ONCOPROTEOMICS: RECENT ADVANCEMENTS AND ITS FUTURE PROSPECTS

Abstract

Oncoproteomics is the field of science which studies cancer samples using 'omics' advancements to identify changes ensnared in tumorigenesis. This will be used to understand how signaling pathways are altered in cancer cells, increasing our understanding of how different pathways can be targeted in cancer therapy. Bioinformatics and multi-omics collaborations provide deeper knowledge of various diseases. Our understanding of cancer biology will be furthered by meta-analyses of sizable cancer data sets and data-driven in silico investigations, and personalized drug response prediction will be made possible by predictive modeling. In this review paper, we shall discuss the development of oncoproteomics, current oncoproteomics research trends and its potential for the future.

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I. INTRODUCTION

Proteomics is the study of the total arrangement of proteins communicated at cell, tissue or life form level. Oncoproteomics is the part of proteomics which manages all protein connections occurring in a malignant cell growth. It includes protein articulation profiling, protein modifications, protein-protein interaction, protein design and capability. This emerging branch will help in reducing disease burden, provide diagnosis and prognosis of disease as well as help in anti-cancer drug discovery. Technologies based on proteomics have assisted in evaluating tumor prognosis, prediction, tumor classification, and probable response to particular therapy. The collection of proteins expressed within a cancer cell is known as a cancer proteome, and it should be thought of as a highly dynamic entity that influences a number of cellular processes. The steps of protein analysis involve protein extraction, protein digestion, peptide fractionation, LC (liquid chromatography)-MS(mass spectroscopy) analysis (refer fig 1). Initially, procedures like centrifugation and filtration are used to separate and purify proteins from tissue or cell lysates. The protein mixture is then typically separated using two-dimensional gel electrophoresis to reduce sample complexity. Next, total protein analysis using LC-MS and the peptides that result from enzymatic digestion are analyzed, and the results are interpreted using a proteome database. The separation is often completed prior to the use of MS by ESI (electrospray ionization), and MS techniques are combined with multidimensional LC to lessen sample complexity. For MS analysis, protein is volatilized and ionized using the ESI technique (Cho & Cheng, 2007). A crucial method for obtaining high-resolution spectra of mixed peptides is liquid chromatography-mass spectrometry (LC/MS), which enables the identification of sensitive and precise biomarkers linked to cancer. It is beneficial for label-based or label-free quantitative analysis.) . Proteins in a sample can be analyzed both quantitatively and qualitatively using the label-based quantitative approach. The techniques involve tagging proteins or peptides with stable isotope labeling of chemical markers like amino acids. However, because reagents are pricey, the proteins are only partially tagged. Proteomics requires careful identification of minute quantities and changes in the expression of particular proteins in order to identify cancer and other disorders.

II. HISTORY

The term *proteomics* was first used in the year 1997. A crucial method for obtaining high-resolution spectra of mixed peptides is liquid chromatography-mass spectrometry (LC/MS), which enables the identification of sensitive and precise biomarkers linked to cancer. It is beneficial for label-based or label-free quantitative analysis.) . Proteins in a sample can be analyzed both quantitatively and qualitatively using the label-based quantitative approach. The techniques involve tagging proteins or peptides with stable isotope labeling of chemical markers like amino acids. However, because reagents are pricey, the proteins are only partially tagged. Proteomics requires careful identification of minute quantities and changes in the expression of particular proteins in order to identify cancer and other disorders. Proteome analysis can be used to analyze the impact of potential treatments on the illness process since it can generate an extensive molecular description of the changes between healthy and diseased states . As will be explained below, oncoproteomics plays a significant part in a number of malignancies (Jain, 2008).

III. CURRENT STATE OF ART

It is being attempted to address some of the drawbacks of conventional drug discovery by using proteomic technology. Proteins are crucial targets for drug discovery, particularly for cancer, as malignant diseases result in defects in the cell's protein machinery. Proteome analysis can be used to examine the impact of potential medications on disease processes since it can offer a thorough molecular description of the changes between healthy and illness states. The "omics" revolution makes it possible to produce, examine, and understand vast quantities of qualitative and quantitative proteomics data and to combine it with data from other fields. A change from the current "one size fits all" approach of illness treatment to one where the right drug at the right dose for the right patient at the right time becomes the new paradigm is represented by precision, customized, or P4 medicine. Over the past ten years, significant technological advances in proteomics, particularly oncoproteomics, have been made. Single cell analysis is now a reality, and our knowledge of the intricate biology underpinning the distinctive features of cancer and disease heterogeneity is fast growing (He et al., 2019).

