AgriCos e-Newsletter
ISSN: 2582-7049
AgriCos e-Newsletter
Open Access Multidisciplinary Monthly Online Magazine
Volume: 04 Issue: 08 August 2023 Article No: 06

Probing the Power of Proteomics: Unraveling the Significance in Vegetable Crop Research

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SUMMARY

Proteomics, the study of proteins and their functions, plays a crucial role in understanding the complex biology of vegetable crops and holds immense significance for crop improvement and nutritional quality. By analyzing the complete set of proteins expressed in vegetable crops, proteomics provides valuable insights into their growth, development, stress responses, and interactions with the environment. Proteomics enables researchers to identify and quantify proteins associated with desirable traits such as yield, disease resistance, and nutritional content. This knowledge can guide breeding programs and facilitate the development of improved vegetable varieties. Additionally, proteomic studies shed light on the underlying mechanisms involved in crop responses to biotic and abiotic stresses, aiding in the development of stress-tolerant cultivars. Moreover, proteomics allows for the assessment of changes in protein composition and abundance during different stages of crop development and post-harvest storage. This information helps optimize crop management practices, enhance post-harvest shelf life, and ensure nutritional quality for consumers.

INTRODUCTION

Proteomics is a recent member of the 'omics' family that has gained rapid momentum at the turn of the century, particularly in the area of therapeutics. In 1994, around 20 years ago, is considered the year of birth for "proteomics", being the term an extension of the word "proteome" first coined by Marc Wilkins while being a Ph.D. student at Australia's Macquarie University (Agrawal *et al*., 2013). Proteomics is the large scale study of proteins particularly their composition, structures, functions, and interactions of the proteins directing the activities of cell (Wilkins *et al*., 1995). The main goal of proteomics is to study, know and understand "how", "where", "when", and "what for" are the several hundred thousand of individual protein forms produced in a living organism, how do they interact with one another and with other molecules to construct the cellular building, how can they be modified and work in order to fit in with programmed growth and development, and to interact with their biotic and a biotic environment (Smith *et al*., 2013). The need for nutritious food is increasing in a developing world, and vegetable crops can supply that need. Vegetable crop production faces ongoing challenges in identifying and adapting to unfavourable changes in their environment to prevent negative effects on growth and development. Throughout their life cycle, plants frequently encounter diverse abiotic stresses. Numerous proteins react to these stresses at the pre, post and translational stages, according to current information. It would be simple to thoroughly explain the processes of stress tolerance in plants if we understood the function of these stress-inducible proteins. The proteomics study provides a novel method for identifying proteins and pathways linked to physiological and stress responses in plants.

What is proteomics?

The term 'proteome' was first coined in 1994 by an Australian post doctoral fellow named Marc wilkins. Proteome refers to the total set of proteins expressed in a given cell at a given time. Proteomics is the large scale study of proteins, particularly their structures and functions or the study of proteome is termed as proteomics.

Aim to study proteomics:

The aim is to study the dynamic protein products of the genome and their interactions.

What proteomics can answer?

- Protein identification
- Protein Expression Studies
- Protein Function
- Protein Post-Translational Modification

- Protein Localization and Compartmentalization
- Protein-Protein Interactions

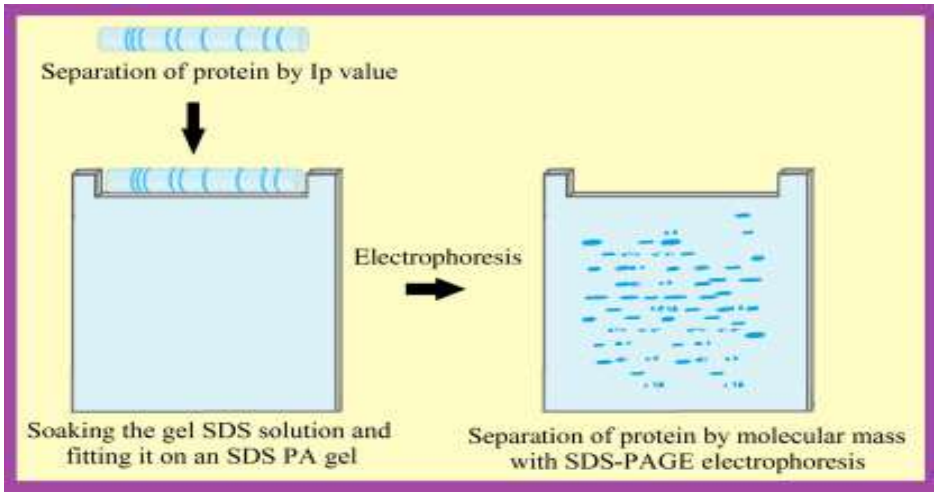
Two major technologies used in proteomics:

2-D gel electrophoresis, mass spectrometry technique were used to observed the protein expressional changes, which is present and absent in tumour tissue, when compared with normal tissue. Which are over expressed and under expressed can be identified and characterized protein activities multi-protein complexes, and signalling pathways (Hinsby *et al*., 2003).

