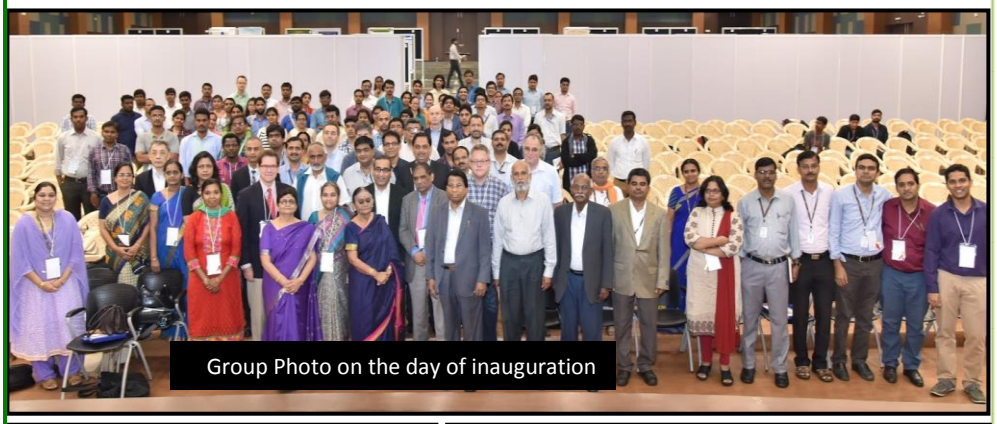
Proteomics Society , India (PSI)

PSI News Letter Vol. 3 (No. 3) December 2015

Glimpses from the 7th Annual Meeting of the Proteomics Society, India Vellore (3rd to 6th Dec. 2015)



Group Photo on the day of inauguration

Panel discussion on "Challenges in Biomarker Proteomics" (Left-Right: Dr. Debasis Dash, Prof. Robert Plumb, Prof. Peter Nilsson)

Poster award winners

PSI travel award winners

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Editors

Abhijit Chakrabarti

K. Dharmalingam

Utpal Tatu

From the Editors

Dear Members,

The last issue of the Newsletter of 2015 brings you an article by Dr. Mahesh Kulkarni, on "Targeted quantification of glycated peptides of Human serum albumin in Diabetes". He describes the use of proteomic tools for using the specific glycated peptides for determining the glycemic diabetic status.

For those of you who missed the 7th Annual meeting of the PSI held in Vellore, held during 3rd to 6th Dec 2015, Dr Krishnan Venkatraman has succinctly summarized the events.

*Ms Sharanya Chatterjee from Dr Utpal Tatu's laboratory, IISc, contributes to the "**Student's Corner**" with her narration of the meeting on "Metabolomics" held in Indian Institute of Science, Bengalure during 12th to 13th Jan. 2015. We look forward to more contributions from students.*

With Best Wishes for the New Year 2016

Editors

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

From the President, PSI

Dear Members,

December 2015 was a very busy time for the PSI community.

The 7th Annual meeting of the PSI, was held at Vellore Institute of Technology, Vellore (3rd to 6th Dec 2015). This was possible due to the valiant efforts of Dr. Vijayalakshmi and Dr. Krishnan Venkatraman who met the challenges of the Chennai floods bravely and ensured that the meeting was on schedule as planned. The meeting was also possible due to the efforts of the speakers and the delegates who found ways and means to reach Vellore when the Chennai route to Vellore was impossible. The pre-meeting workshops were well attended and many youngsters and those new to proteomics technologies learnt the details from the experts in the field. I take this opportunity to thank each one of you for supporting the PSI on this occasion.

IIT Bombay workshop and International Symposium on "Targeted Proteomics" organized by Dr. Sanjeeva Srivastava during 10th -14th Dec 2015 was well attended and appreciated and so was the Education Day on the 10th Dec 2015.

The PSI elects seven new members to its Executive Council each year. I am happy to inform you that the members who join the EC include our renominated members, Dr. Utpal Tatu, Dr. Mahesh Kulkarni, Dr Amol Suryavanshi, Dr. K. Dharmalingam, Dr. Abhijit Chakrabarti, and the new members Dr. Ashok Mohanty and Dr Sharmila Chattopadhya. Their term of three years begins as of

Jan. 2016. I welcome them all in joining the EC team to take PSI to greater heights. PSI would like to thank outgoing members Dr. Abhijit Mitra and Dr. Kalpana Bhargava for their support to the Society activities during their tenure.

PSI embarks on a new venture starting in 2016. The Journal of Proteins and Proteomics (JPP) will now be the official journal of the Society. The first issue of this journal in its new avatar will be released in March 2016. We encourage all our members to contribute their articles to JPP.

The Society is recognized by the Human Proteome Organization (HUPO) and the members of the Society are now Associate members of HUPO.

Remember the Society has designated 18th March each year as Proteomics Day. We encourage members to hold some activities such as lectures/workshop on that day or around that time. This will help in educating students, teachers and researchers who wish to use Proteomic tools in their work.

