BRIEF OVERVIEW OF PROTEOMICS

Advances in molecular biology have led to a better understanding of the genetic and molecular basis of a number of human diseases. The term *'physiological or functional genomics'* has been defined to describe the analysis of changes in gene expression profile in response to experimental or abnormal conditions. Proteomics studies are important for the understanding of the pathogenesis of human diseases. The data obtained solely from gene analysis are limited because they neither provide complete information nor dynamic image between tissues with normal physiology and those with disease pathophysiology. It should be emphasized that *'protein'*, but not *'gene'*, is the molecule that directly determines the cellular functions and responses. Additionally, modification of proteins by a process called *'post-translational modification'* (PTM) cannot be determined by the genetic or genomic approach. Thus, the study on proteins is crucially required.

Western blotting and other immunological methods have been successfully utilized to study proteins for a long time. There are limitations to these conventional methods, i.e. (i) only a small number of proteins can be simultaneously studied in a single experiment; (ii) specific antibody must be available; and (iii) the proteins to be examined are based entirely on *a priori* assumption. To better understand the biology and physiology of a cell, an effective method for global analysis of proteins is required. This ideal technique should have the capability of simultaneous exploring both known (previously determined) and unknown (previously undetermined) components of the *'protein universe'* in the cell, tissue, organ or biofluid.

The post-genomic era has seen development of a number of cutting-edge technologies that utilize genomic information to explain the biology and physiology of cell, tissue or organ. One of these technologies is proteomics, which has been extensively applied to several fields in biomedical research. The field of proteomics began in 1994 when Marc Wilkins first introduced the term **'proteome'** (set of proteins expressed by the genome) to the public during the Siena electrophoresis conference [*Biotechnol Genet Eng Rev* 13:19-50, 1996]. Since then, the term has been defined simply as the subject that involves the study proteins expressed from the whole genome of the cell. One of the most frequently used definitions of proteomics described by Peng and Gygi [*J Mass Spectrom* 36:1083-1091, 2001] is ***"the systematic analysis of proteins for their identity, quantity, and function"***. The rapid progress of the proteomics field is based primarily on the successes in: (i) genomics,

particularly when the Human Genome Project was completed and other Genome Projects are ongoing – because proteins can be identified on the genomic-scale basis; (ii) protein separation sciences, using either gel-based (two-dimensional polyacrylamide gel electrophoresis, 2-D PAGE) or gel-free techniques (liquid chromatography, LC; and capillary electrophoresis, CE); and (iii) mass spectrometry, which is a core technique for protein identification. The data obtained from proteomic analysis are complementary to those obtained from genomic analysis and other 'OMICS' studies (e.g. transcriptomics, metabolomics, interactomics, lipomics, glycomics, etc.).

Proteomic analysis can be applied to examine a large number of proteins simultaneously and does not require the use of antibody. Additionally, protein identification in proteomic analysis is based on molecular mass data, and prior results are not required. Therefore, both known and previously unknown proteins can be explored and characterized using proteomics, a powerful technology which offers rapid determination of proteins that are involved in the pathogenesis and pathophysiology of diseases, rapid identification of new therapeutic targets, and discovery of novel biomarkers.

Visith Thongboonkerd

Faculty of Medicine Siriraj Hospital, Mahidol University