IV. FUTURE PROSPECTS

Proteomics has been shown to provide extra information that complements genomics-based techniques, but it also presents a number of technical, data collection, and interpretation problems. For amplification of low-abundance proteins, for instance, there is no method comparable to polymerase chain reaction, hence a detection range of one to several million molecules per cell is required (Shruthi et al., 2016). The cancer field will have new opportunities thanks to the multi-omics approach, a collective application of the omics-technologies of genomics, transcriptomics, proteomics, and metabolism. Table 3 highlights the application of multi-omics to various cancer types. Collaboration between bioinformatics and multi-omics will increase our understanding of various diseases.

V. CONCLUSION

The ultimate goal of oncoproteomics is the advancement of proteomics technologies for improved usage in clinical laboratories for the classification of cancer stages for diagnostic and prognostic purposes, as well as for the assessment of medication toxicity and efficacy. For the implementation of proteomic technologies in clinical practice, speed and accuracy are crucial. Cancer is characterized by abnormal cell proliferation, in which the normal cell's cell cycle is disturbed by a number of genetic changes. It can happen in any body tissue and is distinguished by its propensity to invade or spread to other organs and tissues. Malignant tumors in particular can acquire resistance to the medications used in therapy, growing quickly, metastasizing to numerous other tissues.Key details, including protein targets and signaling pathways connected to the growth and spread of cancer cells, have been discovered using proteomics techniques. The proteomic approach to cancer research has examined molecular pathways and offered significant new information about the development, metastasis, and treatment of cancer. Proteome databases are widely utilized, available for free access, and integrated with bioinformatics. Recent cancer is essential. Oncoproteomics' development has raised the possibility of finding novel biomarkers for use in screening, early diagnosis, and therapeutic response prediction.

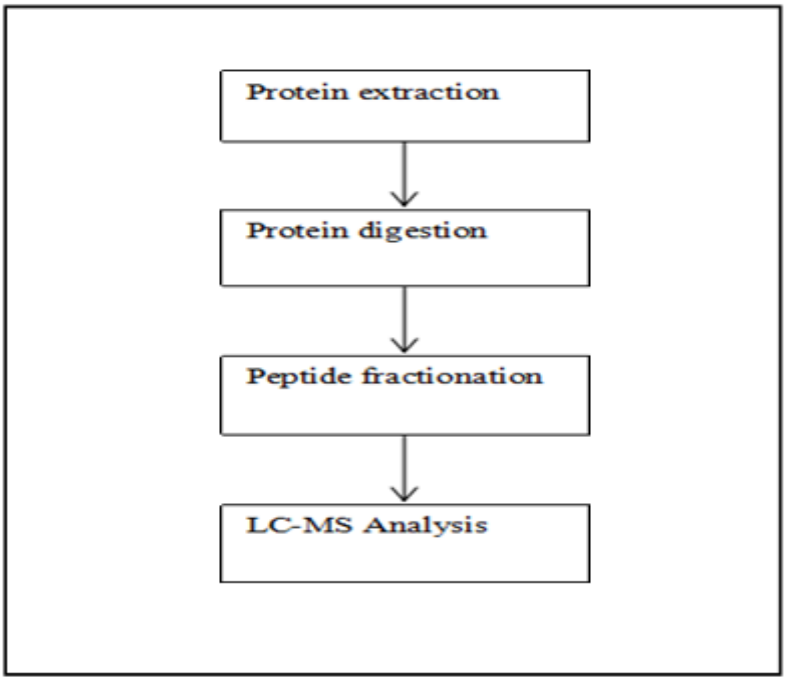

Figure 1: Basic Steps of proteomic analysis

Table 1: Types of methods in quantitative proteomics

Proteomics method	Quantification method	Type	Principle
LC/MS-based proteomics	Labeling	-ICAT -iTRAQ -SILAC -TMT	Isotopic labeling used in quantative proteomics by MS with the help of chemical labeling reagents.
	Label-free	-MRM -SWATH	Method for relatively quantifying differences of concentration between independent samples

Table 2: List of cancers with its biomarker identified by proteomics analysis

Types of cancer	Method of target discovery	Biomarker/target	Type of biomarker
Breast	Proteomics, transcriptomics, phosphoproteomics	GR, PYCR1	Prognostic
Lungs	Proteomics, transcriptomics	Bach1, Ho1, MTOR	Therapeutic
Colon	Proteomics, genomics, phosphoproteomics	Rb phosphorylation	Therapeutic
Prostate	Proteomics, genomics	ACADB	Prognostic
Gastric cancer	Proteomics, genomics, proteogenomics	CTGF, NRP1, RAB23, AXL, RHOA, ARID1, CDH1, TNK	Prognostic
Endometrial carcinoma	Proteomics, genomics,transcriptomics	CTNNB1, AURKA,TP53	Therapeutic
Pancreas	Proteomics	LKB1	Prognostic
Ovary	Proteomics	NNMT	Therapeutic
Myeloid leukemia	Proteomics	IL3RA, CD99	Therapeutic

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