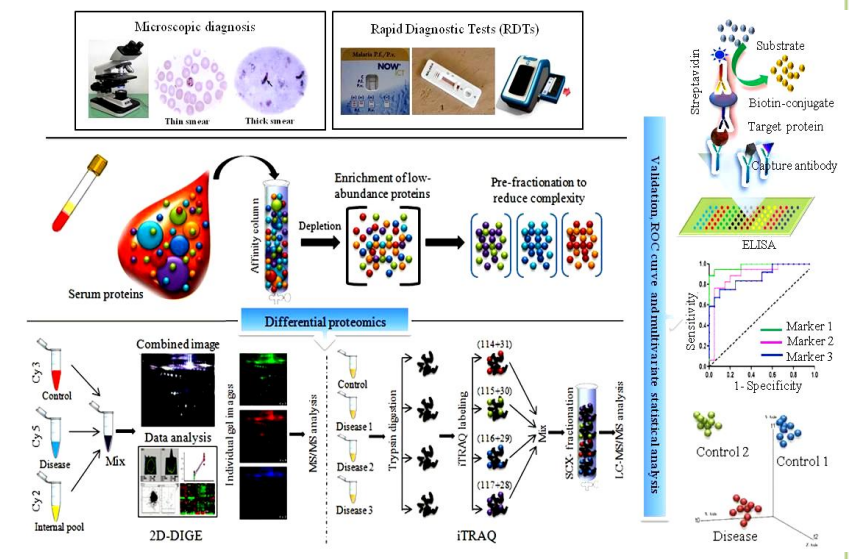
Proteomics Society , India (PSI)

PSI News Letter Vol. 3 (No. 1) April 2015



Editors

Abhijit Chakrabarti

K Dharmalingam

Utpal Tatu

Contents :-

From the Editors

Dear Members,

As promised we are back with the first issue of 2015. This would not have been possible without the timely contributions from our members.

We've celebrated Proteomics Day for the first time in India on March 18th and highlights of such programs held in different Institutes are part of this News Letter.

We have been planning for a column on "perspectives" in the context of proteomics, metabolomics and other omics activities – their future and promises. We think it is high time to have a healthy debate on what could be achieved and what could not in the past decade of proteomics research in India. We welcome Prof. Dharmaligam in this issue for contributing a wonderful article.

An interesting article on Proteomics in Dairy Research by Dr. A. K. Mohanty gives us an insight into the strength of proteomic tools for managing our dairy animals for societal benefit.

In this issue we were really in a quandary with interesting articles on hand with little space left in the News Letter. We have listed the articles to follow at the end in this News Letter. We thank the authors for their contributions and their patience.

*In our next issue we will open up a **"Student's Corner"** and we invite contributions from students and request our faculty colleagues to encourage them to write and contribute articles for the News Letter of PSI.*

We look forward to hearing from you.

With Best Wishes

Editors

PS: Please send your contributions for the News Letter to abhijit.chakrabarti@saha.ac.in

From the President, PSI

Dear Members,

Let me take this opportunity and wish all the PSI members a belated but a Very Happy New Year-2015 as we meet you with the first Newsletter of the year.

December 2014 was an eventful month which started with a bang during the 6th Annual Meeting of the Society at IITB. The outcome of the meeting was that we met the global leaders in Proteomics Research and another step was that Indian Proteomics community was recognized for its contributions. The meeting led to J Proteomics having a special issue on "Proteomics in India". Several of you must have contributed to that. Another one coming up is a focus issue on "Proteomics Research in India" by Nature India in August 2015. The meeting has also brought our Society into the limelight of the Proteomics community.

All this places a responsibility on our shoulders to ensure that the society continues and expands its activities under its mandates. Several of our colleagues have ensured that we do so and as promised organized symposia/workshops to celebrate "Proteomics Day" in March 2015. Their reports provide a glimpse of the events. Further we begin the first Newsletter of the year with a "Perspective". PSI members--faculty and students, do use the PSI News letter to bring to attention Proteomics related news items or to discuss a viewpoint. Dr. Dharmalingam has set the ball rolling this time. Looking forward to this continuing and having articles in waiting for our News letters to follow.

Some of the student members of PSI may require Proteomics related information and help for their research. Do write to me so that you can be connected to our Senior scientists closest to your Institute or those engaged in research of your interest. We are also open to other ideas as to how PSI can help its members.

