

Molecular Responses of Plant Due to Stress Induced by Salt [†]

Shilpi Mishra ^{1,*}, Sunil K. Raman ², Devendra Kumar Mishra ¹ and Areesh Zehra ¹

¹ Ambekeshwar Institute of Pharmaceutical Sciences, Lucknow 226201, India; devendra4747@gmail.com (D.K.M.); areeshzehra3@gmail.com (A.Z.)

² CSIR—Central Drug Research Institute, Lucknow 226031, India; sunil.pharma88@gmail.com

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

[†] Presented at the 2nd International Electronic Conference 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 plant yield, deteriorate the quality of crops and their vigor, and affect plant germination. The regulation of these effects comprises transcriptional factors that control the expression of a gene by requisite to an explicit supporter of DNA sequences. Stress-induced responses due to salt involve transcription factors such as 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 aim for genetic resistance to 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* **2022**, *11*, 37. <https://doi.org/10.3390/IECPS2021-12054>

Academic Editor: Iker Aranjuelo Michelena

Published: 7 December 2021

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



Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed 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 that are outside the normal range and may affect the normal functionality of plants. There are particular environmental conditions that alter specific mechanisms in plants [1]. Some examples could be cited: for example, it has been reported that the reproductive development of plants is hindered by low temperatures, severe dehydration and osmotic imbalance in cells, which occur due to extreme cold stress, and this osmotic imbalance results in an interruption of homeostasis, etc.

The changes in plant, whether physiological or biochemical, are concerned with altered gene expressions [2]. Whenever stress conditions occur, their onset triggers some unknown sensory signals that may initially activate certain signaling pathways such as Ca²⁺ 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 transcriptions signify a vital role in cell functioning against 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 the excessive uptake of ions or due to nutritional imbalance [5].

Metabolic proteins such as TFs or kinases are produced in response to certain abiotic stresses. However, most abiotic responses regulate 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 such as high salinity, drought, etc., are responsible for the signaling of ROS, namely H₂O₂, 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 in these conditions. The Na⁺/K⁺ ratios are reduced as both these ROS genes promote the movement of K⁺ into the cytosol. Na⁺ is also restricted to enter the xylem sap; thus, transpiration occurs and reduces the Na⁺ 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

Transcription factors aim for genetic resistance to 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, is often used to manipulate plant response to a level greater than others. 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 and low temperature is observed, it improves the PSII efficiency, reduces the stomatal conductance or improves 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 the overexpression of 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 that are sensitive to salt stress [10]. A SNF-1 group of serine/threonine kinase in the presence of Spd is shown to activate/phosphorylate OSBZ8 during salinity stress.

4.3. MYB Proteins (*Myeloblastosis oncogene*)

MYB proteins are ABA (abscisic acid)-dependent, which are considered important in the case of various transduction pathways and abiotic stress. MYB transcription factor family, in *Arabidopsis* has improved PSII stability and tolerance to photoinhibition in the case of cold/freezing conditions. 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, the molecular mechanism of response against salt stress is majorly concerned with the identification of salt stress sensors. The front-line area of a plant, i.e., the 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 gene expression and regulate a whole plant in the context of abiotic stress. Systemic studies and their further elucidation are 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.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: 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. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]
3. Thomashow, M.F. Plant cold acclimation: Freezing tolerance genes and regulatory mechanisms. *Annu. Rev. Plant Biol.* **1999**, *50*, 571–599. [[CrossRef](#)] [[PubMed](#)]
4. Zhu, J.-K. Salt and drought stress signal transduction in plants. *Annu. Rev. Plant Biol.* **2002**, *53*, 247–273. [[CrossRef](#)] [[PubMed](#)]
5. Isayenkov, S.V.; Maathuis, F.J. Plant salinity stress: Many unanswered questions remain. *Front. Plant Sci.* **2019**, *10*, 80. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]
9. Liu, C.; Zhang, T. Expansion and stress responses of the AP2/EREBP superfamily in cotton. *BMC Genom.* **2017**, *18*, 118. [[CrossRef](#)] [[PubMed](#)]
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*, 18. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]

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. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]
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. [[CrossRef](#)] [[PubMed](#)]