Editorial

Proteomics Technology – A Powerful Tool for the Biomedical Scientists

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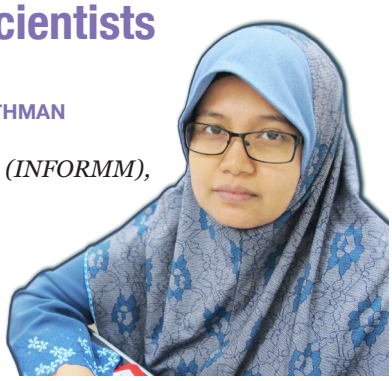

Abstract

"Proteomics" refers to the systematic analysis of proteins. It complements other "omics" technologies such as genomics and transcriptomics in elucidating the identity of proteins of an organism, and understanding their functions. Proteomics is used in many areas of research such as discovery of markers for diagnosis and vaccine candidates, understanding pathogenic mechanisms, in the study of expression patterns at different time points and in response to different stimuli, and in elucidating functional protein networks. Proteomics analysis involves sample preparation, protein separation, and protein identification. The 'heart' of current proteomics is mass-spectrometry, with LC-MS/MS and MALDI-TOF/TOF being commonly used equipment. However, the high costs of the equipment, software, databases, and the need for skilled personnel limit the wide utilization of this technology in the less developed countries. Therefore, there need to be sharing of facilities, better networking and collaborations among our scientists and laboratories to take advantage of this powerful technology.

Keywords: *analysis, mass-spectrometry, proteins, proteomics, technology*

The term 'proteome', originally coined by Mark Wilkins in 1994, describes the entire protein complement expressed by a genome, or by a cell or tissue, and 'proteomics' refers to the systematic analysis of these proteins. Proteomics complements other 'omics' technologies such as genomics and transcriptomics. Although these two prior technologies have provided tremendous and important data, the understanding of genes and messenger ribonucleic acid (mRNA) expressions may not provide the complete or 'real' picture since translational regulations, and post-translational modifications affect the mature type and amount of proteins expressed (1).

There are countless examples and applications of proteomics in the study of diseases -infectious diseases, cancer, heart diseases, neurovascular, diabetes, and many others. It has been used to discover diagnostic markers, vaccine candidates, understand pathogenic mechanisms, study expression patterns at different time points and in response to different stimuli, and elucidate functional protein networks. Other interesting applications include analysing proteomics signatures in the study of mechanism of action of antibiotics in treating bacterial diseases and providing guidance in development of new antibiotics (2).

Proteomics analysis involves three major steps i.e sample preparation, protein separation and protein identification. The interesting subcellular components of potential diagnostic/protective/prognostic proteins of microorganisms are usually either specific cell membrane components, or they circulate in biological fluids at low concentrations, thus appropriate sample preparation is crucial. Complex mixtures of proteins resulting from the prepared sample are then subjected to separation. Traditionally, two-dimensional gel electrophoresis (2-DE) has been a core separation technique in proteomics laboratories. The first-dimensional gel electrophoresis is used to separate proteins according to isoelectric points (pI), and the second dimension separate proteins according to their molecular weights.

With the need for quantitative application, two-dimensional difference in-gel electrophoresis (DIGE) has gained prominence, since it allows for analysis of the relative changes of protein amounts among different samples, for example between drug-treated parasite versus untreated parasite samples. In more advanced laboratories, high-resolution nanoliquid chromatography has

replaced gel-based separation. Other than its superior separation capability, it uses low sample volume with protein analysis performed on an attomole level (3,4).

Protein identification and/or validation are performed by mass-spectrometry (MS), the 'heart' of current proteomics. Proteins are big molecules, thus identification requires proteolytic cleavage prior to the analysis by MS, with trypsin being the most common enzyme used. Two well established methods of introducing samples into the MS are electrospray ionization (ESI) and matrix-assisted laser desorption/ionization (MALDI), and commonly used MS systems are LC-MS/MS and MALDI-TOF/TOF. Validation techniques such as targeted MS and quantitative techniques using isotope-mediated approaches have advanced research applications in proteomics. Raw data from MS/MS are then searched using database search engines and softwares such as MASCOT, ProteinPilot, ProteinLynx Global server (PLGS), PEAKS, and X!tandeem.

Studies using high-end proteomics approaches are rather minimal in Malaysia; this could be partly due to the high cost of the equipment, databases, and softwares; as well as the dearth of expertise. Thus, there need to be sharing of proteomics facilities, better networking and collaborations amongst us. With this in mind, the 1st Malaysian Proteomics Conference was held in September 2012 in Penang, organized by the Institute for Research in Molecular Medicine, in collaboration with Monash University Sunway Campus. It was a huge success with seven foreign invited speakers and 120 scientists from universities and research organizations in Malaysia.

It is hoped that more Malaysian biomedical scientists will take advantage of the tremendous power of proteomics technology in advancing their research.

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