

Transcriptome Analysis of Abiotic Stress Response in Plants

Aryadeep Roychoudhury* and Aditya Banerjee

Post Graduate Department of Biotechnology, St. Xavier's College, 30, Mother Teresa Sarani, Kolkata, West Bengal-700016, India

Editorial

Abiotic stresses like salinity and drought cause a plethora of deleterious impacts at various stages of development in plants. Drought constitutes the central feature of any form of environmental stress. The phytohormone abscisic acid (ABA) is the key regulator in mediating abiotic stress tolerance, since it promotes stomatal closure to conserve water under desiccating conditions [1]. Since plants are sessile, their adaptive features to such hostile situations involve morphological and physiological plasticity and reprogramming their signaling cascades in order to up regulate specific osmotic stress-responsive (OR) genes, most of which are ABA-inducible. The first group of OR genes constitutes those responsible for the accumulation of several classes of compatible solutes (including proline, reducing sugar and higher polyamines like spermidine and spermine), antioxidants (enzymatic and non-enzymatic), together with the different groups of late embryogenesis abundant (LEA) proteins. The second group includes the genes necessary for the regulatory control in the signaling network like the transcription factors (TFs, mostly belonging to the basic leucine zipper, bZIP), mitogen-activated protein kinases (MAPKs), calcium-dependent protein kinases (CDPKs), protein phosphatases and proteinases like phosphoesterases and phospholipase C [2]. Following the two-component signaling pattern, the TFs are activated by these kinases through phosphorylation, thereby triggering covalent modification and stimulating their binding to the upstream regions of their target genes.

Plants exhibit considerable varietal differences at the biochemical, genetic and molecular level with context to their susceptibility/tolerance to salinity and drought stress [3]. At the biochemical level, such differences could be accounted for by the higher level of endogenous accumulation of osmoprotectants and antioxidants and higher activity of reactive oxygen species-scavenging enzymes in the tolerant varieties as compared to the sensitive ones [4]. For almost over a decade, our group has been focusing on such varietal differences in stress tolerance, with indica rice (*Oryza sativa* L.) as the experimental model. Genotypic variation in rice is enormous with the varieties like IR-29, IR-64, M-1-48, etc. being the sensitive ones, while Pokkali, Nonabokra, Oormundakon, etc. being the tolerant varieties. The endogenous ABA level enhanced 10-50 folds in the leaves of salt-tolerant rice varieties like Pokkali and Nonabokra, in comparison to the salt-sensitive variety Taichung Native 1 (TNI) [5]. At the genetic level, such varietal difference is studied by the comparative transcriptome profiling of a wide array of ABA-inducible genes, in response to multiple stresses, focusing on concentration-dependent or time-kinetic analysis. This gives us a holistic approach regarding the behavior and/or effect of the same gene(s) (whose role in tolerance to a particular stress is known) to multiple stresses (which is the actual situation in the agricultural field) [6]. The expression study of a diverse group of such stress-related genes made by our group showed very low transcript levels in the sensitive varieties, inducible only by the stressors, while much higher and constitutive level of gene expression in the tolerant varieties [7]. The generality of stress responses at the transcriptional level was mostly time-dependent [6].

Most of the ABA-inducible genes are characterized by an 8 bp conserved cis-regulatory sequence called the abscisic acid responsive elements (ABREs) with ACGT core, together with certain GC-rich

sequences called coupling elements (CEs), synergistically constituting the abscisic acid responsive complex (ABRC), to which the bZIP factors bind to form a homomeric or heteromeric complex. The multimerization of ABRE or ABRC motifs were found to strengthen the promoter efficiency as analyzed by the assay of the reporter gene *gusA* in transgenic tobacco [8]. Our earlier work has highlighted OSBZ8 as the master regulatory bZIP TF, binding to the Motif I (typical ABRE) and Motif II (CE-like sequences) of the Group II *lea* gene, *Rab16A*, in the vegetative tissues of rice [9]. The *Rab16A* gene from the salt-tolerant rice variety Pokkali, when overexpressed in tobacco showed enhanced salt tolerance through delayed development of oxidative damages and simultaneous increase in osmolytes, antioxidants and a high K^+/Na^+ ratio [10]. The likewise introgression of the same gene in the salt-sensitive indica rice variety, Kshitish contributed towards increased salt tolerance [11]. The overexpression of the trans-acting factors like TRAB-1 and OSBZ8 which target *Rab16A* and regulate its expression also holds a great promise in generating salt/drought-tolerant transgenic plants in future [12]. The casein kinase II (CKII)-like kinases have been shown to phosphorylate OSBZ8 [9], as well as maize Rab17 (which possesses nuclear localization signal), shuttling it from cytoplasm to nucleus following phosphorylation [13].

Approaches like genomic-scale expressed sequence tags (ESTs), genomic sequencing and cDNA microarray analyses have tremendous potentiality in rapidly isolating the candidate genes of the 'osmome', 'xemome' or 'thermome', i.e., the gene complements required to attain tolerance against osmotic stress, desiccation or temperature variation respectively. Datasets emerging from such experiments require to be merged so that comparisons between different cellular and glycothetic, halophytic and xerophytic plant models can be chalked out. Such data mining can be a systematic supply agenda for functional genomics with the use of tagged mutant collections, complementation and overexpression tests, accompanied by microarray analyses to reveal hierarchical relationships between specific signaling components and downstream effector genes [3].

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*Corresponding author: Aryadeep Roychoudhury, Post Graduate Department of Biotechnology, St. Xavier's College, 30, Mother Teresa Sarani, Kolkata, West Bengal-700016, India, Tel: (+91 33) 2255-1101; E-mail: aryadeep.rc@gmail.com

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