We are IntechOpen, the world’s leading publisher of Open Access books
Built by scientists, for scientists

6,600
Open access books available

177,000
International authors and editors

195M
Downloads

154
Countries delivered to

TOP 1%
Our authors are among the most cited scientists

12.2%
Contributors from top 500 universities

WEB OF SCIENCE™
Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com
Abiotic stress is the primary cause of crop loss worldwide, reducing average yields for most major crop plants by more than 50%. Plants as sessile organisms are constantly exposed to changes in environmental conditions. When these changes are rapid and extreme, plants generally perceive them as stresses. However, stresses are not necessarily a problem for plants because they have evolved effective mechanisms to avoid or reduce the possible damages.

The response to changes in environment can be rapid, depending on the type of stress and can involve either adaptation mechanisms, which allow them to survive the adverse conditions, or specific growth habitus to avoid stress conditions. In fact, plants can perceive abiotic stresses and elicit appropriate responses with altered metabolism, growth and development. The regulatory circuits include stress sensors, signalling pathways comprising a network of protein-protein interactions, transcription factors and promoters, and finally the output proteins or metabolites (table 1).

A number of abiotic stresses such as extreme temperatures, high light intensity, osmotic stresses, heavy metals and a number of herbicides and toxins lead to over production of reactive oxygen species (ROS) including $\text{H}_2\text{O}_2$ causing extensive cellular damage and inhibition of photosynthesis.

Normally, ROS are rapidly removed by antioxidative mechanisms, but this removal can be impaired by stresses themselves (Allan & Fluhr, 2007), causing a rise in their intracellular concentration and an increase of the damage. To prevent or repair these damages, plant cells use a complex defence system, involving a number of antioxidative stress-related defence genes that, in turn, induce changes in the biochemical plant machinery. Studies have shown that ROS probably require additional molecules to transduce and amplify defence signals. ROS production and anti-oxidant processes, all act in a synergistic, additive or antagonistic way, related to the control of oxidative stress.

Responses to stress are not linear pathways, but are complex integrated circuits involving multiple pathways and in specific cellular compartments, tissues, and the interaction of additional cofactors and/or signalling molecules to coordinate a specified response to a given stimulus (Dombrowski, 2009). Onset of a stress triggers some (mostly unknown) initial sensors, which then activate cytoplasmic $\text{Ca}^{2+}$ and protein signalling pathways, leading to stress-responsive gene expression and physiological changes (Bressan et al., 1998;
| Stress                     | Consequences                                                                 | Plant Responses                                                                 |
|---------------------------|------------------------------------------------------------------------------|------------------------------------------------------------------------------|
| Heat stress               | High temperature lead to high evaporation and water deficit. The consequent increased turnover of enzymes leads to plant death. | Efficient protein repair systems and general protein stability support survival, temperature can lead to acclimation. |
| Chilling and cold stress  | Biochemical reactions proceed at slower rate, photosynthesis proceeds, carbon dioxide fixation lags, leading to oxygen radical damage. Indeed, freezing lead to ice crystal formation that can disrupt cells membranes. | Cessation of growth in adaptable species may be overcome by changes in metabolism. Ice crystal formation can be prevent by osmolyte accumulation and synthesis of hydrophilic proteins. |
| Drought                   | Inability to water transport to leaves leads to photosynthesis declines. | Leaf rolling and other morphological adaptations. Stoma closure reduces evaporative transpiration induced by ABA. Accumulation of metabolites, consequently lower internal water potential and water attracting. |
| Flooding and submergence  | Generates anoxic or microaerobic conditions interfering with mitochondrial respiration. | Development of cavities mostly in the roots that facilitate the exchange of oxygen and ethylene between shoot and root (aerenchyma). |
| Heavy metal accumulation and metal stress | In excess, detoxification reactions may be insufficient or storage capacity may exceeded. | Excess of metal ions may be countered by export or vacuolar deposition but metal ions may also generate oxygen radicals. |
| High light stress         | Excess light can lead to increased production of highly reactive intermediates and by-products that can potentially cause photo-oxidative damage and inhibit photosynthesis. | Exposure of a plant to light exceeding what is utilized in photochemistry leads to inactivation of photosynthetic functions and the production of reactive oxygen species (ROS). The effects of these ROS can be the oxidation of lipids, proteins, and enzymes necessary for the proper functioning of the chloroplast and the cell as a whole. |

Table 1. Consequences of abiotic stress and plant responses

Xiong et al., 2002). Also, accumulation of abscisic acid (ABA) plays an important role in abiotic stress signalling and transduction pathways, mediating many responses (Wasilewska et al., 2008).

It is well known that abiotic stresses in general, through regulation of both gene expression and protein turnover, alter the abundance of many transcripts and proteins (Wong et al., 2006; Yan et al., 2006; Jiang et al., 2007), indicating that transcriptional and post-transcriptional regulation play an essential role in the adaptation of cellular functions to the environmental changes.

www.intechopen.com
Recent advances in molecular biology, genomics, proteomics and metabolomics have provided insight into plant gene regulatory network system, which is mainly composed of inducible-genes (environmental factors and developmental cues), expression programming and regulatory elements (cis-element and trans-element), corresponding biochemical pathways and diverse signal factors (Tang et al., 2003; Wang et al., 2003; Zhu, 2003; Munns, 2005). Genetic studies revealed that stress tolerance traits are mainly quantitative trait loci (QTLs), which make genetic selection of traits difficult.

Responses to abiotic stress require the production of important metabolic proteins such as those involved in synthesis of osmoprotectants and of regulatory proteins operating in the signal transduction pathways, such as kinases or transcriptional factors (TFs). In addition, new transcripts are made and within a few hours a steady level of stress adaptation has been reached. In general, the transcriptional regulation of genes is directly controlled by a network of TFs and transcription factor binding sites (TFBS) (Chaves & Oliveira, 2004). TFs are proteins with a DNA domain that binds to the cis-acting elements present in the promoter of a target gene. They induce (activators) or repress (repressors) the activity of the RNA polymerase, thus regulating gene expression. TFs can be grouped into families according to their DNA-binding domain (Riechmann et al., 2000). The presence or absence of transcription factors, activators and suppressors regulating transcription of target genes often involves a whole cascade of signalling events determined by tissue type, developmental stage or environmental condition (Wyrick & Young, 2002).

Environmental stress-inducible genes can be mainly divided into two groups in terms of their protein products: one type of genes, whose coding products directly confer to plant cells the resistance to environmental stress such as late embryogenesis abundant (LEA) protein, anti-freezing protein, osmotic regulatory protein, enzymes for synthesizing betaine, proline and other osmoregulators; the other groups of genes, whose coding products play an important role in regulating gene expression and signal transduction such as the transcriptional elements. At least four different regulons can be identified, two ABA independent (1 and 2) and two ABA dependent (3 and 4): (1) the CBF/DREB regulon; (2) the NAC (NAM, ATAF and CUC) and ZF-HD (zinc-finger homeodomain) regulon; (3) the AREB/ABF (ABA-responsive element-binding protein/ ABA-binding factor) regulon; and (4) the MYC (myelocytomatosis oncogene)/MYB (myeloblastosis oncogene) regulon.

Our knowledge of the molecular mechanisms underlying the responses of plants to such environmental stresses is still rather limited, but an increasing number of genes have been identified in recent years that mediate these responses. Some of these genes are induced by stress stimuli and encode products that confer tolerance to adverse conditions, whereas others encode upstream regulators that function within signalling pathways controlling the stress response.

The aim of this book chapter is to describe the regulation of gene expression under abiotic stresses and report recent advances in the stress-response mechanisms.

2. Abiotic stress-inducible genes

The complex plant response to abiotic stress involves many genes and biochemical-molecular mechanisms. The analyze of the functions of stress-inducible genes is an important tool not only to understand the molecular mechanisms of stress tolerance and the responses of higher plants, but also to improve the stress tolerance of crops by gene
manipulation. Hundreds of genes are thought to be involved in abiotic stress responses (Seki, 2003; Avni Öktem et al., 2008).

Many drought-inducible genes are also induced by salt stress and cold, which suggests the existence of similar mechanisms of stress responses.

These genes are classified into three major groups: (1) those that encode products that directly protect plant cells against stresses such as heat stress proteins (HSPs) or chaperones, LEA proteins, osmoprotectants, antifreeze proteins, detoxification enzymes and free-radical scavengers (Bray et al., 2000; Wang et al., 2000); (2) those that are involved in signalling cascades and in transcriptional control, such as Mitogen-activated protein kinase (MAPK), Calcium-dependent protein kinase (CDPK) (Ludwig et al., 2004) and SOS kinase (Zhu et al., 2001), phospholipases (Frank et al., 2000) and transcriptional factors (Cho et al., 2000; Shinozaki et al., 2000); (3) those that are involved in water and ion uptake and transport such as aquaporins and ion transporters (Blumwald et al., 2000).

3. Transcriptional factor genes involved in abiotic stress

Plant growth and productivity are under constant threat from environmental changes in the form of various stress factors. The most common abiotic stresses are drought, flooding or submergence, salinity, extreme temperatures (heat and freezing) and high light. Furthermore, the continued modification of the atmosphere by human activities lead to increase in the concentration of ozone in the troposphere and this can generate oxidative stress, which leads to the destruction of proteins and cells, premature ageing and reduced crop yields.

