Editorial   **Open Access**

Influence of Environmental Factors on Crops

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Editorial

Current agricultural productivity is unable to meet the food demand of a continuously increasing population. Out of over 7 billion people on the planet, 805 million are estimated to be chronically undernourished (http://www.fao.org/publications/sofi/2014/en/). Agricultural productivity is greatly affected by unfavourable environmental factors to which crops are exposed. These environmental factors which decrease agricultural yield are referred to as stress and are divided into two categories – biotic stress and abiotic stress. Abiotic stress, which is the stress caused by non-biological components of the environment such as cold, drought, salinity, heat etc., is responsible for a high percentage of the total decrease in agricultural productivity. Rice is the staple food crop for approximately half the world's population and constitutes approximately 20% of the global daily calorie uptake (http://www.irri.org). Our laboratory, therefore, focuses mainly in elucidating the genetic basis of the response of crops, especially rice, to salinity stress, which along with drought is one of the major problems faced by farmers the world over. We have employed an integrated approach combining transcriptomics, proteomics, metabolmics, ionomics as well as functional genomics to help us obtain an understanding of the osmotic stress response of rice from a systems biology perspective.

Using two contrasting genotypes of rice, IR64 and pokkali, we constructed a subtractive cDNA library and were able to identify over a thousand genes to be salinity regulated, some of which have been found to be localized within the Saltol QTL present in chromosome 1 [1]. Most agronomic traits, including tolerance to abiotic stresses, are quantitative characteristics governed by QTLs. Saltol QTL accounts for 60-80% of phenotypic variation under salinity [2]. Further analysis revealed the possible involvement of many salinity induced factors (SIFs) localized within the Saltol QTL which may putatively function in different processes such as vegetative growth, early flowering, fertility, respectively [3].

One candidate gene in particular, OsCyp2, was identified using the subtracted cDNA library. This gene functions as a molecular chaperone and is regulated by multiple stresses. In lower organisms as *E. coli* and *S. cerevisiae*, overexpression of OsCyp2 increased the tolerance to multiple abiotic stresses [4]. Further, validation of this gene in the endogenous system, i.e Oryza is underway. Our main focus deals with the structural and functional charactization of OsCyp2.

Another candidate gene which we have identified through this approach is OsHK3b. Our analysis using predicted rice interactome network (PRIN), revealed that OsHK3b is the ortholog of the Arabidopsis putative osmosensor, AtHK1 [5]. Functional characterization of OsHK3b with respect to osmotic stress response is currently under progress.

Various other genes identified using the subtractive cDNA library is also currently being characterized. Besides these, various projects currently in progress include 'omics" approach towards understanding osmotic stress response. The lab has also generated IR64 mutants using different doses of gamma- radiation. These mutants are being screened for their tolerance to abiotic stress. Currently, the mutants are at their fifth filial generation and candidate mutant lines have been identified but yet to be characterised.

In conclusion, our research primarily focuses on trying to understand the response of rice to osmotic stress. Using the 'candidate gene' approach, we have raised several transgenic rice plants which exhibit improved tolerance to varied abiotic stresses and a few of them have been transferred to industries for further development of the product from commercialization view point.

References

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This article was originally published in a special issue, entitled: **"Recent Advances in Rice Nutrition and Chemistry",** Edited by Shuvasish Choudhury