

Editorial

Proteomics adds leverage in deciphering plant-pathogen interactions in the post genomics era

Plant biology *per se* needs to be understood in toto, so as to harness the maximum potential of any crop plant to meet out the future food requirements of the growing world population. Genomics research with the phenomenal upsurge to the next generation sequencing platform has proven to be robust enough to decipher complete genetic information coding for useful traits of interest. Proteomics—a complementary tool to genomics is gaining substantial progress in many crop plants like Rice, Maize, Sorghum etc., besides having been well established in the model plant—*Arabidopsis*. There is an unprecedented shift in the pace with which this tool of “*omics*” is carrying forward progressively to address many unresolved issues in agricultural research. It is quite evident that Proteomics is a powerful tool in the post-genomic era and plays a key role in empowering systems biology in plants.

The term proteomics was coined in 1997 and has been defined as the systematic analysis of the proteome, the protein complement expressed by a genome, cell or tissue. Unlike the genome which is static, proteome of an organism dynamically responds to environmental stimuli and intracellular metabolite levels and post translational modifications (PTMs) *viz.* phosphorylation, acetylation, glycosylation, methylation, etc., further add to the inherent complexity of proteome by regulating protein function in cellular processes. It is in this connection that proteomics gains significance as it represents the functional status of an organism, tissue, organelle or cell at any given time point in a given condition. Besides that, genomic sequence editing and annotations mostly depend on algorithms applied to identify genes and under practical situations; the interpretations out of the analysed data might be ambiguous. In order to cross validate the results obtained from the genomics platform, proteomics compliments here, as it certainly has the ability to handle miss-annotations and sequencing errors. This validation of genomics results using proteomics as an alternate tool adds leverage to more precisely understand the complex plant-pathogen interactions.

Though the classical Proteomics started with the initiation of work on isoenzymes during the late 1960s, the impetus gained much later. Introduction of 2D electrophoresis by O’Farrell during 1975 has rejuvenated renewed interest on plant proteomics as evidenced by an influx of research papers during the late 1980’s employing 2DE to study various aspects of plant biology. Subsequently there was an evident slowdown in the pace of proteomics research, probably due to intervention of genomic tools like PCR, that has revolutionized genomics and made it seem more attractive and promising than proteomics at that point of time. However the advancements in protein separation and MS techniques synergistically have made significant contributions especially in crop plants like rice and maize, which serves as model systems for other monocots. Technological advances in Proteomics have taken the science to the pinnacle of glory, particularly due to its invaluable applications in the medical and agricultural sciences. Emergence of gel free techniques like Isotope-coded affinity tag (ICAT), Isobaric tagging for relative and absolute quantitation (iTRAQ) and Multidimensional protein identification technology (MudPIT) has revolutionized the concept to the next level. Proteomics has many different facets *viz.* cellular, organelle, structural, functional, secretomics etc. each of which addresses to specific challenges in crop science. Proteomics *per se* has widened its scope in understanding plant development, regulatory elements, stress-responsive mechanism, etc.

Taking into cognizance the significance of proteomics, it has been applied successfully to understand plant biology during development or in response to various biotic and abiotic factors in many of the model and crop plants. In a plant system, stress response is a dynamic process, where in several stages could be distinguished, each of them could be characterised by its unique proteome composition. Proteome of an organism responds dynamically to environmental stimuli influenced considerably by post translational modifications, unlike genome response. Proteins exhibit diverse functions underlying plant stress tolerance: they act as enzymes, exhibit protective functions, bind water, interact with other proteins and other biomolecules, scavenge ROS either directly *via.* chemical reactions with certain amino acid residues or indirectly *via.* metal cofactors. Better understanding

of physiological mechanisms underlying plant stress response: perception of stress, signalling events leading to changes in gene expression, changes at transcript, protein as well as metabolite levels underlying plant acclimation to a given stress and an acquisition of an enhanced plant stress tolerance can be achieved. Proteomics studies could also significantly contribute to identification and further characterization of key proteins underlying plant tolerance to a given stress, which can be used as protein biomarkers for a given stress. Advancements in these fronts would aid in identification of potential targets to be used in marker-based breeding for all desirable economic traits, which also has the potential to be exploited in the development of transgenics for crop improvement.

TCA/Acetone precipitation-LBT method for efficient extraction of stalk proteins was demonstrated by Amalraj and his group during 2010 and they have established a reference proteome map, which is viewed as a underpinning benchmark in sugarcane stalk proteomics. This pioneering work has laid a solid foundation to further research on Sugarcane stress-related proteomics. Nevertheless, many relevant queries on sugarcane physiology and stress tolerance remain unanswered, due to the paucity of reference genome sequence of Sugarcane, hitherto. Very recently the whole genome of Sugarcane has been published, and the availability of the dataset in public domain has fuelled the interests on employing tools of “*omics*” in unravelling the molecular mechanism behind stress tolerance in Sugarcane. The gained momentum is thus expected to compliment the outcome of MS-based quantitative proteomics research and further catapult sugarcane proteomics to the next level.

Obvious challenges in the field of Proteomics seen as of now are study of PTMs, especially phosphoproteomics and redox proteomics, as well as protein interactions (interactomics) which could play a pivotal role in the field of plant stress proteomics. These approaches will contribute to a detailed protein functional characterization, which will surely help us to better understand the processes of plant stress acclimitization and stress tolerance acquisition. Despite the advent of many robust high throughput proteomic tools, suitability of 2DE coupled with MS especially in plant proteomics remains unchallenged till date, as evidenced by the number of research papers employing this technique to understand various aspects of plant biology. Nevertheless, the progress made in certain areas of abiotic and biotic stress, plant proteomics on several other aspects like organelle, pest resistance and complex interactions of biocontrol agents remain untouched. Further, deliberating PTMs, especially phosphorylation, owing to its significance in regulation of signalling vital cellular process remains to be fully explored. Secretomics, an off-shoot of Proteomics, which focusses on the secreted proteins finds valuable application in the field of effectoromics in Plant Pathology. Integrating these tools of “*Omics*” is inevitable to comprehensively understanding plant disease resistance. In the past decade, evidence on successful application of proteomics to study plant-pathogen interactions is accumulating. These landmark accomplishments in a more closely related host-pathogen system/model system like Arabidopsis and Rice with respective pathogens would help us in furthering through for a critical understanding of many important plant- pathogen encounters.

Considering the developments in plant proteomics, it is appropriate to state that the potential of proteomics to understand plants is being harnessed in a progressive manner. Further harnessing the tools of “*omics*” approaches is likely to enable researchers to reconstruct the whole cascade of cellular events leading to rapid responses and adaptation to the various abiotic/biotic stress stimuli. Proteomics is undergoing a dynamic evolution both in technological and application fronts with the advent of robust and sophisticated platforms. However, the perception and adoption of this technology for understanding plant–pathogen interactions are yet not much encouraging, which is mainly due to lack of expertise, acquaintance and cognizance of scope and potential applications. Hence, a huge impetus is required with path-breaking findings in the form of high impact proteomic publications in challenging crops like sugarcane or complex cellular components to boost the adoption of emerging advanced technologies. The integration of the tools of “*Omics*” would supercharge the ongoing pace of applications of proteomics in all fronts of phyto-pathoproteomics.

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