Tolerance or susceptibility to these abiotic stresses is a very complex phenomenon, both because stress may occur at multiple stages of plant development and more than one stress simultaneously affects the plant. Therefore, the perception of abiotic stresses and signal transduction to switch on adaptive responses are critical steps in determining the survival and reproduction of plants exposed to adverse environments (Chinnusamy et al., 2004).

During the past few years, transcriptome analysis has indicated that distinct environmental stresses induce similar responses. Overlap between stress responses can explain the phenomenon known as cross-tolerance, a capability to limit collateral damage inflicted by other stresses accompanying the primary stress.

Responses to abiotic stresses require the production of important metabolic proteins such as those involved in synthesis of osmoprotectants and regulatory proteins operating in signal transduction pathways, that are kinases or transcription factors (TFs). The regulation of these responses requires proteins operating in the signal transduction pathways, such as transcriptional factors, which regulate gene expression by binding to specific DNA sequences in the promoters of respective target genes. This type of transcriptional regulatory system is called regulon. At least four different regulons that are active in response to abiotic stresses have been identified. Dehydration-responsive element binding protein 1 (DREB1)/C-repeat binding factor (CBF) and DREB2 regulons function in abscisic acid (ABA)-independent gene expression, whereas the ABA-responsive element (ABRE) binding protein (AREB)/ABRE binding factor (ABF) regulon functions in ABA-dependent gene expression (Saibo et al., 2009). In addition to these major pathways, other regulons, including the NAC (or NAM, No Apical Meristem) and Myeloblastosis-Myelocytomatosis (MYB/MYC) regulons, are involved in abiotic stress-responsive gene expression (Fig. 1). Particularly, NAC- type TF OsNAC6 is induced by abiotic stresses, including cold, drought.
Fig. 1. Transcriptional network of abiotic stress responses.

and high salinity. Microarray analysis showed that many abiotic inducible genes were upregulated in rice plants over-expressing OsNAC6 (Nakashima et al., 2007). TFs are powerful targets for genetic engineering in abiotic stress resistance in crop plants and many studies have been done in the last two decades on this topic.

Transcription factors are shown in ovals. Transcription factor-modifying enzymes are shown in circles. The small triangles correspond to post-translational modifications. Green squares with question marks represent putative MYC ICE1-like transcription factors that may activate CBF1/DREB1B and CBF2/DREB1C. The green boxes represent the cis-elements present in stress-responsive genes. The red dot corresponds to the sumoylation modification by SIZ1 of the ICE1 transcription factor. The dashed black line from SIZ1 to HOS1 represents competition for binding places on the ICE1 transcription factor. SIZ1 blocks the access of HOS1 to the ubiquitination sites on the ICE1. CBF4/DREB1D is a DRE cis-element binding factor that is ABA dependent.

4. Drought stress transcriptional factors

The genome controls the regulation of the response to water deficit as well as the effectiveness of the response. Microarrays, largely performed using Arabidopsis thaliana as model plant, have been used to catalogue the many genes that are induced or repressed in
response to conditions that may lead to cellular water-deficit stress (Seki et al., 2002). These genes can be placed in at least four different functional groups: signal transduction, transcriptional regulation, cellular metabolism and transport and protection of cellular structures.

There are at least six different classes of TFs that participate in gene induction or repression in response to water deficit. Homeobox domain and NAC domain containing TFs are induced by multiple treatments that mimic water-deficit stress. Accumulation of proteins which have metabolic or structural functions promote adaptation to stress. One class of genes that could play a role in protection is called the late embryogenesis abundant (Lea) genes. The Lea genes are also developmentally programmed for expression in desiccating seeds. These genes encode small hydrophilic proteins that are predicted to protect proteins and membranes through chaperone-like functions. These proteins were thought to improve the performance of rice plants by protecting cell membranes from injury under abiotic stress (Chandra et al., 2004).

4.1 Gene regulation and transcriptional factors in water deficit
A recent review (Shinozaki & Yamaguchi-Shinozaki, 2007) on analysis of gene expression during drought stress response in plants show and summarize the functions of some genes in both stress response and tolerance. Microarray analysis performed on wheat genome, showed that among 300 unique single expressed sequences tag (ESTs), the 30% of genes were significantly up-regulated and the 18% were down-regulated under drought stress (Way et al., 2005).

Potential functions of approximately 130 genes of *A. thaliana* up-regulated in water-deficit was reported by Bray (2002). These genes are involved in cellular response to drought stress by signalling events, detoxification and other functions. cDNA microarray analysis on 7000 Arabidopsis full-length cDNAs clarify relationship between rehydration-, proline- and water-treatment inducible genes. Among the 152 rehydration-inducible genes, 58 genes contained in their promoter regions the ACTCAT sequence involved in proline- and hypoosmolarity- inducible gene expression, suggesting that this motif is a major cis-activing element involved in rehydration-inducible gene expression (Oono et al., 2003).

Moreover, microarray analysis performed on two moderately drought-tolerant native Andeon potato clones revealed that there was 1713 differentially expressed genes with 186 up-regulated involved in drought tolerance by inducing of osmotic adjustment, changes in carbohydrate metabolism, membrane modifications and cell rescue mechanisms, such as detoxification of oxygen radicals and protein stabilization (Schafleitner et al., 2007). These recent study underline how the expression of genes in response to water deficit is complex and can be regulated at the transcriptional, post-transcriptional and translational levels. Two major transcriptional regulatory pathways of gene expression play an important role in response to water-deficit stress: the ABA-independent pathway and ABA-dependent pathway. The first is controlled largely by a family of TFs called dehydration response element binding protein (DREB), which contains a DNA binding motif originally identified in a flower patterning protein called APETALA2 (AP2) (Fig. 2), while transcription factor families known to be as the most responsive to ABA signalling under drought are NAC, AREB/ABF, and MYB.
4.1.1 ABA-independent pathway

DREB are important TFs which induce a set of abiotic stress-related genes and confer stress resistance to plants. The DREB TFs could be divided into two groups: DREB1, involved in signal transduction pathways under low temperature; DREB2, involved in signal transduction pathways under dehydration. They belong to the ethylene responsive element binding factors (ERF) family of TFs. ERF proteins are a sub-family of the AP2/ethylene responsive element binding protein (EREBP) TFs that is distinctive to plants. ERF proteins share a conserved 58–59 amino acid domain (the ERF domain) that binds to *cis*-elements, the GCC box, found in many pathogens related (PR) gene promoters conferring ethylene responsiveness (Gu et al., 2000), and to the C-repeat CRT/dehydration responsive element (DRE) motif involved in the expression of cold and dehydration responsive genes (Agarwal et al., 2006).

The DREB proteins contain an ERF/AP2DNA-binding domain quite conserved: amino acid alignment shows high sequence similarity in the nuclear localization signal at the N-terminal region and some similarity in the C-terminal acidic domain (Agarwal et al., 2006). Indeed, TFs containing ERF/AP2DNA-binding domain are widely found in many
plants such as Arabidopsis (Okamuro et al., 1997), tomato (Zhou et al., 1997), tobacco (Ohme-Takagi & Shinshi, 1995), rice (Sasaki et al., 1994; Weigel, 1995) and maize (Moose & Sisco, 1996).

Another ABA-independent pathway was identified after the observation that Early Responsive to Dehydration Stress 1 (ERD1) gene transcripts accumulated before any increase of ABA in response to dehydration and high salinity (Nakashima et al., 1997). Promoter analysis of ERD1 revealed TFs belonging to the NAC family and zinc finger homeodomain (ZF-HD) as essential to the activation of the ERD1 gene (Tran et al., 2007). The increased drought tolerance may be due both to the reduced transpiration rate (increased stomatal closure) and to an increased ABA sensitivity.

Many genes (e.g. Aquaporin, ERD10, ERD13 and ERF) already described as being involved in plant response to water stress are down-regulated in drought stress (Cominelli et al., 2005). A member of the A. thaliana family of R2R3-MYB TFs, AtMYB61, is also specifically expressed in guard cells in a consistent manner, being involved in the regulation of stomatal aperture (Liang et al., 2005).

The strong induction of Stress Responsive –NAC1 (SNAC1) gene expression by drought in guard cells suggests an effect in stomatal closure (Hu et al., 2006). It has been reported that modulation of transcription plays an important role in controlling guard cell activity. Recently two MYB-type TFs were identified as regulators of stomatal movements.

### 4.1.2 ABA-dependent pathway

ABA-dependent gene induction during water deficit is controlled by at least five different classes of TFs. The ABA response element (ABRE) with the consensus ACGTGG/TC is bound by basic Leucine Zipper Domain (bZIP-type) TFs (Fig. 2). Three Arabidopsis bZIP TFs (AREB1/ABF2, AREB2/ABF4, and ABF3) are expressed in response to water-deficit stress and ABA treatment. Activation of the TFs requires ABA accumulation and the induction of an ABA-responsive protein kinase which activates the TF through phosphorylation.

