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Perspective

Proteome Profiling in Disease Diagnosis and Prognosis

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DESCRIPTION

Proteome profiling is a low-cost, high-value technique for simultaneously tracking hundreds to thousands of proteins. The examination of a full proteome from complex samples such as complete cells, tissues, or bodily fluids is referred as proteome profiling. It is most commonly used to identify a large number of peptides and proteins. Mass spectrometry (MS)-based proteome profiling study can offer data for high-throughput quantitative proteomics and protein modification analyses. Although tissue samples can be analyzed using both mRNA and proteome profiling, bodily fluids (such as serum, urine, CSF, and synovial fluid) can only be analyzed using proteomics.

The systematic separation, identification, and characterization of proteins present in a biological sample are known as proteomic analysis. It is feasible to find alterations in protein expression that may be connected to organ toxicity by comparing the proteins present in sick patient samples with those present in normal ones. A proteome profile can be used to identify and diagnose an illness or condition, as well as to determine how well the body reacts to the treatment. Identification of protein profiles has been shown to be clinically useful in the development of potential novel medications to treat a variety of diseases. Numerous clinical samples can be used for comprehensive proteome profiling to detect thousands of proteins.

Identification of proteins associated with particular diseases may come by analyzing the proteomes of the patient and the control sample. The circulatory system's proteins represent a person's physiology. Changes in protein profiles reveal much information about various causes of the problem. By evaluating these changes, proteins that have a significant impact on illness progression can be discovered, allowing for the development of specifically designed medications.

The technique of mass spectrometry is used to analyse complicated protein samples in order to detect a specific group of proteins. Its basic idea is to separate ionized molecules based on their mass to charge ratios. Discovering peptide or protein molecular changes in healthy and diseased tissues by proteome profiling may provide insight into the pathophysiology or diagnosis of a condition. When it comes to applying mass spectrometry to clinical biomedicine, Matrix-Assisted Laser Desorption/Ionization- Time of Flight Mass Spectrometry (MALDI-TOF MS), Liquid Chromatography coupled to MALDI tandem Mass Spectrometry (LCMS/MS), and Surface-Enhanced Laser Desorption/Ionization Mass Spectrometry (SELDI MS) are all important.

The resolution of proteins in complex mixtures generated from complete organisms, cell lines, tissues, or physiological fluids is the initial step (sample preparation) in the application of mass spectrometry. Two-Dimensional Gel Electrophoresis (2D-GE) is the most extensively used approach for mass spectrometry resolution and imaging of proteins. For improved separation of proteins of interest, chromatographic techniques could be used.

In the case of protein profiling, 2D-GE is more effective because complex protein mixtures, such as crude cell lysates, might well be resolved better, not only in terms of molecular mass but also in terms of protein isoelectric characteristics. The presence and quantity of proteins in a biological system can be determined using biomedical applications. It offers a lot of potential for increasing throughput. Another technique for detecting differentially expressed proteins is High-Performance Liquid Chromatography-Laser Induced Fluorescence (HPLC-LIF), which involves simultaneously recording spectra and chromatograms of physiological samples in a short amount of time.

CONCLUSION

Prognosis prediction and target identification for the purpose of therapy is the main focus of proteome profiling nowadays. To progress precision medicine, it is necessary to move towards comprehensive proteome profiling of blood. There are now at least two pathways for proteome profiling research. In the first, proteins identified in patient samples can be utilized as disease indicators for diagnosis or prognosis. The second objective is to identify biological proteins linked to therapeutic response. This shows the necessity for multiplex analysis of proteins in blood to endorse precision medicine initiatives aimed at early disease detection as well as stratification and patient monitoring before and during therapeutic interventions. One of the tools that are increasingly transforming our approach to drug development is proteomics.

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