The 8th Annual meeting of the Society is being held in early Dec. 2016 at New Delhi with Dr Subhra Chakraborty as its Convener. Do block this period in your calender.

We would be happy to consider any suggestions for activities to be taken up by our Society. Do contact the Secretary, Dr Shantanu Sengupta (shantanus@igib.res.in) or me with your ideas.

With Best Wishes for the New Year 2016

Dr. Surekha Zingde
(surekha.zingde@gmail.com)

Proteomic Society, India (PSI)

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Vice President: Dr. Utpal Tatu
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Research Article

Targeted quantification of glycated peptides of Human serum albumin in diabetes

Mahesh J. Kulkarni

Proteomics facility, Division of Biochemical Sciences, CSIR-National Chemical Laboratory, Pune-411008, India. E-Mail: mj.kulkarni@ncl.res.in

Diabetes and its complications are becoming global public health problems and posing a serious challenge in disease management. Currently, the diagnosis and treatment of diabetes mainly relies on measurement of glycated hemoglobin (HbA1c). Although, HbA1c is considered as 'gold standard' marker, which reflects the glycemic status over the period of 8-10 weeks, however, factors like anemia, blood loss, splenomegaly, iron deficiency affects the HbA1c levels. Therefore, glycated albumin has been suggested as an additional diagnostic marker for monitoring glycemic status in diabetes. Human serum albumin (HSA) is the most abundant plasma proteins and is a principal target for non-enzymatic reaction with glucose, referred as glycation. Glycated albumin is believed to provide glycemic status over preceding 3-4 weeks and has been preferably recommended in gestational diabetes. In diabetes, the levels of glycated albumin increase and were found to be positively correlated with hyperglycemia. In addition, several recent studies have suggested that the levels of glycated albumin are associated with prediabetic condition, and microalbuminuria. Therefore, quantification of glycated albumin is of utmost clinical significance. Glycated albumin can be quantified by various approaches including, enzyme-linked boronate immunoassay, fluorescence spectroscopy, and mass spectrometry. Amongst these approaches, mass spectrometry offers precise characterization of protein glycation including the amino acid involved in the modification.

Recent developments in targeted mass spectrometric approaches such as such as multiple reaction monitoring (MRM) or selected reaction monitoring (SRM) have enabled absolute quantification. In MRM, specific precursor and fragment ions are monitored for quantitation. MRM is highly reproducible and provides absolute concentration if stable isotope-labeled internal standards are included in the workflows. MRM based targeted quantification is becoming quite popular in the proteomics community, as this

approach is able to replace expensive antibody-based quantification like Western blotting and ELISA. MRM performed on high resolution mass spectrometers such as QTOFs and Orbitraps are called pseudo MRM or high resolution MRM (HR-MRM) or parallel reaction monitoring (PRM). Unlike MRM, in PRM it is not possible to monitor the specific fragment ion during acquisition. Post mass spectral acquisition, extracted ion chromatograms (XIC) for selected ions are used for quantitation. HR-MRM can be also be done by sequential window acquisition of all theoretical mass spectra (SWATH-MS). In SWATH-MS, a spectral library is created by information dependent acquisition (IDA), later the instrument is specifically tuned for the selection of precursor ions from an overlapping window of 25 m/z spread over a precursor mass range of 400-1250 m/z window 25 m/z wide. Peptides are quantitated by targeted data extraction of SWATH-MS data.

Thus, quantitation of glycated albumin heavily relies on the fragment ion library and presence of diagnostic ions specific to glycated peptides. In order to develop ion library, it is important to have good MS/MS spectra. In view of this, we have constructed the fragment ion library for Amadori modified lysine (AML), N(ε)-(carboxymethyl)lysine (CML) and N(ε)-(carboxyethyl)lysine (CEL) modified peptides of the corresponding synthetically modified albumin using high resolution accurate mass spectrometry (Q-Exactive) followed by rigorous manual inspection and validation of MS/MS spectra to construct the spectral library (Fig 1 and 2, Table 1). Furthermore, the fragment ion library was used for quantification of glycated peptides of albumin in the context of diabetes. Targeted SWATH analysis in pooled plasma samples of control, prediabetes, diabetes and microalbuminuria, has led to identification and quantification of 13 glycated peptides comprising of 4 AML, 7 CML and 2 CEL modification representing 9 lysine sites of albumin (K36, K88, K160, K161, K183, K375, K438, K490 and K549). Amongst these sites K549, K438, K490, K88 and K375 were highly sensitive for glycation modification as they had both AML and CML modifications and K549 had additional CEL modification (Fig 3). Precursor ions appertain to K549, K438, K490, K88, K375 could serve as potential novel markers for assessing the degree of glycation or diabetic glycemic status. However, as this is a pilot study involving limited number of samples, it is important to analyze larger patient cohort to consider these peptides as biomarkers.

Reference:

Korwar AM, Vannuruswamy G, Jagadeeshaprasad MG, Ramesha JH. Bhat S, Regin BS, Ramaswamy S, Giri AP, Mohan V, Balasumbramanyam M and **Kulkarni MJ***. Development of diagnostic fragment ion library for glycated peptides of Human serum albumin: Targeted quantification in prediabetic, diabetic and microalbuminuria plasma by PRM, SWATH and MS^E. **Mol Cell Proteom.** 2015 Aug;14(8):2150-9.

