Journal of
Proteomics & Bioinformatics

Xia, J Proteomics Bioinform 2013, S6
DOI: 10.4172/jpb.S6-e001

Editorial Open Access

Microarray Proteomics

Qiangwei Xia

ProQualiX Consultants, Inc., USA

Comparative proteomics, or quantitative proteomics, has followed the footprint of DNA microarray since its infancy. Advancement of proteomics field in the past decade has enabled profiling protein abundance with a similar capacity as what DNA microarray technology provides. As the term "quantitative proteomics" has more general coverage than the specific type of proteomics that pursue after the concept of whole cell or tissue level of comparison, here we come up with this "microarray proteomics" term in order to emphasize this particular type of proteomics research.

In this special issue of "Microarray Proteomics" we have included a total of eight manuscripts, which represent the current status quo of this field from various perspectives. A range of experimental methodology development and data analysis approaches have been described in these manuscripts.

In the research article "Immunosignaturing Microarrays Distinguish Antibody Profiles of Related Pancreatic Diseases", the authors used a peptide array containing 10,000 random sequence 20-mer peptides to differentiate four different diseases that target the same organ; pancreatic cancer, pre-pancreatic cancer (panIN), type II diabetes and acute pancreatitis. As the technology platform takes the format of DNA microarray, the core data analysis in their work has been carried out using software that was designed for DNA microarray. This demonstrates a good example of the influence of DNA microarray technology on peptide microarray platforms.

The research work led by Dr. Kevin Camphausen in the NIH resulted in the identification of 46 compounds in urine samples that differentiated healthy controls from patients with glioblastoma multiforme. This exemplifies the direct clinical impact of microarray proteomics on the molecular diagnosis. The peptide features found in their study may be useful as diagnostic biomarker candidates, which serves as valuable resource for studying the pathophysiology of glioblastoma multiforme.

The authors at Yale University reported the application of a novel statistical approach, Bayesian Variable Partition Model to discover the HBV amino acid sequence mutations in occult Hepatitis B infections. Their work conveys a clear message that there remains a lot more information than that we could possibly interpret at one time. With the development of advanced statistical data analysis approaches, we may be able to disclose what we have been missing.

Another research article "New Insights into the Molecular Mechanisms of Selected Anticancer Metal Compounds through Bioinformatic Analysis of Proteomic Data" further strengthens the argument that bioinformatics plays an increasingly important role in the data analysis of proteomics results. In order to explore the protein pathways thoroughly, the authors applied advanced bioinformatics methodologies to data mine the interactome data. The protein-protein interaction data is unique to proteomics field.

Proteins have post-translational modifications. Phosphorylation is one of the most prevalent PTMs on proteins that are important for many cellular processes. In this special issue, the review article "Phos-tag-Based Microarray Techniques Advance Phosphoproteomics" summarizes the utility of Phos-tag Biotin as a novel phosphate-affinity probe in a range of techniques, including microarray-based methods, for determining the phosphorylation status of large numbers of peptides and proteins. The authors discussed the impact of Phos-tag-based microarray techniques in relation to the detection of protein phosphorylation multiplexes, and compared these techniques with conventional probing procedures on microarrays.

The field of microarray proteomics has progressed rapidly in the past decade. We hope that the research and review articles in this special issue serve as a primer for the audience to understand the current development of this field. While the protein/peptide array and LC-MS based proteomics platforms mature, the researchers are putting more efforts on developing bioinformatics tools to gain deeper understanding of their data. Because of the unique characteristic of proteomics data, such as protein-protein interaction, post-translational modifications, protein pathway analysis, the difficulty in the data analysis necessitates the development of novel statistical or bioinformatics methodologies. Nonetheless, with the improvement on protein sequence coverage and the increasing accessibility of technologies, microarray proteomics is embracing its high-growth era in the coming decade.

***Corresponding author:** Qiangwei Xia, ProQualiX Consultants, Inc., USA, E-mail: qiangwei.xia@gmail.com

Received July 24, 2013; **Accepted** July 25, 2013; **Published** July 28, 2013

Citation: Xia Q (2013) Microarray Proteomics. J Proteomics Bioinform S6: e001. doi:10.4172/jpb.S6-e001