Other TFs are also involved in ABA regulation of gene expression during cellular water deficit. Three genes encoding a class of TFs that is unique to plants, the NAC domain proteins ANAC019, ANAC055, and ANAC072 are induced by water deficit and ABA treatment. The NAC domain is a 60 bp DNA binding domain that is predicted to form a helix-turn-helix motif.

MYB, MYC and homeodomain TFs, and a family of transcriptional repressors (Cys2/His2-type zinc-finger proteins) are also involved in the ABA response to water deficit. Expression of the drought-inducible gene Responsive to Dehydration 22 (RD22) from Arabidopsis was found to be induced by ABA. The promoter region of RD22 contains MYC (CANNTG) and MYB (C/TAACNA/G) cis-element recognition sites. MYC and MYB TFs only accumulate after an increase of ABA concentration. Over-expression of these TFs result in enhanced sensitivity to ABA and drought tolerance (Abe et al., 2003).

### 5. Transcriptional factor involved in response to flooding stress

Flooding and submergence are two conditions that cannot be tolerated by most plants for periods of time longer than a few days. These stresses lead to anoxic conditions in the root system. At a critical oxygen pressure, mitochondrial respiration that provides the energy for growth in the photosynthetically inactive roots will decrease, then cease and the cells will die (Bray, 2004).
Recent reviews on gene expression analysis performed by microarray tools reported as the expression of several transcription factors, such as heat shock factors, ethylene response-binding proteins, MADS-box proteins, AP2 domain, leucine zipper, zinc finger and WRKY factors, increases in response to various regimes of oxygen deprivation in Arabidopsis and rice (Loreti et al., 2005; Lasanthi-Kudahettige et al., 2007).

Recently Licausi et al. (2010), using a qRT-PCR platform (Czechowski et al., 2002; Scheible et al., 2004; Morcuende et al., 2007; Osuna et al., 2007; Barrero et al., 2009), have identified TFs that are differentially expressed by hypoxic conditions. Among the TFs that have been characterized, members of the AP2/ERF-type family are the most commonly represented in the set of up-regulated TFs, followed by Zinc-finger and basic helix-loop-helix (bHLH-type) TFs, while TFs belonging to the bHLH family are the most commonly represented in the set of down-regulated TFs, together with members from the bZIP and MYB families.

*In silico* experiments and trans-activation assays shown that some TFs active in flooding stress are able to regulate the expression of hypoxia responsive genes. Particularly, five hypoxia-induced TFs (At4g29190; LBD41, At3g02550;HRE1, At1g72360; At1g69570; At5g66980) from different TF families [Zinc Finger, Ligand Binding Domain (LBD) or Lateral Organ Boundary Domain, ERF, DNA binding with one finger (DOF), ARF] showed this ability (Licausi et al., 2010).

Accumulation of ROS is a common consequence of biotic and abiotic stresses, including oxygen deprivation. There is evidence of redox-sensitive TFs, at least one of which might be involved in the adaptive response to low oxygen. ZAT12, a putative zinc finger-containing TF, is recognized as a component in the oxidative stress signalling network of Arabidopsis (Rizhsky et al., 2004), promotes expression of other TFs and the upregulation of cytosolic ascorbate peroxidase 1, a key enzyme in the removal of H$_2$O$_2$.

Advances have been made in molecular analyses of cDNAs and genes involved in the anaerobic response. Huq and Hodges (2000) reported early activation of a rice (*Oryza sativa* L.) gene by anoxia, the *aie* (anaerobically inducible early) gene. This gene encodes for a putative protein that shows short stretches of similarities to functionally interesting proteins (e.g. DNA binding proteins and nitric oxide synthase), indicating its putative involvement in signalling.

### 6. Salinity stress

High salinity is a critical environmental factor that inimically affects large areas of cultivated land. Plant growth, physiological and metabolic processes are affected, resulting in significant reductions in global crop productivity (Magomeet al., 2008; Zhang et al., 2009).

Exposure to high levels of NaCl not only affects plant water relations but also creates ionic stress in the form of cellular accumulation of Cl$^-$ and, in particular, Na$^+$ ions. Salt stress also changes the homeostasis of other ions such as Ca$^{2+}$, K$^+$, and NO$_3^-$.

Salt accumulation can modify plant cell plasma membrane lipid and protein composition, cause ion imbalance and hyperosmotic stress and eventually disturb normal growth and development (Fujii & Zhu 2009; López-Pérez et al., 2009). In general, high NaCl concentrations affect plant physiology and metabolism at different levels (water deficit, ion toxicity, nutrient imbalance, and oxidative stress; Vinocur & Altman, 2005), and at least two main responses can be expected: a rapid protective response together with a long term adaptation response. During initial exposure to salinity, plants experience water stress, which in turn reduces leaf expansion. During long-term exposure to
salinity, plants experience ionic stress, which can lead to premature senescence of adult leaves, and thus a reduction in the photosynthetic area available to support continued growth (Cramer & Nowak, 1992).

Salt tolerance determinants are categorized either as effectors that directly modulate stress etiology or attenuate stress effects, or as regulatory molecules that are involved in stress perception, signal transduction, or modulation of effector function. Genomics studies are focused on gene expression analysis following exposure of plants to high salinity, using salt shock experiments to mimic stresses that affect hydration and ion homeostasis.

The stress-responsive genes can be classified into two classes, i.e. early and delayed response genes (Sairam & Tyagi, 2004). The former are induced quickly and transiently, while the latter are activated more slowly and their expression is sustained. The early response genes encode transcription factors that activate downstream delayed response genes (Zhu, 2002).

When microarray expression profiles of wild type plants, a T-DNA insertion knockout mutant of AtNHX1 (nhx1), and a rescued line (NHX1::nhx1) exposed to both short (12 h and 48 h) and long (one and two weeks) durations of a non-lethal salt stress were investigated, 147 transcripts showed both salt responsiveness and a significant influence of AtNHX1. Fifty-seven of these genes showed differential regulation across all salt treatments, while the rest were regulated as a result of a particular duration.

A large number of genes from a variety of biochemical pathways participate in responses conferring salt tolerance. These pathways include notably those involved in: signal transduction; carbon metabolism and energy production; oxidative stress protection; uptake, exclusion, transport and compartmentalization of sodium ions; modifications of structural components of cell walls and membranes.

Several genes have been identified as functional components in the plant response to salt stress, including those encoding detoxifying enzymes like glutathione peroxidase (Roxas et al., 1997), Na+/H+ antiporter AtNHX1 (Apse et al., 1999), osmolytes such as glycine-betaine and LEA (late embryogenesis abundant protein) (Xu et al., 1996), flavoprotein AtHAL3 (Espinosa-Ruiz et al., 1999), signal mediator Ca2+/calmodulin-dependent protein phosphatase (Pardo et al., 1998) and transcription factor Alf1n1 (Bastola et al., 1998). Analyses of complete transcriptomes suggest that systems like synthesis of osmolytes and ion transporters and regulation of transcriptional and translational machineries have distinct roles in salt-stress response. In particular, induction of transcripts of specific TFs, RNA-binding proteins, ribosomal genes and translation initiation and elongation factors has been reported to be important during salt stress (Sahi et al., 2006).

Since not many stress-specific consensus sequences were identified in promoters of stress specific genes to activate or repress transcription, transcription factors must be located in the nucleus, bind DNA and interact with the basal transcription apparatus. Transcription factors involved in stress responses include DRE-related binding factors, leucine zipper DNA-binding proteins, putative zinc finger proteins, myb proteins, bZIP/HD-ZIPs, and AP2/EREBP (Chen et al., 2002; Seki et al., 2002), interact with promoters of osmotic-regulated genes (Abe et al., 1997; Liu et al., 1998; Hasegawa et al., 2000 a-b). Particularly, AP2/ERF domain proteins include the DREB or CBF proteins binding to dehydration response elements (DRE) or C-repeats. A major transcriptional regulatory system is represented by DRE/C-repeat promoter sequences in stress-activated genes and DREBs/CFB factors that control stress gene expression (Stockinger et al., 1997; Liu et al., 1998).
Several stress-inducible genes such as rd29A, Cor6.6, Cor15a and Kin1 are target genes of DREBs/CBFs in Arabidopsis and contain DRE/C-repeat sequences in their promoters. Moreover, basic region leucine zipper (bZIP) proteins contain a DNA binding domain rich in basic residues that bind to an ACGT core sequence. One bZIP subfamily has been linked genetically to an ABA response: AB15 and its homologs, the ABRE binding factors (ABFs/AREBs). ABRE binding factors (ABFs)/ABA-responsive element binding (AREBs) proteins respond at the transcriptional and post-transcriptional level to dehydration and salt stress (Choi et al., 2000; Uno et al., 2000).

