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Opinion Article

Proteomics for Diagnostic and Prognostic Classification of Cancer Diseases

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DESCRIPTION

The scientific identification and measurement of all the proteins present in a biological system like cell, tumor, function, biological fluid, or organism at a given time is known as proteomic analysis or proteomics. Proteomics-based strategies in disease research are viewed as one of the dynamic and innovative tools that can confirm, supplement, or provide more detailed information than can be obtained by other high-throughput approaches. Cancer is characterized by abnormal cellular proliferation, in which the normal cell cycle is disturbed by several numbers of genetic changes. Cancer can develop in any body tissue and is distinguished by its propensity to infiltrate or spread to other tissues. Malignant tumors, in particular, can become resistant to the treatments used in therapy, endangering the lives of patients in addition to growing quickly and metastasizing to different tissues. A crucial scientific method for examining the biochemical alterations in cancer is proteomics. Key details, including protein targets and signaling pathways connected to the growth and spread of cancer cells, have been discovered using proteomics techniques. The ultimate goal of cancer proteomics is to adapt proteomics techniques routinely used in clinical laboratories for the purpose of diagnosing and prognostic classification of disease states, as well as evaluating drug toxicity and efficacy. New techniques enable researchers to comprehensively analyze genomes, transcriptomes and proteomes in health and disease. Another possible mechanism of proteomics in cancer is the result of defects in protein structure and thus its functions.

Mutations in cancer-associated genes can manifest themselves as defects in protein structure. These defects can have mutation by changing protein stability and making the protein more susceptible to degradation. Genomic and proteomic changes in cancer can be further tracked through the recently emerging field of interactome profiling. It focuses on a network-centric approach that yields vast amounts of data showing protein interactions and the effects of protein structure. MALDI Imaging Mass Spectroscopy (MALDI-IMS) provides both patient-specific and cancer-specific information in proteomics-based studies as a tool for biomarker discovery and cancer tissue classification. It also provides basic knowledge of proteomic analysis based on cancer tissue morphology. Detecting cancer in its early stages when it is more likely to be treated is a real challenge for the scientific and medical community, as most clinical blood biomarker assays lack the necessary sensitivity and specificity for this purpose. Combining a panel of circulating biomarkers, rather than a single molecule, with newly developed or updated techniques such as imaging techniques, could provide significant insights into cancer patient's early diagnosis, accurate assessment of prognosis, and response to therapy. As it offers useful information on the identification, amounts of expression, and modification of proteins, proteomics has grown important in the field of cancer sciences. For instance, cancer proteomics revealed important data in experiments on tumor metastasis, which helped to identify treatment targets as well as therapeutically useful indicators. A distinct pattern of biomarkers characterizes different type of cancer. Some biomarkers influence the efficacy of specific new cancer therapies. The information from such technology could soon dramatically transform cancer research and dramatically impact the care of cancer patients. Analysis of tumor-specific proteomic profiles also allows better understanding tumor development and identifying new targets for cancer therapy. Mechanisms such as regulation of protein function by proteolysis, recycling, and segregation in cellular compartments act on gene products rather than genes. Finally, protein-protein interactions and the molecular composition of cellular structures can only be determined at the protein level. Biological variability between patient samples and the large dynamic range of biomarker concentrations are currently major challenges in efforts to derive diagnostic patterns specific to cancer disease states.

New techniques that integrate proteomics and imaging techniques have been used with promising results and better insight in lung cancer pathogenesis at the molecular level. This will hopefully improve the understanding of the efficacy of cancer therapy in terms of its ability to successfully deliver the required dose to solid tumors. A cancer cell line proteomics approach using elastic net analysis which was used to identify markers of drug sensitivity (positive effect size) or resistance (negative effect size). Proteomic approaches for studying many diseases, including cancer, generate data that complement those from other high-throughput techniques. Such techniques do

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more work than other used techniques which only generate a list of differentially expressed macromolecules and their derivatives as causes or consequences of the pathology under study. Detailed evaluation of proteomic data of a patient can reveal underlying mechanisms which are going inside the body leading to cancer development.

Proteomic approaches have become popular in cancer research lately. Proteomics-based techniques have enabled the identification of potential biomarkers and protein expression patterns that can be used to assess tumor prognosis and classification and to identify potential responders to specific therapies. The complexity of proteomic techniques applied to cancer research is further increased by the current concept of cancer heterogeneity. Some researchers consider cancer heterogeneity and biological sample variables to be the most important and challenging issues for all-omics techniques when applied to cancer research.