.6% (30,028/39479) of the genes were found to be expressed in all the maize tissues. Out of the total of 2587 TFs annotated by GRASSIUS in maize (Chen et al., 2013), 54.46% were expressed in all the four tissues while 86.63% of the total TFs were expressed in at least one of the four tissues.

Understanding the mechanisms of gene regulatory networks (GRNs) is vital in gaining insights on how TFs control gene expression in response to various abiotic stresses. Wet lab experiments are technically demanding, time-consuming and financially demanding (Penfold and Wild, 2011). Many machine-learning approaches have been proposed with an aim of reducing costs and time spent in the prediction of GRNs. For instance, recent development of a publicly accessible maize TF ORF collection (TFome) consisting of 2034 clones that correspond to 2017 unique maize TFs and co-regulators (CoREGs), has vastly contributed to the better understanding of GRNs (Burdo et al., 2014). The TFome was generated from a set of full cDNAs (FL-cDNA) obtained from the Arizona Genomics Institute (AGI). The synthesis information, generated sequences, and request links for the maize TFome information are publicly available through GRASSIUS (http://grassius.org/tfomecollection.html). In conclusion, adaptation of available crop databases such as Gramene (Tello-Ruiz et al., 2018), and GRASSIUS for maize in machine learning approaches, as well as developing and adopting new databases for example the Wheat Information System (WheatIS) (Hu et al., 2018) will help in the storage of data at the same time making it more accessible to scientists.

Traditional breeding techniques for selecting desirable traits depend on the observed phenotypic traits which can be misleading sometimes during selection, and this has led to low success in such strategies. Genomic selection is an accurate and efficient approach when it comes to the prediction of genotypic performance in crops. In maize, utilization of genomic techniques in the manipulation and analyses of TFs has been reported in a few studies. For instance, Mittal et al. (2017) utilized genomic selection techniques on 240 subtropical maize lines during exposure to drought by selecting 29,619 SNPs. The study found that 77 out of 1053 SNPs were linked with 10 drought associated TFs located inside a 150 kb area. For example, MYB (149Kb), WRKY (125Kb), NAC (149Kb), bZIP (92Kb), and AP-ERF (148 Kb) among others. Similarly, transcriptome analysis of two maize inbred lines using RNA-Seq showed that a total of 2558 and 555 genes responded to drought in both the sensitive and the tolerant lines respectively (Zhang et al., 2017a). TFs were found to be enriched in the genotype-specific responsive genes, and the genotypic differentially expressed genes. It was postulated that the differential expression of 22 TF genes and the genotype-specific response of 20 TFs in the tolerant line might play an important role in drought tolerance enhancement in maize. Zhang et al. (2017b) utilized RNA-Seq platform to analyze the expression of TFs in response to lead stress in a maize 178 lead-tolerant line. In this study, a total of 464 genes were expressed, among which 262 differentially expressed TFs (DETs) which responded to Pb treatment were identified. More recently, (Zhao et al., 2018) mapped several abiotic stress responsive TFs to QTLs. The results showed that *MYB78* and *hsp70* were mapped to mQTL1-5. On chromosome 6, *pep7* and *mlip15* were both mapped on mQTL6-1. Kusano et al. (1995) demonstrated that *mlip15* was a low-temperature activated gene that encodes a bZIP protein made up of 135 amino acid. Elsewhere, global transcriptome

profiling using RNA-seq on B73 maize seedlings exposed to heat, drought, cold stress, and salinity revealed 5,330 differentially expressed genes (DEGs) (Li et al 2017). Functional annotations of these DEGs suggested that the pathways involving TFs, hormone metabolism and signaling among others controlled the stress responses. Among the 5,330 DEGs obtained, 167 genes were common to the four abiotic stresses; these included two down-regulated TFs (one MYB related and one b-ZIP) and 10 up-regulated TFs (one ARF, five ERFs, one MYB, one HD-ZIP, and two NAC). This study significantly contributes to a deeper understanding of molecular mechanisms involved in maize leaf responses to different abiotic stresses and could eventually contribute to the development of maize cultivars that are tolerant to various abiotic stresses.

Approaches involving genome-editing techniques create possibilities allowing for gene knockouts, point mutations, epigenetic changes, and the activation or repression of genes (Kamburova et al., 2017). Svitashev et al. (2016) reported the use of biolistic delivery of Cas9-gRNA ribonucleoproteins in maize cells, and this approach resulted in plants with both edited and mutated alleles. Recently, (Cox et al., 2017) reported the use of single-effector programmable RNA guided RNases Cas13. This marks a major leap in plant transformation opening new opportunities in accelerated breeding in other main crops such as wheat, soybeans, sorghum, and rice. By using the RNA editing tools, the DNA structure is left intact but the function of the TF genes is manipulated. Utilization of genome editing techniques is still in its infancy and it is yet to be fully explored for abiotic stress tolerance in maize.

Future outlook

Recent advances in genomics, molecular biology, metabolomics and proteomics have yielded fresh insights into the plant gene regulatory network, composed mainly of regulatory elements (*trans*-elements and *cis*-elements) , inducible genes (developmental and environmental cues), varying signal factors and complementary biochemical pathways (Tang et al., 2003; Wang et al., 2003; Zhu., 2002). Sequencing of the whole maize genome has provided a basis for the functional characterization and identification of genetic networks and genes for maize improvement (Schnable et al., 2009). Moreover, recent availability of transcriptome profiling technologies, including genome sequencing and DNA microarrays, has opened new doors for understanding the patterns of transcription in the area of plant growth and development (Sekhon et al., 2011).

Understanding the genetic architecture of the molecular networks involved in maize, by utilizing current “OMICS” technologies is urgently needed to unravel the drought, heat and salt tolerance mechanisms in maize. Numerous genetic studies have shown that abiotic stress tolerance traits are usually polygenic making the selection of such traits extremely difficult (Loredana et al., 2011). With the recent whole-genome sequencing of the B73 maize line, it’s now feasible to identify most maize TFs and systematically estimate their contribution to abiotic stress tolerance. Maize has an increased level of genetic disequilibrium linkage (LD) and genetic diversity making it an ideal plant species since the LD and genetic diversity have been predicted to be within a number of kilobases (kbs) in maize landraces (Tenaillon et al., 2003). This characteristic makes genome-wide association studies (GWAS) at the gene level more accurate when compared to self-pollinated plant species as long as genome-wide and high-density DNA markers are present (Yan et al., 2011; Li et al., 2012). For example, using a Bayesian-based genome-wide association method in which RNA-seq-based systems of transcript buildup were

utilized as explanatory variables (eRD-GWAS), genes linked to 13 traits were discovered from a group of 369 inbred maize lines (Lin et al., 2017). Additionally, TFs were found to be considerably enriched among the trait-associated genes discovered with eRD-GWAS. Similarly, genome-wide analyses carried out on the maize B73 inbred line to identify all the Hsf genes identified 25 non-redundant Hsf genes designated as *ZmHsfs* (Lin et al., 2011). In soybean, an all-inclusive phylogenetic study revealed 58 dehydration responsive genes from the *GmNAC* TF family (Le et al., 2011). RNA sequencing performed on 14-day old maize seedlings of inbred lines Mo17, B73, PH207, B37 and Oh43 under heat, cold and control treatments, revealed a large number of genes that responded differentially between parental inbred lines (Waters et al., 2017). Moreover, 20 of the 57 annotated TF families in maize were enriched for elevated genes in heat and/or cold stress in at least three of the five inbred genotypes. Finally, TF families with TFs that were enriched for up-regulated genes in response to heat stress included MYB and HSF TF families, while 18 TF families with TFs enriched for up-regulated genes in response to cold stress included APETALA2/ (AP2/EREB).

A new approach currently gaining rapid popularity is the field of phenomics. By utilizing high-throughput phenotyping, various physiological parameters such as biomass, internode length, leaf area, chlorophyll content, plant width and height, and growth rate can be accurately determined in real time and noninvasively (Rabara et al., 2014). Large amounts of quality phenomics data can be generated for many transgenic plants. Currently, field phenotyping systems are being developed with the capacity to determine whether the engineering of TFs in plants can improve abiotic stress tolerance (Rabara et al., 2014). For instance, Awlia et al. (2016) demonstrated that the phenotyping of polygenic traits in one experimental study could provide new insights into the mechanisms of plant responses to different abiotic stresses. The establishment of new phenomics technologies will further strengthen the use of forward genetics in the identification of novel TF genes regulating plant responses to different abiotic stresses.

Since TFs tend to regulate multiple pathways as opposed to a majority of the structural genes, they offer a powerful and unique system for use in the control of complex regulatory networks in plants. Over-expression of genes regulating the transcription of several down-stream abiotic/drought stress regulatory genes is a much better approach in the engineering of drought tolerant/resistant plants as opposed to the development of specific functional genes (Bartels and Hussain, 2008). Development of transgenic plants with enhanced abiotic stress tolerance by regulating TFs has become an important aspect of abiotic stress tolerance. Members of the WRKY, MYB, AREB, and bZIP, TF families have recently been utilized in the regulation of abiotic stress responses in major crops (Singh et al., 2002). Many of the members belonging to these TF families have been identified and characterized in *Arabidopsis*, whose genome has been analyzed using microarray analysis, thus leading to the discovery of potential genes (Shinozaki., 2003; Bray., 2004; Denby and Gehring, 2005). Thus TF families offer important targets for use in gene manipulation and regulation which could be vital in understanding responses involved in abiotic stress tolerance. An increasing trend has seen the engineering of TFs involved in stress-signaling networks using biotechnology tools to generate transgenic stress tolerant plants. (Abe et al., 2003; Sakuma et al., 2006).

983

984 **Conclusion**

985 The population in our planet is projected to rise to 9 billion by the year 2050 (Hussain., 2006),
986 together with the rapid changes in climate there is an urgent need to speed up the productivity of
987 major crops. Understanding molecular mechanisms and mining stress-responsive genes that
988 control plant responses to different abiotic stresses is a major prerequisite in the development of
989 stress-resistant and high yielding crop varieties (Khan et al., 2018). To safeguard the global food
990 production, crops (like maize) that are well adapted to adverse environmental conditions should
991 be established (Vinocur and Altman, 2005).

992 Maize is highly affected by abiotic stresses especially drought throughout its growth cycle, with
993 the most damage being seen during the developmental stage and prior to flowering (Claassen and
994 Shaw, 1970). TF mediated research in plants has recently shown progressive improvement since
995 most of the TF encoding genes are early stress-responsive genes which control the expression of
996 various downstream target genes (Lan et al., 2017). This has in turn led to a deeper
997 understanding of the involvement and functions of TFs in plant responses to different abiotic
998 stresses (Bartels and Sunkar, 2005).

999 This review emphasizes on the main TF families and their potential in abiotic stress tolerance in
1000 maize. The majority of the TF genes in the literature are reported to play major roles in multiple
1001 abiotic stress tolerances. Among the target genes for engineering, the utilization of TFs has been
1002 recommended as they have potential to revolutionize biotechnology upon which novel crops with
1003 improved tolerance to abiotic stresses could be successfully generated. There is absence of
1004 literature available on abiotic stress responsive TFs with agronomic traits that have been utilized
1005 in maize in field conditions. Although Monsanto has developed, a biotechnology-derived inbred
1006 maize line that expresses HB17 (ATHB17), a TF from *Arabidopsis* (Park et al., 2013; Hymus et
1007 al., 2013). Expression of ATHB17 in the inbred line is linked with increased ear biomass at the
1008 silking stage compared to the near-isogenic controls (Rice et al., 2014). Increased ear biomass at
1009 the early stage of plant development is associated with increased sink size and greater grain yield
1010 from hybrid maize (Borras and Wetgate, 2006; Lee and Tollenaar, 2007).

1011 TFs are excellent candidates for the development of transgenic crops because of their roles in
1012 plant growth and development. Incorporation of abiotic stress response pathways in the vital
1013 reproductive and vegetative development stages in crops is an efficient strategy to improve
1014 productivity in field conditions (Nelson et al., 2007). TFs can be used to simulate a variety of
1015 developmental and biochemical networks that take part in the regulation of abiotic stresses, thus
1016 increasing the performance of crops in response to multiple plant abiotic stresses. Joshi et al.
1017 (2016) noted that over-expression of several TF genes significantly enhanced abiotic stress
1018 tolerance but at the same time caused a number of negative effects including lower yields, late
1019 flowering and dwarfing in transgenic plants. This should be considered in future studies to
1020 maximize the effectiveness of TF engineering in responses to different abiotic stresses.

1021 Moving forward, identification and characterization of multiple stress regulatory genes should be
1022 given more focus not only in maize but also in other major crops to target the most effective
1023 genes that can be universally used to develop abiotic stress tolerant crop varieties. Machine
1024 learning algorithms can be integrated with transcriptome data and high-throughput phenotyping

data to further increase the automation of the gene discovery processes such as genome annotation and gene regulatory networks (GRNs) predictions.