Figure 1. Overview of the complete study design.

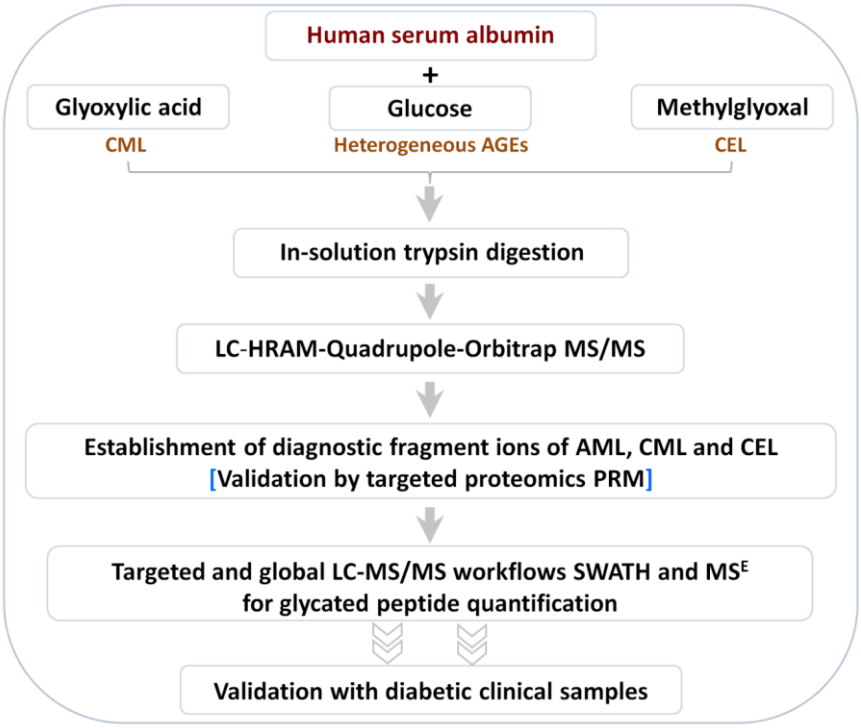


Figure 2. MS/MS annotation of CML modified peptide (m/z- 566.652, K*VPQVSTPTLVEVSR) depicting diagnostic b series fragment ions bearing 58 Da mass shift.