With Best Wishes
Surekha Zingde
(surekha.zingde@gmail.com)

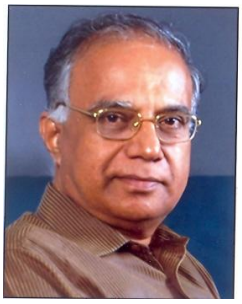
Proteomic Society, India (PSI)

Members of PSI Executive Council

President: Dr Surekha Zingde
Vice President: Dr Abhijit Chakrabarti
Vice President: Dr Utpal Tatu
Secretary: Dr Shantanu Sengupta
Treasurer: Dr Rakesh Mishra
Jt Secretary: Dr Subhra Chakraborty
Jt Secretary: Dr Mahesh Kulkarni
Members: Dr. Ravi Sirdeshmukh
Dr. M A Vijayalakshmi
Dr Abhijit Mitra
Dr Arun Bandyopadhyay
Dr. K Dharmalingam
Dr. Kalpana Bhargava
Dr Niranjan Chakraborty
Dr Amol Suryawangshi
Dr. T. S. Keshava Prasad
Dr. Suman S. Thakur
Dr.Harsha Gowda
Dr. Suman Kundu
Dr. Sanjeeva Srivastava
Dr. Rapole Srikanth

Perspective

MORE THAN ONE WAY TO SKIN A CAT



K.DHARMALINGAM

Aravind Medical Research Foundation, Aravind Eye Hospital, Madurai. 625020

Depth of analysis of a proteome depends on the reduction in the complexity of the starting material as well as the instrument performance. A recent paper from J.J.Coon's lab published in Mol. Cell. Proteomics, (2014,13.1,339-347) showing the identification of 6000 proteins of yeast from an unfractionated lysate is truly an advancement. This is true next generation proteomics, demonstrating identification of 62 proteins per minute, a marvelous thing indeed. Identification of the entire yeast proteome in one hour is certainly an inviting proposition, provided your institution has money to shell out for the instrument. In this case the new Thermo Tribrid mass spectrometer is the key requirement. But, there are more ways than one to skin a cat '(or Catfish/ *Ictalurus punctatus*, lexicographers believe cat in this proverb actually means Catfish, also called American channel Cat and not our *Felis catus*). I always say this to my students that science was done long before the arrival of modern gadgets. Coming to our current discussion, the question is whether we could achieve the depth of analysis by other approaches and how good are they.

U.K. Laemmli improved the one dimensional sodium dodecylsulphate electrophoresis (1D PAGE) to a level that this technique has become the routine method in almost all labs doing experimental biology research. In fact this is the most quoted paper for several years. In proteomics also this technique has become a method of choice, for many labs, for pre fractionation of complex proteins. We routinely use 1D SDS PAGE to separate proteins first and then cut the coomassie blue stained gels into several fractions before trypsin digestion in gel. This method allows us to identify more than 3500 proteins of *E.coli* using Orbitrap velos pro mass spectrometer and using a 15 cm Easy Spray nano- LC column using a gradient of 90 minutes. Similar experiment using complex proteome such as Corneal Epithelial cells from a cell line gives 4000

proteins. The downside here is the time factor. In our labs as of now the identification rate is one protein per minute. A 60 fold less output compared to the one hour yeast proteome achievement. This calculation takes in to consideration the time to do gels, staining, in-gel digestion, extraction and clean up of peptides and mass spectrometry. Obviously there is scope for improvement. Molecular weight based protein level fractionation is easy to perform and has many advantages over solution based protein fractionation techniques, such as ion exchange chromatography.

The next method which many labs follow is pre fractionation at peptide level. The method of choice is isoelectric focusing which separates peptides based on their pI in a pH gradient. Here again there is a solution based IEF using instruments such as Offgel electrophoresis and other similar equipment. We use IEF in IPG strips using conventional equipment used for first dimension electrophoresis in 1 D PAGE. Subsequently the strips were cut into one cm bits and the peptides are eluted in formic acid after clean up the peptides can be analyzed in a mass spectrometer. However, the downside is one should be very careful to clean the eluted peptides to avoid column clogging. Using this approach we could identify 3000 proteins from *E.coli* lysate. These are alternatives to more expensive approaches but will give equally good coverage of the proteome.

Apart from fractionating proteins according to their molecular weight and peptides according to their isoelectric points one could use other options to reduce the sample complexity. One such approach is , fractionation of proteins using their post translational modifications as a handle, e.g. separating glycoproteins from the whole proteome by lectin columns. As it is there are several methods that allow one to reduce the complexity of the proteome. Each investigator can analyze the proteome to a great depth taking advantage of these wet lab exercises and their experimental skill. One precaution is that any bias in the recovery of the analytes should be avoided.

The take home message is that one should not get discouraged by the unaffordable technical advances: Creative ideas still count in good science.