Genetic engineering of multiple stress regulatory TF genes is a strong candidate for the enhancement of stress tolerance in plants when compared to focusing on a single individual gene. Nevertheless, recent advances in maize breeding, genomics and functional analysis of genes combined with high-throughput sequencing technologies have significantly increased the chances of achieving multiple stress tolerances. The identification of commercial transgenic plants with enhanced crop performance under stress conditions is a tedious, expensive and lengthy process. However, the successful genetic engineering of maize for improved abiotic stress tolerance using TFs as reviewed herein confirms this approach is feasible.

Since maize is a major crop in many countries, there is need for more collaboration in both applied and theoretical genomics in order to improve the production of maize. The rapid advancements in TFs genome analysis currently being witnessed are mostly on temperate maize varieties. It is hoped that these technologies can be transferred to subtropical and tropical maize varieties that serve as essential food security crop in developing countries.

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References

Abe H., Urao T., Ito T., Seki M., Shinozaki K., Yamaguchi-Shinozaki K. (2003) *Arabidopsis AtMYC2* (bHLH) and *AtMYB2* (MYB) function as transcriptional activators in abscisic acid signaling. Plant Cell 5:63–78

Abe H., Yamaguchi-Shinozaki K., Urao T., Iwasaki T., Hosokawa D., Shinozaki K. (1997) Role of *Arabidopsis* MYC and MYB homologs in drought- and abscisic acid-regulated gene expression. The Plant Cell 9: 1859-1868.

Agalou A, Purwantomo S, Overnäs E, Johannesson H, Zhu X, Estiati A, de Kam RJ, Engström P, Slamet-Loedin IH, Zhu Z, Wang M, Xiong L, Meijer AH, Ouwerkerk PB. (2008) A genome-wide survey of HD-Zip genes in rice and analysis of drought-responsive family members. Plant Mol. Biol.66: 87–103.

Ahuja I, de Vos RC, and Bones AM. (2010). Plant molecular stress responses face climate change. Trends Plant Sci 15, 664–674.

Allan A.C. & Fluhr R. (2007). Ozone and Reactive Oxygen Species. Encyclopedia of Life Sciences, DOI: 10.1038/npg.els.0001299

Almoguera, C., Rojas, A., Díaz-Martín J., Prieto-Dapena, P., Carranco R. (2002) A seed-specific heat-shock transcription factor involved in developmental regulation during embryogenesis in sunflower. Journal of Biological Chemistry277, 43866–43872. doi:10.1074/jbc.M207330200

1064 Amajová O., Plíhal O., Al-Yousif M., Hirt H., Šamaj J. (2013). Improvement of stress tolerance
1065 in plants by genetic manipulation of mitogen-activated protein kinases. Biotechnol.
1066 Adv.31:118– 128. doi: 10.1016/j.biotechadv.2011.12.002.

1067 Ariel, F.D., Manavella, P.A., Dezar, C.A. and Chan, R.L. (2007) The true story of the HD-Zip
1068 family. Trends Plant Sci.12: 419–426.

1069 Ashburner M,, Bonner JJ. (1979). The induction of gene activity in drosophila by heat shock.
1070 Cell 17: 241-54

1071 Awlia, M., Nigro, A., Fajkus, J., Schmoeckel, S. M., Negrão, S., Santelia, D., Trtílek, M., Tester,
1072 M., Julkowska, M. M., … Panzarová, K. (2016). High-Throughput Non-destructive
1073 Phenotyping of Traits that Contribute to Salinity Tolerance in *Arabidopsis thaliana*.
1074 Frontiers in plant science, 7, 1414. doi:10.3389/fpls.2016.01414

1075 Banti, V., Mafessoni, F., Loreti, E., Alpi, A., & Perata, P. (2010). The Heat-Inducible
1076 Transcription Factor *HsfA2* Enhances Anoxia Tolerance in *Arabidopsis*. Plant
1077 Physiology, 152(3), 1471–1483. http://doi.org/10.1104/pp.109.149815

1078 Bartoli C.G., Casalongué C.A., Simontacchi M., Marquez-Garcia B., Foyer C.H. (2013).
1079 Interactions between hormone and redox signaling pathways in the control of growth and
1080 cross- tolerance to stress. Environ. Exp. Bot.94:73–88. doi:
1081 10.1016/j.envexpbot.2012.05.003.

1082 Bartels D, Sunkar R (2005) Drought and salt tolerance in plants. Crit Rev Plant Sci 24:23–58

1083 Benatti, P., Basile, V., Merico, D., Fantoni, L. I., Tagliafico, E., and Imbriano, C. (2008).
1084 Balance between NF-Y and *p53* governs the pro- and anti-apoptotic transcriptional
1085 response. Nucleic Acids Res. 36, 1415–1428. doi: 10.1093/nar/ gkm1046

1086 Bennetzen, J.L. and Hake, S. (2009) Handbook of Maize: Genetics and Genomics. New York:
1087 Springer.

1088 Boch J, Scholze H, Schornack S, Landgraf A, Hahn S, Kay S, Lahaye T, Nickstadt A, Bonas U.
1089 (2009). Breaking the code of DNA binding specificity of TAL-Type III
1090 Effectors. Science 80, 1509–1512. doi: 10.1126/science.1178811

1091 Borras, L., Slafer, G.A. and Otegui, M.E. (2004) Seed dry weight response to source-sink
1092 manipulations in wheat, maize and soybean: a quantitative reappraisal. Field Crops
1093 Res.86, 131–146.

1094 Bray EA. (2004). Genes commonly regulated by water-deficit stress in *Arabidopsis thaliana*. J
1095 Exp Bot; 55:2331-2341.

1096 Butt, H. I., Yang, Z., Chen, E., Zhao, G., Gong, Q., Yang, Z., … Li, F. (2017). Functional
1097 Characterization of Cotton *GaMYB62L*, a Novel *R2R3* TF in Transgenic *Arabidopsis.*
1098 PLoS ONE, 12(1), e0170578. http://doi.org/10.1371/journal.pone.0170578

1099

1100 Burdo, B., Gray, J., Goetting-minesky, M. P., Wittler, B., Hunt, M., Li, T., … Grotewold, E.
1101 (2014). The Maize TFome development of a transcription factor open reading frame

collection for functional genomics, The Plant Journal (80) 356–366. https://doi.org/10.1111/tpj.12623

Cai, R., Dai, W., Zhang, C., Wang, Y., Wu, M., & Zhao, Y. (2017). The maize WRKY transcription factor *ZmWRKY17* negatively regulates salt stress tolerance in transgenic *Arabidopsis* plants. Planta. https://doi.org/10.1007/s00425-017-2766-9

Cai, R., Zhao, Y., Wang, Y., Lin, Y., & Peng, X. (2014). Overexpression of a maize *WRKY58* gene enhances drought and salt tolerance in transgenic rice. Springer: https://doi.org/10.1007/s11240-014-0556-7

Cao, L., Yu, Y., Ding, X., Zhu, D., Yang, F., Liu, B., Sun, X., Duan, X., Yin, K., Zhu, Y. (2017) The *Glycine soja* NAC transcription factor *GsNAC019* mediates the regulation of plant alkaline tolerance and ABA sensitivity. Plant Mol. Biol. 95, 253–268. doi:10.1007/s11103-017-0643-3

Casaretto, J. A., El-Kereamy, A., Zeng, B., Stiegelmeyer, S. M., Chen, X., Bi, Y. M., & Rothstein, S. J. (2016). Expression of *OsMYB55* in maize activates stress-responsive genes and enhances heat and drought tolerance. BMC genomics, 17, 312. doi:10.1186/s12864-016-2659-5

Chang W and Yin D (2009) Overexpression of maize *ZmDBP3* enhances tolerance to drought and cold stress in transgenic *Arabidopsis* plantsBiologia64/6: 1108—1114, Section Cellular and Molecular Biology DOI: 10.2478/s11756-009-0198-0

Chávez Montes, R. A., Coello, G., González-Aguilera, K. L., Marsch-Martínez, N., de Folter, S., & Alvarez-Buylla, E. R. (2014). ARACNe-based inference, using curated microarray data, of *Arabidopsis thaliana* root transcriptional regulatory networks. BMC Plant Biology, 14, 97. http://doi.org/10.1186/1471-2229-14-97

Chaves M.M. & Oliveira M.M. (2004). Mechanisms underlying plant resilience to water deficits: prospects for water-saving agriculture. Journal of Experimental Botany, 55 (407), 2365-2384

Chen, Y. H., Cao, Y. Y., Wang, L. J., Li, L. M., Yang, J., & Zou, M. X. (2017) Identification of MYB transcription factor genes and their expression during abiotic stresses in maize, Biol Plant. 0006-3134, http://sci-hub.tw/10.1007/s10535-017-0756-1.

Chen, S., Huang, X., Yan, X., Liang, Y., Wang, Y., Li, X., … Liu, G. (2013). Transcriptome Analysis in Sheepgrass (*Leymus chinensis*): A Dominant Perennial Grass of the Eurasian Steppe. PLoS ONE, 8(7), e67974. http://doi.org/10.1371/journal.pone.0067974

Chen H, Lai Z, Shi J, Xiao Y, Chen Z, Xu X (2010) Roles of *ArabidopsisWRKY18*, *WRKY40* and *WRKY60* transcription factors in plant responses to abscisic acid and abiotic stress. BMC Plant Biol 10:281

Chew, W., Hrmova, M., & Lopato, S. (2013). Role of homeodomain leucine zipper (HD-Zip) iv transcription factors in plant development and plant protection from deleterious environmental factors. International Journal of Molecular Sciences, 14(4), 8122–8147. https://doi.org/10.3390/ijms14048122

1141 Christianson, J. A., Dennis, E. S., Llewellyn, D. J., and Wilson, I. W. (2010). ATAF NAC
1142 transcription factors: regulators of plant stress signaling. Plant Signal. Behav. 5, 428–432.
1143 doi: 10.4161/psb.5.4.10847

1144 Claassen MM, Shaw RH (1970) Agron J62:652–655

1145 Cong L, Ran FA, Cox D, Lin S, Barretto R, Habib N, Hsu PD, Wu X, Jiang W, Marraffini LA,
1146 Zhang F. (2013). Multiplex genome engineering using CRISPR/Cas systems. HHS
1147 Public Access, *339*(6121), 819–823. https://doi.org/10.1126/science.1231143

1148 Cox, D. B. T., Gootenberg, J. S., Abudayyeh, O. O., Franklin, B., Kellner, M. J., Joung, J., &
1149 Zhang, F. (2017). RNA editing with CRISPR-Cas13. Science, 358(6366), 1019–1027.
1150 doi:10.1126/science.aaq0180

1151 Cui, S., Youn, E., Lee, J., & Maas, S. J. (2014). An Improved Systematic Approach to Predicting
1152 Transcription Factor Target Genes Using Support Vector Machine. PLoS ONE, 9(4),
1153 e94519. http://doi.org/10.1371/journal.pone.0094519

1154 Cutler SR, Rodriguez PL, Finkelstein RR, Abrams SR (2010) Abscisic acid: Emergence of a
1155 core signaling network. Annual Reviews in Plant Biology 61: 651-679.

1156 Dash, S., Van Hemert, J., Hong, L., Wise, R.P. and Dickerson, J.A. (2012) PLEXdb: gene
1157 expression resources for plants and plant pathogens, Nucleic Acids Res., 40, D1194–201.

1158 Denby K, Gehring C. (2005). Engineering drought and salinity tolerance in plants: lessons from
1159 genome-wide expression profiling in *Arabidopsis*. Trends Plant Sci; 23:547-552.

1160 Dixit S, Biswal AK, Min A, Henry A, Oane RH, Raorane ML, Longkumer T, Pabuayon IM,
1161 Mutte SK, Vardarajan AR, Miro B, Govindan G, Albano-Enriquez B, Pueffeld M,
1162 Sreenivasulu N, Slamet-Loedin I, Sundarvelpandian K, Tsai Y-C, Raghuvanshi S, Hsing
1163 Y-IC, Kumar A, Kohli A. (2015). Action of multiple intra-QTL genes concerted around a
1164 co-localized transcription factor underpins a large effect QTL. Sci Rep 5:15183

1165 Dombrowski J.E. (2003). Salt Stress Activation of Wound-Related Genes in Tomato Plants.
1166 Plant Physiology, 132, 2098-2107

1167 Dong, W., Song, Y., Zhao, Z., Qiu, N.W., Liu, X., Guo, W. (2017). The *Medicago truncatula*
1168 R2R3-MYB transcription factor gene *MtMYBS1* enhances salinity tolerance when
1169 constitutively expressed in *Arabidopsis thaliana*. Biochem. Biophys. Res. Commun. 490,
1170 225–230. doi: 10.1016/j.bbrc.2017.06.025

1171 Dong, Y., Wang, C., Han, X., Tang, S., Liu, S., Xia, X., Yin, W. (2014). A novel bHLH
1172 transcription factor *PebHLH35* from *Populus euphratica* confers drought tolerance
1173 through regulating stomatal development, photosynthesis and growth in Arabidopsis.
1174 Biochem Biophys Res Commun, 450(1), 453–458. doi:10.1016/j.bbrc.2014.05.139

1175 Dou, T., Hu, C., Sun, X., Shao, X., Wu, J., Ding, L., Jie, g., Wei, H.,Manosh, B., Qiao, Y., Yi, G.
1176 (2015). MpMYBS3 as a crucial transcription factor of cold signaling confers the cold
1177 tolerance of banana. Plant Cell, Tissue and Organ Culture (PCTOC), 125(1), 93–106.
1178 doi:10.1007/s11240-015-0932-y

1179 Du, H. A. I., Wang, Y. O. N. G. I. N., Xie, Y. I., Liang, Z. H. E., Jiang, S. A. N. I. E., Zhang, S.
1180 H. H., & Huang, Y. U. I. (2013). Genome-Wide Identification and Evolutionary and
1181 Expression Analyses of MYB-Related Genes in Land Plants, 1(May), 437–448.