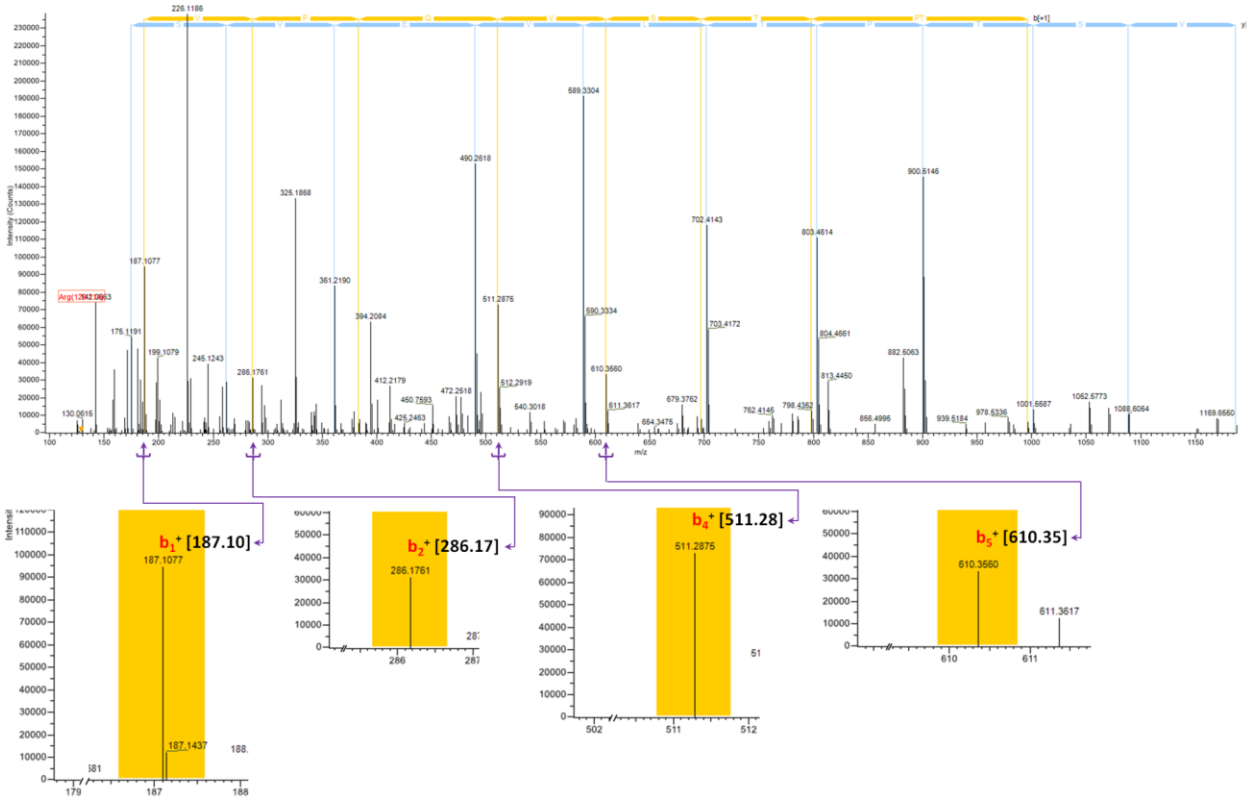
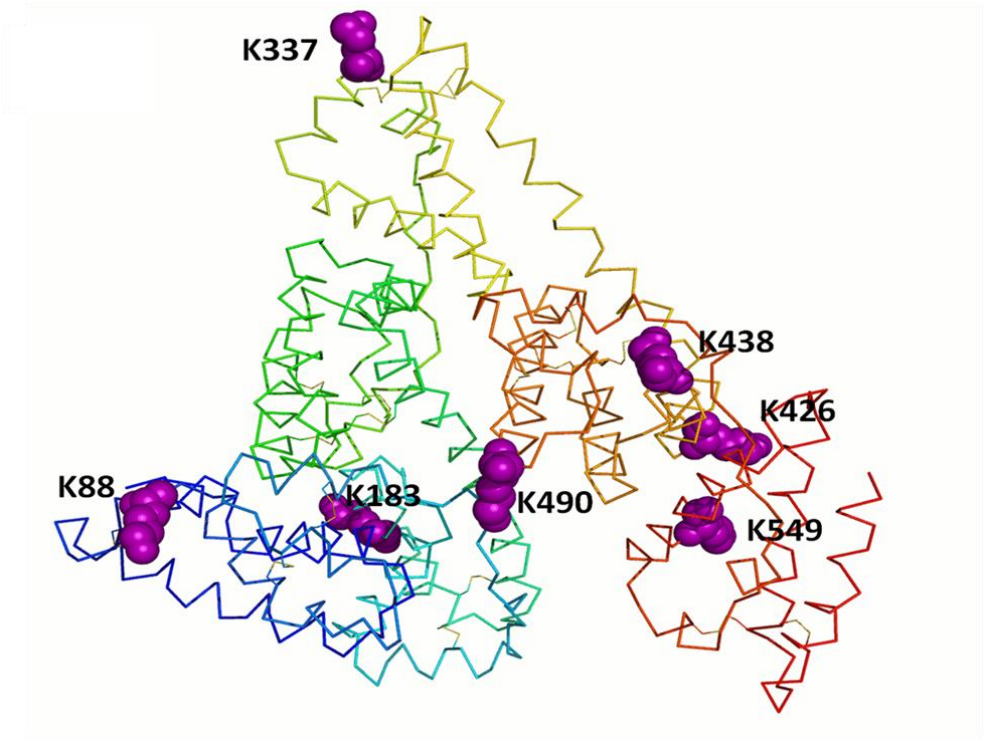


Table 1. A small section of fragment ion library of glycated peptides of albumin, having three consecutive fragment ions retaining modification.

Sl. N	Modified Lysine	Glycated peptide sequence	Peptide MH+ Da	Xcorr,	Modification	Diagnostic fragment ions			
8	438	**K***VPQVSTPTLVEVSR	1697.94	3.53	CML	187.10 [b_1^+]	511.28 [b_4^+]	610.35 [b_5^+]	798.43 [b_7^+]
9	549	**K***QTALVELVK	1186.70	3.46	CML	187.10 [b_1^+]	600.33 [b_5^+]	699.40 [b_6^+]	828.44 [b_7^+]
11	490	MP**C***AEDYLSVVLNQL**C***VLHE**K***TPVSDR	3335.59	3.10	AML	674.34 [y_6^+]	274.12 [y_8^{4+}]	1343.66 [y_{10}^+]	1442.73 [y_{11}^+]
12	88	T**C***VADESAEN**C***D**K***SLHTLFGDK	2659.15	2.96	AML	821.87 [b_{13}^{2+}]	921.87 [b_{15}^{2+}]	948.91 [y_{15}^{2+}]	1114.48 [y_{18}^{2+}]

Static modification: * Carbamidomethyl (57.02146 Da),

Figure 3. Cartoon depicting glycation sensitive lysine residues of human serum albumin



Meeting report

7th Annual Meeting of Proteomics Society, India 2015

Dr. Krishnan Venkatraman, CBST, Vellore;
E-mail; bmkrishna1@yahoo.com ; Krishnan.v@vit.ac.in

