

Chapter 4

Genomics and Proteomic Approach in the Treatment of Various Human Diseases: Applications of Genomics and Proteomics

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ABSTRACT

World wise genomic analysis is beginning to move from the laboratories of basic investigators to large-scale clinical trials. The potential of this technology is to improve diagnosis and tailored treatment of various human diseases. In addition, new data from the emerging proteomics platforms add another layer of molecular information to the study of human disease, as scientists attempt to catalogue a complete list of the proteins encoded by the genome and to establish a 'bio-signature' profile of human health and disease. In the medical sciences identification of human genome sequence is a significant milestone for all the genes and their regulatory regions which provides the required framework for the genetic blueprint of humankind and that will make possible to recognize the molecular premise of disease. It is accepted that, together, these technologies genomic and proteomic will make easier to study all aspects of genes, gene products and signaling pathways so that the objective of personalised molecular medicine can be achieved.

INTRODUCTION

Genomics is an area within genetics that concerns the sequencing and analysis of an organism's genome. Our genomes hold the information and instructions that define how our bodies function. But sometimes there are mistakes, mutations, or variations in our genome that predisposes us to or cause disease. Clini-

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cal genomics is the practice of using DNA sequencing to find these variations to help diagnose disease and find the best treatment or to identify patients at risk for disease to help with prevention.

Gene therapy may provide some clues in the efficient delivery of biologics. For this reason, several studies have focussed to design the vectors, promoter or target gene and testing them in animal models of arthritis, cancer and hepatitis C, and the obtained results concludes that gene therapy can be a convenience procedure in the treatment of provocative and ruinous rheumatoid arthritis as well as in cancer and hepatitis C. Gene therapy is defined as an introduction of nucleic acids into a host cell for therapeutic purposes; one option may be the over expression of a therapeutic gene, another option consist in the repression of a target gene highly expressed in disease {small interfering RNA (siRNA)}. Another approach in gene expression is that it profiles the entire analysis of thousands of gene and its isolation to generate a global picture of biological functions in a specific cell or tissue or even organ. Gene expression profiling has recently been at the forefront of advance in personalized medicine, especially in the field of cancer for the prediction of tumour behaviour in several types of cancer, in arthritis and for hepatitis (Walsh et al., 2004; Tak & Bresnihan, 2000; Bessis et al., 1998; Kim et al., 2002).

The term proteome was introduced in the 1990s, referring to an entire complement of proteins produced. Several metabolic diseases and genetic abnormalities are known to impair the cellular transcription and translation status and thereby creating a variation in proteome (Di Girolamo et al. 2012). These alterations in proteome are an opportunity for development of diagnosis of molecular signatures for several diseases and lead to the development of a new segment of research called 'clinical proteomics'. Proteomics is a study of the structures and functions of the proteins and refers to a large-scale experimental analysis of proteins available in low abundance (Ceciliani et al., 2014). While clinical proteomics is defined as clinical and analytical validation and implementation of novel therapy or diagnosis related markers that originate from preclinical studies designed to identify leads in analogy to drug screening studies (Apweiler et al., 2009).

Early detection, control and prevention of various diseases are difficult (Wulfkuhle et al., 2003). Proteomics provide powerful approach to identify and analyse the normal and transformed cell function from complex mixture (Roy & Shukla, 2008). It is very strong tool for both biomarker discovery and for the observation of biochemical processes involved in diseases. Simply can be said that proteomics includes the inclusive regulation of protein expression levels and consequently allows the regulated pathway for cellular processes. Now a day's three types of proteomics approach have been recognized, (a) Structural proteomics: it analyze the protein structure in large scale, it compares protein structure and help to identify the function of newly discovered gene. (b) Expression proteomics: analysis of protein structure at large scale, it helps identify proteins in normal and diseased condition sample such as healthy vs. diseased tissue. (c) Interaction proteomics: analysis of protein interactions at larger scale, it includes protein-protein analysis or protein-DNA/RNA interactions (Andy et al., 2003). Proteomics and their applications were shown in Figure 1.

The study of human gene and protein helps to identify the new drug for the treatment of diseases. Computer software uses a target for new drugs proteins which are associated with a disease, identified by proteome information. If some of the protein mixed with then its three dimensional (3D) structures provides information to design the drugs to interfere with the action of protein (Vaidyanathan, 2012). Specific proteins as biomarkers were used to diagnose the diseases. Various techniques employed to test for protein produce during a disease and help to diagnose the disease instantly. The proteomics techniques includes secretomics, western blot, ELISA (enzyme linked immuno-sorbent assay) or mass spectrometry, immunohistochemical staining (Klopfleisch et al., 2010; Klopfleisch et al., 2009). Proteomics studied

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