1182 Echevarría-Zomeño, S., Fernández-Calvino, L., Castro-Sanz, A. B., López, J. A., Vázquez, J., &
1183 Castellano, M. M. (2016). Dissecting the proteome dynamics of the early heat stress
1184 response leading to plant survival or death in *Arabidopsis*. Plant, Cell & Environment,
1185 39, 1264–1278. https://doi.org/10.1111/pce.12664

1186 El-Kereamy A., Bi Y.-M., Ranathunge K., Beatty P. H., Good A. G., Rothstein S. J. (2012). The
1187 rice R2R3-MYB transcription factor *OsMYB55* is involved in the tolerance to high
1188 temperature and modulates amino acid metabolism. *PLoS One* 7:e52030.
1189 10.1371/journal.pone.0052030

1190 Faith, J. J., Hayete, B., Thaden, J. T., Mogno, I., Wierzbowski, J., Cottarel, G., … Gardner, T. S.
1191 (2007). Large-Scale Mapping and Validation of *Escherichia coli* Transcriptional
1192 Regulation from a Compendium of Expression Profiles, PLoS Biol. 5 (1).
1193 https://doi.org/10.1371/journal.pbio.0050008

1194 Fornalé, S., Shi, X., Chai, C., Encina, A., Irar, S., Capellades, M., Fuguet, E., Torres, J.L.,
1195 Rovira, P., Puigdomenech, p., Rigau, J., Grotewold, E., Gray, J., Caparrós-Ruiz, D.
1196 (2010). *ZmMYB31* directly represses maize lignin genes and redirects the
1197 phenylpropanoid metabolic flux. Plant Journal, 64(4), 633–644.
1198 https://doi.org/10.1111/j.1365-313X.2010.04363.x

1199 FrancoZorrilla,J.M.,LópezVidriero,I.,Carrasco,J.L.,Godoy,M.,Vera,P,and,Solano,R.(2014). DNA
1200 -binding specificities of plant transcription factors and their potential to define target
1201 genes. Proc. Natl.Acad.Sci.U.S.A. 111, 2367–2372. doi:10.1073/pnas.1316278111
1202 Gahlaut, V., Jaiswal, V., Kumar, A., & Gupta, P. K. (2016). Transcription factors involved in
1203 drought tolerance and their possible role in developing drought tolerant cultivars with
1204 emphasis on wheat (*Triticum aestivum L.*). Theoretical and Applied Genetics.
1205 https://doi.org/10.1007/s00122-016-2794-z

1206 Gaj T, Gersbach CA, and Barbas CF, 3rd. (2013). ZFN, TALEN, and CRISPR/Cas-based
1207 methods for genome engineering. Trends Biotechnol 31, 397–405.

1208 Giraudat J, Parcy F, Bertauche N, Gosti F, Leung J, Morris P, Bouvier-Durand M, Vartanian N
1209 (1994) Current advances in abscisic acid action and signaling. Plant Molecular Biology
1210 26: 1557–1577.

1211 Gong, F., Yang, L., Tai, F., Hu, X., & Wang, W. (2014). "Omics" of maize stress response for
1212 sustainable food production: opportunities and challenges. Omics : a journal of
1213 integrative biology, 18(12), 714-32.

1214 Gupta, K., Jha, B., Agarwal, P.K. (2014). A dehydration-responsive element binding (DREB)
1215 transcription factor from the succulent halophyte *Salicornia brachiata* enhances abiotic
1216 stress tolerance in transgenic tobacco. Mar. Biotechnol. 16, 657–673. doi: http://sci-
1217 hub.tw/10.1007/s10126-014-9582-z

1218 Hu, H., Scheben, A., & Edwards, D. (2018). Advances in Integrating Genomics and
1219 Bioinformatics in the Plant Breeding Pipeline. Agriculture, 8(6), 75.
1220 doi:10.3390/agriculture8060075

1221 Hu H, You J, Fang Y, Zhu X, Qi Z, Xiong L (2008) Characterization of transcription factor gene
1222 *SNAC2* conferring cold and salt tolerance in rice. Plant Molecular Biology 67: 169-18

1223 Hu, H., Dai, M., Yao, J., Xiao, B., Li, X., Zhang, Q., & Xiong, L. (2006). Overexpressing a
1224 NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt
1225 tolerance in rice. Proceedings of the National Academy of Sciences of the United States
1226 of America, 103(35), 12987–12992. http://doi.org/10.1073/pnas.0604882103

1227 Huang, J., Zheng, J., Yuan, H., & McGinnis, K. (2018). Distinct tissue-specific transcriptional
1228 regulation revealed by gene regulatory networks in maize. BMC Plant Biology, 18, 111.
1229 http://doi.org/10.1186/s12870-018-1329-y

1230 Hübel A, SchöfflF (1994). *Arabidopsis* heat shock factor: isolation and characterization of the
1231 gene and the recombinant protein. Plant Molecular Biology26, 353–362.
1232 doi:10.1007/BF00039545

1233 Hussain SS, & Amjad, M. (2011). Transcription Factors as Tools to Engineer Enhanced
1234 Drought Stress Tolerance in Plants. American Institute of Chemical Engineers
1235 Biotechnol. Prog.,27: 297–306, https://doi.org/10.1002/btpr.514

1236 Hussain SS. (2006). Molecular breeding for abiotic stress tolerance: drought perspective. Proc
1237 Pak Acad Sci; 43:189-210.

1238 Hymus GJ, Cai S, Kohl EA, Holtan HE, Marion CM, Tiwari S, Maszle DR, Lundgren MR, Hong
1239 MC, Channa N, Loida P, Thompson R, Taylor JP, Rice E, Repetti PP, Ratcliffe OJ,
1240 Reuber TL, Creelman RA. (2013) Application of HB17, an Arabidopsis class II
1241 homeodomain-leucine zipper transcription factor, to regulate chloroplast number
1242 and photosynthetic capacity.J. Exp. Bot.64, 4479–4490.

1243 Jaglo-Ottosen KR, Gilmour SJ, Zarka DG, Schabenberger O, and Thomashow MF (1998)
1244 *Arabidopsis CBF1* overexpression induces *COR* genes and enhances freezing tolerance.
1245 Science 280:104–106

1246 Jakoby M, Weisshaar B, Dröge-Laser W, Vicente-Carbajosa J, Tiedemann J, Kroj T, Parcy F
1247 (2002) bZIP transcription factors in *Arabidopsis*. Trends Plant Sci 7:106–111

1248 Jia, Z., Lian, Y., Zhu, Y., He, J., Cao, Z., & Wang, G. (2009). Cloning and characterization of a
1249 putative transcription factor induced by abiotic stress in *Zea mays*. African Journal of
1250 Biotechnology, 8(24), 6764–6771.

1251 Jiang Y., Yang B., Harris N.S. & Deyholos M.K. (2007). Comparative proteomic analysis of
1252 NaCl stress-responsive proteins in *Arabidopsis* roots. Journal of Experimental Botany,
1253 58, 3591–3607

1254 Jin, C., Li, K.-Q., Xu, X.-Y., Zhang, H.-P., Chen, H.-X., Chen, Y.-H., Zhang, S.-L. (2017). A
1255 Novel NAC Transcription Factor, *PbeNAC1*, of *Pyrus betulifolia* Confers Cold and
1256 Drought Tolerance via Interacting with PbeDREBs and Activating the Expression of

Stress-Responsive Genes. Frontiers in Plant Science, 8, 1049. http://doi.org/10.3389/fpls.2017.01049

Jin J, Zhang H, Kong L, Gao G, Luo J (2014) Plant TFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. Nucl Acids Res 42:D1182–D1187

Jinhui Song, Qiaoyun Weng, Hailian Ma, Jincheng Yuan, Lingyun Wang & Yinghui Liu (2016) Cloning and expression analysis of the Hsp70 gene *ZmERD2* in *Zea mays*, Biotechnology & Biotechnological Equipment, 30:2, 219-226, DOI: 10.1080/13102818.2015.1131625

Johannesson H, Wang Y, Hanson J, Engstrom P (2003) The *Arabidopsis thaliana* homeobox gene *ATHB5* is a potential regulator of abscisic acid responsiveness in developing seedlings. Plant Mol Biol 51: 719–729

Joshi R, Wani SH, Singh B, Bohra A, Dar ZA, Lone AA, Pareek A and Singla-Pareek SL (2016) Transcription Factors and Plants Response to Drought Stress: Current Understanding and Future Directions. Front. Plant Sci. 7:1029. doi: 10.3389/fpls.2016.01029

Joshi, A., Smet, R. De, Marchal, K., Peer, Y. Van De, & Michoel, T. (2009). Module networks revisited: computational assessment and prioritization of model predictions, Bioinformatics. 25(4), 490–496. https://doi.org/10.1093/bioinformatics/btn658

Kamburova, V. S., Nikitina, E. V., Shermatov, S. E., Buriev, Z. T., Kumpatla, S. P., Emani, C., & Abdurakhmonov, I. Y. (2017). Genome Editing in Plants: An Overview of Tools and Applications. International Journal of Agronomy, 2017, 1–15. doi:10.1155/2017/7315351

Kasuga M, Liu Q, Miura S, Yamaguchi-Shinozaki K, Shinozaki K (1999) Improving plant drought, salt, and freezing tolerance by gene transfer of a single stress-inducible transcription factor. Nat Biotechnol 17:287–291

Khan, S., Li, M., Wang, S., & Yin, H. (2018). Revisiting the Role of Plant Transcription Factors in the Battle against Abiotic Stress. https://doi.org/10.3390/ijms19061634

Kim, C.Y., Vo, K.T.X., Nguyen, C.D., Jeong, D.H., Lee, S.K., Kumar, M., Kim, S.R., Park, S.H., Kim, K., Jeon, S. (2016). Functional analysis of a cold-responsive rice WRKY gene, *OsWRKY71*. Plant Biotechnol. 10, 13–23. doi: 10.1007/s11816-015-0383-2

Kim SH, Hong JK, Lee SC, Sohn KH, Jung HW, Hwang BK. (2004). *CAZFP1*, Cys2/His2-type zinc-finger transcription factor gene functions as a pathogen-induced early-defense gene in Capsicum annuum. Plant Mol Biol; 55:883-904.

Kim, Y. G., Cha, J., and Chandrasegaran, S. (1996). Hybrid restriction enzymes: zinc finger fusions to Fok I cleavage domain. Proc. Natl. Acad. Sci. U.S.A. 93, 1156–1160. doi: 10.1073/pnas.93.3.1156

Kizis, D., & Investigacio, C. De. (2002). Maize DRE-binding proteins *DBF1* and *DBF2* are involved in *rab17* regulation through the drought-responsive element in an ABA-dependent pathway. The Plant Journal 30: 679–689.

Koryachko, A., Matthiadis, A., Ducoste, J. J., Tuck, J., Long, T. A., & Williams, C. (2015). Computational approaches to identify regulators of plant stress response using high-

1295 throughput gene expression data. Current Plant Biology, 3–4, 20–29.
1296 https://doi.org/10.1016/j.cpb.2015.04.001

1297 Kusano T, Berberich T, Harada M, Suzuki N, Sugawara K (1995) A maize DNA-binding factor
1298 with a bZIP motif is induced by low temperature. Mol Gen Genet 248: 507–517.

