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Proteomics Technologies and its Application for Crop Improvement

Harsha Sharma[1]

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Abstract:

The study of protiens and their interactions in a cell is called proteomics. Proteomics is a useful tool and important in shifting from genomics to the protein compliment of the human organism within the wide field of functional OMICS. It is expected from proteomics to produce better disease markers for diagnosis and therapy monitoring because of the proteome reflects more precisely on the dynamic state of cell, tissue, or organism. The present review study is on the technologies of proteomics and their technologies and their applications for crop improvement. New opportunities and challenges for those seeking to gain greater understanding of disease is created by the advent of proteomics technologies for global detection and quantitation of proteins. Mass spectroscopy has become an indispensable tool for molecular and cellular biology and plays a vital role in proteomics.

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Authors:

1. *Atarra Post graduate college Atarra, Uttar Pradesh, INDIA.*

Introduction

In the area of therapeutics, the rapid momentum gaind at the turn of the century by the proteomics which is the recent member of the omics family. Proteomics have the large scale of study of protiens especially the composition, structures, functions and interactionsof the protiens which directs the activity of the cell. Due to the frequent change in the protein expression profile, micro and macro environmental conditions, Proteomics is more complex than genomics (Holman et al., 2013). It is expected to yield more direct understanding of function and regulation than analysis of genes by the global scale analysis of plant protiens. It is necessary to identify the genes and protiens that controls crop architecture or stress resistance to facilitate the biological improvement of crop productivity. Therefore the main aim of this review is proteomics technologies and its application for crop improvements.

Types of Proteomics

Proteomics are classified into different groups as follows which are based on the responses of proteins under stress conditions

1. Expression Proteomics

The qualitative and quantitative expression of total proteins are studied by the expression proteomics under two different conditions. The expressional changes which are present and absent in tumour tissue as compare to normal tissue is observed by the 1-D gel electrophoresis, mass spectrometry techniques.

2. Structural Proteomics

The three dimensional shape and structural complexities of functional protiens is studied by the structural proteomics which can give the details about the structure and function of protein complexes present in a specific cellular organelle. For the determination of Structure, different technologies such as X-Ray crystallography and NMR spectroscopy can be used.

3. Functional Proteomics

Protien functions and unrevealing molecular mechanisms within the cell that depends on the identification of the interacting protein partners are explained by the functional protiens.

Proteomics Technologies

It is very difficult to completely characterize the proteome and the degree of success achieved which is depends on the available methods and their flexibilithy to automation and high amount formats. The parameters which can be used are complexity of the protein mixture, levels of expression and medication and intracellular localization all impact the choice of proteomics technology. Both analytical and bioinformatics tools are used for the characterization of protein structure and functions.

1. Two-Dimensional Polyacrylamide Gel Electrophoresis (2D-PAGE)

For the separation of protiens from a mixture, 2D-PAGE is used which provides the information such as molecular weight, isoelectric point, presence or absence of protiens in a sample. 2D-PAGE of high resolution can resolve upto 10,000 protiens spots per gel and the stains used for the visualization of protiens are Coomassie blue, silver, SYPRO Ruby and Deep Purple. Isoelectric point separate the common protiens in the horizontal direction and in vertical direction by the size and this map of protein spots is called as the protein fingerprint of that particular sample.

2. Mass Spectrometry for Protein Characterization

Application of the mass spectrometry in the field of proteomics research is the new and rapidly growing development which is now being used for the high amount characterization and identification of protiens in addition with the development of comprehensive protein databases and advances in computational methods. Mass spectrometry is the analytical technique which produces spectra of the atomic mass or molecular mass and this spectra is then used to determine the elemental or isotopic signature of the sample.

3. MALDI-TOF-MS

Ionization of peptides of the protiens is done by the MALDI which has its own energy source the laser pulse. Time of flight (TOF) have been developed for use in mass spectrometers and is common because of the ease to operate. TOFs are commonly used coupled with the MALDI ion source and quadrupole analyzers are used coupled with ESI source. For the determination of precised protein molecular weight, MALDI-TOF nstrument is used.

4. Electro Spray Ionization

In ESI mass spectrometry, a potential is applied to create a fine spray of charged droplets that are dried and introduced into the mass analyzer.

5. Chromatographic Techniques

Closely related components of mixtures are separated by the different group of methods of chromatography. It is the technique of separating two components distributed between two phase (mobile and stationary). Due to the capability of analyzing large, fragile bio molecules, Chromatography is very applicable in proteomics research.

6. Protein Microarrays

A small amount of crude sample is needed for the protein biochip or protein microarrays. Through this techniques, thousands of proteins can be analyzed and enables screening for specific types of post transitional modification.

