

# Molecular Responses of Plant Due to Stress Induced by Salt <sup>†</sup>

Shilpi Mishra <sup>1,\*</sup>, Sunil K. Raman <sup>2</sup>, Devendra Kumar Mishra <sup>1</sup> and Areesh Zehra <sup>1</sup>

<sup>1</sup> Ambekeshwar Institute of Pharmaceutical Sciences, Lucknow, Uttar Pradesh 226201, India; mishra.shilpi2014@gmail.com; devendra4747@gmail.com; areeshzehra3@gmail.com

<sup>2</sup> CSIR—Central Drug Research Institute, Lucknow, Uttar Pradesh 226031, India; sunil.pharma88@gmail.com

\* Correspondence: mishra.shilpi2014@gmail.com; Tel.: +91-8544733737

† Presented at the 2nd International Electronic Conferences on Plant Sciences—10th Anniversary of Journal Plants, 1-15 December 2021; Available online: <https://iecps2021.sciforum.net/>.

**Abstract:** Numerous changes in environmental conditions are becoming the main cause of plant stress in the current scenario. Abiotic stress is the most concerning among those as it may affect the efficiency of crops, decrease the plant yield, deteriorate the quality of the crop, its vigour and might affect plant germination too. The regulation of these effects comprises transcriptional factors, that control expression of a gene by requisite to an explicit supporter of DNA sequences. The responses due to stress-induced by salt involves transcription factors viz. AP2/EREBP, bZIP/HDZIPs, myb proteins, putative zinc finger proteins, leucine zipper DNA binding proteins and DRE-associated binding aspects. Principally, AP2/ERF domain proteins consist of DREB or CBF proteins binding to C-repeats or dehydration response elements (DRE). These transcription factors are prevailing to aim for the genetic resistance towards abiotic stress in crops.

**Keywords:** transcriptional factors; gene activation; AP2/ERF domain proteins; salt stress

**Citation:** Mishra, S.; Raman, S.K.; Mishra, D.K.; Zehra, A. Molecular Responses of Plant Due to Stress Induced by Salt. *Biol. Life Sci. Forum* **2021**, *1*, x. <https://doi.org/10.3390/xxxxx>

Academic Editor: Iker Aranjuelo

Published: 2 December 2021

**Publisher's Note:** MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



**Copyright:** © 2021 by the authors. Submitted for possible open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

## 1. Introduction

Abiotic stresses include environmental conditions which are outside the normal range and may affect the normal functionality of plants. There are particular environmental conditions which alter specific mechanism in plants [1]. Some of the examples could be cited like, it has been reported that the reproductive development of plants is hindered by low temperatures, severe dehydration and osmotic imbalance in cells occurs by extreme cold stress and this osmotic imbalance results in interruption of homeostasis etc.

The changes in plant, whether physiological or biochemical, are concerned with the altered gene expressions [2]. Whenever stress conditions occur, its onset triggers some unknown sensory signals initially which may activate certain signaling pathways like Ca<sup>2+</sup> and protein signaling pathways. This activation of signaling pathways lead to many physiological changes and gene expressions in response to salinity stress [3]. As per the reports, abiotic stress conditions modify the richness of many transcripts and proteins by regulating gene expressions and protein turnover. This alteration indicates that post transcriptional regulation and also transcriptions signifies a vital role in cell functioning against the ecological changes [4].

## 2. Abiotic Stress Responses and Transcription Factors

Salt stress affects the growth of plants or crops by inhibiting or disturbing the uptake of nitrogen. As the concentration of ions increases, it becomes toxic for plants and may also lead to plant death. Salinity deteriorates the growth of plants due to excessive uptake of ions or due to nutritional imbalance [5].

Metabolic proteins such as TFs or Kinases are produced in response to certain abiotic stress. However, most of the abiotic responses regulate the gene expressions. TF proteins are basically of DNA domain therefore these, either induce or repress the RNA

polymerase which in turn regulates gene expression [6]. Abiotic stress with regard to Plant responses can be identified by various group of genes regulated by the TF regulatory molecule or by regulons. These regulons are: AP2/EREBP, bZIP/HDZIPs, myb proteins, leucine zipper DNA binding proteins and DRE-associated binding aspects. Principally, AP2/ERF domain proteins consist of DREB or CBF proteins or DRE [7].

