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Importance of Proteomics: A Review

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ABSTRACT
Proteomics is the complete evaluation of the function and structure of proteins to understand an organism's nature. Mass spectrometry is an essential tool that is used for profiling proteins in the cell. However, biomarker discovery remains the major challenge of proteomics because of their complexity and dynamicity. Therefore, combining the proteomics approach with genomics and bioinformatics will provide an understanding of the information of biological systems and their disease alteration. Proteomics is playing an increasingly important role in identifying pathogens, emerging and re-emerging infectious agents, understanding pathogenesis, and diagnosis of diseases. Recently, more advanced and sophisticated proteomics technologies have transformed disease diagnostics and vaccines development.This article provides a brief overview of history, applications, challenges and importance of proteomics.

Key words: *Proteomics, biomarker, drug development, post-translational modifications.*

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I. INTRODUCTION

Proteomics is the large-scale study of proteins, which are essential molecules that perform a vast array of functions within living organisms. Proteins are the final functional products of genes, and understanding their structure, function, and interactions is crucial for comprehending biological processes and disease mechanisms[1,2].

Proteomics is a new type of 'omics' that has rapidly developed, especially in the therapeutics field. The word proteome was created by Marc Wilkins in 1995. Proteomics is the study of the interactions, function, composition, and structures of proteins and their cellular activities. Proteomics provides a better understanding of the structure and function of the organism than genomics. However, it is much more complicated than genomics because the protein expression is altered according to time and environmental conditions. It is estimated that there are almost one million human proteins, many of which contain some modifications such as post-translational modifications (PTMs). However, it is also estimated that the human genome codes for about 26000-31000 proteins. There are a variety of proteomics techniques including one-dimensional (1D) and two-dimensional (2D) gel electrophoresis (2-DE), as well as gel-free high-throughput screening technologies such as multidimensional protein identification technology, stable isotope labeling with amino acids in cell culture, isotope-coded affinity tag, and isobaric tagging for relative and absolute quantitation[3-5].

Proteomics is a multi-step process that requires meticulous control at each stage to prevent non-biological variables from affecting the expression and interaction of proteins. The most crucial stage is sample preparation as it solubilises all of the protein in the sample and gets rid of any lipids or other interfering inhibitory substances. For precise, repeatable, and dependable findings, sample preparation is essential. The most used technique for isolating and separating proteins is PAGE (polyacrylamide gel electrophoresis). Proteins are separated using 1-DE, 2-DE, and high-performance LC (HPLC). 1-DE is used to separate proteins according to their molecular mass. Since proteins are soluble in sodium dodecyl sulphate (SDS), protein solubility is rarely a problem[6-8].

Importance of proteomics

- ➢ *Understanding Cellular Function:* Since proteins are the main effectors in cells, proteomics helps in decoding how cells function in health and disease.
- ➢ *Biomarker Discovery:* Identifying proteins associated with diseases for diagnostics, prognostics, and therapeutic targets.
- ➢ *Drug Development:* Revealing targets for new drugs and understanding drug mechanisms.

- *Post-translational Modifications (PTMs):* Studying modifications like phosphorylation and glycosylation that regulate protein function.
- *Protein-Protein Interactions:* Mapping interaction networks to understand complex biological pathways[9,10].

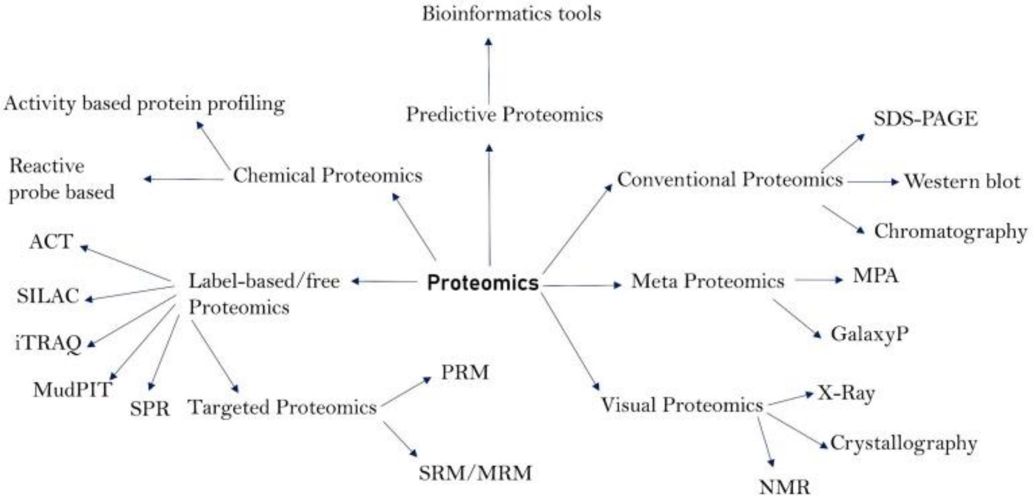

Figure 1: Major proteomics techniques and their subdivisions

Applications of proteomics

Proteomics has a wide range of applications across various fields of biology, medicine, agriculture, and environmental sciences. By studying the complete set of proteins expressed by a genome, proteomics helps in understanding cellular processes, disease mechanisms, and the development of new therapies. Below are some of the major applications of proteomics;

