Editorial

Technologies and Their Applications in Proteomics

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Proteomics involves the applications of technologies for the identification and quantification of overall proteins present content of a cell, tissue or an organism. It supplements the other "omics" technologies such as genomic and transcriptomics to expound the identity of proteins of an organism, and to cognize the structure and functions of a particular protein. Proteomics-based technologies are utilized in various capacities for different research settings such as detection of various diagnostic markers, candidates for vaccine production, understanding pathogenicity mechanisms, alteration of expression patterns in response to different signals and interpretation of functional protein pathways in different diseases. Proteomics is practically intricate because it includes the analysis and categorization of overall protein signatures of a genome. Mass spectrometry with LC–MS-MS and MALDI-TOF/TOF being widely used equipment is the central among current proteomics. However, utilization of proteomics facilities including the software for equipment, databases and the requirement of skilled personnel substantially increase the costs, therefore limit their wider use especially in the developing world. Furthermore, the proteome is highly dynamic because of complex regulatory systems that control the expression levels of proteins. This review efforts to describe the various proteomics approaches, the recent developments and their application in research and analysis. The dynamic role of molecules to support the life is documented since the initial stages of biological research. To demonstrate the importance of these molecules, Berzelius in 1838 given the title "protein", which is originated from the Greek word, proteios, meaning "the first rank". The "proteome" can be defined as the overall protein content of a cell that is characterized with regard to their localization, interactions, post-translational modifications and turnover, at a particular time. The term "proteomics" was first used by Marc Wilkins in 1996 to denote the "PROTein complement of a genOME". Most of the functional information of genes is characterized by the proteome. The proteome of eukaryotic cells is relatively complex and exhibits extensive dynamic range. Moreover, prokaryotic proteins are responsible for pathogenic mechanisms; however, their analysis is challenging due to huge diversity in properties such as dynamic range in quantity, molecular size, hydrophobicity and hydrophilicity.

Proteomics is crucial for early disease diagnosis, prognosis and to monitor the disease development. Furthermore, it also has a vital role in drug development as target molecules. Proteomics is the characterization of proteome, including expression, structure, functions, interactions and modifications of proteins at any stage. The proteome also fluctuates from time to time, cell to cell and in response to external stimuli. Proteomics in eukaryotic cells is complex due to post-translational modifications, which arise at different sites by numerous ways. Proteomics is one of the most significant methodology to comprehend the gene function although, it is much more complex compared with genomic. In the previous several years, tremendously useful advances are made in the field of proteomics. The technologies are rapid, sensitive and provide greater proteome coverage. Furthermore, combination of these technologies has achieved success in purification, analysis, characterization, quantification, sequence and structural analysis and bioinformatics analysis of large number of proteins in all types of eukaryotic and prokaryotic organisms. All fields related to biological sciences have been benefited with increasing use of proteomics techniques. However, further work is still required to improve the reproducibility and performance of well-known proteomics tools.