

Research Journal of Biology

Microarray Proteomics and its Clinical Application

Satya Varali*

Department of Human Genetics, Andhra University, India

Commentary

Received: 12/04/2015
Revised: 22/04/2015
Accepted: 25/04/2015

*For Correspondence

Satya Varali, Department of Human Genetics, Andhra University, India

Keywords: Microarray; metabolome; transcriptomics; proteomics

ABSTRACT

With the development of proteomics, Microarray Proteomics, including protein chip or protein microarray, has received widespread attention because of its characteristics such as high flux, high specificity and sensitivity appeared, and are increasingly used in protein expression spectrum and protein interactions of systemic research. Microarray has also become a tools for the early disease diagnosis and to study the prognosis and treatment of disease, and has been also extended to clinical application.

INTRODUCTION

The principle, classification, preparation, application in the diagnosis of disease, advantages, disadvantages and development prospects of the Microarray Proteomics are introduced in this short commentary [1-3]. Mass Spectrometry is the key technology of proteomics, its advances first was in the development of ionization techniques such as matrix assisted laser desorption ionization (MALDI) [4] and electrospray ionization and secondly was in the ability to conduct tandem MS (MS/MS) [5] to fragment peptides by collision-induced dissociation, paved the way for the development of proteomics as a field.

Characterization of proteins is now done by mass spectrometry i.e from the identification the protein to its quantification, either by studying the post-translation modification [6] or protein interactions. A fragmented protein or an intact protein can be identified by MS either by top-down or bottom-up approach [7-10]. It has been know that the compared to intact proteins, peptides are relatively easy to handle and easy to study physiochemical properties [11,12]. However, the analysis of complex biological matrices by MS is highly dependent on off-line separation technologies such as 2-dimensional gel electrophoresis (2-DGE) or HPLC that simplify such samples prior to mass analysis; and HPLC is also the standard front end on-line separation methodology for many liquid chromatography-MS (LC-MS) based instrumentation platforms [13-17].

CLASSIFICATION OF MICROARRAYS PROTEOMICS

Microarrays Proteomics are divided in two groups:

- a) Functional protein microarrays
- b) Protein-detecting microarrays
- c) Protein Lysate Microarrays

Functional microarrays proteomics

Functional proteomics is used to study a particular proteome by understanding the network of molecular interaction. It is a powerful tool to study proteins of related function [18]; functional protein microarrays allow high-throughput screening and quantification of protein interactions on a proteome-wide scale, thus providing an unbiased perspective on the connectivity of the different protein-protein interaction networks [19,20]. In 2000, Schreiber et al. [21] presented that purified recombinant proteins

could be microarrayed onto chemically derivatized glass slides without seriously affecting their molecular and functional integrity. More recently, Snyder et al. [22] have been able to immobilize $\approx 5,800$ proteins from *Sacharomycescerivisiae* onto microscope glass slides. This protein chip was then probed with different phospholipids to identify several lipid-binding proteins [23-25]. The authors also used this proteome chip for the identification of substrates for 87 different protein kinases. Using this microarray data set in combination with interaction and transcription factor binding data, the authors were able to reveal several novel regulatory modules in yeast.

Protein-Detecting Microarrays

Protein-detecting microarrays are ideal reagents for establishing how this information flows through these interacting networks [26-28], however, requires measuring the abundance and post-translational modifications of many proteins from complex biological mixtures. One of the most frequently used strategies to prepare this type of microarray involves the use of monoclonal antibodies as specific protein capture reagents [29-31].

Protein Lysate Microarrays

An interesting alternative to antibody microarrays is to immobilize cell lysates and then use specific monoclonal antibodies to identify and quantify the presence of a particular analyte in the corresponding lysate [32,33]. This technology was first described by Liotta and co-workers to monitor pro-survival checkpoint proteins as a function of cancer progression. The same approach has recently been used for the discovery and validation of specific biomarkers for disease diagnosis and patient stratification [34,35].