The 7th Annual Meeting of the PSI was held at VIT University, Vellore, India during **December 3rd – 6th , 2015.** This meeting was organized by the Centre for BioSeparation Technology (CBST) at VIT University, Vellore, India with Prof. M. A. Vijayalakshmi as the Convener and Dr. Krishnan Venkatraman as Organizer, under the aegis of Proteomics Society, India (PSI). This annual meeting was themed on Biochromatography, Molecular Recognition hyphenated with Proteomics and it was aimed to integrate cross-disciplinary subjects for better understanding of complexity of proteome, metabolome, glycome, lipidomes of humans, plants, microorganisms, etc. for various applications. This meeting also had a special focus on the applications of Proteomics in pharma-related bioprocess industry. Thus the main themes of this symposium were programmed under

1. Biochromatography, Molecular Recognition and Proteomics
2. Structural and Functional Proteomics
3. Glycomics, Lipidomics, Metabolomics & Metallomics
4. Biomarker Proteomics:- Diseases/Disorders
5. Applications of Proteomics in Biopharma/Bio industries

In addition, there were 4 independent preconference sessions held on 2nd and 3rd of December, 2015, to provide an in depth understanding on various emerging technologies and applications in the field of Proteomics and allied sciences. In addition some of the workshops also provided hands on training for young scientists. The sessions were on:

1. Surface Plasmon Resonance (SPR) hyphenated with proteomics (GE Healthcare, USA & Agilent Technologies, Germany) on December 2, 2015
2. In depth analysis of complex proteomes by benchtop orbitrap MS data with independent analysis (Thermo Fisher Scientific, USA) on December 2, 2015
3. High-throughput spatial proteomics of tissue using rapifleX MALDI tissue typer (Bruker Daltonics, Germany) on December 3, 2015
4. Transomics technologies for integrated analytical technologies for metabolite and protein interaction (Waters, USA) on December 3, 2015.

The whole program had a tenuous start owing to incessant rains in the costal belts of Tamil Nadu and Northern parts of Tamil Nadu including Vellore during the last week of November and during the December 1-2, 2015 leading to heavy floods in Chennai resulting in closure of airports, train, road transport services,

electricity, communication services. Reaching Vellore through Chennai, which is the major hub, was impossible and thus all the participants were requested to come to Vellore either through Bangalore or other routes. Many participants, national and international speakers bravely volunteered to attend the conference despite the anxieties in getting the travel tickets, long wait in the airports or train stations and finally to reach Vellore. Thanks to all the members who attended the conference and this was made possible because of sincere efforts of Prof. M. A. Vijayalakshmi (Conference Convener), Prof. Surekha Zingde (President, PSI), Dr. Shantanu Sengupta (Secretary, PSI), Prof. Utpal Tatu (Vice President, PSI), Dr. Ravi Sirdeshmukh (EC member, PSI), Dr. Harsha Gowda (EC Member, PSI), Prof. Suman Kundu (EC Member, PSI). In addition the organizers of this meeting acknowledge sincere efforts of many participants who supported the success of the conference but could not make it to conference due to difficulties in reaching Vellore.

Since many of the participants could not reach 3rd December, 2015; the inauguration of the conference was held on 4th December 2015.

The meeting comprised of excellent summative review lectures by plenary speakers, oral presentations and poster presentations on current research. The meeting had 180 attendees from 10 different countries including Austria, Australia, France, Germany, India, Israel, Japan, Slovenia, Sweden, United Kingdom (UK) and United States of America (USA) and it was well represented from both academia and industry.

The meeting was inaugurated in the august presence of the Chancellor of Vellore Institute of Technology, Dr. G Vishwanathan, Dr Anand Samuel (Vice Chancellor, VIT University) and Dr Rao Aiyagari (Senior Advisor, Public Health Foundation India) as Chief Guest. Dr Surekha Zingde, President, PSI, Prof.M.A. Vijayalakshmi and Dr Krishnan V were also present. At the inauguration the members felicitated Prof. M. A.Vijayalakshmi (Director, CBST, VIT University) for her efforts in bringing Centre for BioSeparation Technology (CBST) at VIT University, Vellore to its present stature since its founding in 2005. A CD describing her life and scientific achievements was released on the occasion.

The meeting took off on December 4, 2015 immediately after the inauguration in the morning with the opening presentation by Prof. Giulio Superti-Furga (CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria). In this session all the lectures were focused on broad approaches of proteomics for basic understanding of human physiology and pathophysiology towards identifying novel therapeutic or early diagnostic markers. The title of his talk was on “Global analysis of genes and protein that convey the action of drugs”. It evoked the importance of drug resistance and the role played by various membrane transporters with broad goal of understanding the biochemical networks in human physiology and to develop novel therapies. Dr. Kumaran Kandaswamy (Centre for Molecular Medicine of the Austrian Academy of Sciences) delivered a talk on use of proteomics approaches to understand the immune responses and antiviral networks and inflammation.

