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Commentary

Proteom Technology

Yousef Alomi*

Department of Pharmaceutical Care Administration , King Saud University, MOH, Saudi Arabia

ABSTRACT

Proteomics involves the applications of technologies for the identi?cation and quanti?cation of overall proteins present content of a cell, tissue or an organism. It supplements the opposite “omics” technologies like genomic and transcriptomics to expound the identity of proteins of an organism, and to cognize the structure and functions of a specific protein. Proteomics-based technologies are utilized in various capacities for various research settings like detection of varied diagnostic markers, candidates for vaccine production, understanding pathogenicity mechanisms, alteration of expression patterns in response to different signals and interpretation of functional protein pathways in several diseases.

Keywords: Protocell, ELISA; Differential gel electrophoresi;Ion-exchange chromatography;

INTRODUCTION

It It adds perverted "omics" technologies such as genomic and transcriptomics to describe the protein's personality, and the ability to form and structure certain proteins. Proteomics-based technologies are used in a variety of skills in a variety of research settings such as the detection of a variety of diagnostic traits, selections in vaccine production, understanding pathogenicity mechanisms, modification of signaling patterns in various signals and interpretation of effective protein pathways for several diseases Proteomics for all purposes and the marking of general genome protein markers. Mass spectrometry with LC-MS-MS and MALDI-TOF / TOF commonly used hardware is the main focus of current proteomics. however, the use of proteomics resources includes the production of equipment, data sets and thereafter the demand for skilled workers greatly increases costs, thereby reducing their widespread use especially in the developing world. In addition, the proteome is highly potent due to complex regulatory systems that regulate protein production levels.

Low-throughput methods:

1. Antibody-based methods

Strategies such as ELISA (an enzyme-linked immunosorbent assay) and western inhibitors depend on the availability of antibodies targeted to specific proteins or epitopes to identify proteins and measure their production levels.

2. Gel-based methods

Double-dimensional gel electrophoresis (2DE or 2D-PAGE), the main proteomic process performed, uses electrical energy to separate proteins during gel support for their charge (size 1) and size (size 2). Differential gel electrophoresis (DIGE) is a 2DE modified method used in a different fluorescent dye to allow simultaneous comparison of two to three protein samples in the same gel. These gel-based methods do not usually break down proteins before further analysis e.g. mass spectrometry.

3. Chromatography-based methods

Chromatography-based methods often divide and purify proteins into complex natural compounds such as cell lysates. For example, ion-exchange chromatography chromatography classifies proteins produced by proteins, the size of the chromatography release classifies proteins according to their cell size, and chromatography bonds use strong interactions between specific ligands and targeted proteins. lectins purify IgMs and IgA molecules).

High-throughput methods:

1. Analytical, functional and reverse-phase microarrays

Analytical, functional and reverse-phase microarrays

Protein microarrays use small amounts of sample on a "chip" to analyze small amounts of protein. Certain antibodies can be detected on the surface of the chip and used to capture the

Correspondence to: Ferdinando Mannello, Department of Biomolecular Sciences, University Carlo Bo of Urbino, Italy,E-Mail: ferdinando_mannello@gail.com

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targeted proteins in a complex sample. Active protein microarrays are common to express protein functions such as protein-RNA interactions and enzyme-substrate benefits. In the protein-microarray of the retrospective phase, proteins from e.g., healthy or diseased tissue or treated cells are secured to the chip, so the chip is tested by antibodies against antibodies.

2. Mass spectrometry-based proteomics

There are many "non-gel" ways to break down proteins, including the isotope-coded affinity tag (ICAT), a stable isotope label with amino acid in cell culture (SILAC) and isobaric tags for quantitation and relative (TRAQ). others, smaller measurement techniques such as multi-protein identification technology (MudPIT), which offer faster and easier benefits. Other gel-free, chromatographic protein separation techniques include gas chromatography (GC) and liquid chromatography (LC).

CONCLUSION

Several years ago, significant improvements were made in the field of proteomics. The technology is fast, sensitive and provides great protein coverage. In addition, the integration of these technologies has been successful in refining, analyzing, measuring, measuring, sequencing and analyzing the structure and bioinformatics analysis of a large number of proteins completely eukaryotic and prokaryotic species. All the fields associated with biology are benefiting from the increasing use of proteomics techniques. However, more work is still needed to increase the reproduction and performance of well-known proteomics tools.

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CONFLICT OF INTEREST

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