Advantage of Microarrays Proteomics

Microarrays Proteomics is highly parallel, high flux, miniaturization and automation of proteomic detection technology [36-38]. It is on a carrier of the gene chip size, different kinds of fabric density probe protein, protein microarray, experiment with the chip protein mixture under test incubation reaction, then marked the second of the fluorescent antibody reaction with chip protein complex [39,40], on the scanner reads fluorescence intensity, further quantitative analysis the result of the hybrid [41]. The role of protein chip in the proteome research mainly research difference shows the interaction between protein and protein. According to few scientist different production methods and applications, the protein chip can be divided into two kinds: one kind is protein expression chip, it will be a lot of testing with molecules [42-45] (often for antibody) fixed on the surface of the chip and the arrangement of microarray type, so after add sample can find out the presence of these molecules in the sample target; the other is a core of protein function [46-48].

Applications of Microarrays Proteomics

Unlike the DNA/oligo microarray or analytical protein microarrays, functional protein microarrays provide a flexible platform that allows development and detection of a wide range of protein biochemical properties. To date, well-developed assays include detection of various types of protein-ligand interactions [49], such as protein-protein, protein-DNA, protein-RNA, protein-lipid, protein-drug, and protein-glycan interactions [50,51].

Biomarker Identification

Though the applications described above are most useful in basic research, functional protein microarrays may have enormous impacts on clinical diagnosis and prognosis. When proteins on a functional protein microarray are viewed as potential antigens that may or may not associated with a particular disease, it becomes a powerful tool in biomarker identification [52].

Summary

Though there are many advantages and development in Microarray Proteomics. But there are also many of disadvantages and technological barrier and that still need to be overcome. With the progress in technology, we had an optimistical attitude to those difficulties, and the application of Microarray Proteomics will become more extensive in clinic and scientific research.

REFERENCES

1. Saber HB and Elloumi M. Efficiently Mining Gene Expression Data via Novel Binary Biclustering Algorithms. *J Proteomics Bioinform.* 2015;S9: 008.
2. Kitamura N, et al. Statistical Properties and Power Analysis of Cox's Proportional Hazards Model Regularized by Various Penalties for DNA Microarray Gene Expression Survival Data. *J Health Med Informat.* 2015;6:180.
3. Rea F, et al. Eosinophilic Esophagitis and Ige-Mediated Allergy in Children: Specific Ige by Component-Based-Allergen Microarray. *J Allergy Ther.* 2014;5:180.
4. Cimaglia F, et al. Study of a New Gliadin Capture Agent and Development of a Protein Microarray as a New Approach for Gliadin Detection. *J Proteomics Bioinform.* 2014;7:248-255.
5. Hanash SM, et al. Mining the plasma proteome for cancer biomarkers. *Nature.* 2008;452: 571-579.
6. Rifai N, et al. Protein biomarker discovery and validation: the long and uncertain path to clinical utility. *Nat Biotechnol.* 2006;24: 971-983
7. Sawyers CL. The cancer biomarker problem. *Nature.* 2008;452: 548-552.
8. Chin L and Gray JW. Translating insights from the cancer genome into clinical practice. *Nature.* 2008;452: 553-563.
9. Nowell PC. Discovery of the Philadelphia chromosome: a personal perspective. *J Clin Invest.* 2007;117: 2033-2035.
10. King CR, et al. Amplification of a novel v-erbB-related gene in a human mammary carcinoma. *Science.* 1985;229: 974-976.
11. Brodeur GM, et al. Amplification of N-myc in untreated human neuroblastomas correlates with advanced disease stage. *Science.* 1984;224: 1121-1124.
12. Carpten JD, et al. A transforming mutation in the pleckstrin homology domain of AKT1 in cancer. *Nature.* 2007;448: 439-444.
13. Skog J, et al. Glioblastomamicrovesicles transport RNA and proteins that promote tumour growth and provide diagnostic biomarkers. *Nat Cell Biol.* 2008;10: 1470-1476
14. Huixiao H, et al. SELDI Based Proteomic Determination of Hepatic Biomarkers in Mouse Serum Following Acetaminophen Administration. *J Proteomics Bioinform* 2008;1: 424-436.
15. Shukla Y. Concept of Toxicoproteomics in Identifying Biomarkers of Toxicant Action. *J Proteomics Bioinform* 2011;4
16. Narayanan A, et al. Discovery of Infectious Disease Biomarkers in Murine Anthrax Model Using Mass Spectrometry of the Low-Molecular-Mass Serum Proteome. *J Proteomics Bioinform* 2009;2: 408-415.
17. El-Haibi CP, et al. Antibody Microarray Analysis of Signaling Networks Regulated by Cxcl13 and Cxcr5 in Prostate Cancer. *J Proteomics Bioinform* 2012;5: 177-184.
18. Sjöberg R, et al. Biosensor Based Protein Profiling on Reverse Phase Serum Microarray. *J Proteomics Bioinform* 2012;5: 185-189.
19. Zhag ZH, et al. Integrated Bioinformatics for Radiation-Induced Pathway Analysis from Proteomics and Microarray Data. *J Proteomics Bioinform* 2008;1: 047-060.