Other regulatory intermediates that modulate plant salt stress responses include SOS3 (Ca$^{2+}$-binding protein), SOS2 (Suc non-fermenting-like) kinase, Ca$^{2+}$-dependent protein kinases, and mitogen-activated protein kinases (Halter et al., 2000). Genetic and physiological data indicate that SOS3, SOS2, and SOS1 are components of a signal pathway that regulates ion homeostasis and salt tolerance and their functions are Ca$^{2+}$-dependent. In particular, SOS1, encoding a plasma membrane Na$^+$/H$^+$ antiporter, plays a critical role in sodium extrusion and in controlling long-distance Na$^+$ transport from the root to shoot (Liu & Zhu, 1998). This antiporter forms one component in a mechanism based on sensing of the salt stress that involves an increase of cytosolic [Ca$^{2+}$] and reversible phosphorylation with SOS1 acting in concert with SOS2 and SOS3 (Shi et al., 2000). SOS2 encodes a Suc non-fermenting-like (SNF) kinase, and SOS3 encodes a Ca$^{2+}$-binding protein with sequence similarity to the regulatory subunit of calcineurin and neuronal Ca$^{2+}$ sensors (Liu & Zhu, 1998; Liu et al., 2000). In yeast, co-expression of SOS1, SOS2, and SOS3 increases the salt tolerance of transformed yeast cells much more than expression of one or two SOS proteins (Shi et al., 2000), suggesting that the full activity of SOS1 depends on the SOS2/SOS3 complex.

Several studies have shown that reactive oxygen species (ROS) and oxidative stress may be mediating at least some of the toxic effects of NaCl on legumes (Jungklang et al., 2004) and other vascular plants (Attia et al., 2008). ROS are predominantly generated in the chloroplast by direct transfer of excitation energy from chlorophyll to produce singlet oxygen, or by univalent oxygen reduction at photosystem I, in the Mehler reaction (Allen, 1995) and to some extent in mitochondria. ROS have the potential to interact non-specifically with many cellular components, triggering peroxidative reactions and causing significant damage to proteins, lipids, and nucleic acids. To cope with ROS and to maintain redox homeostasis, living organisms evolved antioxidant defense systems, comprised of enzymatic and non-enzymatic components, which normally maintain ROS balance within the cell. Major nonenzymatic antioxidants include ascorbate (vitamin C) and glutathione in plants, although tocopherol (vitamin E), flavonoids, alkaloids, and carotenoids can also act as antioxidants.

Intracellular ROS can also influence the ROS induced MAPK signal pathway through inhibition of phosphatases or downstream transcription factors (Mittler et al., 2004) (Fig. 3).

7. Chilling and cold stress: Gene regulation and transcriptional factor

Cold stress prevents the expression of full genetic potential of plants owing to its direct inhibition of metabolic reactions and, indirectly, through cold-induced osmotic (chilling-induced inhibition of water uptake and freezing-induced cellular dehydration), oxidative and other stresses. Cold stress, which includes chilling (<20°C) and/or freezing (<0°C) temperatures, adversely affects the growth and development of plants. Chilling and freezing
are stresses that show different effects on plants: the first leads to slow biochemical reactions, such as enzyme and membrane transport activities; the second leads to ice crystal formation that can cause the disruption of cell membrane system (Chinnusamy et al., 2007). A large number of studies have used a transcriptional profiling approach to identify genes in Arabidopsis that respond to cold (4°C) and chilling (13°C) temperatures. Results have shown that plants respond to low temperatures by altering mRNA levels of a large number of genes belonging to different and independent pathways. The quantitative and qualitative difference in transcriptional response to low temperature suggests the presence in higher plants of different molecular mechanisms to cold-stress response (Zhu & Provart, 2003). The cold induction of genes involved in calcium signalling, lipid signalling or encoding receptor-like protein kinases are also affected by the ice1 mutation (Lee et al., 2005). Controlled proteolysis of transcriptional regulators also plays an important role in shaping the cold-responsive transcriptome in plants.

TFs that bind to the DRE/CRT are named DREB1/CTR-binding factor (CBF) and DREB2. Cold stress induces the expression of AP_2/ERF family TFs, that is, CBFs, which can bind to cis-elements in the promoters of COR genes and activate their expression (Fig. 4). CBFs regulate the expression of genes involved in phosphoinositide metabolism, transcription, osmolyte biosynthesis, ROS detoxification, membrane transport, hormone metabolism and signalling and many others with known or presumed cellular protective functions (Fowler et al., 2002; Maruyama et al., 2004; Lee et al., 2005).

The first isolated cDNAs encoding DRE binding proteins were DREB1A and DREB2A (Liu et al., 1998) from Arabidopsis and then, DREB genes have been isolated from a wide variety of plants. In wheat and barley, a number of CBF homologs have been mapped to low temperature QTLs, Fr-2 chromosomal region (Skinner et al., 2005; Vágújfalvi et al., 2005; Miller et al., 2006). Thus, it is clear that the DREB1/CBF regulon is ubiquitous within higher plants. Expression of DREB1 genes was extensively investigated in various crops with regard to different abiotic stresses. It was found that the expression of AdDREB1 gene is induced by cold, but not by dehydration, or high salt stress (Liu et al., 1998; Shinwari et al., 1998). Similarly, CBF genes also showed high expression in response to low temperature treatment and its transcript was detectable after 30 min of exposure to 4°C, and showed maximum expression at 1 h (Medina et al., 1999). Indeed, CBF regulon could be sub-regulated by cold-responsive transcription factor genes RAP2.1 and RAP2.7 as shown by microarray analysis of transgenic Arabidopsis plants ectopically expressing CBFs (Fowler et al., 2002).
Fig. 4. Cold-responsive transcriptional network in Arabidopsis. CBFs regulate the expression of COR genes that confer cold tolerance. CBFs might cross-regulate each other’s transcription. CBFs induce the expression of ZAT10 which might downregulate the expression of COR genes. Constitutive expressed ICE1 is activated through sumoylation and phosphorylation induced by cold stress. ICE1 activated induce the transcription of CBFs and repress MYB15. The expression of CBFs is negatively regulated by MYB15 and ZAT12. HOS1 mediates the ubiquitination and proteolysis of ICE1, thus negatively regulates CBF regulons. Lines ending with bar indicate negative regulation; question mark (?) indicate unknown cis-elements; broken arrows indicate post-translational regulation; solid arrows indicate activation; lines ending with bar indicate negative regulation.

In Arabidopsis, ICE1 (Inducer of CBF Expression1), a MYC-type bHLH TF, can bind to MYC recognition elements in the CBF3 promoter and is important for the expression of CBF3 during cold acclimation. ICE1 is constitutively expressed and localized in the nucleus, but it induces expression of CBFs only under cold stress (Fig. 4). This suggests that cold stress-
induced post-translational modification is necessary for ICE1 to activate downstream genes in plants (Chinnusamy et al., 2003). Two important post-translational protein modifications are the ubiquitination and the sumoylation. Ubiquitination is mediated by High Expression of Osmotically Responsive1 (HOS1). For HOS1 encodes for a RING finger ubiquitin E3 ligase that physically interacts with ICE1 and mediates the ubiquitination of ICE1 to regulate negatively the expression of ICE1 target genes (Fig. 4) and is thus critical for the desensitization of plant cells to cold stress (Dong et al. 2006). Sumoylation is induced by SUMO (Small Ubiquitin-related Modifier) proteins that are conjugated to proteins substrates in a process dependent on SUMO E3 ligases. Sumoylation might protect target proteins from proteasomal degradation preventing the ubiquitination (Ulrich, 2005).

8. Heavy metal accumulation and metal stress

Uptake of excess metal ions is toxic to most plants. Phytotoxicity of heavy metals can be attributed to symplastic accumulation of heavy metals, particularly in the plasmatic compartments of the cells, such as the cytosol and chloroplast stroma (Brune et al., 1995). Metal-induced changes in development are the result of either a direct and immediate impairment of metabolism (Van Assche & Clijsters, 1990) or signalling processes that initiate adaptive or toxicity responses that need to be considered as active processes of the organism (Jonak et al., 2004). The detoxification of heavy metals by plants is achieved by uptake and translocation, sequestration into the vacuole and metabolization, including oxidation, reduction or hydrolysis and conjugation with glucose, glytanyl cysteine syntase (GSH) or amino acids (Salt et al., 1998; Meagher, 2000; Dietz & Schnoor, 2001).

So, in order to determine genes involved in response to heavy metal, recently, several studies, based on use of A. thaliana as model plant, performed the analysis of global gene expression after exposure to salts of lead (Pb) and cadmium (Cd). The analysis revealed 65 and 338 up- and down-regulated genes by Cd and 19 and 76 by Pb (Kovalchuk et al., 2005). Particularly, it was found that ABC transporters were differentially regulated after Cd treatments, suggesting for some plant ABC transponders a key role in glutathione-Cd or phytochelatins-Cd complex transport both into cellular compartments and outside of the cell (Bovet et al., 2005).

Subsequently studies performed on Arabidopsis, using microarray tools, demonstrated that exist a complex regulatory network which differentially modulates gene expression in a tissue-specific manner. Responses observed in roots included the induction of genes involved in sulphur assimilation-reduction and glutathione metabolism. Therefore, it was suggested that plants activate the sulphur assimilation pathway by increasing transcription of related genes to provide an enhanced supply of glutathione for phytochelatin biosynthesis (Fig. 5).

Non specific defense mechanisms include accumulation of osmolytes, antioxidants, aminoacids and changes in hormonal balances.