Prof. Peter Nilsson (KTH-Royal Institute of Technology Stockholm, Sweden) spoke on Human Proteomics Atlas which enabled neuroproteomic profiling of body fluids. The talk focused on antibody based neuroproteomic profiling of body fluids with analysis both within and between different neurological disorders using various platforms. Prof. Akhilesh Pandey (Johns Hopkins University School of Medicine, Baltimore, USA) talked on Quantitative proteomics to study oncogenic signaling pathways especially focusing on tyrosine kinase and Tyr-phosphorylation-proteome profiling and interactions in triple negative (ER, PR, HER2) breast cancers, which may have implications in addressing biomedical questions in health and disease. Dr. Sudhir Srivastava (National Cancer Institute, USA) spoke on Proteomics and Precision Health and the talk concentrated on the approaches to precision cancer detection by both nucleic acid and protein array platforms to identify early novel biomarkers of cancer. Dr. A.K.Yadavv (THSTI) presented the use of various quantitative proteomics approaches and their limitations to study temporal dynamics of host responses to mycobacterial infections.

The second session focused on pre-fractionation for proteomics, essentially focusing on various pre-fractionation and newer emerging technologies in miniaturization methods available for effective and sensitive proteomic analysis of complex biological samples and therapeutic antibodies. Prof. Alois

Jungbauer (Austrian Centre of Industrial Biotechnology and BOKU, Vienna, Austria). The talk focused on various chromatographic and precipitation strategies for purifying therapeutic antibodies, followed by proteomic analysis which could be used at industrial scales for obtaining high value therapeutic products. Dr. Mark McDowall (Waters Corporation, UK) spoke on the integration of microfluidics with UPLC and its utility in peptide quantitation especially useful for biomarkers by MS/MS (MRM) detection. Dr. Kishore Tetala (CBST, VIT University, Vellore) spoke on the use of Immobilized Metal Affinity Chromatography systems and its utility in the pre-fractionation of complex biological samples for effective proteomic analysis. In addition, how these chromatographic supports could be used in developing novel microfluidics for analytical purposes in proteomics platform was also discussed.

Dr. Andreas Huhmer (Thermo Fisher Scientific) explained about Protein Quantitation by various approaches such as SRM (single reaction monitoring); PRM (parallel reaction monitoring) and TMT (Tandem mass tag) and DIA (Data independent methods).

At the end of the day, the delegates enjoyed a cultural feast of Indian classical dance and music, performed by children from a dance school and a batch of enthusiastic youngsters whose musical performance made the audience drum and sway to the melodies emanating from the different instruments

The second day of the meeting (5th of December 2015) was focused on Lipidomics, Metabolomics and Glycomics. The first lecture was delivered by Prof. Tony Futerman (Weizmann Institute of Science, Israel). His lecture focused on “So many sphingolipids-What do they all do” He gave an overview of lipids and lipidome and particularly the role sphingolipids in cellular physiology and pathophysiology. Following which Prof. Robert Plumb (Imperial College, London, UK and Waters Corporation) talked about “Understanding Human Health and Disease with LC/MS metabolic phenotyping”. The talk focused on approaches to identify polar and non-polar metabolites and the workflow for their identification, validation and quantification. It was discussed with targeted LC/MS approaches to quantify various small molecules such as bile acids, amino acids, eicosanoids etc.

Prof. Abhijit Mitra (International Institute of Information Technology, Hyderabad, India) talked about computational core for plant metabolomics and the need for newer computational approaches to quantify and characterize the metabolites as there is a surge in generation of large volume of high quality data.

Dr.Jim Thorn (SCIEX) spoke about Capillary Electrophoresis systems coupled to MS with special reference to characterization of biologics, biosimilars and in biomarker discovery. Dr. Jaran Jainhuknan spoke on Glycoproteins Analysis challenges and solutions with special reference to use of MALDI-TOF and TOF/TOF approaches.

The Clinical and Biomarker Proteomics session was initiated with a talk by Dr. Rakesh Mishra (CCMB, Hyderabad) on Nuclear Matrix (NuMat) which supports the nuclear processes including transcription, replication and mitotic chromosome proteomics for better understanding of nuclear architecture. Further, two talks by Dr. Sagarika Biswas (IGIB, New Delhi) and Dr. Arun Bandopadhyay (ICGEB, Kolkata) focused on the pathogenesis of coronary heart diseases and Rheumatic Heart Disease respectively. Dr. Kalpana Bhargava (DRD), New Delhi) presented a lecture on the redox modulating properties of nanoceria in exercised muscle with an emphasis on mitochondrial function.

Dr. Shannon Cornet of Bruker Daltonics presented extensive analysis of tissues by MALDI-TOF and its utility in identification and characterization of biomarkers of diseases. Dr. Sharmistha Dey, AIIMS, New Delhi, presented the use of SPR technologies in characterizing protein-protein interaction and the development of peptide inhibitors of p38MAPK which serves as a marker pancreatic cancer.

The final day of the conference focused on Biosimilar and Biopharamaceutical analysis and characterization by various analytic tools including LC/MS based approaches. Prof. Ales Podgornik (University of Ljubljana, Slovenia) and Dr. Matjaz Peterka (COBIK, Slovenia) discussed about Process Analytical Technologies which is highly required by the regulatory agencies such as Food and Drug Administration (FDA) for Critical Process Parameters (CPP) and Critical Quality Attributes (CPP) which

affect the Critical Quality attributes. They presented PAT systems using Monolith based approaches for Biopharmaceuticals, Viral particles etc.,

Dr. Jaran Jain Hukknan (Bruker Daltonics) spoke about the biosimilar characterization with the use of UHR-Q-TOF. Dr. Vikas Halan (Theramyt Novobiologics, Bangalore) gave a general overview on high throughput screening of therapeutic proteins in the early stage development.

