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Commentary

Clinical Proteomics in Diagnosis of Breast Cancer

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DESCRIPTION

Proteomics technologies are generating important information in the discovery and confirmation of breast cancer diagnostic, prognostic and predictive biomarkers, detecting genetic aberrations at the proteome level, describing functional and regulatory pathways, and focusing specific protein and peptide profiles in human tissues, among other things. Breast cancer is a complex, multi-faceted, and chameleonic illness that poses an ongoing struggle for the new era of precision diagnostics and tailored onco-medicine. Proteomics, the study of a large set of proteins expressed by an organelle, a cell type, a tissue or an organism at a given time, has grown increasingly significant in both diagnosis and treatment as time has passed. Breast cancer genetic classifications, such as the *PAM50* RNA-based gene signature are becoming more popular as a gold standard for identifying intrinsic subtypes and recommending biomarkers for therapeutic usage. For cancer classification and prognosis, genomic expression profiling is a highly reliable technique. Genes lack any catalytic or signaling properties, and instead depend on translation to produce active proteins. Furthermore, important natural biological processes like RNA post-translational modification and alternative splicing of Phosphorylation, glycosylation, and ubiquitination are examples of protein modifications. Acetylation, nitrosylation, methylation, and proteolysis result in the formation of genomic discovery investigations limitations. As a result, post-genomic "proteomic" efforts connecting protein expression profiles to cancer are critical for a better understanding of the disease. Breast cancer is represented in a way that is both complementary and thorough biology of cancer. Variations in gene expression patterns determined from cDNA microarrays have been used to create a new breast cancer classification. Luminal A type tumors now have highest ERa gene expression; b) Luminal subtype B has similar ERa gene expression with PR positive or HER2 positive tendencies; c) ERBB2 positive group has high expression of several genes in the ERBB2 amplicon at 17q22.24, including ERBB2 and GRB; d) Basal-like subtype has high expression of keratins, laminin, and fatty acid binding. Proteomic research into disease prognostic indicators and treatment stratification in breast cancer are less common. Quiescin sulfhydryl oxidase-1 is an enzyme that converts quiescin to sulfhydryl oxidase (QSOX1) has been identified as a novel biomarker for Luminal B breast cancer that predicts relapse risk and poor survival, as well as having a proliferative, pro-invasive role in malignant breast cancer progression. Mass Spectrometry (MS) proteome investigations in breast cancer diagnoses, revealing protein patterns distinct to patients with breast cancer in early or late stages of the disease. MS studies of the blood proteome revealed patterns distinct to breast cancer patients with varying outcomes and therapeutic responses. Proteomics studies in breast cancer reached the level of biomedical research with high aspirations of discovering new disease indicators and therapeutic targets. In addition, modern proteome methods primarily MS, allowed for large-scale, high-throughput investigations for the detection, identification, and functional analysis of very low-abundance proteomic targets. As a result, a large amount of proteomic data was created in the attempt to learn more about breast cancer's molecular properties. The use of MS-based proteome studies to characterize breast cancer has provided us with an important tool for distinguishing a number of subgroups linked to clinical outcome. MS proteome method has led to the identification of proteins and protein profiles that help to refine breast cancer subtypes, as well as the discovery of novel protein biomarkers that hint to diagnostic and prognostic potential or therapy resistance in a certain subtype. In order to more accurately identify the functional phenotypic distinctions that cause breast cancer heterogeneity, newer classifications based on protein expression profiling have been proposed.

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