Editorial

Proteomics

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Mass spectrometry-based proteomics has played an increasing role in biological and biomedical research as gauged by the ever increasing numbers of thousands of publications arising each year. With advances in proteomic technology, bioinformatics and different experimental approaches, sampling of near complete proteomes for some organisms, assessment of entire signaling pathways, and discovery of biomarkers of disease have become possible. The broad range and ease of implementation of various workflows combined with access to robust instrumentation has allowed for continued crossover of proteomics to many diverse biological and even clinical areas. Here, the Journal of Biomedicine and Biotechnology presents the “Proteomics 2011” special issue. Although only representing a small fraction of the contribution of mass spectrometry to many research fields, the articles presented here definitely encompass the excitement that proteomics research can provide to complement traditional biological studies.

To start this special issue, we have five contributions that review several aspects of proteomic research. W. Zhu et al. discuss the different contributing factors for accurate label-free quantification, while challenges that remain for proteomic SELDI experiments to be successful in biomarker discovery are covered by M.-P. Merville and coworkers. Two more specialized reviews cover parts of the biology of translation in eukaryotes mediated by internal ribosome entry sites and intrinsically disordered protein structures (Pecheco et al. and V. N. Uversky, resp.). Lastly, how

proteomics may play a role in crop disease prevention by understanding the pathogenesis of fungi is covered by J. V. Jorrín-Novó and coworkers.

Articles describing the development of methods and computational approaches are also well represented in this special issue. On the methods side, we have J. Hou et al. demonstrating improved MALDI-MS of phosphopeptides by an optimized matrix. Improved sample preparations including separations are utilized by M. Centlow et al. and E. Gamelin and coworkers to uncover potential biomarkers of preeclamptic placenta and to improve proteome coverage of plasma, respectively. 2D liquid chromatography coupled to mass spectrometry is used to determine proteomic response to cadmium stress in plants by G. Visioli et al. Identifying released bioactive proteins from human platelets is addressed by G. Cagney and coworkers. Dealing with the computational end of proteomic studies, T. H. Corzett et al. describe statistical measures for determining variation resulting from quantification of the human plasma proteome separated by 2D difference gel electrophoresis. Enhanced peptide and protein identification is addressed by L. Pattini and coworkers who present a novel method for preprocessing proteomic data, and by K. Macur et al. who utilize peptide retention time as an extra indication of false positives.

Lastly, we showcase the application of mass spectrometry-based proteomics for the determination of potential biomarkers from various biological and clinical conditions. J. Svasti and coworkers investigate the secretomes from

different carcinoma cell lines by GeLC-MS to find potential tumor biomarkers. In search of an elusive Down's syndrome (DS) protein marker, S. Hahn and coworkers use iTRAQ labeling to screen plasma from DS pregnancies. Campostrini et al. look to quantify the iron regulating hepcidin protein isoforms in patients afflicted by chronic haemodialysis. Overall, we hope this special issue brings to light the potential that proteomic experiments possess and the impacts that could be made to health and disease.

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