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Proteomics in Agriculture

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Introduction

Proteins are large biological molecules or macromolecules, consisting of one or more long chains of amino acid and are the work horses of biological systems. They play key roles in constructing and maintaining living cells. The end product of our genes is proteins. The term “proteome” was first used by Wilkins *et al*. (1994) to describe the protein complement to the genome. A genome has multiple proteomes. It links the static information contained in the organism’s DNA to the dynamic physiology of the whole cell and whole organism i.e. its phenotype. Analogous to Genomics, the term "Proteomics" was first introduced by Marc Wilkins in 1994, as a data-rich discipline that uses Mass Spectrometry (MS) and bioinformatics to characterize the proteome of a cell (Wilkins, 2009).Knowing the identity, abundance, turnover rate, Post-Translational Modifications (PTMs) and interactions within a cell, as well as understanding the mechanism are the benefits of this proteomics science (Hirano *et al.*, 2004*).*

Why Proteomics?

The high-density genomic maps are available. Additionally, a genome-wide scan of the loci responsible for trait variability is being conducted. There is a wealth of information available about desirable genes and their functions. Candidate genes for a variety of qualities have been discovered, but they have yet to be used. As a result, we entail this science. The Nobel Laureate Edmond H. Fischer quoted that, genome sequencing might enable us to predict the proteins that can potentially be generated, but not where, when, or at what level’. Gene product behaviour is difficult, if not impossible, to anticipate from gene sequences. Even if a gene is transcribed, it may be controlled at the translational level. The sequence of

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proteins is revealed by the genome sequence, but not by post-translational modification. These changes are not explained by genomics. Proteomics fills in the voids between genomic sequencing and cellular behavior (Fischer, 1997).

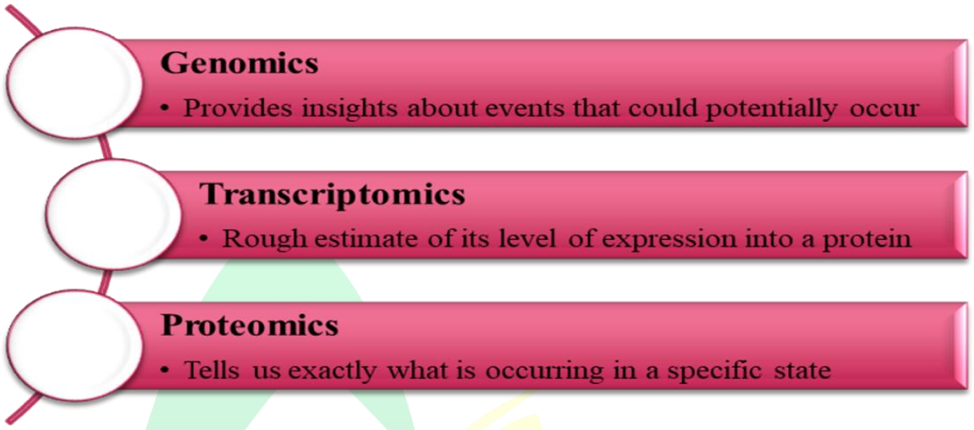

Fig: Roles of Omics

1. **Classification of Proteomics**

1.1 Structural Proteomics:- The goal is to figure out the 3D structure of proteins and protein complexes. X-ray crystallography and NMR spectroscopy are employed. Using bioinformatics, it will aid in comparative modelling and protein fold recognition.

1.2 Functional Proteomics:- The study of protein interactions at a bigger scale is known as functional proteomics. Protein-protein interactions must be characterized in order to determine the activities of the proteins. It also describes how proteins get together to form larger complexes. In interaction proteomics, technologies like affinity purification, mass spectrometry and the yeast two-hybrid system are particularly useful.

1.3 Expression Proteomics:-The study of protein expression at a wider scale is known as expression proteomics. It aids in the identification of key proteins in a sample as well as proteins that are differently expressed in similar samples. 2D-SDS PAGE, MALDI-TOF, Liquid chromatography, MS-MS, SELDI and Protein microarray are the most common techniques used in expression proteomics.

2. **Steps in Proteomic Studies**

The proteins of interest should be isolated from the relevant organ, tissue or cell. Proteins must be separated using a variety of methods, including 2D gel electrophoresis, non-

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gel-based electrophoresis and chromatographic techniques, to reduce the complexity of the protein extract. After trypsin digestion on the Maldi-TOF, proteins must be identified using Peptide Mass Fingerprinting (PMF), which can be done using databases.

3. Application of Proteomics in Agriculture in Crop Improvement

- Rice under drought stress was shown to have proteins involved in photosynthesis, cell elongation, antioxidant metabolism and lignifications. Drought-responsive proteins, APX and Cu-Zn SOD, have been identified and can be used as markers to research plant responses to drought stress (Salekdeh *et al.,* 2002).
- OsCYP2, a salt-induced rice cyclophilin was isolated and identified and having Peptidyl-Prolyl cis-trans Isomerase activity. Cyclophilin 2 (OsCYP2) transgenic rice seedlings were found to be more resistant to salt stress than wild-type seedlings.
- During *Magnaporthe* infestation in rice, an apoplast localized cyclophilin group protein was discovered, suggesting that its activity is critical for dealing with most cellular stressors (Shenton *et al.,* 2012).
- The investigation of the process of programmed cell death during salt stress begins with the mitochondrial proteome (Chen *et al.,* 2009).
- Now, the proteomic technique attempts to characterize the proteins responsible for resistance caused by PAMPs, which will be critical in the plant defence era.
- Characterization of the process with the final gene product responsible for the bio control features, such as lytic enzymes and plant resistance elicitors, can be done directly (Massart*et al.,* 2015).
- Identification of bacteria might be done accurately and has been utilized for taxonomic studies by acquiring the profile of those proteins and analyzing quantitatively.
- Ekramoddoullah and Hunt in 1993 used 2D PAGE to differentiate between susceptible and resistant seedlings of *Pinus lambertiana* (sugar-pine) to white pine blister rust *Cronartium ribicola*.
- The Pierre de Wit research group's pioneering work on the *Cladosporium fulvum* and tomato interaction from 1985 exemplifies the importance of proteomics in plant fungal diseases research.

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- The first avirulence gene product (Avr9) was characterized using preparative polyacrylamide gel electrophoresis by De Wit et al in 1986 from extraction of tomato apoplastic fluids.
- Meiotic proteomics can provide you a lot of information on how meiocytes work. It reveals the recombination mechanism, highlighting the effects of male sterility genes and elucidating cell cycle regulation.

4. Challenges

- Proteins cannot be amplified like DNA. So, it is more difficult to detect less abundant species.
- Difficulty, as some proteins have over 1000 different variations. For detecting a wider spectrum of unwanted outcomes, more sensitive approaches are required.
- Unknown proteins will be encountered often in proteomics, necessitating deeper structural genomics and interaction research.
- Difficult to access the genomic regions simply based on proteomics as frequent encounter of unknown proteins in Proteomics will occur, such cases need further structural genomics and interaction studies.
- Protein-Protein interactions are quite complicated.
- It's nearly impossible to detect a cell's entire programmed protein complement.

5. Future Prospect

- Integrated approach of omics techniques and system biology should be approached.
- Contribute to the development of functional genomics.
- An efficient tool to identify and characterize isolates.
- New types of proteomics technologies combined with advanced bioinformatics will enhance its efficiency.
- Creates new possibilities in the elucidation of host pathogenmechanisms and will have throughput knowledge of various stages.

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