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Applications of Microarrays in Different Fields of Science

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Commentary

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INTRODUCTION

The large scale study of proteins their structure function is called proteomics. Proteins are the building blocks of any organisms and also play a very important and vital part of an organism either human, plants or microbes. With the development in the science scientists around the sequenced the whole genome of organisms but researchers were not able to know the actual cause of a particular disease as most of the genetic disorders are due to post-translation modifications or due to defective gene expression in the particular genetic trait. Together with the advancements in genomics and proteomics the root cause of a disease can be identified and accordingly the ways to prevent or to reduce the genotype of the disease. The modification of protein, its complement and the translation depends on the time environment of that particular cell or organisms.

DRUG INDUCED TOXICITY BIOMARKER DISCOVERY

Adults over the age 50 in US are subjected to drug induced toxicities especially in patients with acute liver failure. It is due a drug acetaminophen (APAP) as this drug is available in drug stores and supermarkets and can be purchased without a prescription [1-3]. There are many cases reported to FDA for unintentional overdose of the drug- acetaminophen associated with hepatotoxicity [4]. Hence the study of this drug toxicity has been an interest among the scientific community. SELDI based proteomics analysis was performed on the samples obtained from the mice that were treated with APAP to discover the hepatic toxicity biomarkers from the serum [5, 6].

Individuals are subjected to environmental toxins and these toxins cause variety of disease such as neurological disorders and cancers. Thus researchers are now using new toxicological approach for effective screening of environmental risk. Application of proteomics, bioinformatics to study the toxicity is toxicoproteomics. Scientist use mass spectrometry to detect, separate and identify proteins that cause certain disease, specific to toxins and to forecast carcinogenicity along with 2D gel electrophoresis. Biomarkers can be identified using this toxicoproteomics for these environmental pollutants [7-9].

HOST-DERIVED BIOMARKERS

Until now the biomarkers were used to study the detection and study of cancer. Biomarkers can be also used to study the host-pathogen interaction at various stages of anthrax progression. Candidate biomarkers were discovered specific to murine anthrax model to compare the toxigenic and non-toxigenic strains response. Proteomics analysis of body fluids is an obstacle because of the presence of abundant proteins that interferes with the proteome profiling technologies such as SELDI with the resolution and sensitivity [10-13]. Thus the body fluids of the mice used in the experiment are fractionated into groups of proteins to separate analysis of groups. The experiment was carried out to estimate the relevance of the murine biomarker that were identified with the *B. anthracis* infected animal models using virulent

challenge strains in blinded validation studies. The results propose that SELDI investigation can be used for initial detection of hepatotoxicity based on the expression pattern of the biomarker peaks [14, 15].

CONCLUSION

Proteomics goes for comprehension of protein status under certain physiological or unhealthy conditions in an expansive scale. Protein microarray innovation has risen as a promising methodology for a wide mixture of utilizations for investigative and clinical research on an entire proteome scale. In this, the point of this survey is to condense the latest advancements in the uses of protein microarrays for biomarker profiling, catalyst substrate profiling, little atom profiling, protein-protein communication profiling, and neutralizer specificity profiling.

Protein microarray has been a phenomenal high-throughput technique used to test proteins for a particular capacity or organic chemistry on a huge scale. They have a principle advantage by following expansive quantities of proteins in parallel, which are additionally quick, mechanized, practical, profoundly touchy, and sparing examples and reagents. At this point, it is a promising methodology with a wide assortment of utilizations for experimental and clinical exploration.

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