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Editorial

Introduction to Diagnosis of Diseases *via* Proteome Profiling

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EDITORIAL

The examination of a full proteome from complex samples such as complete cells, tissues, and bodily fluids is referred to 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 reference data for high throughput quantitative proteomics and protein modification analyses. Proteome profiling is a low-cost, high-value technique for simultaneously tracking hundreds to thousands of proteins. Proteins can now be analyzed using high throughput, automated approaches thanks to proteomics. Although tissue samples can be analysed using both mRNA and proteome profiling, bodily fluids (such as serum, urine, CSF, and synovial fluid) can only be analysed using proteomics. One of the tools that are increasingly transforming our approach to drug development is 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 samples with those present in normal ones. Proteomics is a technology that is related to genomics. At particular times, all proteins generated in blood, other body fluids, or tissues are recorded. 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 treatment. Protein expression profile and protein signature are other terms for the same thing. Identification of protein profiles has been shown to be clinically useful in the development of potential novel medications to treat a variety of diseases. 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. 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. 2-DE 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, 2-DE 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. Protein mixtures can be resolved using two distinct features of proteins: their net charge in the first dimension and their molecular mass in the second dimension. Protein microarray is a technology that is employed in the majority of studies. 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. Proteomic studies despite the fact that analytical microarrays. Protein microarrays are currently employed in three different ways: functional microarrays, reverse phase microarrays, and hybrid microarrays. Analytical microarrays are commonly used to profile a complex combination of proteins in terms of measuring binding affinities, specificities, and protein expression in order to analyse the biochemical activity of proteins. It is a powerful approach for monitoring differential protein expression in the context of clinical diagnosis. 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. Prognosis prediction and target identification for the purpose of therapy In general, start with an antibody library. These methods are time demanding and Labour expensive for the investigation of proteins. Secondly, 2-DE lacks the sensitivity to detect small amounts of a substance. As a result, a large amount of protein is required of biological substance. Low quantity proteins may be degraded during sample purification due to interactions with other high-quantity proteins; consequently, all purification processes must be examined.

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