Proteomics and Dairy Research: An Insight

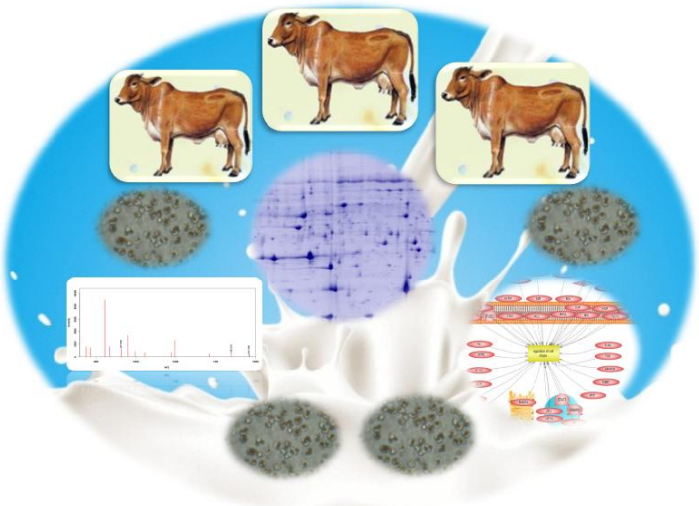
Dr. Ashok Kumar Mohanty
Animal Biotechnology Centre, National Dairy Research Institute,
Karnal 132001, Haryana, India; ashokmohanty1@gmail.com

Milk is a nutritious product secreted by the mammary gland. It serves an important role in human daily diet. Milk is a complex biological fluid containing a high amount of proteins, lipids and minerals. Milk from all species is dominated by the presence of a few primary proteins (O'Donnell *et al*., 2004) that contribute to the nutritional value of milk and milk produts (Lonnerdal, 2003). Cow, buffalo, goat, and sheep milk accounts for more than 87% of global milk production (Yang et al., 2013). India harbours highest population of livestock (512.057 million) that constitutes 190.904 million cattle and 108.702 million buffaloes and rest constituting sheep, goat, pig, horses and ponies, mules, donkeys, camels, mithun and yak. India is currently the highest milk producer in the world and total milk production stands at 132.4 million tons according to 2012-13 statistics released by Government of India. Around 56% of the milk is contributed by the buffaloes and rest is contributed by crossbred and indigenous cows. There is substantial variation in milk yield within and between various breeds of cows and buffaloes. This dramatic difference can be attributed to various factors such as genetics, physiology, management and environmental influence etc. The key mechanism behind this variability has direct correlation with the expression of different genes encoding signalling proteins, transcription factors, cell survival and death factors in the mammary gland at different stages of lactation and involution. Conventional breeding is routinely followed to improve the milk production of animals by selection of high milk producing animals. With the advancement of proteomics, identification of proteins influencing milk yield and lactation persistency is a distinct possibility, which can be used as biomarkers for assessing the lactation potential in farm animals. In this article, application of proteomics in different areas of dairy research has been discussed.

Proteomics of mammary gland involved in milk yield and lactation persistency:

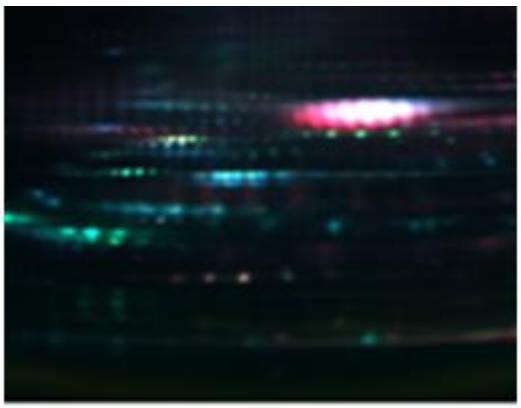
The mammary gland provides an excellent system to study questions pertaining to organogenesis, cell differentiation and oncogenesis. Mammary gland is made up of a branching network of ducts that ends in alveoli. Terminally differentiated mammary epithelial cells (MECs), which constitute the innermost layer of alveoli are involved in the synthesis and secretion of milk proteins during lactation. MECs reflect the milk producing ability in animals. Our

group at NDRI has used deciphered the proteome map of functionally differentiated MECs (isolated from milk) in lactating cows using 2-DE-MALDI-TOF/MS and 1D-GE-LC-MS/MS (Shotgun proteomics). We have identified 497 proteins in MECs, which reflect their role during physiological lactation. Extensive bioinformatics analysis revealed involvement of novel proteins that works at the cellular level for milk synthesis and secretion. We have built the protein interaction network of MEC associated proteins to understand their functional significance during lactation. The proteins regulating few important cellular processes e.g. positive regulators of lactation, cell shape, cell survival, cell differentiation, negative regulators of apoptosis, and proteins involved in cholesterol export have been reported. A number of antimicrobial proteins / peptides involved in innate immune response was also observed (Janjanam et al., 2013).



