

Editorial

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

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The agricultural productivity across the globe is severely disturbed by varying environmental conditions. Due to these climatic situations, plants frequently observe various unexpected biotic and abiotic stress conditions [1, 2]. Crops are being subjected to various abiotic stress conditions such as drought, heat, cold, radiation, salinity and ion toxicity that restrict their growth and genetic potential of higher yield. Plants being sessile have developed an intricate signaling network for stress perception and tolerance. The plant's responses to combination of stress conditions are genetically controlled to a great extent by different interacting signaling pathways [3, 4]. Determination of these molecular mechanisms governing stress mediated signaling in plants and underlying regulatory network of interacting proteins has been a major focus of research in the past decades. Functional elucidation of genes involved in these regulatory pathways is intended towards generating stress tolerant crops.

Recent development of various omics based approaches has considerably facilitated the identification of various stress-responsive components of complex molecular regulatory and developmental systems in plants [5-7]. These comprehensive approaches including genomics, transcriptomics, proteomics and metabolomics are now extensively employed to understand the coordination among various regulatory pathways. Genomics involves elucidation of sequence and structure of a genome. Transcriptomics deals with structural and functional study of complete RNA transcripts generated under specific conditions by microarray analysis and RNA sequencing methodologies; proteomics involves extensive study of proteins and their regulatory pathway including post-translational modifications. Subsequent to transcriptomic and proteomic study that reveals the expressing gene set in a given environment within the cell, metabolic profiling identify and measure metabolites composition to reveal a different aspect of cellular function. The collective term for all the chemicals that are produced during a cellular process is metabolome and study of these metabolites at global or tissue level is known as metabolomics [8]. The integration of all systems biology techniques can truly contribute towards understanding complex cellular biology in plants such as undetermined gene functions, pathways such as diurnal fluctuation in metabolite levels, response and tolerance to biotic or abiotic stresses, to observe the growth and performance of transgenic plants and to evaluate the genetic improvement of crops [5, 9].

The integration of omics based techniques have given rise to a new era of systematic investigations that offer much more deep insights into the functionality of a gene altogether with its effect on the phenotype in a given biological context.

Plants adapt to varying environmental conditions by modifying their transcript profiles. The primary purpose of omics based studies is to investigate at the transcript levels that includes molecular interaction, their correlation with the signaling cascade and to process the evidences in order to elucidate the interaction network that set off with the specific signals and gets over with a definite response.

Elucidation of the biological processes governing plant regulatory networks requires detailed information of plant responses at genome level towards different stress and developmental stimuli. In comparison to the previous 'gene-by-gene' method, the introduction of high-throughput approaches such as microarray, RNA sequencing, Expressed Sequence Tags (EST) analysis, site-directed mutagenesis, loss- and gain-of-function analysis have contributed to precisely identify the location of a candidate gene in the signaling cascade and its role in abiotic and biotic stress tolerance [5, 6, 10]. Omics based technologies are often exercised in a high throughput mode, therefore, generate huge amount of data. This is due to these approaches that we have been able to considerably scale down the cost as well as time to perform large-scale endeavors such as whole genome sequencing and transcriptome analysis among others. To improve crop production efficiency, previous attempts to increase plant tolerance to drought, high salinity and cold stress through traditional methods such as breeding were inadequate due to extreme complexity of stress responses. Progress towards achieving crops species capable of acclimatizing to environmental stress is anticipated through comparative study of model plants using functional genomics approaches. The identification of novel genes and their expression in response to different stress stimuli and a better understanding of their involvement in stress tolerance mechanism will provide the means to effectively plan strategies to raise stress tolerant transgenic crops.

In this special issue on 'Genomics and Functional Genomics of Stress Signaling in plants', we propose to include two volumes (Vol. 1 and 2) with 8 review articles in volume I and 6 research articles in volume II from several plant biologists across the globe. The articles comprised of both research and review in the field of genomics and functional genomics of stress signaling in plants.

In the volume I, the first review article by *Tiwari et al.* emphasizes on the functional genomics perspective of molecular mechanism of drought signaling and its cross talk with several phytohormone-signaling pathways implicated in abiotic stress responses. Transcription factors regulate the expression of stress responsive genes under adverse conditions. *Hoang et al.* describes the role and potential application of transcription factors in signal transduction and their importance in stress tolerance improvement in crop plants. The review article by *Pareek et al.* discusses the molecular mechanisms underlying cold sensing and signaling with an aim for the development of efficient strategies to obtain cold tolerant plants. Like cold stress, increase in temperatures (heat stress) causes havoc on the plant growth and development. The next review article by *Shukla et al.* describes the genomics and functional genomics of metal stress mediated signaling and adaptive responses. Here, authors emphasize on the role of signaling networks and various signaling components such as phytohormones, reactive oxygen species and reactive nitrogen species in generating defense responses during metal stress. The subsequent review article by *Jha et al.* elaborates the advancement of several methodologies in identification of substrates of protein kinases. In addition, the role of protein kinases and their substrates in regulating different stress signaling pathways have also been discussed. *Nikalje et al.* present a review article on perspective of salt stress adaptation. Here, authors focus on the sensing and signaling components involved in mediating tolerance to saline conditions as adaptive mechanisms of halophytes through the genomic approaches. Subsequently, the review article by *Wan et al.* describes the role of osmotin and osmotin like proteins in salt stress mitigation in plants. The last article of this volume also discusses the problem of salinity stress and its mitigation in leguminous crop chickpea. In this review article, *Kashyap et al.* elaborates the usage of genetic and genomics based tools to understand the problem of salt stress in chickpea and possible approaches to tackle the problem of crop loss under salt stress condition.

The intricacies of abiotic stress responses generally impede the detailed experimental investigation of individual stresses. A 'broader' approach equipped with all omics based methods may enable plant scientists to dissect and describe these stress responses in detail. This knowledge will be useful in the manipulation of these responses and integration in cereal crops through transgenic approach.

Nonetheless, it is not possible to include various aspects of stress signaling components and pathway but the review articles in this special issue certainly add valuable information in this emerging field of genomics and functional genomics of stress signaling.

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