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Proteomics in Cancer Biomarkers Discovery

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Genes/proteins have modified depend on pathological condition of biologically system of human. Deciferable of molecular pathway have provided the opportunity to detect of new over-expressed biomolecules with extra-, inter-and intra-signals. At the last decade researchers have stressed change of biomolecule expression on tissue or body fluids respectively, which their expression were induced regularly by the other biomolecules (for example TNF-alpha) and they have affected for expressing new biomolecules as abnormal profile for example over-expression of caspases or interleukins.

Proteins have dynamic structure which are represented protein binding to its ligand/receptor or protein-protein interaction, can be subjected to extensive functional regulation by various processes such as proteolytic degradation, post translational modification and, compartmentalization. Therefore proteins on biological fluids and tissue have changed due to type of diseases and can be detected by analyzing the genetic, proteomic, or metabolomic structure of samples [1].

Proteomics are high-throughput technologies which involved a vast amount of data of hundreds or thousands of proteins. Structure of proteins are modified depend on intensity of pathological events for example cancer and non-cancer -bearing individuals and, analysis of data have to be extra-cautious for possible erroneous outcomes [2]. Biomarkers have involved patterns of single nucleotide polymorphisms (SNPs), changes in mRNA, protein, or metabolite amount and DNA methylation. All patterns should provide relationship between the specifity and the disease [3].

Discovery of cancer biomarkers have some limited to describe of the methods, hovewer, are also usable/applicable to detect cancer prognosis-diagnosis. Samples of various biomolecules such as saliva, body fluids, and plasma/serum have obtained from cancer patients for the proteomics studying to detect of tumor pathogenesis and developing new approach for use in clinical platforms, as well as to support various cancer therapeutic regimens.

Proteomics technologies have utilized in identifying protein differential expression in various human cancers [4,5]. In the United States of American's National Institutes of Health (NIH) have published a set of "best-practices" for MS-based assay development and utilization of targeted proteomics assays. The set have involved combined applications for example protein microarray and imaging methods such as 2D gel electrophoresis and MS [6,7].

Electrophoresis of polyacrylamide gel (PAGE) and isoelectric focusing (IEF) have steamed with the techniques of 2D PAGE which are based on the molecular weight and isoelectric points of resolving proteins, respectively. Cancer cells proteins have analyzed with this technique for long time [8].

MS-based techniques have utilized for further advancement with addition fluorescent dyes and gel comparative proteomic analysis. Plasma and other biofluids have been abundant proteins such as albumin and immunoglobulins, therefore low-abundance proteins of biofluids can be hiding due to entity of high abundant proteins. Preclearing step of initial samples might be application to clear the high abundance proteins from biofluids and tissues [4]. Hovewer this technique have involved some potential risk such as depletion of low-abundance proteins. Depletion of these proteins allows for the detection of low abundant proteins resulting in the loss of potentially important information. To identify of low abundance proteins might be choice bead-based immunoassay as a nother way [9].

In the global analysis of serum proteins have different approaches; one of them is global serum proteome analysis using two and three dimentional HPLC/MS [7,10]. Recently, in cancer diagnosis and therapy will be focused to study of epigenetic biomarkers on proteomics approach [11]. One of the high-throughput technologies is microarray which thousands of proteins can measure and detection of proteomic biomarkers via protein microarray [12]. Immunohistochemistry/immunocytochemistry based proteomics identifiying of cancer samples have been described as other approaches in the literature [13].

Proteomic biomarker studies for cancer prognosis-diagnosis and therapies have been extended with different applications and approaches. All techniques have stressed to some implications such as sample preaparation, storage, fractionation, purification and so on. Clinically use of proteomic biomarkers need to standardization, validation and verification improved that are contributed to analyze of samples with double check. Proteomics research tools at the molecular level such as imaging and quantitative methods can be applied to explain the effectiveness of therapeutic agents of cancer diseases and find their way into targeted cells.

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