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Proteomics Technologies and its Application for Crop Improvement

Harsha Sharma¹

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Abstract:

Proteomics is defined as the study of interaction of cell and proteins. Proteomics is a useful tool in shifting from genomics to the complimentary protein of human within the wide field of functional OMICS. Proteomics is expected to produce better abberation markers for diagnosis and therapy of various deadly diseases because the proteome reflects more precisely on the basis of 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. Mass spectroscopy has become an significant tool in the field of molecular and cellular biology and plays an important role in proteomics. The advent of proteomics has opened new doors for opportunities and challenges for those who are keen to know the depth of this field.

Keywords: Bioinformatics, Mass Spectroscopy, Proteomics.





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

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Introduction

In the area of therapeutics, the rapid momentum gaind in certain years is with the help of proteomics developed recently. Proteomics study protiens especially the composition, structures, functions and their interactions 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 provide direct understanding of functions and regulation. It is necessary to identify the genes and protiens that controls crop architecture or stress resistance to facilitate the biologically driven improvement in crop productivity. Therefore the main aim of this review is proteomics technologies and its application for crop improvements.

Types of Proteomics

Proteomics are divided into different categories which are based upon 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

Stuctural proteomics studies three dimensional shape and structure of complex functional protiens. This helps in determining the same in differet cell organelles. X-Ray crystallography and NMR spectroscopy can be used in this.

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 quite difficult to completely characterize the proteome and the proximity of success, which rely on the available methods and their flexibility. The factors like complexity of the protein mixture, levels of expression and medication and intracellular localization affect 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)

The segregation 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 ten thousand protiens marks per gel and then 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 or linear direction and in vertical direction with respect to the size and this chart of protein marks is called as the protein fingerprint.

2. Mass Spectrometry for Protein Characterization

Application of mass spectrometry in the field of proteomics research is new and growing rapidly. This is being now applied`when large amount of proteins are to be characterized and identified. Mass spectrometry is the analytical technique which produces spectra of the atomic mass or molecular mass and this spectra is then used to evaluate the principle signature of the given protein 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) has been made for mass spectrometers and is common because it is easy to operate. For the determination of precised protein molecular weight, MALDI-TOF instrument is used which is coupled with each other.

4. Electro Spray Ionization

In ESI mass spectrometry, a fine spray of charged particles or drops are created which are then dried amd then subjected to 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

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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- A New Tool for Plant Biotechnology

In the development and proper growth of crop plants proteins, proteins paly a key role. The cellular environment is maintained by these proteins by controlling physiological and biochemical passage. Genomics and proteomics discoveries in the fieldof genology. Crop proteomics has become a significant part of the integrated omics.

1. Two-Dimensional Maps of Different Plant Tissues

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

Organ Specific Proteome Analysis: Biotic Stress Response in Crop Plants

- 1. Proteomics of leaf during photosynthesis and senescence in order to determine crop productivity.
- **2.** Proteomics of xylem and phloem of roots and leaves during stress.
- **3.** Proteomics of symbiotically associated root legumes to enhance 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

Chandrasekhar *et al.*, (2014) studied on a review of proteomics and its applications and emphasized on various techniques for analyzing the expressed proteins. He has also put a strain on the application of proteomics in the area of biomedical, agriculture and food industries. This resulted into a conclusion proteomics can be used in any field of biology.

Katam, Jones and Sakata, (2015) studied the advances in proteomics in recent years which includes protein isolation methods, mass spectrometry, protein- protein interactions and post translational modification.

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) studied the function of proteomics in stress tolerance in plants.

Conclusion

The changes of protein which are induced by various conditions are investigated by the proteomics which is the powerful and useful tool. It. 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.



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