

Elucidating Diversity of Transcription Factors to Develop Stress-Tolerant Crops: An Overview

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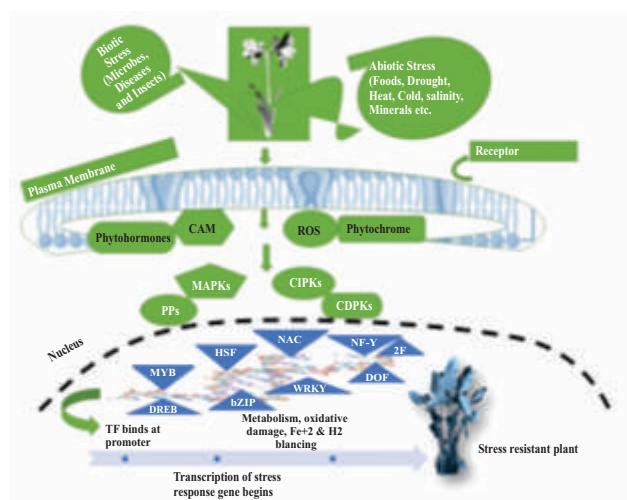
With more than 21 years of experience in research and teaching, Professor Dinesh Yadav holds specialization in molecular biology, bioinformatics, plant biotechnology, and enzyme technology. Presently he is working on Plant specific transcription factor-DOF (DNA binding with one finger) and Nuclear Factor-Y (NF-Y) for developing biotic and abiotic stress tolerance crops and pectinases group of enzymes with potential applications in different industries. He has served

as Head, Department of Biotechnology, D.D.U. Gorakhpur University and as Associate Professor in the Department of Molecular Biology and Genetic Engineering at G.B Pant University of Agriculture and Technology, Pantnagar. He has availed DST-BOYSCAST Fellowship at Australian Centre for Plant Functional Genomics (ACPFG), University of Adelaide, South Australia. He is also recipient of Dr. Pushpendra Kumar Gupta Vishisht Krishi Vaigyanik Puraskar-2015 in the field of Agricultural Sciences by Uttar Pradesh Academy of Agricultural Sciences (UPAAS), Lucknow, and Young Scientist Award-2008 by Uttarakhand State Council of Science & Technology in the discipline Biotechnology, Biochemistry, and Microbiology. With more than 130 research publications to his credit and more than 230 GenBank accession numbers, he has guided 12 doctorate students and mentored DST and SERB fellows. Currently, he is the Coordinator of Centre for Genomics and Bioinformatics and Nodal officer IPR cell, DDU Gorakhpur University. His areas of specialization include Molecular biology,

Over the years agriculture has witnessed several technological innovations to achieve the goal of global food and nutritional security. The omics-driven research has substantially influenced the pace of traditional plant breeding approaches for crop improvement and several varieties with desired traits are being developed. Plant genome sequences have revealed a large complement of transcription factors (TFs) genes accounting for more than 6% of the total ESTs. Transcription factors (TFs) are sequence-specific DNA-binding proteins playing a significant role in the regulation of diverse genes by targeting unique DNA sequences known as cis-elements present in the gene promoters. The variability among transcription factors is due to different DNA binding domains. Several families of TFs exist, some of which

are ubiquitously observed in all eukaryotic systems while many of them are plant-specific with unique DNA binding domains. Families of TFs predominately observed in plants are zinc fingers, DNA binding with One Finger (DOF), basic-region leucine-zipper (bZIP), basic-region helix-loop-helix (bHLH), MYB, NAC, MADS-box, HMG-box, AP2/EREBP, and WRKY family. Engineering of transcription factors is preferred because a single TF can control the expression of many downstream genes by binding to the cis-acting element in the promoters of the many target genes. The diversity of TF families across eukaryotes especially in plants is a matter of systematic research to harness the immense potential for developing tolerant crops. These TF genes are essential for controlling plant development processes

and responses to the environment, including functions that have a key role in agronomy. It is associated with several functions like morphology, inflorescence/flower formation, reproduction, embryogenesis, fruit development, and ripening, plant morphology, organ development, senescence, signaling, metabolism, and abiotic and biotic stress responses. Each of the transcription factors has different promoter recognition sequences. The action of TFs can be seen by binding their target site within the promoter region, which has cis-acting elements for desired traits. The binding of TFs can initiate the formation of complexes that show various types of responses, viz., physiological, biochemical, and molecular responses. The stress-responsive TFs influence the expression of several genes associated with biotic and abiotic stresses by a cascade of events as shown in Fig.1. The receptors present on the membrane recognize the signals of different stresses and are modulated in the presence of several intracellular elements like ROS (Reactive oxygen species), phytochrome, phosphatase, Ca²⁺, and protein kinase. The presence of phytohormones coordinates the signal transduction pathway which culminates with either upregulation or downregulation by binding specific TFs to cis-elements of stress-responsive genes.



Schematic representation of the general mechanism revealing the role of stress-responsive transcription factors.

As FAO statistics, nearly 20,000 species of legumes (Fabaceae) make up the third-largest family of angiosperms with varied morphology and ecology. In addition to their symbiotic relationship with specific diazotrophic bacteria, legumes exhibit interesting ecological and agricultural properties. Several studies elucidating the potential role of TF genes in developing biotic and abiotic stress tolerant legumes have been reported recently. At present, 20 legume genomes are accessible, containing many TF genes. The role of many of the TFs like Dof, WRKY, NF-Y, HSF, and NAC for biotic and abiotic stress tolerance is being studied. A list of available TFs observed in different legume genomes is depicted in Fig. 1. Keeping in view of the enlisted transcription factor of seven legumes, transcription factor families like Zinc-finger, Dof, WRKY, MYB, NAC, and NF-Y seems to have immense potential for developing abiotic stress-tolerant crops.

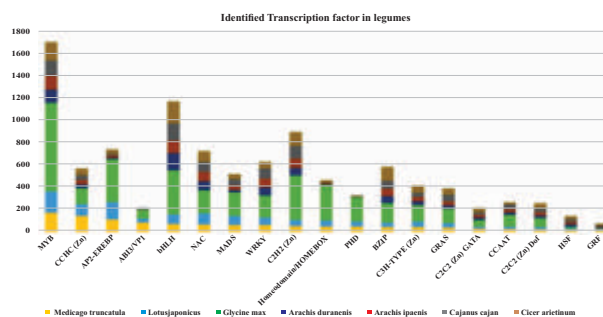


Fig. 1. Diversity of transcription factors in legumes based on available TF databases.

The diversity of these TFs gene families in plants is deciphered using bioinformatics tools and genome-wide prediction, identification, structural and functional characterization of several TFs gene families in different crops have been reported. These serve as important resources for its utilization in crop improvement especially for stress tolerance using approaches like transgenic, genome-editing, and RNAi silencing.

ACKNOWLEDGEMENT

Figure made by Ph.D. Scholar Varsha Rani is duly acknowledged.