1299 Lan, X., Hoang, T., Ngoc, D., Nhi, H., Binh, N., Thu, A., Tran, L. P. (2017). Transcription
1300 Factors and Their Roles in Signal Transduction in Plants under Abiotic Stresses, 483–
1301 497. https://doi.org/10.2174/1389202918666170227150057

1302 Lata, C., Yadav, A., & Prasad, M. (2007). Role of Plant Transcription Factors in Abiotic Stress
1303 Tolerance. Physiological, Biochemical and Genetic Perspectives; www.intechopen.com

1304 Le, D. T., Nishiyama, R., Watanabe, Y., Mochida, K., Yamaguchi-Shinozaki, K., Shinozaki, K.,
1305 & Tran, L.-S. P. (2011). Genome-Wide Survey and Expression Analysis of the Plant-
1306 Specific NAC Transcription Factor Family in Soybean During Development and
1307 Dehydration Stress. DNA Research: An International Journal for Rapid Publication of
1308 Reports on Genes and Genomes, 18(4), 263–276. http://doi.org/10.1093/dnares/dsr015

1309 Lee, E.A. and Tollenaar, M. (2007) Physiological basis of successful breeding strategies for
1310 maize grain yield.Crop Sci.47, S202–S215.

1311 Lee, Y.-H., Oh, H.-S., Cheon, C.-I., Hwang, I.-T., Kim, Y.-J., & Chun, J.-Y. (2001) Structure
1312 and expression of the *Arabidopsis thaliana* homeobox gene *Athb-12*. Biochem Biophys
1313 Res Commun 284: 133–141.

1314 Li Z, Srivastava R, Tang J, Zheng Z and Howell SH (2018) Cis-Effects Condition the Induction
1315 of a Major Unfolded Protein Response Factor, *ZmbZIP60*, in Response to Heat Stress in
1316 Maize. Front. Plant Sci. 9:833. doi: 10.3389/fpls.2018.00833

1317 Li P, Cao W, Fang H, Xu S, Yin S, Zhang Y, Lin D, Wang J, Chen Y, Xu C and Yang Z (2017)
1318 Transcriptomic Profiling of the Maize (Zea mays L.) Leaf Response to Abiotic Stresses at
1319 the Seedling Stage. Front. Plant Sci. 8:290. doi: 10.3389/fpls.2017.00290

1320 Li, H. C., Zhang, H. N., Li, G. L., Liu, Z. H., Zhang, Y. M., Zhang, H. M., & Guo, X. L. (2015).
1321 Expression of maize heat shock transcription factor gene *ZmHsf06* enhances the
1322 thermotolerance and drought-stress tolerance of transgenic *Arabidopsis*. Functional Plant
1323 Biology, 42(11), 1080–1091. https://doi.org/10.1071/FP15080

1324 Li, H., Gao, Y., Xu, H., & Dai, Y. (2013). *ZmWRKY33*, a WRKY maize transcription factor
1325 conferring enhanced salt stress tolerances in *Arabidopsis*, 207–216.
1326 https://doi.org/10.1007/s10725-013-9792-9

1327 Li Q, Yang X, Xu S, Cai Y, Zhang D, Han Y, Li L, Zhang Z, Gao S, Li J, Yan J. (2012)
1328 Genome-wide association studies identified three independent polymorphisms associated
1329 with alphatocopherol content in maize kernels. PLoS One 7: e36807

1330 Lin, H., Liu, Q., Li, X., Yang, J., Liu, S., Huang, Y., Schnable, P. S. (2017). Substantial
1331 contribution of genetic variation in the expression of transcription factors to phenotypic
1332 variation revealed by eRD-GWAS, 1–14. https://doi.org/10.1186/s13059-017-1328-6

1333 Lin, Y., Jiang, H., Chu, Z., Tang, X., Zhu, S., & Cheng, B. (2011). Genome-wide identification ,
1334 classification and analysis of heat shock transcription factor family in maize.BMC
1335 Genomics 2011,12:76 http://www.biomedcentral.com/1471-2164/12/76

1336 Lin, Z., Hong, Y., Yin, M., Li, C., Zhang, K. and Grierson, D. (2008) A tomato HD-Zip
1337 homeobox protein, LeHB-1, plays an important role in floral organogenesis and ripening.
1338 Plant J.55: 301–310.

1339 Liu, B., Hong, Y.B., Zhang, Y.F., Li, X.H., Huang, L., Zhang, H.J., Li, D.Y., Song, F.M.
1340 (2014a). Tomato WRKY transcriptional factor *SlDRW1* is required for disease
1341 resistance against *Botrytis cinerea* and tolerance to oxidative stress. Plant Sci. 227,
1342 145–156. https://doi.org/10.1016/j.plantsci.2014.08.001
1343 Liu, T. K., Song, X. M., Duan, W. K., Huang, Z. N., Liu, G. F., Li, Y., Hou, X. (2014b).
1344 Genome- wide analysis and expression patterns of NAC transcription factor family
1345 under different developmental stages and abiotic stresses in Chinese Cabbage.
1346 Plant Mol. Biol. Report. 32, 1041–1056. doi: 10.1007/s11105-014-0712-6

1347 Liu, S., Wang, X., Wang, H., Xin, H., Yang, X., Yan, X., Li, J., Tran, L.P, Shinozaki, K., Qin, F.
1348 (2013) Genome-Wide Analysis of ZmDREB Genes and Their Association with
1349 Natural Variation in Drought Tolerance at Seedling Stage of *Zea maysL.*. PLoS Genet
1350 9(9): e1003790. doi:10.1371/journal.pgen.1003790

1351 Liu, L., Hao, Z., Weng, J., Li, M., Zhang, D., Bai, L., & Wang, L. (2012). Identication of
1352 drought-responsive genes by cDNA-amplied fragment length polymorphism in maize,
1353 Annals of Applied Biology, https://doi.org/10.1111/j.1744-7348.2012.00565.x

1354 Liu C., Ruan Y., Lin Z., Wei R., Peng Q., Guan C., Ishii H. (2008). Antagonism between
1355 acibenzolar-S-methyl-induced systemic acquired resistance and jasmonic acid-induced
1356 systemic acquired susceptibility to Colletotrichum orbiculare infection in cucumber.
1357 Physiol. Mol. Plant Pathol. 72:141–145. doi: 10.1016/j.pmpp.2008.08.001.

1358 Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamaguchi-Shinozaki K, Shinozaki K. (1998).
1359 Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding
1360 domain separate two cellular signal transduction pathways in drought- and low
1361 temperature-responsive gene expression, respectively, in *Arabidopsis*. Plant Cell;
1362 10:1391–1406.

1363 Loredana F. Ciarmiello, Pasqualina Woodrow, Amodio Fuggi, Giovanni Pontecorvo and
1364 Petronia Carillo (2011). Plant Genes for Abiotic Stress, Abiotic Stress in Plants -
1365 Mechanisms and Adaptations, Prof. Arun Shanker (Ed.), ISBN: 978-953-307-394-1,
1366 InTech, Available from: http://www.intechopen.com/books/abioticstress-in-plants-
1367 mechanisms-and-adaptations/plant-genes-for-abiotic-stress

1368 Lowder, L. G., Zhou, J., Zhang, Y., Malzahn, A., Zhong, Z., Hsieh, T. F., Qi, Y. (2018). Robust
1369 Transcriptional Activation in Plants Using Multiplexed CRISPR-Act2.0 and
1370 mTALE-Act Systems. Molecular Plant, 11(2), 245–256.
1371 https://doi.org/10.1016/j.molp.2017.11.010

1372 Lu., M, Sun., QP, Zhang., DF, Wang., T, Pan., T. (2015) Identification of 7 stress related NAC
1373 transcription factor members in maize (*Zea mays L.*) and characterization of the

expression pattern of these genes, Biochemical and Biophysical Research Communications, doi: 10.1016/j.bbrc.2015.04.113.

Lu, M., Ying, S., & Shi, D. Z. Y. (2012). A maize stress-responsive NAC transcription factor, *ZmSNAC1*, confers enhanced tolerance to dehydration in transgenic *Arabidopsis*, 1701–1711. https://doi.org/10.1007/s00299-012-1284-2

Luan, M., Xu, M., Lu, Y., Zhang, L., Fan, Y., & Wang, L. (2014). Expression of zma-miR169 miRNAs and their target ZmNF-YA genes in response to abiotic stress in maize leaves. Gene, 1–8. https://doi.org/10.1016/j.gene.2014.11.001

Ma, H., Liu, C., Li, Z., Ran, Q., Xie, G., Wang, B., Fang, S., Chu, J., … Zhang, J. (2018). *ZmbZIP4* Contributes to Stress Resistance in Maize by Regulating ABA Synthesis and Root Development. Plant physiology, 178(2), 753-770.

Ma, X., Zhu, X., Li, C., Song, Y., Zhang, W., Xia, G., & Wang, M. (2015). Overexpression of wheat *NF-YA10* gene regulates the salinity stress response *in Arabidopsis thaliana*. Plant Physiol. Biochem. 86, 34–43. doi: 10.1016/j.plaphy. 2014.11.011

Mahalingam, R. (ed.) (2015). "Consideration of combined stress: a crucial paradigm for improving multiple stress tolerance in plants," in Combined Stresses in Plants, (Cham: Springer International Publishing), 1–25. doi: 10.1007/978-3-319-07899-1_1

Manavella, P. A., Arce, A. L., Dezar, C. A., Bitton, F., Renou, J.-P., Crespi, M., & Chan, R. L. (2006) Cross- talk between ethylene and drought signaling pathways is mediated by the sunflower Hahb-4 transcription factor. Plant J.48: 125–137.

Mantovani, R. (1999). The molecular biology of the CCAAT-binding factor NF-Y. Gene 239, 15–27. doi: 10.1016/S0378-1119(99)00368-6

Mao, H., Yu, L., Han, R., Li, Z., & Liu, H. (2016). Plant Physiology and Biochemistry *ZmNAC55*, a maize stress-responsive NAC transcription factor, confers drought resistance in transgenic *Arabidopsis*. Plant Physiology et Biochemistry, 105, 55–66. https://doi.org/10.1016/j.plaphy.2016.04.018

Mao, H., Wang, H., Liu, S., Li, Z., Yang, X., Yan, J., Li, J., Tran LS, Qin, F. (2015). A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. Nature Communications. 6: 8326. https://doi.org/10. 1038/ncomms9326 PMID: 26387805.

Margolin, A. A., Nemenman, I., Basso, K., Wiggins, C., Stolovitzky, G., Favera, R. D., & Califano, A. (2006). ARACNE : An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context. BMC Bioinform. 7 (1) 15, 1–15. https://doi.org/10.1186/1471-2105-7-S1-S7

M'mboyi F, Mugo S, Mwimali M, Ambani L. (2010) Maize Production and Improvement in Sub-Saharan Africa. Nairobi: African Biotechnology Stakeholders Forum (ABSF).

Misra, A., & Sriram, G. (2013). Network component analysis provides quantitative insights on an Arabidopsis transcription factor-gene regulatory network. BMC Systems Biology, 7, 126. http://doi.org/10.1186/1752-0509-7-126

1414 Mittler, R. (2006). Abiotic stress, the field environment and stress combination. Trends Plant Sci.
1415 11, 15–19. doi: 10.1016/j.tplants.2005. 11.002

1416 Moon, S.J., Han, S.Y., Kim, D.Y., Yoon, I.S., Shin, D., Byun, M.O., Kwon, H.B., Kim, B.G.
1417 (2015) Ectopic expression of a hot pepper bZIP-like transcription factor in potato
1418 enhances drought tolerance without decreasing tuber yield. Plant Mol. Biol. 89, 421–431.
1419 doi: 10.1007/s11103-015-0378-y.

1420 Nakashima K, Ito Y, Yamaguchi-Shinozaki K (2009) Transcriptional Regulatory Networks in
1421 Response to Abiotic Stresses in *Arabidopsis* and Grasses. Plant Physiology 149: 88– 95.

1422 Nardini, M., Gnesutta, N., Donati, G., Gatta, R., Forni, C., Fossati, A., Vonrhein,C., Moras, D.,
1423 Romier, M., Matovani, R. (2013). Sequence-specific transcription factor NF-Y displays
1424 histone-like DNA binding and H2B-like ubiquitination. Cell 152, 132–143. doi:
1425 10.1016/j.cell.2012.11.047

1426 Nelson DE, Repetti PP, Adams TR, Creelman RA, Wu J, Warner DC, Anstrom DC, Bensen RJ,
1427 Castiglioni PP, Donnarummo MG, Hinchey BS, Kumimoto RW, Maszle DR, Canales
1428 RD, Krolikowski KA, Dotson SB, Gutterson N, Ratcliffe OJ, Heard JE. (2007). Plant
1429 nuclear factor Y (NF-Y) B subunits confer drought tolerance and lead to improved corn
1430 yields on water-limited acres. Proc Natl Acad Sci USA; 104:16450–16455.

