



## Plant Abiotic Stress: 'Omics' Approach

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Abiotic stress is the major threat towards the living world more precisely the plant kingdom whose development and productivity is negatively hampered. It is considered as the major cause behind plant damage and reduced crop yield [1]. Plants have developed several biochemical, physiological and metabolic strategies in order to combat such abiotic stresses. Often it is difficult to predict the complex signaling pathway that are activated or deactivated in response to different abiotic stresses [2]. The attempt to integrate multidimensional biological information in a network and model leads to the development of system biology. Most of the plant system biology approaches relies on four main axes, viz., genomics, proteomics, transcriptomics and metabolomics, which provide us with a detailed knowledge about the topology and dynamic function of a molecular system [3]. The complex molecular regulatory system involved in stress tolerance and adaptation in plants can be easily deciphered with the help of different 'omics' study [2]. Genomics involves study of genome; transcriptomics includes structural and functional analyses of coding and non-coding RNA or transcriptome, proteomics deals with protein and post-translational protein modification along with their regulatory pathway and metabolomics, which provide a powerful tool to analyze about various metabolites when analyzed in an integrated way can be a very powerful tool in identifying the complex network involved in stress tolerance. The advent of omics technologies led to the development of well designed experiments that provides much more deep insight about the functionality of the gene along with their effect on the phenotype in a specified biological context. Plant modifies their 'omics' profiles to cope with the changing environment for their survival. The main objective of this 'omic' approach is to find out the molecular interaction, their relationship with the signaling cascade and to process the information which in turn connects specific signals with specific molecular responses. Thus Linus Pauling rightly said that "Life is a relationship among molecule and not a property of any molecule".

Knowledge about the plant regulatory network and the biological principle by which they are governed requires detailed information regarding the genome-scale responses during developmental and environmental stimuli. Before the introduction of the omics approach, genetic approach was termed as "candidate gene- by-gene" which involves identification and study of a single gene in different regulatory pathways in order to determine its position in the signaling cascade and its contribution towards stress tolerance. The understanding of plant response towards abiotic stress is enhanced with the application of genomic techniques such as high- throughput analysis of expressed sequence tags (EST), large scale parallel analysis of gene expression, targeted or random mutagenesis, and gain- of- function or mutant complementation [4,5]. Previous workers carried out a comparative genomic analysis between the model plant *Arabidopsis thaliana* and *Thellungiella halophila*, a species showing remarkable cold, drought and salinity tolerance [5]. *Thellungiella* appears as 'stress anticipating' because it shows elevated pre- stress expression of genes, some of which are paralogous versions and alleles that might be stress-inducible in *A. thaliana*, which in turn elevates metabolites that either act as a signaling molecule or osmolytes. In a work carried out by Cushman and Bohnert [4] ESTs from leaf

tissues of a well-watered and salt- stressed *Mesembryanthemum crystallinum* were sampled. It was observed that 15% more unknown genes were expressed in the plant subjected to salt stress than in the unstressed plant. Their study suggested that the exposure of plant to salt stress results in the increase in gene expression.

In response to various abiotic stresses plant continuously needs to adjust their transcriptome profile. The transcriptome of different organs and developmental stages of *Arabidopsis* and Rice were examined under different environmental condition in various laboratories. This contributes a major step towards the understanding and identification of plant gene regulatory network. In order to find out groups of coexpressed genes different clustering algorithms were used. The genes that belong to the coexpressed cluster under different internal and external condition and were regulated by similar transcription factor forming a transcription sub-network were hypothesized as co-regulated genes [6]. Furthermore integration of coexpressed data, gene ontology annotations and cis motifs link the gene with its biological function. Reconstruction of transcriptional network requires nodes (gene) and edges (interactions between the genes). Narsai et al. [7] identified an entire new set of reference genes in Rice that remain stable during development, stress and hormonal treatment. This work provides a new set of reference genes that are of immense importance for future studies in *Oryza*. Nineteen microRNA genes of eleven microRNA families in *Arabidopsis thaliana* were identified that were upregulated in response to cold stress. A further analysis of their promoter sequence shows the prevalence of some stress regulatory cis-element [8]. These cold responsive micro RNA genes directly or indirectly affect different signaling pathways during the period of stress. Stress response in *Arabidopsis thaliana* was associated with a co-ordinated re-programming of the energy-associated transcriptome. The result from this study shows a sharp decrease in the rate of photosynthesis while other energy promoting networks were activated [9].

Similar to transcriptional network protein and metabolites network can be constructed using nodes and edges. In case of protein networks, nodes are represented by proteins while edges are represented by protein-protein interaction (interactome) whereas in case of metabolic network, nodes are represented by the metabolites and the edges are represented by enzymatic reactions or biochemical modifications.

