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Editorial

Editorial Note on Introduction and Types of Proteomics

Sathvik Arava*

Department of Modern Chemistry, Acharya Nagarjuna University, Guntur, India

EDITORIAL

The term “proteome" refers to the entire proteome of a cell. Proteomics refers to the large-scale characterization of all protein supplementation of cells, tissues, and even whole organisms. Modern proteomics research involves many different fields. These include studies of protein-protein interaction, protein function, and protein localization. The development of proteomics is a direct result of advances in large-scale nucleotide sequencing of various genomes. Without this development, protein identification would be difficult. Obtaining information about proteins is important because they determine the phenotype of the cell. It is impossible to understand the mechanisms of disease, aging, etc. Only by understanding the function of protein and its modification can drug targets for various diseases be determined. One of the main goals of proteomics is to create a three-dimensional map of the cell that indicates the location of the protein.

The proteome of a given cell is dynamic. In order to respond to internal and external signals, protein environment at a specific moment. It is speculated that in organisms with known the cell's biochemical mechanisms can be adjusted. This may lead to various changes in the protein, such as post-translational modifications, changes in cell location, and effects on its synthesis or degradation. Therefore, examining the proteome is like taking a snapshot of the genome sequences, approximately one-third of the gene sequences cannot be assigned any function. The complete identification of the proteins in the genome will help structural genomics projects. The goal of these projects is to obtain the 3D structure of all the proteins in the genome. Structural analysis will help to assign functions to many of these proteins. In addition to protein identification, one of the main goals of proteomics is to characterize post-translational modifications of proteins.

Types of proteomics

Expression proteomics: The quantitative study of the expression of proteins between samples that are different due to certain variables is called expression proteomics. With this method, you can compare the protein expression of the entire proteome or sub proteome between samples. This can be used to identify disease-specific proteins. For example, it is possible to analyze the differential expression of proteins from tumor samples from cancer patients and similar tissue samples from normal individuals. Using two-dimensional gel electrophoresis, followed by mass spectrometry, it is possible to identify proteins that are overexpressed or under-expressed in cancer patients compared to normal individuals. This can be compared to the microarray data. Identifying these can provide clues to understanding the basis of tumors development.

Structural proteomics: Unlike the comparison of the same cells or tissues in normal and diseased states in expression proteomics, structural proteomics aims to map the structure and properties of protein complexes that exist specifically in specific organelles. The objective is to identify all the proteins present in the complex and to characterize all the protein interactions that occur between these proteins. Purification and isolation of specific subcellular organelles or protein complexes can help gather information about cell structure and explain how the expression of certain proteins gives cells their unique characteristics.

Functional proteomics: Functional proteomics is a very broad term for many targeted specific proteomics methods. It can be defined as the use of proteomics methods to analyze the characteristics of molecular networks involved in living cells. One of the main goals is to identify the molecules participating in these networks. One of the successes of functional proteomics is the identification and analysis of protein networks involving nuclear pore complexes. This discovery led to the identification of new proteins that are important for moving important molecules from the cytoplasm of the cell to the nucleus and vice versa.

Correspondence to: Sathvik Arava, Department of Modern Chemistry, Acharya Nagarjuna University, Guntur, Andhra Pradesh, India, Tel: +32-466-90-04-51; E-mail: sathvikraj38@gmail.com

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