The significance of glutathione and the metal-induced phytochelatins (PCs) in heavy metal tolerance has been summarized intensely in excellent reviews (Rauser, 1995, 1999; Hall, 2002). Depletion of glutathione appears to be a major mechanism in short-term heavy metal toxicity and in accordance with this hypothesis, a good correlation between glutathione contents and tolerance index was observed with 10 pea genotypes differing in Cd sensitivity (Metwally et al., 2005).
In roots, after Cd exposure, three categories of genes were identified from transcriptome analysis: (1) common responses conserved across species; (2) metallophyte-specific responses representing candidate genes for Cd hypertolerance; (3) specific responses to Cd (Weber et al., 2006).

In leaves, instead, was reported an early induction of several genes encoding enzymes involved in the biosynthesis of phenylpropanoids (Herbette et al., 2006).

9. High light stress

Light plays a critical role in regulating plant growth and development through the modulation of expression levels of light-responsive genes that regulate developmental and metabolic processes. Light signals are perceived through at least four distinct families.
of photoreceptors, which include phytochromes (Phy), cryptochromes, phototropins and unidentified ultraviolet B (UVB) photoreceptor(s). For each developmental response, more than one photoreceptor can contribute to the perception of light signals, indicating that signal integration points for different light signals must exist in transcriptional hierarchies. Light can modulate photoreceptor activity by inducing changes that alter their cellular localization. The best characterized light receptor is Phy, which exists in two photochemically interconvertible forms, Pr and Pfr, and is encoded by a small family of genes in angiosperms. Phytochromes are synthesized in the inactive Pr form, that absorbs red light, (660 nm), and are activated on light absorption by conversion to the biologically active Pfr form, that absorbs far-red light (730 nm). The photoconversion of phytochromes results in their translocation from the cytoplasm into the nucleus, which is crucial for allowing them to interact with transducers in initiating downstream transcriptional cascades (Quail, 2002).

The responses of plants to light are complex: seed germination, seedlings photomorphogenesis, chloroplast development and orientation, photodinesis, stem growth, pigment biosynthesis, flowering and senescence (Kendrick & Kronenberg, 1994). Collectively these processes are known as photomorphogenesis. Besides excess light, a range of abiotic environmental conditions such as O₃, salt, toxic metals, and temperature can induce increased production of ROS by limiting the ability of a plant to utilize light energy through photosynthesis (Shinozaki & Yamaguchi-Shinozaki, 2000). Exposure of a plant to light exceeding what is utilized in photochemistry leads to inactivation of photosynthetic functions and the production of reactive oxygen species (ROS) such as hydrogen peroxide (H₂O₂), superoxide (O₂⁻), hydroxyl radicals, and singlet oxygen (¹O₂; Niyogi, 1999). Indeed, high light drove change in the redox potential of plastoquinone (PQ) regulating the expression of two cytosolic peroxidases during HL stress (Karpinski et al., 1999). Furthermore, the redox state of PQ has been shown to be involved in the expression of chloroplast encoded genes (Pfannschmidt et al., 1999).

Classical genetic and molecular approaches have identified various regulators downstream of photoreceptors. Many of these encode TFs, as well as kinases, phosphatases and degradation-pathway proteins. Although some of these regulators are specific for light quality, others regulate signal transduction networks in response to various light signals, representing potential signal integration points. Several basic post-translational mechanisms are involved in regulating TF activities and the subcellular localization in response to light. The phosphorylation of TFs is a common modification that can influence their ability to bind to promoters. For example, the level of G-Box Binding Factor 1 (GBF1) is constant, but its affinity for the G-box is modulated by its phosphorylation status: its phosphorylation by nuclear Casein Kinase II (CKII) enables G-box binding (Klimczak et al., 1995).

In the dark, some TFs that positively regulate gene expression in response to light, such as Long After Farred Light 1 (LAF1), are ubiquitylated by Constitutive Photomorphogenic 1 (COP1), a ring-finger-type ubiquitin E3 ligase. In darkness, COP1 acts as E3 ligase in the nucleus, targeting TFs like Long Hypocotyl5 (HY5) and LAF1 to degradation via the 26S proteasome. Upon exposure to light, COP1 migrates from the nucleus to the citosol. The study by Ulm and coworkers (2004) established that HY5, a bZIP transcription factor that is one of the key regulators of cryptochrome and phytochrome controlled photomorphogenesis, is an important component of the UVB-induced signalling network. UVB promotes rapid transcriptional activation of HY5 (and its interacting partner Long
Hypocotyl5-Like (HYH) independently of all known photoreceptors, and loss of HY5 results in the impairment of the transcriptional induction of a subset of UVB-responsive genes. Taken together, these observations demonstrate that UVB up-regulates HY5 transcription by yet-unknown signalling pathway(s), and that the signalling cascades that mediate responses to visible light and long-wavelength UVB (300–320 nm) use shared components. Additional studies suggested that HY5 also regulates the transcription of several photosynthesis-related genes, such as the ribulose bisphosphate carboxylase small subunit (RbcS1A) (Lee et al., 2007). Given that HY5 appears to regulate the expression of several Arabidopsis genes known to respond to abiotic stress conditions (e.g. CBF1, DREB2A, RD20 and MYB59) (Lee et al., 2007), it is inferred that HY5 could also be involved in the regulation of photosynthesis by adverse environmental conditions.

In vitro analysis showed that HY5 directly binds to the promoters of several light-inducible genes (Hiltbrunner et al., 2006) and a recent chromatin immuno-precipitation analysis in combination with a whole-genome tiling microarray revealed that HY5 binds directly to a large number of genomic sites, mainly at the promoter regions of annotated genes. HY5 interacts specifically with the G-box (CACGTG) and is required for normal control by light of promoters bearing this sequence (Lee et al., 2007).

Recently, some review showed as DNA cis-elements responsible for light regulated transcription are located within 5' upstream sequences. The evolution of regulatory sequences, which determine where, when, and the level at which genes are transcribed, has been largely neglected. In the case of the photosynthesis-associated nuclear genes (PhANGs) from higher plants, interesting evolutionary aspects of the molecular mechanisms by which transcription is activated by light receptors (e.g. phytochrome) could be addressed through the comparative analysis of promoter sequences. For instance, why does light profoundly affect transcription of PhANGs in monocotyledonous and dicotyledonous plants, while PhANG promoters in conifers, ferns, and mosses are either light insensitive or, at most, weakly photosensitive (Mukai et al., 1992).

Light-responsive Transcriptor Factors (TFs) have been identified through screens for light-responsive cis-element (LRE)-binding proteins and through genetic analyses of mutants that are deficient in their response to specific types of light. A combination of various methods has been used to identify these LREs. Such analyses have been successfully performed in identifying cis-acting elements involved in the light responsiveness of PhANGs, such as the G-box and I-box elements from rbcS genes (Giuliano et al., 1988) and the GATA motifs of Lhcb1 genes (Gidoni et al., 1989; Millar et., 1994).

Although many LREs and their binding proteins have been identified, no single element is found in all light-regulated promoters, suggesting a complex light-regulation network and a lack of a universal switch (Jiao et al., 2007). Sequence heterogeneity of regulatory elements may be functionally overcome if multiprotein regulatory complexes facilitate binding to imperfect target sites (Miner et. 1991). The individual elements found within a multipartite cis-regulatory region are termed phylogenetic footprints (PFs); they share high conservation over a segment of 6 contiguous base pairs in alignments of orthologous upstream sequences and represent potential binding sites for transcription factors (Gumucio et al., 1993).

The “phylogenetic-structural method” is based on the search of “homologous” (rather than “similar”) DNA sequences of a functionally characterized promoter. Two sequences are homologous when they share common ancestry, regardless of the degree of similarity between them (Doolittle et al., 1987).
10. References

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. Plant Cell, 9, 1859–1868

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. The Plant Cell, 15, 63–78

Agarwal P.K., Agarwal P., Reddy M.K. & Sopory S.K. (2006). Role of DREB transcription factors in abiotic and biotic stress tolerance in plants. Plant Cell Rep, 25, 1263–1274, DOI 10.1007/s00299-006-0204-8

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

Allen R. (1995). Dissection of oxidative stress tolerance using transgenic plants. Plant Physiol, 107, 1049–1054

Apse M.P., Aharon G.S., Sneddon W.A. & Blumwald E. (1999). Salt tolerance conferred by overexpression of a vacuolar Na+/H+ antiporter in Arabidopsis. Science, 285, 1256–1258

Attia H., Arnoud N., Karray N. & Lachaâl M. (2008). Long-term effects of mild salt stress on growth, ion accumulation and superoxide dismutase expression on Arabidopsis rosette leaves. Physiologia Plantarum, 132, 293–305

Avni Öktem H., Eyidoğan F., Selçuk F., Tufan Öz M., da Silva J.A.T. & Yücel M. (2008). Revealing Response of Plants to Biotic and Abiotic Stresses with Microarray Technology. Genes, Genomes and Genomics, pp 14-48

Barrero J.M., Millar A.A., Griffiths J., Czechowski T., Scheible W.R., Udvardi M., Reid J.B., Ross J.J., Jacobsen J.V. & Gubler F. (2009). Gene expression profiling identifies two regulatory genes controlling dormancy and ABA sensitivity in Arabidopsis seeds. Plant Journal, 61, 611–622

Bastola D.R., Pethe V.V. & Winicov I. (1998). A1fin1, a novel zincfnger protein in alfalfa roots that binds to promoter elements in the salt-inducible MsPRP2 gene. Plant Mol. Biol, 38,1123–1135