20. Chen B, et al. Protein Microarrays in Proteome-wide Applications. *J Proteomics Bioinform* 2014;S12:001
21. MacBeath G, Schreiber SL (2000) Printing proteins as microarrays for high-throughput function determination. *Science* 289:1760-1763.
22. Hudson ME, Pozdnyakova I, Haines K, Mor G, Snyder M (2007) Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays. *ProcNatlAcadSci USA* 104:17494-17499.
23. Nicolini C, et al. SpADS and SNAP-NAPPA Microarrays towards Biomarkers Identification in Humans: Background Subtraction in Mass Spectrometry with E.coli Cell Free Expression System. *J MolBiomarkDiagn*. 2015;6: 214.
24. Greetham D. Presence of Low Concentrations of Acetic Acid Improves Fermentations using *Saccharomyces cerevisiae*. *J Bioprocess Biotech*. 2014;5: 192
25. Paul S and Amundson SA. Differential Effect of Active Smoking on Gene Expression in Male and Female Smokers. *J Carcinog Mutagen*. 2014;5: 198.
26. Mathivanan S. Quest for Cancer Biomarkers: Assaying Mutant Proteins and RNA That Provides the Much Needed Specificity. *J Proteomics Bioinform*. 2012;5: xiii-xvii.
27. Hamrita B et al. Proteomic Analysis of Human Breast Cancer: New Technologies and Clinical Applications for Biomarker Profiling. *J Proteomics Bioinform*. 2012;3: 091-098.
28. Tadashi K. Cancer Proteomics for Biomarker Development. *J Proteomics Bioinform* 2008;1: 477-484
29. Cheng F. Blood MicroRNAs: Novel "Omics" Biomarkers for Ovarian Cancer Early Detection. *J Proteomics Bioinform*. 2012;5: xx-xxi.
30. Holubek WJ, et al. Acetaminophen- induced acute liver failure: Results of a United States multicenter, prospective study. *Hepatology* 2005;42: 1364-72.
31. [http:// www.fda.gov/fdac/features/2003/103_pain.html](http://www.fda.gov/fdac/features/2003/103_pain.html)
32. Ruddock MW, et al. Immunodetection of Cytoplasmatic Membrane-Bound Thrombomodulin in Formalin-Fixed Paraffin-Embedded Human Tissue Microarrays. *J Mol Genet Med*. 2014;8: 140.
33. Aziz MA, et al. Mucin Family Genes are Downregulated in Colorectal Cancer Patients. *J CarcinogeneMutagene*. 2014;S10: 009.
34. An LTT, et al. Statistical Analysis of Protein Microarray Data: A Case Study in Type 1 Diabetes Research. *J Proteomics Bioinform*. 2014;S12: 003.
35. Srivastava A, et al. Personalized Radioproteomics: Identification of a Protein Biomarker Signature for Preemptive Rescue by Tocopherol Succinate in CD34+ Irradiated Progenitor Cells Isolated from a Healthy Control Donor. *J Proteomics Bioinform*. 2015;08:023.
36. Mishra N. A Framework for associated pattern mining over Microarray database. *Journal of Global Research in Computer Science*. 2011;2.
37. Huang P, et al. Developing Prospects of Microarray Proteomics. *J Proteomics Bioinform*. 2014;S12:002.
38. Kikkawa Y, et al. Gene Expression Profiling and Bioinformatic Analysis of Rabbit Basilar Artery after Experimental Subarachnoid Hemorrhage. *J NeurolNeurophysiol*. 2014;5:201.
39. Sirdeshmukh R. Integrated Approach to Study Mouse Embryonic Stem Cell Proteome. *Proceedings of The Joint 2nd Pacific Rim International Conference on Protein Science and 4th Asian-Oceania Human Proteome Organization, Cairns- Australia (2008)*.
40. Selvaraj D, Loganathan A, Sathishkumar R (2010) Molecular Characterization and Phylogenetic Analysis of BZIP Protein in Plants. *J Proteomics Bioinform* 3: 230-233.
41. Nahalka J (2011) Quantification of Peptide Bond Types in Human Proteome Indicates How DNA Codons were Assembled at Prebiotic Conditions. *J Proteomics Bioinform* 4: 153-159.