Proteomics is associated with two types of studies, first one is the

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characterization of a proteome which involves identification of all the proteins expressed and second one is differential proteomics which involves comparison between proteome of a control and plant subjected to stress. Proteomic approach has been largely adopted to investigate the protein profiles in plants in response to abiotic stress that might lead to the development of new strategies for improving stress tolerance. Two major laboratory techniques that are mostly used for this approach are protein electrophoresis and protein identification with mass spectrometry. Sanchez-Bel et al. [10] performed a comparative proteomic analyses between a control and cold stressed bell pepper fruit to understand the alterations of protein profile associated with redox homeostasis and carbohydrate metabolism. It was observed that the protein abundance in ascorbate-glutathione cycle was altered and catalase was down-regulated. Some of the key proteins involved in glycolysis and Kelvin cycle were also inhibited in chilled fruit. Jasmonate, a cyclopentanone signal involved in plant response to abiotic and biotic stress plays a key role in regulating plant metabolism. A plant when treated with methyl jasmonate shows a remarkable change in its protein profile. About 194 differentially expressed proteins were identified that participates in various plant physiological processes. Functional analyses of the result showed repression of carbohydrate anabolism and photosynthesis whereas carbohydrate catabolism was upregulated along with some proteins involved in jasmonic acid biosynthesis pathway, stress, defense and secondary metabolism [11]. [12] analyzed the effect of salt and cold stresses on the leaf transcriptome and proteome of potato which shows a large number of differentially regulated genes and proteins. It was observed that when the plant was subjected to salt stress a large number of genes associated with primary metabolism, signal transduction and detoxification apparatus were down regulated whereas when the plant was exposed to cold stress the number of genes showing up-regulation and down regulation was equal. But on contrary proteome analyses reveals a rise in protein expression in almost every protein except those that were involved in photosynthesis. This study reflects the accuracy of proteomic approach in comparison to transcriptomics approach.

Huge amounts of chemically diverse compound with different biological activity are synthesized by the higher plants that help to combat stresses. Thus metabolomics plays a significant role to gather information not only about the phenotype but changes in it induced by stress thereby bridging the gap between phenotype and genotype. This is one of the most rapidly developing technologies. The major approaches that are used in plant metabolomics research includes metabolic fingerprinting which involves separation of metabolites based on the physical and chemical properties using various analytical tools and technologies, metabolite profiling which includes the study of the alterations in metabolites pool that are induced by stress and finally target analyses. Sicher et al. [13] conducted an experiment in maize to understand the combined effect of enhanced atmospheric CO<sub>2</sub> and drought response by monitoring foliar metabolites. The concentration of leaf metabolites were found to be altered. The amount of soluble carbohydrate, aconitate, shikimate, serine, glycine, proline and eight other amino acid increases whereas leaf starch, malate, fumarate, 2-oxoglutarate and seven other amino acid decreases in response to drought. Thus water stress in maize results in the inhibition of C4 photosynthesis and activation of photorespiration.

System biology approaches have given a more holistic view of the molecular response in plants when exposed to abiotic stress and the integration of various omics studies has revealed a new area of interactions and regulations [14,15]. This approach of research requires close interaction of biologists and mathematicians in all steps of experimental design, data collection, analysis and mining. The three main domains that must be addressed to take full advantage of plant

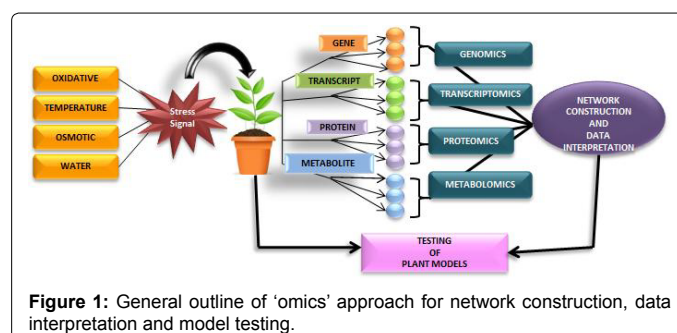


Figure 1: General outline of 'omics' approach for network construction, data interpretation and model testing.

systems biology are development of omics technology, integration of data in a usable formats and analysis of data within the domain of bioinformatics (Figure 1). The limitation of system biology is greatly tied to data modeling, in which analysis always involves generalization, simplification and assumptions. Although, networks in systems biology might never completely represent the dynamic biological system but proper applications of these techniques will provide significant insight in the field of plant abiotic stress.

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