Recent trends and applications of cancer proteomics.

Dogan Tamayo*

Department of Medicine, University of Washington, Seattle, WA, USA

Accepted on November 6, 2021

Description

Cancer proteomics involves the identification and quantitative analysis of variously expressed proteins compared to their counterparts in healthy tissues at various stages from pre-neoplastic to neoplasm formation. Cancer is a complex disorder resulting from a dysregulated, normal cell signalling network that controls cell behavior such as proliferation and apoptosis caused by genetic, genomic, and metamorphic changes at the cellular or tissue level. More than 11 million people develop cancer each year. It is estimated that there will be 16 million new cases each year until 2020. Of the total of 58 million deaths worldwide in 2005, 7.6 million (13%) of the world's deaths were due to cancer. The number of deaths from cancer is expected to continue to increase worldwide, with 9 million people dying from cancer in 2015 and 11.4 million in 2030.

Key techniques include 2D gel electrophoresis, mass spectrometry, laser capture microdissection, detection of molecular markers and protein patterns in cancer. Proteomics holds great promise in the prevention and treatment of cancer because it provides unique tools for discovering biomarkers and therapeutic targets. As such, proteomics helps transform basic scientific discoveries into clinical practice in personalized medicine. Cancer can occur in any tissue in the body and is characterized by its ability to invade or spread to other tissues and organs. Various cancers and metastases that occur during the course of cancer are serious obstacles to the successful development of treatments.

Metastases in particular are the most common feature of malignancies. However, the exact mechanism by which the transition cascade occurs is not well defined. Recently, several proteomics studies have been conducted to determine the cause of increased cancer metastasis. In one such study that examined a heterologous transplanted mouse model of patient origin using multiple omics such as transcriptomics, proteomics, and phosphoproteomics, TMT marker analysis was performed on stress hormone levels associated with breast cancer progression. Increases have been shown to increase the activity of glucocorticoid-causing receptors (GR) in the metastatic region, which ultimately results in decreased viability. Cancer may recur despite treatment such as surgery or chemotherapy, suggesting that recurrent cancer may contain cells that are resistant to anticancer drugs.

Proteomics approaches can be used to characterize drug-resistant cancer cells and discover targets that can overcome drug resistance that develops during cancer treatment. Some reports show that cells that survive treatment with anticancer drugs, such as breast, pancreatic, and lung cancer, have specific protein expression and molecular mechanisms that correlate with reduced patient survival. These studies may offer the opportunity to maximize the effectiveness of chemotherapy by using additional drugs that control the major proteins involved in drug resistance.

Proteomics provides valuable information in several areas, including protein profiles, protein levels, sites of modification, and protein interactions in pathophysiological conditions. Because of this, cancer proteomics identified clinically applicable, novel biomarkers and therapeutic targets. The proteomics approach in cancer research has investigated molecular mechanisms and provided key information on cancer growth, metastasis, and therapy. Importantly, recent cancer proteome databases are established globally and can be freely accessed and used through the integration with bioinformatics. In this paper, we have reviewed the current state of proteomics in multiple cancers. In the case of cancer, the databases are well-organized; however, various diseases the organization of the database information is suboptimal compared to the cancer research database. To address this shortfall, systematic proteomics approaches should be carried out in a variety of diseases, and appropriate databases should be established to provide disease-related information.

*Correspondence to

Dogan Tamayo,

Department of Medicine,

University of Washington,

Seattle, WA, USA

E-mail: dogan@tamayo.edu

Citation: *Tamayo D. Recent trends and applications of cancer proteomics. J Syst Biol Proteome Res. 2021;2(2):2*