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Short Communication on Microarray

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Short Communication

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INTRODUCTION

Study of the proteins produced and expressed in the genome of an organism is the proteome. Proteomics deals with the study of these proteins its structure and function. Genomics is the study of the whole genome of an organism which is consistent but the proteome of organisms depends on the environment, life cycle and it also differs from cell to cell.

Proteins play an important part in the day to day activity of the organism, formation of these proteins its quality and quantity depends on the different elements such as life cycle, environment like stress, stimulus and gene expression. Thus these proteins can be used as biomarkers which indicate a particular disease. The Human Genome Project led to the finding that the protein coding genes are far less than the proteins that are found in humans. This diversity in the protein is due to alternative splicing and the post-translational modifications of the proteins. Thus the proteins are very good biomarkers for different diseases.

APPLICATION OF PROTEOMICS FOR DISCOVERY OF PROTEIN BIOMARKERS

In the development of drug biomarkers have become very important [1]. For the discovery of protein biomarkers the usage of mass spectrometry and quantitative proteomics has increased widely. The protein identification helps to understand the mechanism of the tumor metastasis and thus facilitates the drug development/interventions of cancer. Along with the other branches of science like biochemistry, molecular genetics, cell biology with proteomics help in studying the cancer metastasis and improvement of the methodologies [2]. Thus, helping researchers in the discovery of biomarkers and pathogenetic studies. A measurable biological indicator of a specific biological state which has the potential to improve the patient survival rate affectively is biomarkers. These biomarkers are used for diagnostic, predictive, prognostic and for pharmacodynamics purposes. The biomarkers used in the identification of a particular disease state are diagnostic biomarkers, whereas biomarkers which predict the progression of the disease, its severity are prognostic biomarkers [3-6]. Predictive biomarker will provide us the drug efficacy or the response to a particular therapy; while to measure the forthcoming effect of the drug and to assist the dosage selection pharmacodynamic biomarkers are used. Metabolites and antibodies are also used as biomarkers in genomics, transcriptomics. DNA anomalies in chromosomes, gene amplification, mutations in somatic cells are detected by genomic biomarkers. However these genomic analyses are not reflected at RNA and protein levels as the epigenetic changes and the post transcriptional changes ad post-translation changes affect the amount of proteins and alter the RNA. Proteins and RNA are most abundantly found in the body fluids and these are most readily affected by diseases, thus these are considered as promising biomarker [7 - 10].

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CANCER BIOMARKERS

Detection, prognosis, diagnosis and therapy of breast cancer is now possible with the advancements in the field of proteomics along with the use of mass spectrometry. The discovery of the protein patterns has enabled researchers to distinguish the disease and disease free-state associated with breast cancer has been uncovered with the development of proteomics technologies. This discovery leads to personalized therapy for the patients. Proteins expressed or found in the serum, plasma and the tumor cells using the novel methodologies provide a better view of the heterogeneity of the cancers [11 - 14].

With the study of cilical-pathological parameters and proteomics, researchers identified proteins of clinical relevance to cancer patients. They developed a new method with the combination of 2D gel electrophoresis and a sensitive fluorescent dye for laser microdissection to study the proteome data. With the study of comprehensive proteomics study of 1000 surgical specimens, scientists concluded that the proteome reflects the major cancer phenotypes like prognosis, response to treatment and histological differentiation. The study also concludes that a single protein can predict the clinical response in different types of tumors such lung adenocarcinoma, esophageal cancer. These protein biomarkers can enhance the therapeutic methods. This can be used as a tool to develop personalized medicine [15 - 18].

Ovarian Cancer is the major cause of death in US, due to poor diagnosis. Studies reveal that blood microRNA, a noncoding RNA which can be used as non-invasive biomarkers for the diagnosis of ovarian cancers. Pathogenesis of cancer could be involved in many types of Cancer like ovarian cancer. It is also observed that, microRNA expressions were also observed in ovarian cancer. Origin of cancer could be found in Micro RNA tissue specific could identify the origin of cancer [19 - 21]. One of the important features of Micro RNA is their stability in Biological Conditions. The stability of Micro RNA could also be found in formalin fixed, paraffin embedded tissue samples. Thus, the features of MicroRNA are acts as biomarkers for Cancer diagnosis. Ovarian cancer is also associated with many micro RNA from blood cells or serums. Investigation of microRNA and their targets genes significantly enhances the understanding of molecular mechanism of ovarian cancer [22].

CONCLUSION

Over the years the field of proteomics has expanded with the development of mass-spectrometry to a broad and varied research areas of science. Incredible progress in instrumentation of mass-spectrometry has led to the sensitivity, accuracy and quick analysis and identification of proteins. With the advancement in science qualitative and quantitative differences in protein profiles of particular diseased vs. normal can be analyzed. Application of proteomics to study the clinical samples like tissues, cell lysates and body fluids led to the discovery of novel biomarker for specific diseases. The research in the field of biomarkers is also used to develop drugs targets against specific disease

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