42. Neha S, Vrat BS, Kumud J, Thakur PD, Rajinder K, et al. (2011) Comparative In silico Analysis of Partial Coat Protein Gene Sequence of Zucchini Yellow Mosaic Virus Infecting Summer Squash (*Cucurbitapepo* L.) Isolated From India. *J Proteomics Bioinform* 4: 068-073.
43. Sharma DK, Rawat AK, Srivastava S, Srivastava R, Kumar A (2010) Comparative Sequence Analysis on Different Strains of Swine Influenza Virus Sub-type H1N1 for Neuraminidase and Hemagglutinin. *J Proteomics Bioinform* 3: 055-060.
44. Saravanan V (2010) Mass Blaster V1.0 – A Perl Gui Tool for Mass Sequence Blast and Gene Prediction. *J Proteomics Bioinform* 3: 302-304.
45. Mohammed A, Guda C (2011) Computational Approaches for Automated Classification of Enzyme Sequences. *J Proteomics Bioinform* 4: 147-152.
46. Kumar S, Sahu BB, Tripathy NK, Shaw BP (2009) In Silico Identification of Putative Proton Binding Sites of a Plasma Membrane H⁺-ATPase Isoform of *Arabidopsis Thaliana*, AHA1. *J Proteomics Bioinform* 2: 349-359.
47. Ghosh S, Ghosh P, Basu K, Das SK, Daefler S (2011) A Discrete Event Based Stochastic Simulation Platform for 'In silico' Study of Molecular-level Cellular Dynamics. *J Biotechnol Biomaterial* S6: 001.
48. Pyatnitskiy M, Karpova M, Moshkovskii S, Lisitsa A, Archakov A (2010) Clustering Mass Spectral Peaks Increases Recognition Accuracy and Stability of SVM-based Feature Selection. *J Proteomics Bioinform* 3: 048-054.
49. Wu XL, Gianola D, Hu ZL, Reecy JM (2011) Meta-Analysis of Quantitative Trait Association and Mapping Studies using Parametric and Non-Parametric Models. *J Biomet Biostat* S1: 001.
50. Zaman Q, Strasak AM, Pfeiffer KP (2011) Exact Waiting Time Survival Function. *J Biomet Biostat* 2: 117.
51. Alessandro A, Di Serio C (2009) Vectors and Integration in Gene Therapy: Statistical Considerations. *J ComputSciSystBiol* 2: 117-123.
52. Pinto FR (2009) A Probabilistic Approach to Study Yeast's Gene Regulatory Network. *J ComputSciSystBiol* 2: 044-050.