1431 Nepolean T, Kaul J, Mukri G and Mittal S (2018) Genomics-Enabled Next-Generation Breeding
1432 Approaches for Developing System-Specific Drought Tolerant Hybrids in Maize. Front.
1433 Plant Sci. 9:361. doi: 10.3389/fpls.2018.00361

1434 Ni Y, Aghamirzaie D, Elmarakeby H, Collakova E, Li S, Grene R and Heath LS (2016) A
1435 Machine Learning Approach to Predict Gene Regulatory Networks in Seed Development
1436 in Arabidopsis. Front. Plant Sci. 7:1936. doi: 10.3389/fpls.2016.01936

1437 Nuruzzaman, M., Manimekalai, R., Sharoni, A. M., Satoh, K., Kondoh, H., Ooka, H., kikuchi, S.
1438 (2010). Genome-wide analysis of NAC transcription factor family in rice. Gene 465, 30–
1439 44. doi: 10.1016/j.gene.2010.06.008

1440 Ogawa., O, Yamaguchi., K and Nishiuchi., T. (2007) "High-level overexpression of the
1441 *Arabidopsis HsfA2* gene confers not only increased themotolerance but also
1442 salt/osmotic stress tolerance and enhanced callus growth, " Journal of Experimental
1443 Botany, vol. 58, no. 12, pp. 3373–3383.

1444 Ooka H, Satoh K, Doi K, Nagata T, Otomo Y, Murakami K, Matsubara K, Osato N, Kawai J,
1445 Carninci P, Hayashizaki Y, Suzuki K, Kojima K, Takahara Y, Yamamoto K, Kikuchi S
1446 (2003) Comprehensive analysis of NAC family genes in *Oryza sativa* and *Arabidopsis*
1447 *thaliana*. DNA Res 10:239–247

1448 Pandey, P., Ramegowda, V., and Senthil-Kumar, M. (2015). Shared and unique responses of
1449 plants to multiple individual stresses and stress combinations: physiological and
1450 molecular mechanisms. Front. Plant Sci. 6:723. doi: 10.3389/ fpls.2015.00723

1451 Park, M.Y., Kim, S.A., Lee, S.J. and Kim, S.Y. (2013) ATHB17 is a positive regulator of
1452 abscisic acid response during early seedling growth. Mol. Cells, 35, 125–133.

1453 Paz-Ares J, Ghosal D, Wienand U, Peterson PA, Saedler H (1987) The regulatory cl locus of *Zea*
1454 *mays* encodes a protein with homology to myb proto-oncogene products and with
1455 structural similarities to transcriptional activators. EMBO f. 6: 3553-3558.

1456 Pérez-Rodríguez P, Riaño-Pachón DM, Corrêa LG, Rensing SA, Kersten B, Mueller-Roeber B
1457 (2010) PlnTFDB: updated content and new features of the plant transcription factor
1458 database. Nucl Acids Res 38:D822–D8227

1459 Perlack, R.D., Wright, L.L., Turhollow, A.F., Graham, R.L., Stokes, B.J. and Erbach, D.C.
1460 (2005) Biomass as Feedstock for a Bioenergy and Bioproducts Industry: The Technical
1461 Feasibility of a Billion-Ton Annual Supply. Oak Ridge, TN: Oak Ridge National
1462 Laboratory.

1463 Phukan UJ, Jeena GS and Shukla RK (2016) WRKY Transcription Factors: Molecular
1464 Regulation and Stress Responses in Plants. Front. Plant Sci. 7:760. doi:
1465 10.3389/fpls.2016.00760

1466 Phukan, U.J., Mishra, S., Timbre, K., Luqman, S., and Shukla, R.K. (2014). *Mentha arvensis*
1467 exhibit better adaptive characters in contrast to *Mentha piperita* when subjugated
1468 to sustained water logging stress. Protoplasma 251, 603–614.doi: 10.1007/s00709-013-
1469 0561-4

1470 Prasad, P. V. V., Pisipati, S. R., Momcilovic, I., and Ristic, Z. (2011). Independent and combined
1471 effects of high temperature and drought stress during grain filling on plant yield and
1472 chloroplast EF-Tu expression in spring wheat. J. Agron. Crop Sci. 197, 430–441. doi:
1473 10.1111/j.1439-037X.2011.00477.x

1474 Qin, F., Kakimoto, M., Sakuma, Y., Maruyama, K., Osakabe, Y., Tran, L.-S. P., Yamaguchi-
1475 Shinozaki, K. (2007). Regulation and functional analysis of ZmDREB2A in response to
1476 drought and heat stresses in Zea mays L. The Plant Journal, 50(1), 54–69.
1477 doi:10.1111/j.1365-313x.2007.03034.x

1478 Qin F, Sakuma Y, Li J, Liu Q, Li Y, Shinozaki K, Yamaguchi-Shinozaki K (2004) Cloning and
1479 Functional Analysis of a Novel *DREB1/CBF* Transcription Factor Involved in Cold-
1480 Responsive Gene Expression in *Zea mays L*. Plant Cell Physiol. 45(8): 1042–1052 (2004)

1481 Qing, M and Wei, D. (2018). Functional Analysis of Mam-Resistant Candidate Gene *Zmhdz12*.
1482 Science Online.

1483 Rabara, R. C., Tripathi, P., & Rushton, P. J. (2014). The potential of transcription factor-based
1484 genetic engineering in improving crop tolerance to drought. Omics: a journal of
1485 integrative biology, 18(10), 601-14.

1486 Ramakrishna, C., Singh, S., Raghavendrarao, S., Padaria, J. C., Mohanty, S., Sharma, T. R.,
1487 Solanke, A.U. (2018). The membrane tethered transcription factor *EcbZIP17* from finger
1488 millet promotes plant growth and enhances tolerance to abiotic stresses. Sci. Rep.
1489 8:2148. doi: 10.1038/s41598-018-19766-4

1490 Ramegowda, V., and Senthil-Kumar, M. (2015). The interactive effects of simultaneous biotic
1491 and abiotic stresses on plants: mechanistic understanding from drought and pathogen
1492 combination. J. Plant Physiol. 176, 47–54. doi: 10.1016/j.jplph.2014.11.008

1493 Rasmussen S., Barah P., Suarez-Rodriguez M.C., Bressendorff S., Friis P., Costantino P., Bones
1494 A.M., Nielsen H.B., Mundy J. (2013). Transcriptome responses to combinations of
1495 stresses on Arabidopsis. Plant Physiol. 161:1783–1794. doi: 10.1104/pp.112.210773.

1496 Renau-Morata, B., Molina, R. V., Carrillo, L., Cebolla-Cornejo, J., Sánchez-Perales, M.,
1497 Pollmann, S., Nebauer, S. G. (2017). Ectopic Expression of CDF3 Genes in Tomato
1498 Enhances Biomass Production and Yield under Salinity Stress Conditions. Frontiers in
1499 Plant Science, 8, 660. http://doi.org/10.3389/fpls.2017.00660

1500 Riechmann JL, Heard J, Martin G, Reuber L, Jiang CZ, Keddie J, Adam L, Pineda O, Ratcliffe
1501 OJ, Samaha RR, Crelman R, Pilgrim M, Broun P, Zhang JZ, Ghandehari D, Sherman
1502 BK, Yu GL. (2000). *Arabidopsis* transcription factors: genome-wide comparative
1503 analysis among eukaryotes. Science; 290:2105-2110.

1504 Riechmann, J. L., and Meyerowitz, E. M. (1998). The AP2/EREBP family of plant transcription
1505 factors. Biol. Chem. 379, 633–646.

1506 Rice, E. A., Khandelwal, A., Creelman, R. A., Griffith, C., Ahrens, J. E., Taylor, J. P., … Loida,
1507 P. J. (2014). Expression of a truncated ATHB17 protein in maize increases ear weight at
1508 silking. PloS one, 9(4), e94238. doi:10.1371/journal.pone.0094238

1509 Rushton PJ, Somssich IE, Ringler P, Shen QXJ (2010) WRKY transcription factors. Trends
1510 Plant Sci 15:247–258

1511 Rushton, P. J., Bokowiec, M. T., Han, S., Zhang, H., Brannock, J. F., Chen, X., Laudeman, T.
1512 W., … Timko, M. P. (2008). Tobacco transcription factors: novel insights into
1513 transcriptional regulation in the Solanaceae. Plant physiology, 147(1), 280-95.

1514 Saibo NJM, Lourenc¸o T, Oliveira MM (2009) Transcription factors and regulation of
1515 photosynthetic and related metabolism under environmental stresses. Annals of Botany
1516 103: 609-623.

1517 Sakuma Y, Maryyama K, Qin F, Osakabe Y, Shinozaki K, Yamaguchi-Shinozaki K. (2006) Dual
1518 function of an *Arabidopsis* transcription factor *DREB2A* in water-stress-responsive and
1519 heat-stress-responsive gene expression. Proc Nat Acad Sci USA 2006;103:18822-18827.

1520 Saleh A, Lumreras V, Pages M (2005) Functional role of DRE binding transcription factors in
1521 abiotic stress. In: Tuberosa R, Phillips RL, Gale M (eds) Proceedings of the International
1522 Congress 'In the Wake of the Double Helix From the Green Revolution to the Gene
1523 Revolution', 27–31 May 2003, Bologna, Italy, 193–205, 2005 Avenue media. Italy,
1524 Bologna

1525 Sato, H., Mizoi, J., Tanaka, H., Maruyama, K., Qin, F., Osakabe, Y., Morimoto, K., Ohori, T.,
1526 Kusakabe, K., Nagata, M., Shinozaki, K., Yamaguchi-Shinozaki, K. (2014). *Arabidopsis*
1527 DPB3-1, a DREB2A interactor, specifically enhances heat stress induced gene expression
1528 by forming a heat stress-specific transcriptional complex with NF-Y subunits. Plant Cell
1529 26, 4954–4973. doi: 10.1105/tpc.114. 132928

1530 Scharf., K, Berberich., T, Ebersberger., I, and Nover., L. (2012). Plant heat stress
1531 transcription factor (Hsf) family: structure, function and evolution, Biochimica et
1532 Biophysica Acta—Gene Regulatory Mechanisms, vol. 1819, no. 2, pp. 104–119.

1533 Scharf KD, Rose S, Zott W, SchöfflF, Nover L. (1990) Three tomato genes code for heat stress
1534 transcription factors with a region of remarkable homology to the DNA-binding domain
1535 of the yeast HSF.EMBO Journal 9, 4495–4501.

1536 Schnable, P. S., Ware, D., Fulton, R. S., Stein, J. C., Wei, F., Pasternak, S., … Graves, T. A.
1537 (2009). The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science,
1538 326(5956), 1112–1115. doi:10.1126/science.1178534.

1539 Schuetz, T., Gallo, G., Sheldon H., empst P., Kingston R. (1991) "Isolation of a cDNA for
1540 HSF2: Evidence for two heat shock factor genes in humans," Proceedings of the
1541 National Academy of Sciences of the United States of America, vol. 88, no. 16,
1542 pp. 6911–6915.

1543 Sekhon, R.S., Lin H, Childs K.L., Hansey C.N., Buell C.R., de Leon N., Kaeppler S.M. (2011)
1544 Genome-wide atlas of transcription during maize development The Plant Journal 66,
1545 553–563 doi: 10.1111/j.1365-313X.2011.04527.

1546 Shang Y, Yan L, Liu Z-Q, Cao Z, Mei C, Xin Q, Wu F-Q, Wang X-F, Du S-Y, Jiang T, Zhang
1547 X-F, Zhao R, Sun H-L, Liu R, Yu Y-T, Zhang D-P (2010) The Mg-chelatase H subunit
1548 of *Arabidopsis* antagonizes a group of WRKY transcription repressors to relieve ABA-
1549 responsive genes of inhibition. Plant Cell 22:1909–1935

1550 Shao, H., Wang, H and Tang, X. (2015) NAC transcription factors in plant multiple abiotic stress
1551 responses: progress and prospects. Front. Plant Sci. 6:902. doi: 10.3389/fpls.2015.00902

1552 Shen, Q., Zhang, P., Ho T-HD (1996) Modular nature of abscisic acid (ABA) response
1553 complexes: composite promoter units that are necessary and sufficient for ABA
1554 induction of gene expression in barley. Plant Cell 8:1107–1119

1555 Shim, D., Hwang, J.U, Lee, J, Lee, S, Choi, Y. (2009) Orthologs of the class A4 heat shock
1556 transcription factor *HSFA4a* confer cadmium tolerance in wheat and rice. The Plant
1557 Journal21, 4031–4043.

1558 Shinozaki, K., & Yamaguchi-Shinozaki, K. (2006). Gene networks involved in drought stress
1559 response and tolerance. Journal of Experimental Botany, 58(2), 221–227.
1560 doi:10.1093/jxb/erl164

1561 Shinozaki K, Yamaguchi-Shinozaki K, Seki M. (2003). Regulatory network of gene expression
1562 in the drought and cold stress responses. Curr Opin Plant Biol; 6:410-417.

1563 Shiriga, K., Sharma, R., Kumar, K., & Kumar, S. (2014). Genome-wide identification and
1564 expression pattern of drought-responsive members of the NAC family in maize.
1565 MGENE, 2, 407–417. https://doi.org/10.1016/j.mgene.2014.05.001

1566 Siefers, N., Dang, K. K., Kumimoto, R. W., Bynum, W. E., Tayrose, G., Holt, B. F. (2009).
1567 Tissue-specific expression patterns of *Arabidopsis* NF-Y transcription factors suggest
1568 potential for extensive combinatorial complexity. Plant Physiol. 149, 625–641. doi:
1569 10.1104/pp.108.130591

1570 Singh K, Foley RC, Oñate-Sánchez L. (2002). Transcription factors in plant defense and stress
1571 responses. Curr Opin Plant Biol.5:430-436.