Proteome Analysis of Mammary Epithelial Cells isolated from Cow milk

In an effort to identify potential biomarkers involved in milk yield and lactation persistency, we performed 2D-DIGE in functionally differentiated MECs isolated from milk of high *vis-à-vis* low producing cows during early, peak and late lactation stages. We identified 22 proteins in high and low milk yielding cows and 41 differentially expressed proteins (DEPs) during different stages of lactation. Bioinformatics analysis of DEPs showed that a majority of the proteins are associated in metabolic process, catalytic and binding activity. The differentially expressed proteins were mapped to the available biological pathways and networks involved in lactation. The proteins up-regulated during late stage of lactation were found to be associated with NF-kB stress induced signalling pathways and whereas Akt, PI3K and p38/MAPK signalling pathways were associated with high milk production mediated through insulin hormone signalling (Janjanam et al., 2014). After validation of few selected proteins, we identified the role of MFGE8 as a potential biomarker of milk yield in cows. shRNA based knockdown of this gene in buffalo mammary epithelial cell line (Anand et al. 2012) revealed that MFGE8 is involved in cell shape maintenance and regulation of β-casein in mammary gland (unpublished data). In India, Buffaloes are prized animals, which contribute substantially to the total milk pool of India. We performed 2D-DIGE in mammary gland tissue of virgin (heifer) *vis-à-vis* lactating buffalo and identified ~43 differentially proteins in lactating buffalo mammary gland tissue that gives exclusive reflection of association of



Differential proteome of lactating vis-à-vis heifer (non-lactating) mammary tissue

various proteins in milk synthesis and secretion (Jena et al., 2015). Various other groups have profiled the comparative profiling of milk from different species. Differential proteome analysis of milk whey proteins in different species such as cow, Yak, Buffalo, Goat and Camel has been reported (Yang et al. 2013). Proteomic characterization and comparison of mammalian milk fat globule proteomes by iTRAQ analysis in Holstein, Jersey, yak, buffalo, goat, camel, horse, and human revealed 520 proteins (Yang et al., 2015)

Proteomics for Biomarker Discovery for Detection of Sub-clinical Mastitis:

Mastitis is a multifactorial disease in lactating cows and buffaloes, which encompasses infection and inflammation of the mammary gland. Mastitis causes major economic losses, has negative impact on animal health and welfare and has implications on food safety through lower quality milk. Clinical mastitis can be detected by visual observation of red and swollen mammary gland and production of either clotted or curdled milk. But, subclinical mastitis is difficult to detect due to the absence of any visible indications, and it has major cost implications. Farmers do not have an option to detect milk of animals having sub-clinical mastitis. Recent development in Mass Spectrometry based techniques has promised crucial advancement in diagnosis of subclinical mastitis. In bacterial infection, the overall protein profile in milk changes, which includes some bacterial origin proteins and some endogenous proteins from animal body whose normal expression level is altered. By using 2D-proteomics and MS-based techniques many proteins have been identified. Some of them are Lipocalin-type prostaglandin D synthase, transferrin, microsomal triglyceride protein, apolipoprotein A-1, cathelicidin-1, heat shock protein 70kD protein, peptidoglycan recognition receptor protein (PGRP), calgranulin B and C, and serum amyloid A (SAA), which are present in excess in mastitic milk. NDRI has taken up this research in a big way to identify potential biomarkers for development of ready to use diagnostic kit against subclinical mastitis.

Proteomics of Dairy Animal Reproduction:

Biomarkers for early detection of pregnancy and estrus: A very potential application of research in identification of urine based protein biomarker for detection of pregnancy and oestrous. Unlike human being, where human chorionic gonadotropin (HCG) based detection kits are available, the same is not applicable in bovine. Our group at NDRI is involved in identification of early pregnancy biomarkers in cows and buffaloes by employing proteomics approaches. We have profiled more than thousand proteins in cow urine for the first time (unpublished data) and have identified potential biomarkers for early detection of pregnancy.

Bull Fertility**:** High reproductive performance and factors that influence this have a significant impact on the economics of animal production. Proteomics has been used to show that variation in protein types and amounts in seminal fluid and sperm regulates fertility indexes in dairy bulls. These findings can be used to identify potential biomarkers to select dairy bulls of high fertility at an early age. Research at NDRI, Karnal is also focussed to find potential biomarkers in spermatogonial cells for early selection of high fertile bulls.

