

Editorial

Genomics and Functional Genomics of Stress-mediated Signaling in Plants: Volume II

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Plants repeatedly combat abiotic stresses such as drought, high salinity, extreme temperatures, nutrient deficiency and toxicity in their natural environment. Often plants are exposed to a combination of stresses such as drought and high temperature attributable to excessive irradiation and low water availability. In comparison to the normal growth conditions abiotic stresses reduce the overall yield significantly amidst the varieties of crops cultivated worldwide [1]. Different abiotic stresses affect the plant growth and responses at various stages eventually leading to cessation of growth. Following stress perception activation in the transcription of key enzymes, perturbation in metabolic flux, changes in biomolecules activity invoke tolerance response against adverse environmental conditions [2].

Plants possess an astonishing ability to sense change in the environmental conditions. The knowledge of molecular signaling of stress tolerance mechanism would help in developing strategies for the survival of plants under adverse conditions. Any external environmental stimulus when sensed by the plants activates downstream signaling cascades that amplify the signal as well as alert analogues pathways. Several methodologies have been used to identify the genes that are involved in the stress tolerance [3-5]. Isolation of these stress responsive genes will allow recognition of their associating cellular functions. However, functional integration of large number of stress responsive genes is a big challenge that can potentially create a complete understanding of the stress response pathways [6].

In the post genomic era, development of a range of tools such as proteomics, metabolomics, transcriptomics, phenomics have empowered the functional elucidation of proteins governing vital processes in plants. The practice of various omics based tools for the functional characterization of a gene/s is termed as 'functional genomics' [3-5]. The broad genetic studies in various crops have revealed the extensive variation in abiotic stress responsive genes among them. However, exploitation of this knowledge to generate stress tolerant crops is difficult due to existence of relatively limited information about molecular response pathway in these plants. Previous studies on complex and interconnected signal transduction pathways have been arduous and challenging using traditional approaches. The advent of functional genomics approaches has simplified the analysis of large number of genes and gene products involved in several defense and developmental processes in plants. Functional genomics is now considered as a viable tool to examine abiotic stress response in crops such as rice and wheat, through which process of stress perception, signaling cascade and tolerance responses can be analyzed from gene expression to protein complements of cells, to comparative metabolite profiling of stressed tissue *versus* controlled tissue [7-9]. Using this background, plant biologists are working to transfer the knowledge gained from model plants to the field crops to enhance their tolerance ability and productivity.

In volume II of our special issue, we have attempted to cover the latest, methodical, practical and successful use of functional genomics approaches to divulge the molecular details of tolerance response. Volume II of this special issue comprises of 6 articles and the first research article by Kim *et al.* describes the whole transcriptome analysis of rice root and shoot under ABA and JA. This article enlightens us about the phytohormones ABA and JA and suggests that they might have common gene expression regulation system. Their study also aims to shed light on the conundrum why JA could respond for both abiotic and biotic stress tolerance?

The second research article by Lee *et al.* elaborate the results of genome-wide analysis of alternate splicing on inbred lines of cabbage under heat stress. This study primarily identify that number of alternate splicing events markedly increased under heat stress and among these are heat shock transcription factor (Hsf) and heat shock protein (Hsp) genes. The third article of this volume identifies the possible role of microRNA (miRNA) in glyoxylase overexpressing transgenic plants of rice under salt stress. Based on the Next Generation Sequencing (NGS) analysis, the role of miRNAs and their involvement in the glyoxalase-regulated metabolism pathway during salt stress response is explored by Tripathi and co-workers.

Followed by this is an interesting report describing the affects of widely used herbicide glyphosate. Lu *et al.* describes the impact of glyphosate on the rhizosphere microbial communities of an *EPSPS*-transgenic soybean line by metagenome sequencing. From this study, authors concluded that glyphosate did not significantly affect the alpha and beta diversity of the rhizobacterial community of the soybean line ZUTS31, whereas it significantly influenced some functional genes involved in plant growth-promoting traits in the rhizosphere.

The next research article by Kumar *et al.* covers a detailed analysis of one of the CBS domain containing protein widely known as sensors of cellular energy. The functional characterization of rice cystathionine- β -synthase domain-containing protein, OsCBSCBSPB4 suggest that it impart abiotic stress tolerance.

Previously, genetic basis of salt tolerance has been well defined in model plant Arabidopsis by identification of Salt-Overly Sensitive pathway (SOS). After the discovery of this SOS pathway in Arabidopsis, several researchers investigated the presence of SOS pathway components in crop plants as well. The abiotic stress signals trigger the change in cellular calcium (Ca^{+2}) levels, which is then perceived by various calcium sensors such as CBLs to regulate the downstream signaling cascades. The last research article by Nutan *et al.* studied the role of BjsOS3 (also known as calcineurin B-like 4, CBL4) from *Brassica juncea* in salt stress tolerance by complementation of Arabidopsis *sos3* mutant.

Henceforth, this volume of our special issue comprising of several research articles will aware readers about the potential areas of abiotic stress signaling with genomics and functional genomics perspectives. In this post-genomic era, huge amount of data and information is generated. This required unified attention of plant biologists to make holistic and successful efforts in order to develop new technologies, to enhance the crop yield under these prevailing stressful conditions.

The articles in this special issue put forward several potential problems, which need to be addressed using the tools of multidisciplinary fields of genomics and functional genomics. We hope that this special issue will provide a practical update on our knowledge of plant's abiotic stress response and will prompt contemplation and promotion of superior approaches for sustainable crop production.

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