1572 Soderman E, Hjellstrom M, Fahleson J, Engstrom P (1999) The HD-Zip gene *ATHB6* in
1573 *Arabidopsis* is expressed in developing leaves, roots and carpels and up-regulated by
1574 water deficit conditions. Plant Mol Biol 40: 1073–1083.

1575 Soderman E, Mattsson J, Engstrom P (1996) The *Arabidopsis* homeobox gene *ATHB-7* is
1576 induced by water deficit and by abscisic acid. Plant J 10: 375–381

1577 Song,X., Li,Y., and Hou,X.(2013). Genome-wide analysis of the AP2/ERF transcription factor
1578 super family in Chinese cabbage (*Brassicarapa ssp. pekinensis*). BMC Genomics 14:573.
1579 doi:10.1186/1471-2164-14-573

1580 Su, H., Cao, Y., Ku, L., Yao, W., Cao, Y., Ren, Z., … Chen, Y. (2018). Dual functions of
1581 *ZmNF-YA3* in photoperiod-dependent flowering and abiotic stress responses in maize.
1582 Journal of Experimental Botany. doi:10.1093/jxb/ery299

1583 Sun, X.C., Gao, Y.F., Li, H.-R., Yang, S.Z., Liu, Y.S. (2015) .Over-expression of *SlWRKY39*
1584 leads to enhanced resistance to multiple stress factors in tomato. J. Plant Biol. 58, 52–60.
1585 doi: http://sci-hub.tw/10.1007/s12374-014-0407-4

1586 Sun H, Huang X, Xu X, Lan H, Huang J, Zhang, HS, (2012) ENAC1, a NAC transcription
1587 factor, is an early and transient response regulator induced by abiotic stress in rice (*Oryza sativa*
1588 *L.*). Mol Biotechnol 52:101–110

1589 Suzuki, N., Rivero, R. M., Shulaev, V., Blumwald, E., and Mittler, R. (2014). Abiotic and biotic
1590 stress combinations. New Phytol. 203, 32–43. doi: 10.1111/nph. 12797

1591 Svitashev, S., Schwartz, C., Lenderts, B., Young, J. K., & Cigan, A. M. (2016). Genome editing
1592 in maize directed by CRISPR – Cas9 ribonucleoprotein complexes: 13274, Nature
1593 Communications. 1–20.

1594 Tang W., Harris L. & Newton R.J. (2003). Molecular mechanism of salinity stress and
1595 biotechnological strategies for engineering salt tolerance in plants. Forestry Studies in
1596 China, 5(2), 52-62

1597 Tello-Ruiz, M. K., Naithani, S., Stein, J. C., Gupta, P., Campbell, M., Olson, A., Ware, D.
1598 (2018). Gramene 2018: unifying comparative genomics and pathway resources for plant
1599 research. Nucleic Acids Research, 46 (Database issue), D1181–D1189.
1600 http://doi.org/10.1093/nar/gkx1111

1601 Tenaillon, M. I., Sawkins, M. C., Long, A. D., Gaut, R. L., Doebley, J. F., & Gaut, B. S. (2001).
1602 Patterns of DNA sequence polymorphism along chromosome 1 of maize (*Zea mays ssp.*
1603 *mays L.*). Proceedings of the National Academy of Sciences of the United States of
1604 America, 98(16), 9161–9166. doi:10.1073/pnas.151244298.

1605 Todaka, D., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2015). Recent advances in the
1606 dissection of drought-stress regulatory networks and strategies for development of
1607 drought-tolerant transgenic rice plants. Front. Plant Sci. 6:84. doi:
1608 10.3389/fpls.2015.00084

1609 Tran L-SP, Nakashima K, Sakuma Y, Osakabe Y, Qin F, Simpson SD, Maruyama K, Fujita Y,
1610 Shinozaki K, Yamaguchi-Shinozaki K (2007) Co-expression of the stress-inducible zinc

finger homeodomain *ZFHD1* and NAC transcription factors enhances expression of the *ERD1* gene in *Arabidopsis*. Plant J 49:46–63

Tripathi P, Rabara RC, Rushton PJ (2014) A systems biology perspective on the role of WRKY transcription factors in drought responses in plants. Planta 239:255–266

Ulker B, Somssich IE (2004) WRKY transcription factors: from DNA binding towards biological function. Curr Opin Plant Biol 7:491–498

Ullah, A., Sun, H., Yang, X., Zhang, X. (2017). A novel cotton WRKY gene, *GhWRKY6*-like, improves salt tolerance by activating the ABA signaling pathway and scavenging of reactive oxygen species. Physiol. Plant. 162, 439–454. https://doi.org/10.1111/ppl.12651.

Umezawa T, Fujita M, Fujita Y, Yamaguchi-Shinozaki K, and Shinozaki K (2006) Engineering drought tolerance in plants: discovering and tailoring genes to unlock the future. Current Opinion in Biotechnology 17: 113-122.

Vermeirssen, V., Clercq, I. De, Parys, T. Van, Breusegem, F. Van, & Peer, Y. Van De. (2014). *Arabidopsis* Ensemble Reverse-Engineered Gene Regulatory Network Discloses Interconnected Transcription Factors in Oxidative Stress. Plant Cell, tpc-114. https://doi.org/10.1105/tpc.114.131417

Vinocur B, and Altman A. (2005). Recent advances in engineering plant tolerance to abiotic stress: Achievements and limitations. Curr Opin Biotech 16, 123–132.

Wang, C. T., Ru, J. N., Liu, Y. W., Yang, J. F., Li, M., Xu, Z. S., & Fu, J. D. (2018). The Maize WRKY Transcription Factor *ZmWRKY40* Confers Drought Resistance in Transgenic Arabidopsis. International journal of molecular sciences, 19(9), 2580. doi:10.3390/ijms19092580

Wang B, Li Z, Ran Q, Li P, Peng Z and Zhang J. (2018b) *ZmNF-YB16* Overexpression Improves Drought Resistance and Yield by Enhancing Photosynthesis and the Antioxidant Capacity of Maize Plants. Front. Plant Sci. 9:709. doi: 10.3389/fpls.2018.00709

Wang C.-T., Ru, J.-N., Liu, Y.-W., Li, M., Zhao, D., Yang, J.-F., … Xu, Z.-S. (2018c). Maize WRKY Transcription Factor *ZmWRKY106* Confers Drought and Heat Tolerance in Transgenic Plants. International Journal of Molecular Sciences, 19(10), 3046. doi:10.3390/ijms19103046

Wang C., Lu, G., Hao, Y., Guo, H., Guo, Y., Zhao, J., & Cheng, H. (2017). *ABP9*, a maize bZIP transcription factor, enhances tolerance to salt and drought in transgenic cotton. Planta, 246(3), 453–469. https://doi.org/10.1007/s00425-017-2704-x

Wang D., Yanchong Y., Liu., Z, Shuo., L, Wang., Z, Xiang., F. (2016a) Membrane-bound NAC transcription factors in maize and their Contribution to the oxidative stress response, Plant Science http://dx.doi.org/10.1016/j.plantsci.2016.05.019

Wang H, Shao H and Tang X (2016b) Recent Advances in Utilizing Transcription Factors to Improve Plant Abiotic Stress Tolerance by Transgenic Technology.Front.PlantSci.7:67. doi: 10.3389/fpls.2016.00067

Wang, Z., Su, G., Li, M., Ke, Q., Kim, S. Y., Li, H., … Kwak, S.-S. (2016). Overexpressing *Arabidopsis* ABF3 increases tolerance to multiple abiotic stresses and reduces leaf size in alfalfa. Plant Physiology and Biochemistry, 109, 199–208. doi:10.1016/j.plaphy.2016.09.020

Wang N (2014). Analysis of Abiotic Stress Related Functions of Genes *ZmWRKY50* and *ZmWRKY44* in Maize (*Zea Mays L.*).Globe Thesis, 2180330485996209

Wang, C., Shi, X., Liu, L., Li, H., Ammiraju, J. S., Kudrna, D. A., … Luo, M. (2013). Genomic resources for gene discovery, functional genome annotation, and evolutionary studies of maize and its close relatives. Genetics, 195(3), 723–737. doi:10.1534/genetics.113.157115

Wang B., Zheng, J., Liu, Y., Wang, J., & Wang, G. (2012). Cloning and characterization of the stress-induced bZIP gene *ZmbZIP60* from maize. Molecular Biology Reports, 39(5), 6319–6327. https://doi.org/10.1007/s11033-012-1453-y

Wang CT, Yang QA, Yang YM. (2011) Characterization of the *ZmDBP4* gene encoding a CRT/DRE-binding protein responsive to drought and cold stress in maize. Acta Physiologiae Plantarum. 33: 575± 583. https://doi.org/10.1007/s11738-010-0582-y

Wang, W., Vinocur, B., Shoseyov, O., & Altman, A. (2004). Role of plant heat-shock proteins and molecular chaperones in the abiotic stress response. Trends in Plant Science, 9(5), 244–252. doi:10.1016/j.tplants.2004.03.006

Wang W.X., Barak T., Vinocur B., Shoseyov O. & Altman A. (2003). Abiotic resistance and chaperones: possible physiological role of SP1, a stable and stabilizing protein from Populus. In: Vasil IK (ed.) Plant biotechnology 2000. Kluwer, Dordrecht, pp 439-43

Waters, A. J., Makarevitch, I., Noshay, J., Burghardt, L. T., Hirsch, C. N., Hirsch, C. D., & Springer, N. M. (2017). Natural variation for gene expression responses to abiotic stress in maize. Plant Journal, 89(4), 706–717. https://doi.org/10.1111/tpj.13414

Wei, H., Zhao, H., Su, T., Bausewein, A., Greiner, S., Harms, K., & Rausch, T. (2017). Chicory R2R3-MYB transcription factors *CiMYB5* and *CiMYB3* regulate fructan 1-exohydrolase expression in response to abiotic stress and hormonal cues. Journal of Experimental Botany, 68(15), 4323–4338. http://doi.org/10.1093/jxb/erx210

Wei, T., Deng, K., Liu, D., Gao, Y., Liu, Y., Yang, M., Zhang, L., Zheng, X., Wang, C., Song, W., Chen, C., Zhang, Y. (2016). Ectopic Expression of DREB Transcription Factor, *AtDREB1A*, confers tolerance to drought in transgenic *Salvia miltiorrhiza*. Plant Cell Physiol. 57, 1593–1609. https://doi.org/10.1093/pcp/pcw084

Wei, K. A., Chen, J. U. A. N., Wang, Y. A., Chen, Y. A., Chen, S. H., Lin, Y. I. N. A., … Zhong, X. I. (2012a). Genome-Wide Analysis of bZIP-Encoding Genes in Maize, (October), DNA Research 19, 463–476. doi:10.1093/dnares/dss026.

Wei, K.-F., Chen, J., Chen, Y.-F., Wu, L.-J., & Xie, D.-X. (2012b). Molecular Phylogenetic and Expression Analysis of the Complete WRKY Transcription Factor Family in Maize. DNA Research: An International Journal for Rapid Publication of Reports on Genes and Genomes, 19(2), 153–164. http://doi.org/10.1093/dnares/dsr048

1689 Wong, C. E., Li, Y., Labbe, A., Guevara, D., Nuin, P., Whitty, B., … Moffatt, B. A. (2006).
1690 Transcriptional profiling implicates novel interactions between abiotic stress and
1691 hormonal responses in *Thellungiella*, a close relative of A*rabidopsis*. Plant physiology,
1692 140(4), 1437–1450. doi:10.1104/pp.105.070508

1693 Wu, J., Zhou, W., Gong, X., & Cheng, B. (2016). Expression of ZmHDZ4, a Maize
1694 Homeodomain-Leucine Zipper I Gene, Confers Tolerance to Drought Stress in
1695 Transgenic Rice. Plant Molecular Biology Reporter, 34(4), 845–853.
1696 doi:10.1007/s11105-015-0970-y

1697 Wurzinger B., Mair A., Pfister B., Teige M. (2011). Cross-talk of calcium-dependent protein
1698 kinase and MAP kinase signaling. Plant Signal. Behav. 6:8–12. doi:
1699 10.4161/psb.6.1.14012.

1700 Xiong L., Schumaker K.S., Zhu J.K. (2002). Cell signaling during cold; drought; and salt stress.
1701 Plant Cell. 14:165–183. doi: 10.1105/tpc.010278.