Proteomics in Dairy Processing:

A large number of bacterial species are used in the production of dairy products. Milk processing methodologies are highly dependent on the total repertoire of milk proteins. The presence of bacteria in milk may change the quality of

milk that might critically impact the manufacturing processes. Bacterial behaviour itself changes drastically when it is moved from laboratory to manufacturing environment presenting challenges to the manufacturing strategies. A proteomic approach can yield information regarding the global changes in protein expression to understand the adaptations that these bacteria undergo. The proteomes of *Lactobacillus bulgaricus*, *Lactococcus lactis*, and *Streptococcus thermophilus* have been examined for protein changes. These data provide food scientists with new information to modify/select these bacteria for optimum dairy food production practices. Research on probiotics is currently one of the potential areas of food biotechnology, where friendly bacteria are in use. But looking at the rate of their application in industry, it is felt that a screening and identification of probiotics is needed. The latest innovation and development in proteomics will enable rapid characterization of a large number of candidate bacterial species to qualify as probiotic. Proteome data for probiotic and pathogenic bacteria can be generated so that future research attempts for quality milk product and processing could find an informative platform to move on.

Future Perspective in Dairy Animal Proteomics:

Dairy animal proteomics has major implications in understanding the physiological process in a better way. Therefore, it is highly required to build the proteome map of indigenous bovine in consonance with human proteome project. Major emphasis must be given on the generation of bovine protein reference data base (BPRD), which will lay foundation to the future research endeavours towards understanding animal production, reproduction and quality attributes.

References:

1. Anand, V., Dogra, N., Kaushik, J. K., Singh, S., Jena, M. K., Kumar, S., Malakar, D., Dang, A. K., Mishra, B. P Mukhopadhyay, T. and Mohanty, A. K (2012). Establishment and Characterization of a Buffalo (*Bubalus bubalis*) Mammary Epithelial Cell Line. *PLosOne.*2012; 7(7): e40469.

2. Janjanam, J., Jamwal, M., Singh, S., Kumar S., Panigrahi, AK., Hariprasad, G., Jena MK., Anand, V., Kumar, S., Kaushik., JK., Dang, AK., Mukesh., M., Mishra ., BP., Alagiri, S., , Reddy, VS. and Mohanty, A. K (2013). Proteome analysis of functionally differentiated bovine (*Bos indicus*) mammary epithelial cells isolated from milk. *Proteomics 13*, 3189–3204).

3. Janjanam, J., Singh, S., Jena, M., Varshney, N., Kola, S., Kumar, S., Kaushik, J.K., Grover, S., Dang, A.K., Mukesh, M., Prakash, B.S. and Mohanty, A.K. (2014). Comparative 2D-DIGE Proteomic Analysis of Bovine Mammary Epithelial Cells during Lactation Reveals Protein Signatures for Lactation Persistency and Milk Yield. *PlosOne* DOI: 10.1371/journal.pone.0102515.

4. Jena, M.K., Janjanam, J., Naru, J., Kumar, Saravanan, Kumar, Sudarshan, Singh S., Mohapatra, S. K., Kola, S., Anand, V., Jaswal, S., Verma, A. K., Malakar, D., Dang, A. K., Kaushik, J. K., Reddy, V. S., Mohanty, A. K (2015). DIGE based proteome analysis of mammary gland tissue in water buffalo (*Bubalus bubalis*): Lactating *vis-a-vis* heifer. *J. Proteomics*. 119: 100 – 111.

5. Yang Y., Bu, D., Zhao, X., Sun, P., Wang, J., and Zhou, L (2013). Proteomic Analysis of Cow, Yak, Buffalo, Goat and Camel Milk Whey Proteins: Quantitative Differential Expression Patterns. *J. Proteome Res.* 2013, 12, 1660−1667.

6. Yanga, Y., Zhenga, N., Zhao, X., Zhang, Y., Han, R., Maa, L., Zhao, S., Li, S., Guo, T and Wang, J (2015). Proteomic characterization and comparison of mammalian milk fat globule proteomes by iTRAQ analysis. *J. Proteomics*. 116: 34 – 4 3.

7. O'Donnell, R., Holland, J. W., Deeth, H. C., (2004). Milk Proteomics. *Int. Dairy J.* 14 (12): 1013-1023.

8. Lönnerdal, B (2003). Nutritional and physiologic significance of human milk proteins. *Am. J. Clin. Nutr.* 77 (6): 1537S-1543S.

Proteomics Day Celebrations

Recent Advances in Proteomics

18th March 2015

A mini symposium organized by National Centre for Cell Science (NCCS), Pune on the occasion of "Proteomics Day" in association with Proteomics Society, India.

Convener: Dr. Srikanth Rapole, Scientist, Proteomics Lab, NCCS, Pune.