Blumwald E. (2000). Sodium transport and salt tolerance in plants. Curr Opin Cell Biol, 12, 431-4

Bovet L., Feller U. & Martinoia E. (2005). Possible involvement of plant ABC transporters in cadmium detoxification: a cDNA sub-microarray approach. Environment International, 31, 263–267

Bray E.A. (2002). Classification of genes differentially expressed during water- deficit stress in Arabidopsis thaliana: an analysis using microarray and differential expression data. Annals of Botany, 89, 803-811

Bray E.A. (2004). Genes commonly regulated by water-deficit stress in Arabidopsis thaliana. Journal of Experimental Botany, 55, 2331–2341

Bray E.A., Bailey-Serres J. & Weretilnyk E. (2000). Responses to abiotic stresses. In: Gruissem W, Buchanan B, Jones R (eds.) Biochemistry and molecular biology of plants. American Society of Plant Physiologists, Rockville, MD pp 1158-249

Bressan R.A., Hasegawa P.M. & Pardo M. (1998). Plants use calcium to resolve salt stress. Trends in Plant Science, 3, 411–412
Brune A., Urbach W. & Dietz K.J. (1995). Differential toxicity of heavy metals is partly related to a loss of preferential extraplasmic compartmentation: a comparison of Cd-, Mo-, Ni-, and Zn-stress. New Phytologist, 129, 404-409

Chandra Babu R., Jingxian Z., Blumc L. David Hod T-H., Wue R. & Nguyenf H.T. (2004) HVA1, a LEA gene from barley confers dehydration tolerance in transgenic rice (Oryza sativa L.) via cell membrane protection. Plant Science, 166, 855-862

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 W., Provart N.J., Glazebrook J., Katagiri F., Chang H.S., Mauch F., Luan S., Zou G., Whitham S.A., Budworth P.R., Tao Y., Xie Z., Chen X., Lam S., Kreps J.A., Harper J.F., Si-Ammour A., Mauch-Mani B., Heinlein M., Kobayashi K., Hohn T., Dangl J.L., Wang X. & Zhu T. (2002). Expression profile matrix of Arabidopsis transcription factor genes suggests their putative functions in response to environmental stresses. Plant Cell, 14,559–574

Chinnusamy V., Ohta M., Kanrar S., Lee B.-H., Hong X., Agarwal M., & Zhu J.-K. (2003). ICE1: a regulator of cold-induced transcriptome and freezing tolerance in Arabidopsis. Gene Deco, 17, 1043-1054

Chinnusamy V., Schumaker H. & Zhu J-K. (2004). The Arabidopsis LOS5/ABA3 Locus Encodes a Molybdenum Cofactor Sulfurase and Modulates Cold Stress- and Osmotic Stress-Responsive Gene Expression. J Exp Bot, 55 (395), 225-236

Chinnusamy V., Zhu J. & Zhu J-K. (2007). Cold stress regulation of gene expression in plants. TREND in Plant Science, 12 (10), Doi: 10.1016/j.tplants.2007.07.002

Choi H.I., Hong J.H., Ha J., Kang J.Y. & Kim S.Y. (2000). ABFs, a family of ABA-responsive element binding factors. J Biol Chem, 275, 1723-30.

Cominelli E., Galbiati M., Vavasseur A., Conti L., Sala T., Vuylstekte M., Leonhardt N., Dellaporta S.L. & Tonelli C. (2005). A guard-cell-specific MYB transcription factor regulates stomatal movements and plant drought tolerance. Current Biology, 15, 1196–1200. doi: 10.1093/jxb/erh005

Dietz A.C. & Schnoor J.L. (2001). Advances in phytoremediation. Environ Health Perspect, 109, 163–168

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

Dong C.H., Agarwal M., Zhang Y., Xie Q. & Zhu J.K. (2006). The negative regulator of plant cold responses, HOS1, is a RING E3 ligase that mediates the ubiquitination and degradation of ICE1. Proc Natl Acad Sci USA, 103, 8281-8286

Doolittle R.F. (1987). Of URFs and ORFs. A Primer on How to Analyze Derived Amino Acid Sequences. Mill Valley, CA: Univ. Sci. Books

Espinosa-Ruiz A., Belles J.M., Serrana R. & Culianez-Macla F.A. (1999). Arabidopsis thaliana AtHAL3: a flavoprotein related to salt and osmotic tolerance and plant growth. Plant J, 20, 529-539

Fowler S. & Thomashow M.F. (2002). Arabidopsis transcriptome profiling indicates that multiple regulatory pathways are activated during cold acclimation in addition to the CBF cold response pathway. Plant Cell, 14, 1675-1690
Frank W., Munnik T., Kerkmann K., Salamini F. & Bartels D. (2000). Water deficit triggers phospholipase D activity in the resurrection plant *Craterostigma plantagineum*. *Plant Cell*, 12, 111-24

Fujii H. & Zhu J-K. (2009). An autophosphorylation site of the protein kinase SOS2 is important for salt tolerance in Arabidopsis. *Mol. Plant*, 2, 183–190

Gidoni D., Brosio P., Bond-Nutter D., Bedbrook J. & Dunsmuir P. (1989). Novel cis acting elements in petunia Cab gene promoters. *Mol. Gen. Genet.*, 215, 337–44

Giuliano G., Pichersky E., Malik V.S., Timko M.P., Scolnik P.A. & Cashmore A.R. (1988). An evolutionarily conserved protein binding sequence upstream of a plant light-regulated gene. *Proc. Natl. Acad. Sci. USA*, 85, 7089–93

Gu Y.Q., Yang C., Thara V.K., Zhou J. & Martin G.B. (2000). *Pt4* is induced by ethylene and salicylic acid, and its product is phosphorylated by Pto kinase. *Plant Cell*, 12, 771–786

Gumucio D.L., Shelton D.A., Bailey W.J., Slightom J.L. & Goodman M. (1993). Phylogenetic footprinting reveals unexpected complexity in trans factor binding upstream from the b-globin gene. *Proc. Natl. Acad. Sci. USA*, 90, 6018–22

Halfter U., Ishitani M. & Zhu J-K. (2000). The Arabidopsis SOS2 protein kinase physically interacts with and is activated by the calcium-binding protein SOS3. *Proc Natl Acad Sci USA*, 97, 3735–3740

Hall J.L. (2002). Cellular mechanisms for heavy metal detoxification and tolerance. *Journal of Experimental Botany*, 53, 1–11

Hasegawa P.M., Bressan R.A. & Pardo J.M. (2000a). The dawn of plant salt tolerance genetics. *Trends Plant Sci.*, 5, 317–319

Hasegawa P.M., Bressan R.A., Zhu J-K. & Bohnert H.J. (2000b). Plant cellular and molecular responses to high salinity. *Annu Rev Plant Physiol Plant Mol Biol*, 51, 463–499

Herbette S., Toconnat L., Hugouvieux V., Piette L., Magniette M.L.M., Cuine S., Auroy P., Richaud P., Forestier C., Bourguignon J., Renou J.P., Vavasseur A. & Leonhardt N. (2006). Genome-wide transcriptome profiling of the early cadmium response of Arabidopsis roots and shoots. *Biochimie*, 88, 1751-1765

Hiltbrunner A., Tscheuschler A., Viczi´an A. et al. (2006). FHY1 and FHL act together to mediate nuclear accumulation of the phytochrome A photoreceptor. *Plant Cell Physiol*, 47, 1023–34

Hu H., Dai M., Yao J., Xiao B., Li X., Zhang Q. & Xiong L. (2006). Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. *Proceedings of the National Academy of Sciences USA*, 103, 12987–12992

Huq E. & Hodges T.K. (2000). An anaerobically inducible early (aie) gene family from rice. *Plant Molecular Biology*, 40, 591-601

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

Jiao Y., Lau O.S. & Wang D.X. (2007). Light-regulated transcriptional networks in higher plants. *Nature Reviews Genetics*, 8, 217

Jonak C., Nakagami H. & Hirt H. (2004). Heavy metal stress. Activation of distinct mitogen-activated protein kinase pathways by copper and cadmium. *Plant Physiology*, 136, 3276–3283.
Jungklang J., Sunohara Y. & Matsumoto H. (2004). Antioxidative enzymes response to NaCl stress in salt-tolerant Sesbania rostrata. *Weed Biology and Management*, 4, 81-85

Karpinski S., Reynolds H., Karpinska B., Wingsle G., Creissen G. & Mullineaux P. (1999). Systemic signaling and acclimation in response to excess excitation energy in Arabidopsis. *Science*, 284, 654-657

Kendrick R.E. & Kronenberg G.H.M., eds. (1994). Photomorphogenesis in Plants. Dordrecht: Kluwer. 2nd ed

Klimczak L.J., Colline M.A., Farini D. et al. (1995). Reconstitution of Arabidopsis casein kinase II from recombinant subunits and phosphorylation of transcription factor GFB1. *Plant Cell*, 7, 105-115

Kovalchuk I., Titov V., Hohn B. & Kovalchuka O. (2005). Transcriptome profiling reveals similarities and differences in plant responses to cadmium and lead. *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis*, 570 (2), 149-161