- **Disease Diagnosis and Biomarker Discovery:**Identification of disease-specific proteins that serve as biomarkers for early detection, diagnosis, and prognosis of diseases like cancer, cardiovascular diseases, neurodegenerative disorders, and infectious diseases.Example: Discovery of cancer biomarkers such as PSA (Prostate-Specific Antigen) for prostate cancer.
- **Drug Development and Therapeutics:**Identification of novel drug targets by studying proteins involved in disease pathways.Monitoring the effect of drugs at the protein level to understand drug mechanisms and off-target effects.Development of personalized medicine approaches by analyzing individual proteomes to tailor treatments.Example: Targeting specific kinases in cancer therapy based on proteomic profiling.
- **Understanding Cellular and Molecular Mechanisms:**Elucidating signaling pathways, protein-protein interactions, and regulatory networks involved in normal and diseased states.Studying post-translational modifications (PTMs) like phosphorylation, ubiquitination, glycosylation, which regulate protein activity.
- **Agriculture and Plant Research:** Improving crop yield, stress resistance, and disease resistance by analyzing plant proteomes.Understanding plant responses to environmental stress (drought, salinity, temperature) at the protein level.Example: Identifying stress-responsive proteins in rice or wheat under drought conditions.
- **Microbial Proteomics:** Characterization of pathogenic organisms to identify virulence factors and potential vaccine targets.Understanding antibiotic resistance mechanisms through protein analysis.Example: Studying Mycobacterium tuberculosis proteome to identify drug resistance markers.
- **Environmental Proteomics (Ecoproteomics):** Studying environmental effects on organisms at the protein level.Monitoring pollution impacts and understanding adaptation mechanisms of organisms to environmental stress.Example: Analyzing fish liver proteome to assess water pollution effects.
- **Proteogenomics:** Integrating proteomics with genomics and transcriptomics to improve gene annotations and understand the functional output of genomes.Example: Validating gene expression data at the protein level in cancer studies.
- **Vaccine Development:** Identification of antigens and immune response-related proteins for vaccine formulation.Example: Discovery of protein antigens for COVID-19 vaccine development.
- **Personalized and Precision Medicine:** Analyzing individual proteomes to design personalized therapeutic strategies.Example: Customizing cancer therapy based on the patient’s tumor proteome profile.

- **Nutritional and Food Science:** Studying food allergens, protein content, and nutritional value of different food sources.Identifying bioactive peptides and understanding digestion and metabolism of dietary proteins[11-14].

Role of proteomics in identifying pathogens

The first stage in diagnosing a disease is to identify the causal agent, since their precise and detailed identification and confirmation aids in the prevention of illness transmission and knowledge of its epidemiology. Biochemical features, Gram staining, and carbohydrate metabolism are some of the traditional methods for identifying bacteria that have been used for a long time.

Proteomics technologies, such as Mass Spectrometry (MS), have recently become popular for precisely identifying and confirming bacterial infections. Proteomics methods are commonly used to identify pathogen structure and other components that contribute to virulence. Proteomics methods are being used to describe the structures of both bacterial and viral pathogens, with the goal of not only identifying structural and non-structural proteins involved in virulence, but also investigating metabolic and physiological factors. Classification of un-sequenced microorganisms has been made easier by using capLC-MS/MS on an Orbitrap[15-17].

Identification of diagnostic markers

Proteins are a significant source of biomarkers and are used for illness diagnosis, prognosis, staging, and monitoring. Hormones, carbohydrate epitopes, enzymes, genetic alterations, and receptors are examples of biomarkers. Pathogen proteins have been shown to be responsible for virulence and infections, and hence can be used to find useful biomarkers for illness detection. The fact that they are important diagnostic indicators has piqued the interest of scientists all around the world in using proteomics technologies to uncover specific disease markers.

Pasteurellosis and pneumonia in sheep have been proven to have biomarkers in the form of proteins and cytokines. Proteomics, both traditional and modern, is playing an increasingly important role in diagnostics, providing trustworthy and meaningful results. Since the last decade, mass spectrometry-based techniques have advanced significantly and are becoming increasingly useful in the search for promising diagnostic markers. Recent advances in quantitative proteomics, as well as increased accuracy, have paved the road for the discovery of effective diagnostic markers for a variety of disorders. The LC-MS-MS method is commonly used to diagnose diseases such as TB and periodontitis[2,18,19].

Challenges

There are many challenges in proteomics. The major challenge is the broad change in protein expression with the environment and cell type. In addition, there is no comparable proteomics method, unlike genomics, that uses polymerase chain reaction. Moreover, protein activities are highly regulated post-transnationally, which adds difficulty is proteomics. Finally, the type of samples and sample preparation techniques are other challenges in proteomics that can significantly change the quality of MS data. For example, the protein and phosphoprotein levels in breast cancer tumor samples were affected by the sample manipulation technique and bio-specimen type[1,20,21].

Conflict-of-interest statement

All authors declare no conflict of interest.

II. CONCLUSION

In the past several years there have been very important extremely useful advances in proteomics methods based on bottom-up display and bottom-up identification using peptides.Proteomics has played a vital role in identifying and distinguishing bacterial infections, as well as understanding and diagnosing their pathophysiology. Using a combination of methods, researchers were able to more effectively detect infections as well as identify and characterize the proteins involved in pathogenicity.Proteomics is a fast, sensitive technology that provides high proteome coverage. Expression proteomics, functional proteomics, and structural proteomics are the three major types of proteomics. There are two different workflows in proteomics: top-down and bottom-up proteomics. In addition, there are increasing uses of proteomics in the majority of biological sciences. Finally, proteomics can assist in finding new biomarkers in different diseases and discover new therapies.

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