The world of 'proteomics' technologies is increasing day by day with the introduction of new technologies, thereby enhancing the scope of scientific research related to 'proteomics'. Current progress in proteomics has been largely due to recent developments in mass spectrometry based technologies. 'Proteomics' technologies are not new to scientist in the research community, but majority of the young students, undergraduates, college faculties and clinicians are not so familiar. A mini symposium on "Recent advances in Proteomics" on the occasion of Proteomics Day was organized at the National Centre for Cell Science, Pune on 18th March 2015 in association with the Proteomics Society, India. The main objective behind this mini symposium was to make aware the local scientific community, students, faculty from NCCS, and neighboring institutions including colleges about the recent advancements in the proteomics world. The mini symposium was comprised of a series of lectures from eminent scientists working in various genres of proteomics research in India. The mini symposium was attended by more than two hundred and fifty participants including teachers, students, and clinicians from Pune.

Dr. Srikanth Rapole, Scientist, NCCS, Pune and the Convener of this event briefed the audience about the importance and objectives behind organizing this event. He expressed the need for awareness about the new technological advances in the Proteomics for undertaking world class research. He emphasized the fact that improvements in mass spectrometry techniques permit studying in detail the proteome including post-translational modifications. This was followed by the series of five lectures by the eminent scientists from India working on various areas of proteomics and two lectures from representatives of world leader mass spectrometry companies.

The inaugurating lecture was delivered by **Dr. Surekha Zingde**, President, Proteomics Society, India (PSI). In her presentation, Dr. Zingde elaborated on the importance of Human Proteomics Project of the Human Proteome Organization (HUPO) and technological advancements in mass spectrometry, bioinformatics (knowledge base), the Human Protein Atlas and finally proteomics research in India. In the second part of her talk she discussed on the research carried out by her lab in the area of oral cancers. She emphasized on the fact that diagnosis of oral cancer is not an issue but there is a need for predictive and prognostic biomarkers. She spoke about some aspects of her research which involved tissue proteomics, keratins and autoantibodies in circulation. In addition, she also briefed about Proteomics Society, India and its activities among the proteomics researchers.

Dr. Harsha Gowda from Institute of Bioinformatics, Bangalore, very elegantly presented his recent work about a draft map of human proteome using high resolution mass spectrometry. He also discussed about phosphoproteomics and its capabilities to characterize signaling pathways. He emphasized on the revolutionizing capabilities of the modern mass spectrometry which has made high-throughput research in proteomics possible. He discussed about the power of phosphoproteomics approach used for characterizing aberrantly activated signaling pathways in cancers.

Dr. Geetanjali Sachdeva from National Institute for Research in Reproductive Health, Mumbai, delivered her talk about the role of endometrium in women reproductive health. She spoke on the need to identify molecules that are differentially expressed in the receptive phase endometrium which subsequently will help in the understanding of the mechanisms by which endometrium becomes receptive and also the identity of the markers of receptivity for infertility management. She briefed about her research involving the various proteomics approaches undertaken to identify the proteins present in uterine fluid during the receptive phase. She also discussed about need to profile the uterine secretome using proteomic approaches, considering the potential of uterine secretome in determining the functional status of the endometrium.

Dr. Mahesh Kulkarni from National Chemical Laboratory, Pune, explained about chemical and biological strategies to reduce Advanced Glycation End (AGEs) products. He talked about the process of glycation leading to the formation of heterogeneous advanced glycation end products (AGEs) and its implication in various diseases including aging, diabetic complication, and neurodegenerative diseases. He discussed about protein aggregation and formation of protease resistant proteins (PRPs) as a result of glycation. He demonstrated from his research findings that the accumulation of protein aggregates is an inevitable consequence of impaired proteasomal activity and protease resistance due to AGE modification. He emphasized that these findings will provide a new dimension for developing intervention strategies for the treatment of glycation associated diseases such as diabetes complications, atherosclerosis, and aging.

Dr. P. Babu from Centre for Cellular and Molecular Platforms, Bangalore, deliver his lecture on a recent aspect of proteomics namely, identifying glycan modifications in proteins. His talk was on structural characterization of N- and O-Glycans and their role in Hydra Regeneration. He very elegantly described about the diversity of glycans attached to glycoconjugates which drive many of the processes involved in development, homeostasis and diseases. Structural characterization of the glycans is foremost step in understating their functions and

recent advances in mass spectrometry play an important role in this area. Cell-cell communications, cell-matrix interactions and cell migrations play a major role during regeneration. However, little is known about the molecular players involved in these critical events, especially the cell surface glycans. He presented the data related to the role of polyfucosylated glycan-receptor interactions in the regeneration.

