



Proteomics: A Trending Approaches in Plant Breeding

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A sharp decline in natural resources such as arable land and water along with a continuous steep increase in global food demands have exerted a pressure on farmers to produce more with fewer resources. A viable solution to release this pressure is to speed up the plant breeding process by employing biotechnology in breeding programs. Proteomics has progressed at a tremendous pace since the year 2000, and that has resulted in establishing and understanding the proteomes of tissues, organs, and organelles under both normal and abnormal (adverse) environmental conditions. Established proteomes have also helped in re-annotating the genome of many crops and revealing the new role of previously known proteins. The word “proteome” is derived from PROTEins expressed by a genOME. Analogous to genomics, the term “proteomics” describes the study and characterization of the complete set of proteins present at a given time in the cell (Wilkins *et al.*, 1995). Proteomics refers to the systematic analysis of protein profiles of entire cells, tissues, organisms, or species. It represents the protein counterpart to the analysis of gene function..

Proteomics vs Genomics and interrelation of Genomics and Proteomics

DNA sequence does not predict if the protein is in an active form or not so to study of proteomics is important for analyzing the function of protein i.e in functional proteomics. RNA quantitation does not always reflect corresponding protein levels. Multiple proteins can be obtained from each gene due to alternative splicing. Genomics cannot predict post-translational modifications and the effects there of DNA/RNA analysis.

Aim of proteomics

Proteomics aiming to the Detect the different proteins expressed by the tissue, cell culture, organism using 2-Dimensional Gel Electrophoresis .by using the 2 dimensional gel electrophoresis it enables to know the expression of proteins within cell as well as in cell culture. It Store those information in a database. It also helps to compare expression profiles between a healthy cell vs. a diseased cell. Data comparison also study aids for testing and drug design rationally.

Types of proteomics

1. **Structural proteomics:** The Structural proteomics concerns with mapping out the 3-D structure and nature of protein complexes present specifically in a particular cell/organelle. The ultimate aim of structural proteomics is to build a body of structural information that will help predict the probable structure and potential function for almost any protein from knowledge of its coding sequence. This branch of proteomics helps in assembling information about protein-protein interactions and about architecture of cells to explain how the expression of certain proteins contributes in cells unique characteristics.

- 2. Functional Proteomics:** It refers to the use of proteomics techniques to analyze the characteristics of molecular protein-networks involved in a living cell. One of the recent successes of functional proteomics is the identification and analysis of molecular protein-networks involved in the nuclear pore complex (NPC) in yeast. This success helps to understand the translocation of molecules from nucleus to the cytoplasm and vice-versa.
- 3. Expressional proteomics:** The pattern of expression of the complete proteome or of its part (sub-proteome) between samples can be compared with the help of this approach. Expression proteomics is quite useful in identifying disease specific proteins.
- 4. Interaction proteomics:** It concern with the investigation of protein interaction on the atomic, molecular and cellular levels.
- 5. Cellular proteomics:** It deals to map the location of proteins and protein- protein interaction in whole cells during key cell events. This method centers on the use of techniques such as x-ray tomography and optical fluorescence microscopy.
- 6. Proteomic analysis (Analytical protein chemistry):** It deals with the characterization of proteins and their post translational modifications.

Techniques used for structural proteomics

It aims the determination of three-dimensional protein structures in order to better understand the relationship between protein sequence, structure and function. NMR and x-ray crystallography are used to determine the structure of macromolecule. Nuclear magnetic resonance spectroscopy, most commonly known as NMR spectroscopy or magnetic resonance spectroscopy (MRS) is a spectroscopic technique to observe local magnetic fields around atomic nuclei. To obtain optimal results, protein should possess minimum 95% purity.

Domains: Discrete portions of the proteins that fold independently from the rest of protein and they have their own function and serve as the building blocks of proteins.

Motif: Domains contain a region of conserved pattern of amino acids or conserved combinations of the structural elements formed.

Applications of proteomics:

1. Protein Mining: Proteomics study helps to catalog all the proteins present in a tissue, cell, organelle, etc.
2. Differential Expression Profiling: Identification of proteins in a sample as a function of a particular state i.e differentiation, stage of development, disease state, response to stimulus or environments.
3. Network Mapping – Identification of proteins in functional networks of biosynthetic pathways, signal transduction pathways, multiprotein complexes.
4. Mapping Protein Modifications: Characterization of posttranslational modifications viz, phosphorylation, glycosylation, oxidation etc.

References

1. Abdalla KO, Rafudeen MS. (2012). Analysis of the nuclear proteome of the resurrection plant *Xerophyta viscosa* in response to dehydration stress using iTRAQ with 2DLC and tandem mass spectrometry. *J Proteomics*, 75: 2361–74.
2. Agrawal GK, Pedreschi R, Barkla BJ, Bindschedler LV, Cramer R, Sarkar A, *et al.* (2012). Translational plant proteomics: a perspective. *J Proteomics*, 75:4588–601
3. Baggerman, G., Vierstraete, E., Loof, A. D., and Schoofs, L. (2005). Gel based versus gel-free proteomics: areview. *Comb. Chem. High Throughput Screen.* 8: 669–677.
4. Buell CR, Joardar V, Lindeberg M, Selengut J, Paulsen IT, Gwinn ML, *et al.* The complete genome sequence of the Arabidopsis and tomato pathogen *Pseudomonas syringae* pv. tomato DC3000. *Proc Natl Acad Sci U S A* 2003;100:10181–6.
5. Cooper B, Campbell KB, Feng J, Garrett WM, Frederick R. (2011). Nuclear proteomic changes linked to soybean rust resistance. *Mol Biosyst*, 7: 773–83.