1702

1703 Xu, Z., Ali, Z., Xu, L., He, X., Huang, Y., Yi, J., Zhang, D. (2016). The nuclear protein
1704 *GmbZIP110* has transcription activation activity and plays important roles in the response
1705 to salinity stress in soybean. Scientific Reports, 6, 20366.
1706 http://doi.org/10.1038/srep20366

1707 Yamaguchi-Shinozaki K, Shinozaki K. (2006). Transcriptional regulatory networks in cellular
1708 responses and tolerance to dehydration and cold stresses. Annu Rev Plant Biol 57:781–
1709 803

1710 Yamaguchi-Shinozaki K, Shinozaki K (1994) A novel cis-acting element in an *Arabidopsis* gene
1711 is involved in responsiveness to drought, low-temperature, or high-salt stress. Plant Cell
1712 6:251–264

1713 Yamanouchi U, Yano M, Lin HX, Ashikari M, Yamada K. (2002) Rice spotted leaf gene, *Spl7*,
1714 encodes a heat stress transcription factor protein. Proceedings of the National Academy
1715 of Sciences of the United States of America 99, 7530–7535. doi:10.1073/pnas.112209199

1716 Yamasaki, K., Kigawa, T., Seki, M., Shinozaki, K., & Yokoyama, S. (2013). DNA-binding
1717 domains of plant-specific transcription factors: structure, function, and evolution. Trends
1718 in Plant Science, 18(5), 267–276. doi:10.1016/j.tplants.2012.09.001

1719 Yan J, Warburton M, Crouch J (2011) Association Mapping for Enhancing Maize (*Zea mays L.*)
1720 Genetic Improvement. Crop Sci 51: 433–449.

1721 Yanhui C, Xiaoyuan Y, Kun H, Meihua L, Jigang L, Zhaofeng G, Zhiqiang L, Yunfei Z,
1722 Xiaoxiao W, Xiaoming Q, Yunping S, Li Z, Xiaohui D, Jingchu L, Xing-Wang D,
1723 Zhangliang C, Hongya G, Li-Jia Q (2006) The MYB transcription factor superfamily of
1724 *Arabidopsis*: expression analysis and phylogenetic comparison with the rice MYB
1725 family. Plant Mol Biol 60:107–124

1726 Ying, S., & Jing, D. Z. (2012). Cloning and characterization of a maize bZIP transcription factor,
1727 *ZmbZIP72*, confers drought and salt tolerance in transgenic *Arabidopsis*, 253–266.
1728 https://doi.org/10.1007/s00425-011-1496-7

1729 Yu, X., Liu, Y., Wang, S., Tao, Y., Wang, Z., Shu, Y., Peng, H., Mijiti, A., Wang, Z., Zhang, H.
1730 (2016). *CarNAC4*, a NAC -type chickpea transcription factor conferring enhanced
1731 drought and salt stress tolerances in *Arabidopsis*. Plant Cell Rep. 35, 613–627

1732 Yu, S., Liao, F., Wang, F., Wen, W., Li J., Mei, H., and Luo, L. (2012). Identification of rice
1733 transcription factors associated with drought tolerance using the Ecotilling method. PLoS
1734 One 7, e30765.

1735 Zhang, X., Liu, X., Zhang, D., Tang, H., Sun, B., Li, C., … Li, Y. (2017). Genome-wide
1736 identification of gene expression in contrasting maize inbred lines under field drought
1737 conditions reveals the significance of transcription factors in drought tolerance. PLOS
1738 ONE, 12(7), e0179477. doi:10.1371/journal.pone.0179477

1739 Zhang, Y., Ge, F., Hou, F., Sun, W., Zheng, Q., Zhang, X., Shen, Y. (2017b). Transcription
1740 factors Responding to Pb stress in Maize. Genes, 8(9), 1–13.
1741 https://doi.org/10.3390/genes8090231

1742 Zhang, X., Liu, X., Wu, L., Yu, G., Wang, X., & Ma, H. (2015). The SsDREB Transcription
1743 Factor from the Succulent Halophyte *Suaeda salsa* Enhances Abiotic Stress Tolerance in
1744 Transgenic Tobacco. International Journal of Genomics, 2015, 875497.
1745 http://doi.org/10.1155/2015/875497

1746 Zhang X, Wang L, Meng H, Wen H, Fan Y, Zhao J (2011) Maize *ABP9* enhances tolerance to
1747 multiple stresses in transgenic *Arabidopsis* by modulating ABA signaling and cellular
1748 levels of reactive oxygen species. Plant Mol Biol 75:365–378

1749 Zhao, X.,Peng, Y.,Zhang, J., Fang, P., & Wu, B. (2018). Identification of QTLs and Meta-
1750 QTLs for Seven Agronomic Traits in Multiple Maize Populations, 520 (april), 507–520.
1751 https://doi.org/10.2135/cropsci2016.12.0991

1752 Zhao, Y., Ma, Q., Jin, X., Peng, X., Liu, J., Deng, L., Sheng, L. (2014). A Novel Maize
1753 Homeodomain – Leucine Zipper (HD-Zip) I Gene , *Zmhdz10* , Positively Regulates
1754 Drought and Salt Tolerance in Both Rice and *Arabidopsis.* Oxford Academic, 1, 1–33:
1755 https:// doi.org /10.1093/pcp/pcu054.

1756 Zhao, Y., Zhou, Y., Jiang, H., Li, X., Gan, D., Peng, X., & Zhu, S. (2011). Systematic Analysis
1757 of Sequences and Expression Patterns of Drought-Responsive Members of the HD-Zip
1758 Gene Family in Maize, 6(12), 20–21. https://doi.org/10.1371/journal.pone.0028488

1759 Zhao JF, Sun ZF, Zheng J, Guo XY, Dong ZG, Huai JL, Gou M, He J, Jin Y, Wang J, Wang G.
1760 (2009). Cloning and characterization of a novel CBL-interacting protein kinase from
1761 maize. Plant Molecular Biology. 69: 661±674. https://doi.org/ 10.1007/s11103-
1762 008-9445-y PMID: 19105030.

1763 Zhou W, Jia C, Wu X, Hu R, Yu G , Zhang X, Liu J, Pan H. (2016). *ZmDBF3*, a Novel
1764 Transcription Factor from Maize (*Zea mays L.*), Is Involved in Multiple Abiotic Stress
1765 Tolerance, Plant Mol Biol Rep DOI 10.1007/s11105-015-0926-2

1766 Zhu, Q., Zhang, J., Gao, X., Tong, J., Xiao, L., Li, W., Zhang, H. (2010). The *Arabidopsis*
1767 AP2/ERF transcription factor *RAP2.6* participates in ABA, salt and osmotic stress
1768 responses.Gene.457:1–12. https://doi.org/10.1016/j.gene.2010.02.011

1769 Zhu J. K. (2002). Salt and drought stress signal transduction in plants. Annu. Rev. Plant Biol.,
1770 53, 247

1771 Zhuang, J., Deng, D.-X., Yao, Q.-H., Zhang, J., Xiong, F., Chen, J.-M., & Xiong, A.-S. (2010).
1772 Discovery, phylogeny and expression patterns of AP2-like genes in maize. Plant Growth
1773 Regulation, 62(1), 51–58. doi:10.1007/s10725-010-9484-7

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Figure 1

A diagrammatic representation of gene expression and abiotic stress signal perception in plants via ABA-independent and ABA-dependent pathways.

Figure.1 A diagrammatic representation of gene expression and abiotic stress signal perception in plants via ABA-independent and ABA-dependent pathways (Modified from Gahlaut et al., 2016; Khan et al., 2018). Abbreviations: Abscisic acid (ABA), Reactive oxygen species (ROS), myeloblastosis oncogene (MYB), myelocytomatosis oncogene (MYC), Zinc-finger homeodomain (ZF-HD) regulon, ABA-responsive element binding protein (AREB), ABA-independent regulons include; the NAC (CUC, NAM and ATAF), The cis-acting element (DRE), ABA-binding factor (ABF), The cis-acting element (CRE), Dehydration responsive element binding proteins (DREBs), C-repeat (CRT), (ZFR) zinc finger RNA binding protein, (NARC) NAC recognition site, (MYBRS) MYB recognition site, (MYCRS) MYC recognition site, Nuclear transcription factor Y (NF-Y), Heat Shock Factors (HSFs), Inducer of CBF Expression (ICE).

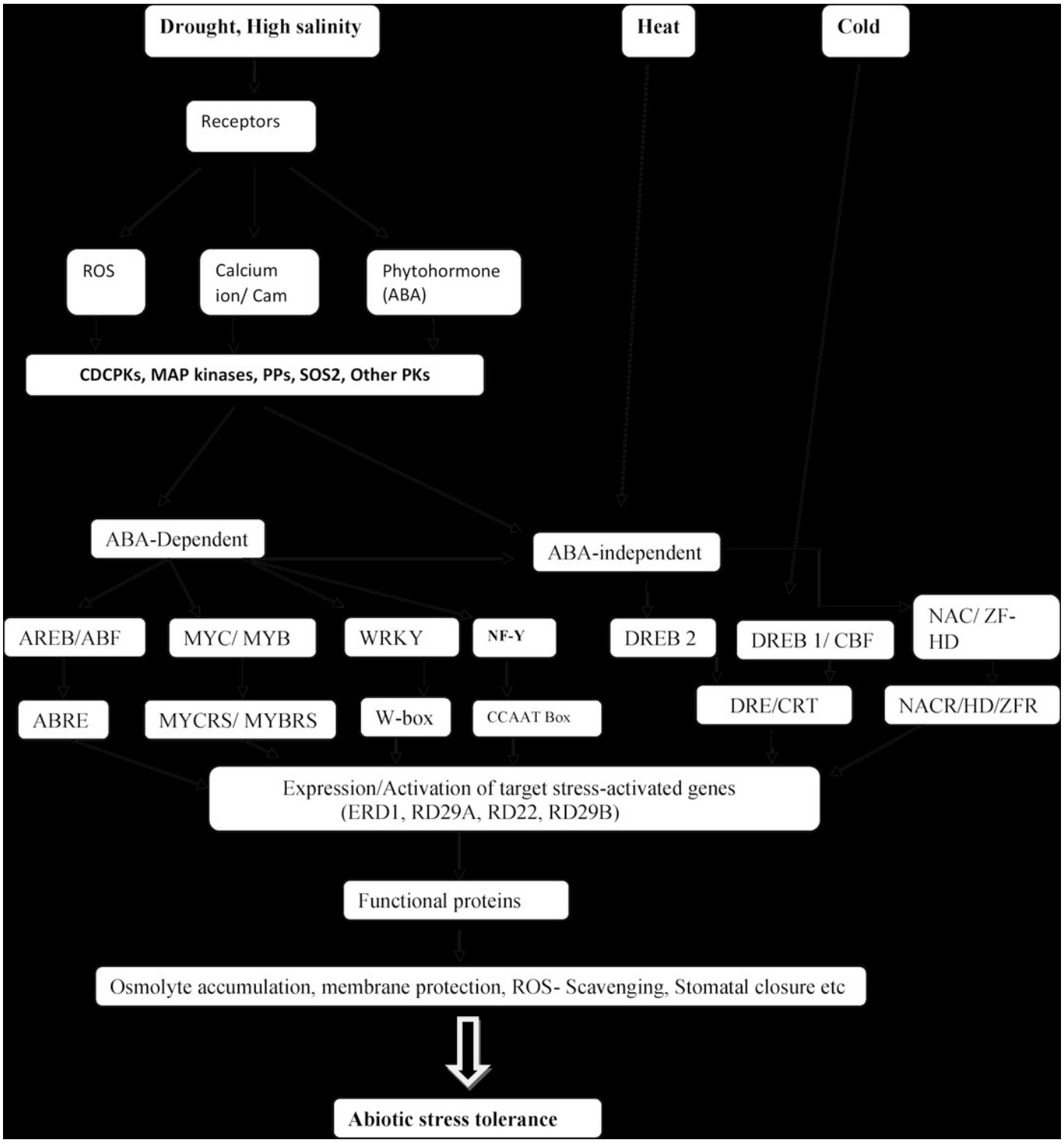
Drought, High salinity
Heat
Cold
Receptors
ROS
Calcium ion/ Cam
Phytohormone (ABA)
CDCPKs, MAP kinases, PPs, SOS2, Other PKs
ABA-Dependent
ABA-independent
AREB/ABF
MYC/ MYB
WRKY
NF-Y
DREB 2
DREB 1/ CBF
NAC/ ZF-HD
ABRE
MYCRS/ MYBRS
W-box
CCAAT Box
DRE/CRT
NACR/HD/ZFR
Expression/Activation of target stress-activated genes (ERD1, RD29A, RD22, RD29B)
Functional proteins
Osmolyte accumulation, membrane protection, ROS- Scavenging, Stomatal closure etc
Abiotic stress tolerance

Figure 2

Cross-talk network between *cis*-acting elements and TFs in the ABA-independent and ABA-dependent pathways during abiotic stress

Cross-talk network between *cis*-acting elements and TFs in the ABA-independent and ABA-dependent pathways during abiotic stress. Broken arrows indicate the protein-protein interactions. Thick green arrows show the major pathways which regulate many downstream genes (modified from Yamaguchi-Shinozaki and Shinozaki, 2006).