Proteomics Techniques Offer New Tools for Plant Biotechnology

The critical role played by the knowledge of key proteins in the proper growth and development of the plant which are critical to drive the biotechnological improvement of crop plants. The cellular homeostasis are maintained by these proteins under the given environment by controlling physiological and biochemical pathways. Genomics and proteomics are the two major wheels that keep the discovery of novel genes rolling, it is revealed by the published research literature which can be placed into the pipelines for the crop improvement programs. Crop proteomics become an essential part of the integrated omics approaches.

1. Two-Dimensional Maps of Different Plant Tissues

Several articles have been published by the Jacoby *et al*. (2013) in which proteomes of different plant tissues from rice and Arabidopsis is discussed and mapped. There are many plant proteomics studies have been published focusing on the specific sub cellular proteomes or protein complexes including plasma membrane, roots, mitochondria and chloroplasts.

Organ Specific Proteome Analysis of a Biotic Stress Response in Crop Plants

1. Proteomics of Leaf Photosynthesis and Senescence to Understand Crop Productivity
2. Xylem and Phloem Proteomics of Root-to-Leaf Signalling Pathways during Stress
3. Root Proteomics of Symbiotic Systems to Improve Legume Productivity
4. Progress in Crop Proteomics for Stress Responses
5. Post-translational modification
6. Analyses of Food Quality, Safety and Nutritional Values

Review of Literature

Lilley and Dupree, (2006) worked on methods of quantitative proteomics and their applications to plant organelle characterization and concluded that 2D-difference gel electrophoresis as well as differential isotope tagging strategies coupled to non gel based LC-MS are proving useful in this area of research.

Chandrasekhar *et al.*, (2014) studied on a review of proteomics and its applications and focused on different types of techniques for analyzing the expressed proteins, also concentrated on applicative perspective of proteomics in the fields of biomedical, agriculture and food finally concluded that applications for proteomics are relevant to all of the biological process.

Katam, Jones and Sakata, (2015) studied on advances in proteomics and bioinformatics in agriculture research and crop improvement. The advances in proteomics in recent years includes protein isolation methods, mass spectrometry, protein- protein interactions and post translational modification and concluded that advances in protein interactions and bioinformatics will have an increasing impact on better understanding the various functional aspects in plants.

Aslam *et al.*, (2016) worked on the technologies of proteomics and their applications, and said that although all fields related to biological science have been benefited with increasing use of proteomics techniques still further work is required in the improvement of the producibility and performance of well known proteomics tools.

Ahmad *et al.*, (2016) discussed the role of proteomics in crop stress tolerance and also different types of abiotic stresses and their effects on plants particularly with stress induced expressions of proteins and concluded that proteomics have gained attention due to the ease in handling the proteomic analysis tools and accuracy of the results.

Komatsu and Hossain, (2017) discussed on plant proteomic research and this includes four reviews and 13 original articles on environmental proteomic studies. Six articles highlight iTRAQ based proteomic approaches among the 13 original articles

Conclusion

The changes of protein which are induced by various conditions are investigated by the proteomics which is the powerful and useful tool. It is expected to yield more direct understanding of function and regulation than analysis of genes by the global scale analysis of plant protiens. The explanation related to the compound relationship that exists between stress tolerance and crop productivity has contributed to various proteomic studies. The existence of this relationship enables to generate the strategies of development of novel breeding that results in productivity of crop and environmental performance. From this review it is concluded that all the biological process are relevant to the applications of proteomics and provides an effective way to utilize the expressed protein data.

References:

Ahmad, Parvaiz, *et al.* “Role of Proteomics in Crop Stress Tolerance.” *Frontiers in Plant Science*, vol. 7, Aug. 2016.

Aslam, Bilal, *et al.* “Proteomics: Technologies and Their Applications.” *Journal of Chromatographic Science*, vol. 55, no. 2, Oct. 2016, pp. 182–196.

Beyene, Belachew, *et al.* “Review on Proteomics Technologies and Its Application for Crop Improvement.” *Innovative Systems Design and Engineering*, vol. 7, no. 6, 2016, pp. 7–15.

Chandrasekhar, K., *et al.* “A Short Review on Proteomics and Its Applications.” *International Letters of Natural Sciences*, vol. 17, 2014, pp. 77–84.

Holman, J. D., Dasari, S. and Tabb, D. L., 2013. Informatics of protein and posttranslational modification detection via shotgun proteomics. *Methods Mol. Biol.*1002, 167–179.

Jacoby, R. P., Millar, A. H. and Taylor, N. L., 2013b. Application of selected reaction monitoring mass spectrometry to field-grown crop plants to allow dissection of the molecular mechanisms of a biotic stress tolerance. *Front. Plant Sci.*4:20.

Komatsu, Setsuko, and Zahed Hossain. “Preface—Plant Proteomic Research.” *International Journal of Molecular Sciences*, vol. 18, no. 1, Apr. 2017, p. 88.

Lilley, K. S, and Paul Dupree. “Methods of Quantitative Proteomics and Their Application to Plant Organelle Characterization.” *Journal of Experimental Botany*, vol. 57, no. 7, 2006, pp. 1493–1499.