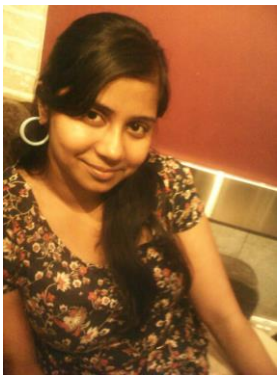
During the conference, two animated and very interactive panel discussions were held and they were :
(i) The importance of pre-fractionation for proteomics of complex biological samples. (Panel discussion was headed by Prof. Shuichi Yamamoto, and the panel members comprised of Prof. Alois Jungbauer, Prof. M. A. Vijayalakshmi, Dr. Shantanu Sengupta.
(ii) Challenges in biomarker discovery and their utility (Discussion panel was headed by Prof. Peter Nilsson and the panel members included Prof. Robert Plumb and Dr. Debasis Dash.

On all the three days, 82 posters (74 young scientists and 8 company posters) were presented on different Proteomic themes. The organizers presented three awards to the best Posters, while PSI, gave 10 travel awards to students who participated in the meeting. The meeting concluded with a hearty appreciation for the involvement of academia and industry delegates to disseminate the information and the tremendous enthusiasm shown by young scientists towards exchange of ideas during poster presentation and during the panel discussions in emerging areas of Proteomics and allied sciences how it was impacting basic understanding of living systems and the emerging technologies and methods for various applications benefitting mankind.

Please note;

1. The conference proceedings are published in the Journal of Proteins and Proteomics (ISSN:0975-8151); Volume 6, Number 4, 2015. (http://jpp.org.in/index.php/jpp/issue/archive)
2. Some of the conference pictures are uploaded at https://goo.gl/photos/5e9Gu1rAVS7ubCGt8

Students Corner



Sharanya Chatterjee, Prof Utpal Tatu's laboratory, Biochemistry Department, Indian Institute of Science, Bengaluru 560012.

Report on the Metabolomics Meeting at Indian Institute of Science

Groundbreaking innovations in the field of science often arise from an amalgamation of novel tools and concepts. On the same note, the year 2015 embarked with a metabolomics symposium which gave a comprehensive coverage of the progress the field has made in the past decade. Metabolomics is the next

generation omics tool for medical diagnostics, research and drug development and it is currently in the exponential phase of its growth across the globe. The symposium which commenced on January 12 to13 at Indian Institute of Science, Bangalore was the first of its kind wherein we saw a close collaboration of the academia and industry. It was organized by Prof. Utpal Tatu, Department of Biochemistry, Indian Institute of Science together with Agilent Technology, Bangalore and was attended by about 300 participants from various scientific areas including medicine, life science research and biotechnology. The scientific session included 15 enriching talks by eminent national and international scientists with the main focus on how metabolomics is changing the landscape of research. These talks covered vibrant areas such as profiling the metabolite catecholamine in arthropods to understand its regulation in defense; application of metabolomics to study disease biology such as malaria, Alzheimer's disease and lysosomal storage disorders as well as the current trends and advances in LCMS and MS/MS based metabolite identifications. The daylong session was combined with a poster presentation session which served as a good platform for students to exchange their scientific ideas with the leading professionals in the field. The event had a lucky coincidence with 80th birthday of Prof. N Appaji Rao, one of the most prolific researchers in the field of enzymology. A small celebration was organized to honor his excellent scientific contribution by the symposium team. This was followed by a panel discussion held at Agilent Technologies, Bangalore wherein experts in the field outlined the current state of art, success stories and the challenges in metabolomics.

Metabolomics is the identification and quantification of metabolites of an organism and thereby it completes the omics triad by providing a holistic picture of the complex biological processes. In targeted metabolomics approach, a set of biochemically defined metabolites are quantitated in context of any physiological cue. The metabolome is the downstream product of gene expression thereby it reflects the functional status of the cell more precisely and hence changes in the metabolome are expected to be amplified relative to the proteome or transcriptome. Additionally since the function of both genes and proteins are subject to epigenetic regulation and post translational modifications respectively, metabolites serve as direct biochemical signature of an organism. It is now being successfully applied in functional genomics, environmental toxicology such as pesticide analysis, systems biology, infectious disease research, pharmacogenomics and biomarker discovery for drug development and therapy monitoring. While conventional clinical assays are limited both in terms of the number and diversity of compounds, metabolomics is highly sensitive and hence can be applied to diverse areas. A single compound may not be the best biomarker (diagnostic, prognostic, or predictive) and hence it is necessary to determine the global metabolic profile to determine a set of clinical biomarkers in assessing the true pathophysiological status of patients.