### 3. Salt Stress

Environmental stresses like high salinity, drought etc. are responsible for the signaling of ROS namely H<sub>2</sub>O<sub>2</sub> etc. which are produced in the apoplast, peroxisomes, chloroplast and mitochondria. ROS production is mediated by respiratory burst oxidase homologs, which are localized by plasma membrane, *AtRbohD* and *AtRbohF* respectively. These are upregulated under salt stress showing hypersensitivity to the same. The Na<sup>+</sup>/K<sup>+</sup> ratios are reduced as both these ROS genes promote the movement of K<sup>+</sup> into the cytosol. Na<sup>+</sup> is also restricted to enter the xylem sap, thus transpiration occurs and reduces the Na<sup>+</sup> transport from roots to shoots. The mechanism helps in triggering the environmental stimuli at the initial stage of salt stress and helps in reduced oxidative damage to cells [8].

### 4. Genetic Resistance Towards Abiotic Stress

The transcription factors are prevailing to aim for the genetic resistance towards abiotic stress in plants and crops. Here, we are going to discuss those various transcription factors.

#### 4.1. AP2/EREBP

The AP2/EREBP family which is a stress responsive gene and is often used to manipulate plant response in a level greater than other. Abiotic stress related transcription factors confer stress tolerance and improve photosynthesis in different plants. Some of which are cited as follows: The AP2/EREBP TF family in tobacco, lowers the loss of chlorophyll contents if high salt stress tolerance occurs. In Tomato, chilling stress tolerance is overcome as it improves maximum quantum efficiency of PSII/chlorophyll accumulation. The drought tolerance and recovery in case of *Arabidopsis* results in reduced transpiration probably. In case of rice if the stress tolerance of drought, high salt, low temperature is observed, it improves the PSII efficiency, reduces the stomatal conductance or improved photosynthesis adaptation and efficacy. Abiotic stress involves the transcriptional responses, having a substantial role in regulating various aspects in response to salt stress [1].

#### 4.2. bZIP/HDZIPs

In various studies it has been observed that the gene expression of bZIP when exposed to salinity, is upregulated in salt-sensitive wheat cultivar but the salt tolerance variety is decreased. However, salt tolerance is conferred by overexpression of a NAC transcription both in rice and wheat. This predicts their role in stress mitigation [9].

OSBZ8, a bZIP class of ABRE binding transcription factor, identified from rice, is shown to be highly expressive in response to tolerance against salt stress cultivars as compared to those which are sensitive to salt stress [10]. A SNF-1 group of serine/threonine kinase within the presence of Spd is shown to activate/phosphorylate OSBZ8, during salinity stress.

#### 4.3. MYB Proteins (*Myeloblastosis Oncogene*)

The MYB proteins are ABA (abscisic acid) dependent, which are considered important in case of various transduction pathways and abiotic stress. MYB transcription factor family, in *Arabidopsis* has improved PSII stability and tolerance to photoinhibition in case of cold/freezing. These transcription factors play a vital role in response from both stomatal and non-stomatal. MYB regulates either the numbers and size of stomata or

regulates the metabolic components [1]. These TFs if overexpressed, may result in greater sensitivity to abscisic acid (ABA) and against drought [11].

#### 4.4. DREB or CBF Proteins

The C-repeat binding factor (CBF) or dehydration responsive element binding protein (DREB) are the two transcription factors which are known to be master regulators for salt stress. CBF1/2/3 proteins, belonging to the AP2/ERF (Ethylene-Responsive Factor) family, are responsive in low temperatures [12,13]. Overexpression of CBF3/DREB1A boosts the tolerance of the plant against salinity [14]. An optimistic role of CBF proteins, in response to stress due to salt is indicated.