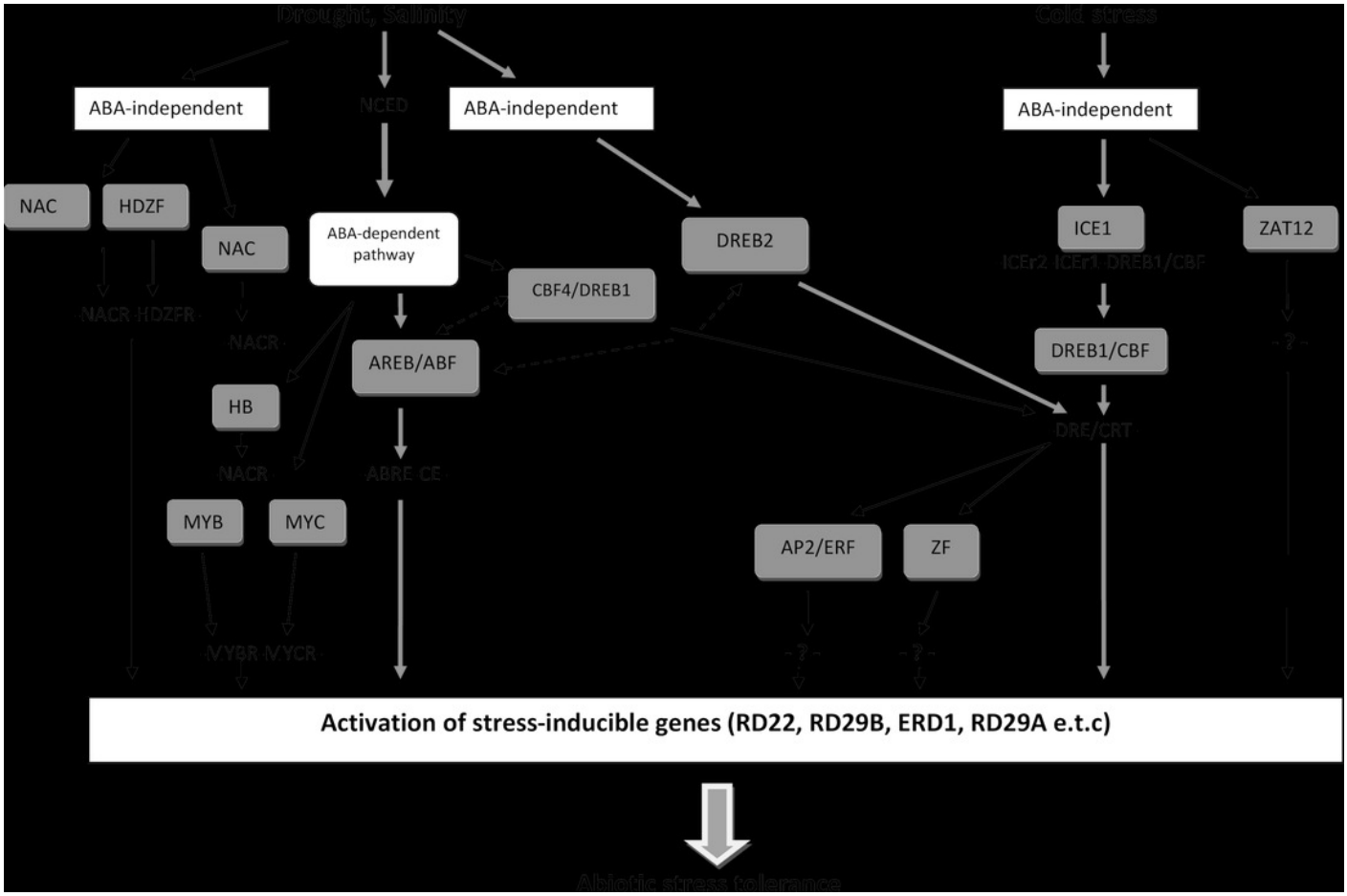

Table 1(on next page)

Abiotic stress- related TF families, together with the specific TFs in Maize.

Abiotic stress- related TF families, together with the specific TFs, their characteristics, the regulons they control and their regulatory functions in the abiotic stress responses in Maize.

Table 1 Abiotic stress- related TF families, together with the specific TFs, their characteristics, the regulons they control and their regulatory functions in the abiotic stress responses in Maize.

Family	TFs in Maize	Cis-element recognition	Stress response	Downstream genes	References
DREB/CBF	*ZmDREB2A*	(DRE) TACCGACAT	Salt, Heat, Drought, Cold	*rd29A*, *rd29B,ZmGOLS2*	Qin et al., 2007
	ZmDBP3	(DRE) TACCGACAT	Cold, salt	U	Wang and Dong., 2009
	ZmDREB1A	(DRE/CRT) G/ACCGAC	Drought, cold	*KIN1*, *KIN2*,*COR15A* etc	Qin et al., 2004
	ZmDBF3	N/A	Salt, drought, freezing	U	Zhou et al., 2015
	ZmDBP4	(DRE/CRT) G/ACCGAC	Cold, drought	U	Wang et al., 2011
	ZmDREB2.7	(DRE) A/GCCGAC	Drought	U	Liu et al., 2013
MYB/ MYC	*ZmMYB30*	(MYBR) TAACNA/G	Salt, drought, ABA	*RD20*, *RD29A*, *RbohD* e.t.c	Chen et al., 2015
	ZmMYB36	N/A	Salt, drought, ABA	U	Chen et al., 2015
	ZmMYB95	N/A	Salt, drought, ABA	U	Chen et al., 2015
	ZmMYB53	N/A	Cold	U	Chen et al., 2015
	ZmMYB31	N/A	Sensitivity to UV radiation	*ZmF5H*, *ZmCOMT, C3H*, and *ZmActin*	Fornale et al., 2010
	ZmMYB-R1	N/A	Cold, high salinity, drought, ABA and heat	U	Liu et al., 2012
bZIP	*ZmbZIP60*	(ABRE) ACGTGGC	Dehydration, high salinity, ABA	U	Wang et al., 2012
			Heat stress	U	Li et al., 2018
	ZmbZIP17	N/A	Drought, ABA, heat, Salt	U	Jia et al., 2009
	ZmbZIP54 and *ZmbZIP107*	(ABRE) ACGTGGC	Lead (Pb)	U	Zhang et al., 2017
	mlip15	(ABRE) ACGTGGC	Low temperature, salt, ABA	U	Kusano et al., 1995
	ZmbZIP72	(ABRE)	ABA, drought,	*Rab18*, *rd29B*,	Ying and Jing .,

		ACGTGGC	high salinity,	*HIS1-3* e.t.c	2012
	ABP9	(ABRE) (C/T) ACGTGGC	ABA, drought, H_2O_2, salt	*KIN1, COR15A, PP2C, AZF2* e.t.c	Zhang et al., 2011
	ZmbZIP4	(ABRE) (C/T) ACGTGGC	Heat, cold, salinity and ABA	*ZmLEA2, ZmRD20, ZMRab18, ZmGEA6* e.t.c	Ma et al., 2018
NAC	*ZmSNAC1*	N/A	Low temperature, ABA, high salinity, drought	U	Lu et al., 2012
	ZmNAC55	N/A	High salinity, cold, drought, ABA	*RD29B*, *LEA14*, *RD17*, *ZAT10* e.t.c	Mao et al., 2016
	Zma006493	N/A	Drought	U	Min et al., 2015
	Zma000584	N/A	Drought, cold	U	Min et al., 2015
	Zma001259	N/A	Drought, salt, cold	U	Min et al., 2015
	ZmSNAC052	N/A	Drought, cold	U	Min et al., 2015
	Zma029150	N/A	Drought, salt	U	Min et al., 2015
WRKY	*ZmWRKY17*	(W-box) TTGACC/T	Drought, salt, ABA	*bHLH92, KIN1, DREB1F* e.t.c	Cai et al., 2017
	ZmWRKY33	(W-box) TTGACC/T	High salinity, dehydration, cold, ABA	*RD29A* and *DREB1B*	Li et al., 2013
	ZmWRKY44	(W-box) TTGACC/T	Salt, high temperature, ABA, H_2O_2	U	Wang., 2014
	ZmWRKY58	(W-box) TTGACC/T	Drought, ABA, Salt	U	Cai et al.,2014
	ZmWRKY106	(W-box) TTGACC/T	Drought, high temperature, ABA, Salt	*CuZnSOD, DREB2A, NCED6* and *RD29A*	Wang et al., 2018c
	ZmWRKY40	(W-box) TTGACC/T	Drought, High salinity, High temperature, ABA	*DREB2B, STZ* and *RD29A*	Wang et al., 2018a
Others					
HD-Zip	*Zmhdz10*	CAATAATTG	Salt, ABA	*ABI1, RD22, P5CS1*e.t.c	Zhao et al., 2018
	ZmHDZ4	CAATAATTG	Drought	U	Wu et al., 2016
HSP	*ZmERD2*	N/A	Heat, salinity, cold, PEG,	U	Jinhui et al., 2015

			dehydration		
NF-Y	*ZmNF-YB16*	CCAAT	Dehydration, Drought	*P5CS*, *Atj3*, *AtDJC82*, *HSP70* e.t.c	Wang et al., 2018b
	ZmNF-YB2	CCAAT	Drought	*U*	Nelson et al., 2007
	ZmNF-YA3	CCAAT	Drought, high temperature	*ZmbHLH92, ZmMYC4* and *ZmFAMA*	Su et al., 2018

N/A- The *cis*-acting element is unknown, U- unknown

Table 2(on next page)

Abiotic stress responses of over-expressing Maize TFs in transgenic plants.

Represents the abiotic stress responses of over-expressing Maize TFs in transgenic plants.

Table 2 Represents the abiotic stress responses of over-expressing Maize TFs in transgenic plants.

Family	Gene	Stress Tolerance	Transgenic Plant	References
MYB/ MYC	*ZmMYB30*	Salt	*Arabidopsis*	Chen et al., 2015
	ZmMYB31	Sensitivity to UV irradiation	*Arabidopsis*	Fornale et al., 2010
DREB/CBF	*ZmDREB2A*	Drought, heat	*Arabidopsis*	Qin et al., 2007
	ZmDBP3	Cold, salt	*Arabidopsis*	Wang and Dong., 2009
	ZmDBF3	Salt, freezing	yeast (*Saccharomyces cerevisiae*)	Zhou et al., 2015
	ZmDREB1A	Drought, Freezing	*Arabidopsis*	Qin et al., 2004
	ZmDREB2.7	Drought	*Arabidopsis*	Liu et al., 2013
	ZmDBP4	Drought, cold	*Arabidopsis*	Wang et al., 2011
bZIP	*ZmbZIP60*	Dithiothreitol (DDT)	*Arabidopsis*	Wang et al., 2012
	ZmbZIP72	Drought, partial salinity	*Arabidopsis*	Ying and Jing ., 2012
	Abp9	Salt, osmotic stress	Cotton (*Gossypium hirsutum*)	Wang et al., 2017
		Drought, ABA, Salt	*Arabidopsis*	Zhang et al., 2011
NAC	*ZmSNAC1*	Sensitivity to ABA, osmotic stress	*Arabidopsis*	Lu et al., 2012
		Tolerance to dehydration		
	ZmNAC55	Sensitivity to ABA	*Arabidopsis*	Mao et al., 2016
		Tolerance to drought		
	ZmNAC111	Drought	Maize (*Zea mays*)	Mao et al., 2015
WRKY	*ZmWRKY17*	Sensitivity to salt	*Arabidopsis*	Cai et al., 2017

		Tolerance to ABA		
	ZmWRKY33	Salt	*Arabidopsis*	Li et al., 2013
	ZmWRKY44	Sensitivity to salt	*Arabidopsis*	Wang., 2014
	ZmWRKY58	Enhanced tolerance to drought, salt	Rice (*Oryza sativa*)	Cai et al., 2014
	ZmWRKY106	Drought, heat stress	*Arabidopsis*	Wang et al., 2018c
	ZmWRKY40	drought	Arabidopsis	Wang et al., 2018a
Others				
HSF	*ZmHsf06*	Drought, thermotolerance	*Arabidopsis*	Li et al., 2015
HD-Zip	*Zmhdz10*	Drought, salt Sensitivity to ABA	Rice (*Oryza sativa*)	Zhao et al., 2018
		Drought, salt	*Arabidopsis*	
	ZmHDZ4	Drought	Rice (*Oryza sativa*)	Wu et al., 2016
	Zmhdz12	Drought	*Arabidopsis*	Qing and Wei., 2018
NF-Y	*ZmNF-YB2*	Drought	Maize (*Zea mays*)	Nelson et al., 2007
	ZmNF-YB16	Drought, Dehydration	Maize (*Zea mays*)	Wang et al., 2018b

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