Mr. Sangram Pattanaik from Thermo Fisher Scientific India Pvt. Ltd., Mumbai, spoke about recent advancement in Orbitrap Mass spectrometry for complex Proteomics. He introduced the audience to the orbitrap fusion tribrid mass spectrometer which has three mass analysers working together to produce unmatched analytical performance. He made the audience understand the capabilities and power of orbitrap fusion tribrid mass spectrometer for those facing the most difficult analytical challenges in cell biology, proteomics and structural analysis.

Dr. Manoj Pillai from AB Sciex India, New Delhi, spoke about the Next-Gen Proteomics Platform. He introduced the audience to the SWATH acquisition on Triple TOF mass spectrometer to overcome the limitations in shotgun proteomics and targeted proteomics. He demonstrated the technology of SWATH-MS through his lecture and conveyed the advantages of SWATH-MS including broader dynamic range, improved mass accuracy stability, and high resolution. He also introduced new swath proteomics cloud toolkit to combine genomics information with proteomics information.

The event was formally concluded by vote of thanks from **Dr. Jyoti Rao**, Scientist, NCCS, Pune. She thanked all the invited speakers, participants, the Proteomics Society, India and the volunteers of the event for making it a success.

The invited speakers and the team of volunteers for the event at NCCS Pune.

PROTEOMICS DAY" AT INDIAN INSTITUTE OF TECHNOLOGY, BOMBAY.

Ghantasala Saicharan, Proteomics Laboratory, Dept of BioSciences
and Bioengineering, IIT B, Mumbai

On 18th March 2015, --" Proteomics Day" the proteomics lab at IIT Bombay under the guidance of Dr.Sanjeeva Srivastava (Assoc.Prof, Biosciences & Bioengineering, IITB) introduced the students from NMIMS School of Science, Mumbai , the techniques and potential of various proteomics technologies. The students were given live demostration for techniques like 2D-DIGE, Protein Microarray, Mass Spectrometry and SPR with an intention of helping them appreciate their importance in science.

The day began with a lecture by Dr. Srivastava where the students were introduced to the different proteomics techniques which have revolutionized the field over the last two decades. This lecture was followed by sessions from Dr. Veenita Gover Shah and Ms. Tumpa Das who explained the principle, applications and advantages of Surface Plasmon Resonance (SPR) and Matrix-assisted laser desorption ionisation (MALDI) in the field of proteomics.

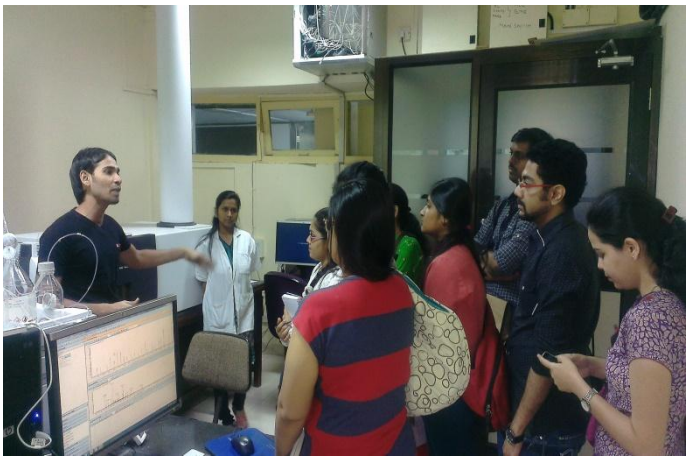
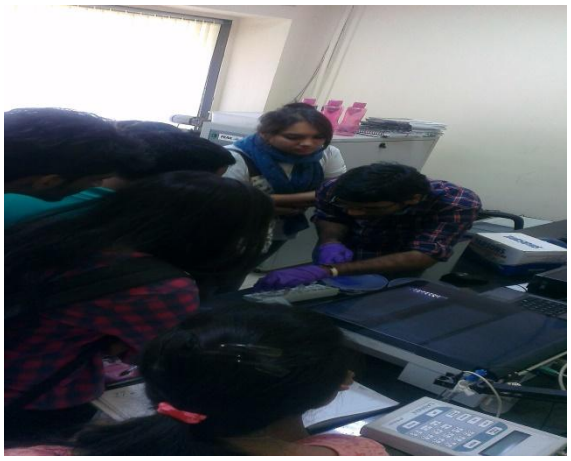
Dr. Srivastava introducing the different proteomics techniques to students

Dr. Veenita (left) and Ms. Tumpa (right) explaining SPR and MALDI.

The 2D-DIGE demo introduced the students labelling of proteins with CyDyes, isoelectric focussing, gel electrophoresis and Scanning. Demos at the SPR and MALDI facility managed further increased the interest among the students who had by then familar with three different techniques. When the students were introduced to the protein microarray technology, a relatively new technique among the Indian scientific community, they could not help but marvel at the robustness and the amount of data this technique was able to generate in a single experiment alone.


