
EDITORIAL

Time to Rethink Healthcare Research!

Nikhat Ahmed Siddiqui¹

Medical research must translate into improved treatments for patients with advancement in proteomics technology. This will allow us to measure thousands of molecules at a given point in time. These molecules in form of biomarkers give clues about underlying biological processes in health and disease as they are used to monitoring a disease or predict the outcome of a treatment. The resulting insights will provide novel drug targets and protein-based markers contributing towards a futuristic basis for personalized medicine.

The emerging field of proteomics and the spectacular progress of proteomic technologies is a mainstay of biological research and clinical translation, for more effective analysis of human disease and for the identification and validation of biomarkers. It is only recently that post-genomic research, with evolving new fields in science, provides insights that will benefit both basic medical research and clinical applications by permitting deeper understanding of the genotype-phenotype relationship, mechanistic and functional insights capturing the details of physiological states.

In last couple of years, hundreds of proteins have been characterized using LC-MS to produce for example, a reference map of urine, based on analysis using combinatorial peptide ligand libraries and 2-DE/MS analysis. Additionally, with proteins it is the post-translational modifications which could result in aberrant protein misfolding leading to a dysfunctional protein. Therefore an understanding of the molecular mechanisms involved in post-translational modifications (PTMs) of proteins is indispensable for targeted drug development as it plays a pivotal role in unveiling diverse phenotypes of normal and disease physiology.

The current proteomic advancement in functional and structural profiling also analyse PTMs of specific biomarkers, using CID (collision –induced fragmentation) and electron transfer dissociation (ETD). This approach offers differential stage biomarker status before and after their clinical manifestations are perceptible and assessable. PTM of proteins will provide a better understanding of mechanism of action and protein drug or protein-protein interactions. Additionally proteomics relies heavily on high resolution MS and bioinformatics tools to identify the protein of interest. Protein indicators observed in osteoblast differentiation cells may have a diagnostic, prognostic therapeutic value for tumors and dysfunctions of bone as they reflect various state of cells both temporally and spatially. Similarly in body fluids, label free quantitative proteomic technique and Selected reaction monitoring (SRM) technique reveals a promising outlook for clinical applications for routine analysis of relevant protein markers.

Proteomics is now also being vastly applied in various field of medical sciences like obstetrics and neuroscience to name the few, providing insights in the pathogenesis of preeclampsia, and identifying makers associated with disease diagnosis. Protein–drug interaction is another major field where proteomics has left the foot mark, how drug treatment can be mapped onto affected biological functions and the prediction of potential side effects using such mapping.

¹ Nikhat Ahmed Siddiqui

Dean Research, Ziauddin University & Hospitals, Karachi.

Advances on these various fronts obviously depend on different types of research, ranging from investigations on fundamental aspects of human biology to the more clinically oriented applications. We witness that biomedical research is entering the most exciting phase of its development of effective health delivery strategies according to the needs of the countries. Medical research must therefore continue to provide better preventive measures to control diseases with the application of discoveries in these new fields of science with the balance between discoveries and its bedside applications.

A major transformation in outlook of those educating medical scientists and doctors in developing countries is crucial. The research community of biomedical research has to face the challenge put forward by the medical practitioners as to why do we need research? This challenge can be met by educating government and non-government organizations on evidence based medicine training and on boarding the public about the activities and the faith in medical research endeavor. Dissemination of knowledge about the recent advancement in mass-spectrometry-based proteomics and collaboration between researchers, clinicians and statisticians should be promoted as it help researchers and clinicians better understand and detect complex disease phenotypes.

The need for good science, with a complete change of attitude towards health care research and practice is vital, ranging from studies of molecules to communities. The transformation of the mindset can only be achieved if the education programs of the universities can emphasize a global perspective of health and disease for the future medical scientists. This would lead to large networking of universities and related bodies for the establishment of sustainable research programs relevant to the need of the country, much progress will be made toward distributing the benefits of biomedical research and good practice to the population of this country.

REFERENCES

- ¹ Mary S, Patil GV, Kulkarni AV, Kulkarni MJ, Joshi SR, Mehendale SS, Giri AP. Dynamic proteome in enigmatic preeclampsia: an account of molecular mechanisms and biomarker discovery. *Proteomics Clin Appl* 2012; 6(1-2): 79-90
- ² Dutta B, Yan R, Lim SK, Tam JP, Sze SK. Quantitative Profiling of Chromatome Dynamics Reveals a Novel Role for HP1BP3 in Hypoxia-induced Oncogenesis. *Mol Cell Proteomics* 2014; 13: 3236-3249.
- ³ Halim A, Carlsson MC, Madsen CB, Brand S, Møller SR, Olsen CE, Vakhrushev SY, Brimnes J, Wurtzen PA, Ipsen H, Petersen BL, Wandall HH. Glycoproteomic Analysis of Seven Major Allergenic Proteins Reveals Novel Post-translational Modifications 2015. *Mol Cell Proteomics* 2015; 14: 191-204.
- ⁴ Marimuthu A, O'Meally RN, Chaerkady R, Subbannayya Y, Nanjappa V, Kumar P, Kelkar DS, Sneha M, Sharma PR, Renuse S, Goel R, Christopher R, Delanghe B, Cole RN, Harsha HC, Pandey A. A Comprehensive Map of the Human Urinary Proteome. *J Proteome Res* 2011; 10(6): 2734–2743.