Lasanthi-Kudahettige R., Magneschi L., Loreti E., Gonzali S., Licausi F., Novi G., Beretta O., Vitulli F., Alpi A. & Perata P. (2007). Transcript profiling of the anoxic rice coleoptile. *Plant Physiology*, 144, 218–231

Lee B-H., Henderson D.A. & Zhu J-K. (2005). The Arabidopsis cold-responsive transcriptome and its regulation by ICE1. *Plant Cell*, 17, 3155-3175

Lee J., He K., Stolc V., Lee H., Figueroa P., Gao Y., Tongprasit W., Zhao H., Lee I. & Deng X.W. (2007). Analysis of transcription factor HY5 genomic binding sites revealed its hierarchical role in light regulation of development. *The Plant Cell*, 19, 731–749

Liang Y.K., Dubos C., Dodd I.C., Holroyd G.H., Hetherington A.M. & Campbell M.M. (2005). AtMYB61, an R2R3-MYB transcription factor controlling stomatal apertute in *Arabidopsis thaliana*. *Current Biology*, 15, 1201–1206

Licausi F., Daan A., Weits D.A., Scheible W.R., Geigenberger P. & van Dongen J.T. (2010). Hypoxia responsive gene expression is mediated by various subsets of transcription factors and miRNAs that are determined by the actual oxygen availability. *New Phytologist*, doi: 10.1111/j.1469-8137.2010.03451.x

Liu J., Ishitani M., Halfter U., Kim C-S. & Zhu J-K. (2000). The *Arabidopsis thaliana* SOS2 gene encodes a protein kinase that is required for salt tolerance. *Proc Natl Acad Sci USA*, 79, 3730-3734

Liu J. & Zhu J-K. (1998). A calcium sensor homolog required for plant salt tolerance. *Science*, 280, 1943–1945

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

Loreti E., Poggio A., Novi G., Alpi A. & Perata P. (2005). A genome-wide analysis of the effects of sucrose on gene expression in Arabidopsis seedlings under anoxia. *Plant Physiology*, 137, 1130–1138

Ludwig A., Romeis T. & Jones J.D. (2004). CDPK mediated signalling pathways: specificity and cross-talk. *Journal of Experimental Botany*, 55,181-188
López-Pérez L. et al. (2009). Changes in plasma membrane lipids, aquaporins and proton pump of broccoli roots, as an adaptation mechanism to salinity. *Phytochemistry*, 70, 492–500

Magome H., Yamaguchi S., Hanada A., Kамиya Y. & Oda K. (2008). The DDF1 transcriptional activator upregulates expression of a gibberellin-deactivating gene, GA2ox7, under high-salinity stress in Arabidopsis. *Plant J.*, 56, 613–626

Maruyama K., Sakuma Y., Kasuga M., Yto Y., Seki M., Godi H., Shimado Y., Yoshida S., Shinozaki K. & Yamaguchi-Shinozaki K. (2004). Identification of cold-inducible downstream genes of the Arabidopsis DREB1A/CFB3 transcriptional factor using two microarray systems. *Plant J.*, 38, 982-993

Meagher R.B. (2000). Phytoremediation of toxic elemental and organic pollutants. *Curr Opin Plant Biol.*, 3, 153–162

Medina J., Bargues M., Terol J. Perez-Alonso M. & Salinas J. (1999). The Arabidopsis CBF gene family is composed of three genes encoding AP2 domain-containing proteins whose expression is regulated by low temperature but not by abscisic acid or dehydration. *Plant Physiol.*, 119, 463-469

Metwally A., Safronova V.I., Belimov A.A. & Dietz K.J. (2005). Genotypic variation of the response to cadmium toxicity in *Pisum sativum*. *Journal of Experimental Botany*, 56, 167–178

Millar A.J., McGrath B. & Chua N-H. (1994). Phytochrome phototransduction pathways. *Annu. Rev. Genet.*, 28, 325–49

Miner J.N. & Yamamoto K.R. (1991). Regulatory crosstalk at composite response elements. *Trends Biochem. Sci.*, 16, 423–26

Mittler R. (2006). Abiotic stress, the field environment and stress combination. *Trends in Plant Science*, 11(1), 15-19

Mittler R., Vanderauwera S., Gollery M. & Breusegem F.V. (2004). Reactive oxygen gene network of plants. *Trends Plant Sci.*, 9, 490–498

Moose S.P. & Sisco P.H. (1996). *Glossy15*, an APETAL2-like gene from maize that regulates leaf epidermal cell identity. *Genes Dev.*, 10, 3018–3027

Morcuende R., Bari R., Gibon Y., Blasing O., Usadel B., Czechowski T., Udvardi M.K., Stitt M. & Scheible W.R. (2007). Genome-wide reprogramming of metabolism and regulatory networks of Arabidopsis in response to phosphorus. *Plant, Cell & Environment*, 30, 85–112

Mukai Y., Tazaki K., Fujii T. & Yamamoto N. (1992). Light-independence expression of three photosynthetic genes, cab, rbcS, and rbcL, in coniferous plants. *Plant Cell Physiol.*, 33, 859–66

Munns R (2005). Genes and salt tolerance: bringing them together. *New Phytologist*, 167, 645-663

Nakashima K., Kiyosue T., Yamaguchi-Shinozaki K. & Shinozaki K. (1997). A nuclear gene, *emd1*, encoding a chloroplast-targeted Clp protease regulatory subunit homolog is not only induced by water stress but also developmentally up-regulated during senescence in *Arabidopsis thaliana*. *The Plant Journal*, 12, 851–861

Nakashima K., Tran L.S.P., Van Nguyen D., Fujita M., Maruyama K., Todaka D., Ito Y., Hayashi N., Shinozaki K. & Yahaguchi-Shinozaki K. (2007). Functional analysis of NAC-type transcription factor OsNAC6 involved in abiotic and biotic stress-responsive gene expression in rice. *The Plant Journal*, 51, 617-630
Niyogi K.K. (1999). Photoprotection revisited: genetic and molecular approaches. *Annu Rev Plant Physiol Plant Mol Biol*, 50, 333–359

Ohme-Takagi M. & Shinshi H. (1995). Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element. *Plant Cell*, 7, 173–182

Okamuro J.K., Caster B., Villarroel R., Van Mantagu M. & Jofuku K. D. (1997). The AP2 domain of APETELA2 defines a large new family of DNA binding proteins in *Arabidopsis*. *Proc Natl Acad Sci USA*, 94, 7076-7081

Oono Y., Seki M., Nanjo T., Narusaka M., Fujita M., Satoh R., Satou M., Sakurai T., Ishida J., Akiyama K., Iida K., Maruyama K., Satoh S., Yamaguchi-Shinozaki K. & Shinozaki K. (2003). Monitoring expression profiles of Arabidopsis gene expression during rehydration process after dehydration using ca. 7000 full-length cDNA microarray. *The Plant Journal*, 34, 868-887

Osuna D., Usadel B., Morcuende R. et al. (2007). Temporal responses of transcripts, enzyme activities and metabolites after adding sucrose to carbon-deprived Arabidopsis seedlings. *Plant Journal*, 49, 463–491

Pardo J.M., Reddy M.P., Yang S. et al. (1998). Stress signaling through Ca2+/calmodulin-dependent protein phosphatase calcineurin mediates salt adaptation in plants. *Proc. Natl. Acad. Sci.*, 95, 9681–9686

Pfannschmidt T., Nilsson A. & Allen J.F. (1999). Photosynthetic control of chloroplast gene expression. *Nature*, 397, 625–628

Quail P.H. (2002). Phytochrome photosensory signalling networks. *Nature Rev Mol Cell Biol*, 3, 85–93

Rauser W.E. (1995). Phytochelatins and related peptides. Structure, biosynthesis, and function. *Plant Physiology*, 110, 1141–1149

Rauser W.E. (1999). Structure and function of metal chelators produced by plants. *Cell Biochemistry and Biophysics*, 31, 19–48

Riechmann J.L., Heard J. & Martin G. (2000). Arabidopsis transcription factors: genome-wide comparative analysis among eukaryotes. *Science*, 290 (5499), 2105-2110

Rizhsky L., Davletova S., Liang H. & Mittler R. (2004). The zinc finger protein Zat12 is required for cytosolic ascorbate peroxidase 1 expression during oxidative stress in Arabidopsis. *Journal of Biological Chemistry*, 279, 11736–11743

Roxas V.P., Smith R.K., Allen E.R., Allen Jr. & R.D. (1997). Overexpression of glutathione S-transferase/glutathione peroxidase enhances the growth of transgenic tobacco seedlings during stress. *Nat. Biotechnol.*, 15, 988–991

Rushton P.J. & Somssich I.E. (1998). Transcriptional control of plant genes responsive to pathogens. *Curr Opin Plant Biol*, 1, 311-315

Sahi C., Singh A., Blumwald E. & Grover A. (2006). Beyond osmolytes and transporters: novel plant salt-stress tolerance-related genes from transcriptional profiling data. *Physiologia Plantarum*, 127, 1-9

Saibo N.J.M., Lourenco T. & Oliveira M.M. (2008). Transcription factors and regulation of photosynthetic and related metabolism under environmental stresses. *Annals of Botany*, 103, 609–623