Prof. Utpal Tatu spearheaded the panel discussion on the need for Metabolomics forum to discuss, deliberate and raise the issues/concerns and solutions across different fields of research and industry. He also referred the success on other similar forums/societies in India viz. Proteomics society. Applicability of the tool is still a challenge in our country owing to its expensive nature. He emphasized that there is a need for R&D in metabolomics which immediately and directly correlates to our society. Dr. Yajnik, KEM Hospital, Pune, continued on the same line and his emphasis was to measure both short term and long term gains. He also discussed about the status of diabetes in India and his initiative on "Fetal Programming". The study of metabolomics can be very well integrated to diabetes treatment and prevention.

Dr. Gautam, Milann, discussed about the conventional approach of the infertility treatments in India and also indicated a few areas where metabolomics can be of use. He pointed out the changes in the levels of

metabolites in culture fluids and its correlation with implantation and child birth rate. This approach can indeed provide a good model for diagnosis and increase the success rate of the treatment as well. Dr. Kamath presented the pharma perspective of the Metabolomics approach. He indicated the need for metabolomics research to identify potential biomarkers from the body fluids viz. blood, saliva; urine etc. which will reduce the pain associated with sample collection. He also suggested profiling of the secretome of microbiota w.r.t. Indian foods for properly channelizing its benefits. Dr. Sarvanan, Mitra Biotech, Bengaluru, highlighted the need for personalized pre-clinical cancer drug treatment approach. He shared the challenges of cancer treatments in terms of both time and money to arrive at systematic treatment with a suitable drug. He also urged to have some sort of methodology wherein drug susceptibility profiling can be done using metabolomics approach. Dr. Akash, Acquity Labs, Bengaluru, discussed about the application of MS technology to human healthcare and diagnostics. He shared his personal experience on the applicability of metabolomics in neonatal disorder screening. Mr. Chandan Mithra, c-CAMP, Bengaluru, highlighted the analytical aspects of the technique and also elaborated on various approaches for analysis viz. targeted and untargeted metabolomics.

Since a metabolic pathway encompasses diverse metabolites such as precursors, end products, derivatives and degradation products with varying concentrations ; accurate metabolite profiling demands sophisticated systems and detection methods to resolve this complexity. Among the various techniques available for metabolite detection, MS is the method of choice owing to its comprehensiveness, selectivity, and sensitivity. Meanwhile, the advent of versatile mass analyzers (tandem or hybrid) has further augmented metabolite identification by acquiring highly resolved and accurate MS/MS spectra. This has been achieved through ion fragmentation by collision-induced dissociation (CID) in either quadruple-based tandem in-space instruments [e.g., triple quadrupole (QqQ) or quadrupole time-of-flight (QTOF)], or ion-trap-based tandem in-time instruments [e.g., quadrupole-ion trap (QIT), linear trap quadrupole (LTQ)-Orbitrap, or linear trap quadrupole Fourier-transform ion cyclotron resonance (LTQ-FT-ICR)]. Triple quad has been the gold standard for absolute quantitation of small molecules. Owing to its sensitivity and specificity using selected reaction monitoring (SRM), it has been applied for quantitation of trace-level metabolites with low detection limit of ng/mL in sample matrices (e.g., plasma, serum, or media). Another approach to bypass the problem of sample complexity and allowing metabolite separation prior to detection is coupling of liquid chromatography (LC) to MS (LC-MS). Coupling HPLC separation with MS detection not only improves MS sensitivity and signal reproducibility but also alleviates matrix interferences in the ionization process.

Proper integration of the metabolome data with other systems wide data is the need of the hour. Hence development of publicly available databases with systematic annotation of the metabolites is crucial. Another major challenge in the field is *de novo* metabolite identification i.e. unknown analytes. Combination of NMR and MS can be used for structure elucidation to overcome this issue. Nevertheless, the accurate identification and quantification of all metabolites in a pathway makes it possible not only to study dynamic networks but also to understand the mechanisms by which these networks are regulated with respect to environmental or genetic perturbations. This will indeed open up new avenues towards the discovery of new correlations among existing biochemical pathways as well as pathways hitherto unknown. The general consensus of the meeting was to align these technological advancements to address biological problems by the integration of metabolomics data to the currently available transcriptomics and proteomics data. The next obvious step will be to fit these data in global models of cellular framework to get a complete systems view of biology !

Upcoming Events

1.

Workshop on Mass Spectrometry based Quantitative Proteomics for Beginners. : Institute of Bioinformatics, Bengaluru. 1st-4th Feb.2016,
workshop@ibioinformatics.org

2.

8th Annual Meeting of the Proteomics Society, India (PSI), combined with the 3rd meeting of Asia Oceania Agricultural Proteomics Organization (AOAPO) and 8th International Symposium on Frontiers in Agricultural Proteome Research is being organized by PSI, AOAPO and National Institute of Plant Genome Research in early Dec. 2016 at New Delhi. **Final dates will be announced shortly. Keep track on the PSI website for more details**

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proteomicsociety@ccmb.res.in
www.psindia.org