Interactive demos for MALDI (left) and Microarray (right) techniques

The LC-MS/MS facility at CRNTS, IIT Bombay introduced the students to the dynamic ability of mass spectrometry. The students were given demos for in-gel digestion, off-gel fractionation, instrumentation and analysis of the obtained mass spectrometric data.

Interactive demos at the LC-MS/MS facility, CRNTS IIT Bombay.

The students were finally introduced to the Remote Triggered Virtual Laboratory (RT-Vlab) developed by IIT Bombay. This unique effort showed the students how the experiments could be performed at a click of the mouse.

The interactive sessions between students and the instructors during the demo sessions were able to get the best out of the students who by the end of the day carried home concepts of different proteomics techniques, their applications and their usefulness in understanding and development of science. The success of the whole exercise was evident from the words of Dr. Purvi Bhatt, Assistant professor NMIMS School of science who had accompanied the students for each of the above mentioned sessions.

"We had a fruitful learning experience and we gained a lot of knowledge regarding the use of various techniques in the field of Proteomics. In fact the theoretical knowledge complemented the instrument demonstration. Your team of students and the scientific staff were very dynamic and explained every instrument clearly. Our students were happy to visit on the 'India Proteomics Day' and everyone received both practical and theoretical knowledge"

All in all the Proteomics Day workshop was a huge success and the lab looks forward to educating and spreading awareness on proteomics to young students, researchers and faculty alike in the years to come and help India become a major force in Proteomics research.

Workshop on fundamentals of mass spectrometry-based proteomics for beginners, March 11-14, 2015, conducted at Institute of Bioinformatics, Bangalore

Convenor, Dr. T.S. Keshava Prasad,
Instititute of Bioinformatics, Bengaluru

Institute of Bioinformatics conducted a four days workshop (March 11-14, 2015) on fundamentals of mass spectrometry-based proteomics. The objective of the workshop was to share the expertise of IOB investigators in using high-resolution mass spectrometry proteomic technologies with young researchers in India. Six participants from different institutes, i.e. Dr. Pinky Agarwal from National Institute of Plant Genome Research (NIPGR), New Delhi, Mr. Kaushal K. Bhati and Mr. Prateek Jain from National Agri-food Biotechnology Institute (NABI), Mohali, Ms. Shrilaxmi V. Joshi from Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), Bangalore, Ms. Pramila Sharma from Indian Institute Technology (IIT), Ganhinagar and Mr. Suhas Mhaske from National Centre for Cell Science (NCCS), Pune participated in the workshop.

The workshop started with a talk on 'Introduction to proteomics and mass spectrometry' by Dr. Keshava Prasad, Faculty Scientist at IOB and Coordinator of this workshop, followed by talk and hands-on training in sample preparation and fractionation strategies. A talk on LC-MS/MS analysis by Dr. Sneha Pinto included fundamentals of mass spectrometry and quantitative proteomics, followed by hands-on training in sample preparation strategies for quantitative proteomics. Dr. Harsha Gowda discussed proteomics strategies for analysis of post

Workshop participants getting hands-on training in sample preparation strategies

translational modifications. Participants were then provided with series of demo and hands-on training in data analysis for both qualitative and quantitative proteomics. Participants were highly motivated and found the workshop significant and essential for basic knowledge of mass spectrometry-based proteomics. Hands-on training in sample preparation, fractionation strategies and data analysis answered multiple queries of the participants. However, the participants felt that the frequency and duration of such workshops could have been increased for a complete training and better practice of proteomic technologies.

In the next issue:

Research Article:

Integrative Approaches for Discovery of Protein-Protein Interactions

Padma P. Nanaware, Centre for Biotechnology, Anna University, Chennai-600025, India

Students Corner

A Decade of Proteomics Activity at Saha Institute of Nuclear Physics

Avik Basu, Saha Institute of Nuclear Physics, Kolkata 700064, India

Upcoming Events

7th Annual Meeting of the Proteomics Society, India, December 3-6, 2015, Vellore Institute of Technology. **Abstract submission: 1st May – 31st July 2015. www.psivellore2015.org**

This conference is themed on **BioChromatography, Molecular Recognition and Proteomics** and it aims to integrate cross disciplinary subjects for better understanding of complexity of proteome, metablome, glycome, lipidomes of humans, plants, microorganisms, etc for various applications.

Proteomics Society, India

Registered under Andhra Pradesh Societies Registration Act. (35/2001)

(Regd. No. 286/2009)

proteomicsociety@ccmb.res.in

www.psindia.org