2-D electrophoresis:

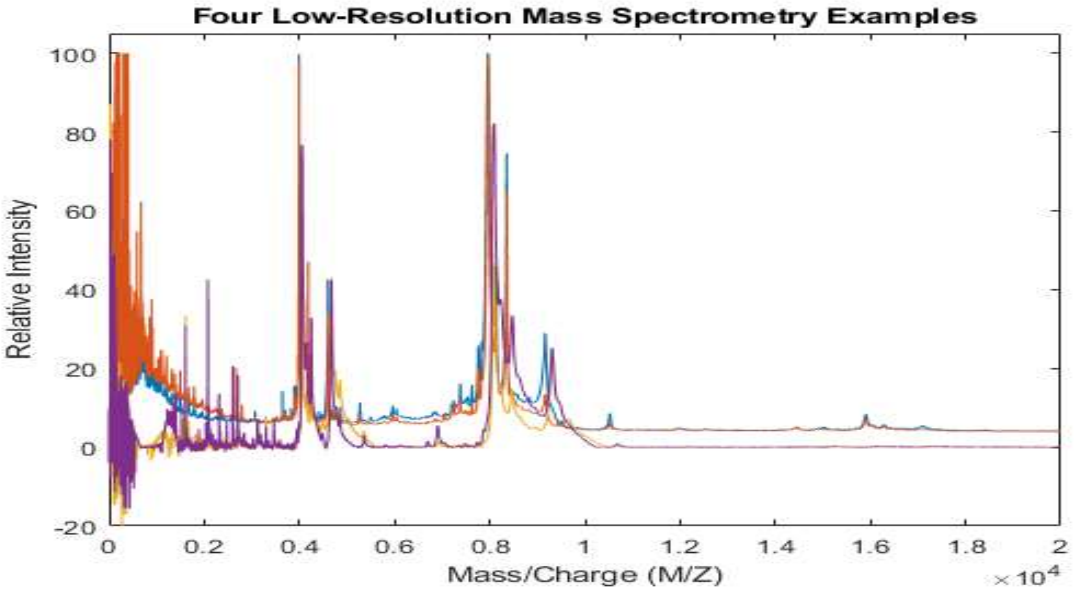
2-D gel electrophoresis is a powerful and widely used method for the analysis of complex protein mixtures extracted from cells, tissues, or other biological samples. It is the method available which is capable of simultaneously separating thousands of proteins.

2-D electrophoresis separates proteins depending on two different steps: the first one is called isoelectric focusing (IEF) which separates proteins according to isoelectric points (pI); the second step is SDS-polyacrylamide gel electrophoresis (SDS-PAGE) which separates proteins based on the molecular weights.



Mass spectrometry:

- Mass spectrometry is used for protein identification
- It is useful to obtain structural information like peptide mass sequence
- Identification of chemical modification (PTM in proteins after synthesis)
- Identification of organisms (identifying bacteria by finger printing proteins)



Principle:

Mass spectrometry (MS) is an analytical technique that separates ionized particles such as atoms, molecules, and clusters by using differences in the ratios of their charges to their respective masses (mass/charge; m/z), and can be used to determine the molecular weight of the particles.

Stages of mass spectrometry:

Ionization

Before being introduced into an ionisation chamber, the sample is vaporised before being pounded by a barrage of electrons released by a metal coil that has been electrically heated. The particle loses one or more electrons as a result of the violent collisions, creating a positively charged ion. Due to the inherent difficulties of extracting a second electron from an ion that is already positive, the majority of them have a positive charge.

Acceleration

The positively charged ionization chamber repels the positively charged ions, which accelerate towards three negatively charged slits with progressively decreasing voltage. The speed at which they accelerate depends on their mass so the lighter ions move faster than the heavier molecules.

Deflection

The stream of positively charged ions are deflected by a magnetic field in this stage. The extent of the deflection depends on the mass and charge of the ion. The lighter the mass of the ion, the more the deflection. Ions with a charge greater than +1 will also be deflected more.

Detection

In the last step, a detector using the mass-to-charge ratio (m/z) of the ions flowing through the mass analyzer detects the beam of ions. An electron that has jumped from the metal onto the ion when the ion strikes the detector balances the charge. This produces an electrical current that is inversely proportional to the ion's abundance. After all four phases are complete, the mass spectrum is produced. It is then transferred to a computer for analysis, where it reveals the various m/z values of the ions present and their relative abundance.

Applications of proteomics

- **Protein Mining:** Catalogue all the proteins present in a tissue, cell, organelle etc.
- **Differential Expression Profiling:** Identification of proteins in a sample as a function of a particular state: differentiation, stage of development, disease state, response to stimulus or environments.
- **Network Mapping:** Identification of proteins in functional networks: biosynthetic pathways, signal transduction pathways, multiprotein complexes.
- **Mapping Protein Modifications:** Characterization of posttranslational modifications: phosphorylation, glycosylation, oxidation, etc.

Challenges in applying the proteomics study:

- Complexity in studying variants of protiens due to large number.
- Broad study of cellular proteins is required.
- Detailed analysis is required.
- Post transcriptional modification of proteins.
- Many transcripts give rise to more than one protein.

CONCLUSIONS

Proteomics is a composite study of set of proteins. The detailed protein studies will shed light on the role of protein modification in protein function. The development of proteomics renders us with a powerful tool to examine biochemical processes at the molecular level and identify sets of protein. During plant life sometimes in adverse conditions it can passes through biotic or abiotic stresses, at that time proteomics can be useful to identify sets of protein.

Future prospective

Integration of vegetable crops proteomics-related datasets accumulated from various tissue sources, employing different proteomic tools is a daunting challenge, but would result in obtaining comprehensive snapshots on crops proteomes and pave way for establishment of reference proteomes and protein databases for many vegetable crops. Creation of a comprehensive and integrated database, consisting information on vegetable proteomes, though as of now seems unrealistic, would be possible by synergistic contribution by various academic consortia working on vegetable proteomics around the world. In the future, integration of advanced high through put approaches, such as microarray, genomics, and proteomics, in various developmental stages and stress conditions will provide us with transgenic plants developed for combating with High stress.

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