Sairam R. K. & Tyagi A. (2004). Physiological and molecular biology of salinity stress tolerance in plants. *Curr. Sci.*, 86, 407–420

Salt D.E., Smith R.D. & Raskin I. (1998). Phytoremediation. *Annu Rev Plant Physiol Plant Mol Biol*, 49, 643–668
Abiotic Stress in Plants – Mechanisms and Adaptations

Sasaki T., Song J., Koga-Ban Y. et al. (1994). Toward cataloguing all rice genes: large scale sequencing of randomly chosen rice cDNAs from a callus cDNA library. *Plant J.*, 6, 615–624

Schafleitner R., Rosales R.O.G., Gaudin A., Aliaga C.A.A., Martinez G.N., Marca L.R.T., Bolivar L.A., Delgado F.M., Simon R. & Bonierbale M. (2007). Capturing candidate drought tolerance traits in two native Andean potato clones by transcription profiling of field grown plants under water stress. *Plant Physiology and Biochemistry*, 45, 673–690

Scheible W.R., Morcuende R., Czechowski T. et al. (2004). Genome-wide reprogramming of primary and secondary metabolism, protein synthesis, cellular growth processes, and the regulatory infrastructure of Arabidopsis in response to nitrogen. *Plant Physiology*, 136, 2483–2499

Seki M., Kamei A., Yamaguchi-Shinozaki K. & Shinozaki K. (2003). Molecular responses to drought, salinity and frost: common and different paths for plant protection. *Current Opinion in Biotechnology*, 14, 194-199

Seki M., Narusaka M., Ishida J., Nanjo T., Fujita M., Oono Y., Kamiya A., Nakajima M., Enju A., Sakurai T., Satou M., Akiyama K., Taji T., Yamaguchi-Shinozaki K., Carninci P., Kawai J., Hayashizaki Y. & Shinozaki K. (2002). Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. *Plant J.*, 31, 279–292

Shi H., Ishitani M., Kim C. & Zhu J-K. (2000). The Arabidopsis thaliana salt tolerance gene SOS1 encodes a putative Na+/H+ antiporter. *Proc Natl Acad Sci USA*, 97, 6896–6901

Shinozaki K. & Yamaguchi-Shinozaki K. (2000). Molecular responses to dehydration and low temperature: differences and cross-talk between two stress signalling pathways. *Curr Opin Plant Biol.*, 3, 217-223

Shinozaki K. & Yamaguchi-Shinozaki K. (2007). Gene networks involved in drought stress response tolerance. *Journal of Experimental Botany*, 58, 221-227

Shinozaki K. & Yamaguchi-Shinozaki K. (2000). Molecular responses to dehydration and low temperature: differences and cross-talk between two stress signaling pathways. *Curr Opin Plant Biol.*, 3, 217–223

Shinwari Z.K., Nakashima K., Miura S. et al. (1998). An Arabidopsis gene family encoding DRE/CRT binding proteins involved in low-temperature-responsive gene expression. *Biochem Biophys Res Commun*, 250, 161-170

Skinner J.S., Zitzewitz J., Szücs P. et al. (2005). Structural, functional, and phylogenetic characterization of a large CBF gene family in barley. *Plant Mol Biol*, 59, 533-551

Stockinger E. J., Gilmour S. J., & Thomashow M. F. (1997). *Arabidopsis thaliana* CBF1 encodes an AP2 domain-containing transcriptional activator that binds to the C-repeat/DRE, a cis-acting DNA regulatory element that stimulates transcription in response to low temperature and water deficit. *Proc. Natl. Acad. Sci. USA*, 94, 1035-1040

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

Tran L.S., Nakashima K., Sakuma Y. et al. (2007). Co-expression of the stress-inducible zinc finger homeodomain ZFHD1 and NAC transcription factors enhances expression of the ERD1 gene in Arabidopsis. *The Plant Journal*, 49, 46–63
Ulm R., Baumann A., Oravecz A. et al. (2004). Genome-wide analysis of gene expression reveals function of the bZIP transcription factor HY5 in the UV-B response of Arabidopsis. *Proc Natl Acad Sci USA*, 101, 1397-1402

Ulrich H.D. (2005). Mutual interactions between the SUMO and ubiquitin systems: A plea of no contest. *Trends Cell Biol*, 15, 525-532

Uno Y., Furuhata T., Abe H., Yoshida R., Shinozaki K. & Yamaguchi- Shinozaki K. (2000). Arabidopsis basic leucine zipper transcription factors involved in an abscisic acid-dependent signal transduction pathway under drought and high-salinity conditions. *Proc. Natl. Acad. Sci. USA*, 97, 11632-11637

Vágúifalvi A., Aprile A., Miller A. et al. (2005). The expression of several Chf genes at the Fr-A2 locus is linked to frost resistance in wheat. *Mol Genet Genomics*, 274, 506-514

Van Assche F. & Clijsters H. (1990). Effects of metals on enzyme activity in plants. *Plant, Cell and Environment*, 13, 195–206

Vinocur B. & Altman A. (2005). Recent advances in engineering plant tolerance to abiotic stress: achievements and limitations. *Curr Opin Biotech.*, 16, 123-122

Wang W.X., Barak T., Vinocur B., Shoseyov O. & Altman A. (2003). Abiotic resistance and chaperones: possible physiological role of SPI, a stable and stabilizing protein from Populus. In: Vasil IK (ed.) Plant biotechnology 2000. Kluwer, Dordrecht, pp 439-453

Wang W.X., Vinocur B. & Altman A. (2003). Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. *Planta*, 218, 1-14

Wasilewska A., Vlad F., Sirichandra C. et al. (2008). An update on abscisic acid signaling in plants and more. *Molecular Plant*, 1, 198–217

Way H., Chapman S., McIntyre L., Casu R., Xue G.P., Manners J. & Shorter R. (2005). Identification of differentially expressed genes in wheat undergoing gradual water deficit stress using a subtractive hybridisation approach. *Plant Science*, 168, 661-670

Weber M., Trampczynska A. & Clemens S. (2006). Comparative transcriptome analysis of toxic metal responses in Arabidopsis thaliana and the Cd^{2+} -hypertolerant facultative metallophyte Arabidopsis halleri. *Plant Cell and Environment*, 29, 950-963

Weigel D. (1995). The APETELA2 domain is related to a novel type of DNA binding domain. *Plant Cell*, 7, 388-389

Wong C.E., Li Y., Labbe A. et al. (2006). Transcriptional profiling implicates novel interactions between abiotic stress and hormonal responses in Thellungiella, a close relative of Arabidopsis. *Plant Physiology*, 140, 1437–1450

Wyrick J.J. & Young R.A. (2002). Deciphering gene expression regulatory network. *Current Opinion in Genetic and Development*, 12, 130–136

Xu D., Duan X., Wang B., Hong B., Ho T.D.D. & Wu R. (1996). Expression of a late embryogenesis abundant protein gene, HVA1, from barley confers tolerance to water deficit and salt stress in transgenic rice. *Plant Physiol.*, 110, 249-257

Yan S.P., Zhang Q.Y., Tang Z.C., Su W.A. & Sun W.N. (2006). Comparative proteomic analysis provides new insights into chilling stress responses in rice. *Molecular and Cellular Proteomics*, 5, 484–496

Zhang L. et al. (2009). Identification of an apoplastic protein involved in the initial phase of salt stress response in rice root by twodimensional electrophoresis. *Plant Physiol.*, 149, 916–928

www.intechopen.com
Zhou J.M., Tang X. & Martin G.B. (1997). The Pto kinase conferring resistance to tomato bacterial speck disease interacts with proteins that bind a cis-element of pathogenesis-related genes. *EMBO J*, 16, 3207–3218

Zhu J.K. (2001). Cell signaling under salt, water and cold stresses. *Curr Opin Plant Biol.*, 4, 401-406

Zhu J.K. (2001). Plant salt tolerance. *Trends Plant Sci.*, 6, 66–67

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

Zhu J.K. (2003). Regulation of ion homeostasis under salt stress. *Current Opinion in Plant Biology*, 6(5), 441-445

Zhu T. & Provart N.J. (2003). Transcriptional responses to low temperature and their regulation in Arabidopsis. *Canadian Journal of Botany- Revue Canadienne de Botanique*, 81, 1168-1174
World population is growing at an alarming rate and is anticipated to reach about six billion by the end of year 2050. On the other hand, agricultural productivity is not increasing at a required rate to keep up with the food demand. The reasons for this are water shortages, depleting soil fertility and mainly various abiotic stresses. The fast pace at which developments and novel findings that are recently taking place in the cutting edge areas of molecular biology and basic genetics, have reinforced and augmented the efficiency of science outputs in dealing with plant abiotic stresses. In depth understanding of the stresses and their effects on plants is of paramount importance to evolve effective strategies to counter them. This book is broadly dived into sections on the stresses, their mechanisms and tolerance, genetics and adaptation, and focuses on the mechanic aspects in addition to touching some adaptation features. The chief objective of the book hence is to deliver state of the art information for comprehending the nature of abiotic stress in plants. We attempted here to present a judicious mixture of outlooks in order to interest workers in all areas of plant sciences.

How to reference
In order to correctly reference this scholarly work, feel free to copy and paste the following:

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