### 5. Future Perspective

Salt stress or abiotic stress due to environmental conditions is a major concern with regard to plant growth, germination and development. However, understanding the whole mechanism of abiotic stress and gene expression is very challenging. Here we have tried to review certain transcriptional factors and molecular responses of plant during salt induced stress. In plants, molecular mechanism of response against salt stress is majorly concerned to the identification to salt stress sensors. The front line area of plant i.e., cell wall is clearly associated with the sensor of salt stress, as it is directly exposed to the stress. As far as transcriptional factors are concerned it is hard to understand the gene expressions and regulate the whole plant in context to abiotic stress. Systemic studies and their further elucidation is suggested.

**Author Contributions:** S.M., S.K.R., D.K.M. and A.Z.; Conceptualization, Methodology, Data Collection, Writing—Original draft preparation. S.M., S.K.R., D.K.M. and A.Z.; Writing—Reviewing and Editing. All authors have read and agreed to the published version of the manuscript.

**Funding:** This review received no external funding.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** Please refer to suggested Data Availability Statements in section “MDPI Research Data Policies” at <https://www.mdpi.com/ethics>.

**Acknowledgments:** Not applicable.

**Conflicts of Interest:** The authors declare no conflict of interest.

### References

1. Saibo, N.J.; Lourenco, T.; Oliveira, M.M. Transcription factors and regulation of photosynthetic and related metabolism under environmental stresses. *Ann. Bot.* **2009**, *103*, 609–623.
2. Imin, N.; Kerim, T.; Weinman, J.J.; Rolfe, B.G. Low temperature treatment at the young microspore stage induces protein changes in rice anthers. *Mol. Cell. Proteom.* **2006**, *5*, 274–292.
3. Thomashow, M.F. Plant cold acclimation: freezing tolerance genes and regulatory mechanisms. *Annu. Rev. Plant Biol.* **1999**, *50*, 571–599.
4. Zhu, J.-K. Salt and drought stress signal transduction in plants. *Annu. Rev. Plant Biol.* **2002**, *53*, 247–273.
5. Isayenkov, S.V.; Maathuis, F.J. Plant salinity stress: many unanswered questions remain. *Front. Plant Sci.* **2019**, *10*, 80.
6. Seki, M.; Ishida, J.; Narusaka, M.; Fujita, M.; Nanjo, T.; Umezawa, T.; Kamiya, A.; Nakajima, M.; Enju, A.; Sakurai, T.; et al. Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. *Funct. Integr. Genom.* **2002**, *2*, 282–291.
7. Riechmann, J.L.; Heard, J.; Martin, G.; Reuber, L.; Jiang, C.Z.; Keddie, J.; Adam, L.; Pineda, O.; Ratcliffe, O.J.; Samaha, R.R.; et al. Arabidopsis transcription factors: genome-wide comparative analysis among eukaryotes. *Science* **2000**, *290*, 2105–2110.
8. Zhao, C.; Zhang, H.; Song, C.; Zhu, J.-K.; Shabala, S. Mechanisms of plant responses and adaptation to soil salinity. *Innovation* **2020**, *1*, 100017.
9. Liu, C.; Zhang, T. Expansion and stress responses of the AP2/EREBP superfamily in cotton. *BMC Genom.* **2017**, *18*, 1–16.
10. Mukherjee, K.; Choudhury, A.R.; Gupta, B.; Gupta, S.; Sengupta, D.N. An ABRE-binding factor, OSBZ8, is highly expressed in salt tolerant cultivars than in salt sensitive cultivars of indica rice. *BMC Plant Biol.* **2006**, *6*, 1–14.

11. Abe, H.; Urao, T.; Ito, T.; Seki, M.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. *Plant Cell* **2003**, *15*, 63–78.
12. Liu, Q.; Kasuga, M.; Sakuma, Y.; Abe, H.; Miura, S.; Yamaguchi-Shinozaki, K.; Shinozaki, K. 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* **1998**, *10*, 1391–1406.
13. Stockinger, E.J.; Gilmour, S.J.; Thomashow, M.F. 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* **1997**, *94*, 1035–1040.
14. Kasuga, M.; Liu, Q.; Miura, S.; Yamaguchi-Shinozaki, K.; Shinozaki, K. Improving plant drought, salt, and freezing tolerance by gene transfer of a single stress-inducible transcription factor. *Nat. Biotechnol.* **1999**, *17*, 287–291.