

Conference Report on 6th Congress of Swiss Proteomics Society, Lausanne, Switzerland (3-5 December, 2007)

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General Introduction

The 6th Congress of Swiss Proteomics Society (SPS07) was organized in the city of Lausanne, the most beautiful place I have ever visited. The city with its snow capped mountains, huge lake and ample scenic beauty can impress even the most aesthetic person on earth. It is hard to resist oneself from coming here again and again.

This year the theme of the congress was, “**Proteomics: Pushing the Limits**”. The theme was chosen to highlight two most important aspects of proteomics science i.e. reproducibility and limitations. More than 150 professionals including scientists from both academia and industry, and research scholars from all over the world have attended this congress. The second important objective of this conference was to establish and strengthen the connections among different groups, which is crucial for evaluation, harmonization and dissemination of knowledge on global level to improve and develop the science of proteomics.

Advance Courses

Before the congress started, two short advance courses were scheduled. Both courses were organized in order to make the researchers more aware about the informatics tools. The instructor of the first course was Dr. Marie-Claude Blatter from Swiss Institute of Bioinformatics, Geneva. This course dealt with different protein sequence databases in order to do mass spectrometry (MS) identification more efficiently. Since I am involved in bioinformatics based research, hence I felt this course was a bit elementary for me. Hence I had opted not to attend the course. But after participating in entire congress, I can vouch about its worthiness for a bioinformatics novice. The second course entitled ‘**Introduction to Computational Proteomics**’ was taught by Dr. Jacques Colinge from CeMM, Austrian Academy of Science, Wien, Austria. The course was neatly divided in following modules (a) Introduction to proteomics, (b) Peptide mass fingerprinting, (c)

Raw spectra processing, (d) Tandem MSs and different applications of MS such as differential proteomics, genome annotations and molecular interactions. It also described different software packages used for MS data analysis like MASCOT, Sequest, X!Tandom, Phenyx. Any bioinformatics course/talk is incomplete without reference to 'Open Source Resources'. Dr. Colinge has concluded his talk by introducing different open source resources to process and analyze MS data.

Congress Proceedings

The conference started with a welcome address by Dr. Dario Neri, Hilal Lashuel (both from EPFL, Lausanne) and Dr. Jean-Charles Sanchez (Geneva University Hospital). The whole congress was divided into six sessions. In total, the sessions covered several informative sections ranging from pre-analytical topics to many core aspects such as important issues related to proteomics of post-translational modifications, membrane proteomics, biomarker discovery and bioinformatics. A brief description of some interesting and useful topics covered during the symposium is as follows:

- i. Identification of post-translational modifications:** Protein complexity and regulation in higher eukaryotes is governed by co- and post-translational modifications and splicing events. Dr. Bruno Domon highlighted different aspects of MS based proteomics. A number of posters describing the methods to systematically identify post-translational modifications during protein identification studies were also presented.
- ii. Identification of pathways for diagnostic purposes:** A study was presented which can be used to identify activated pathways from expression proteomics data using database of genes, molecules and their interactions. The data shown during presentation made it quite clear that the proposed method is very rapid and can be used for identification of pathways activated at a given condition. It also unravelled the potential to become a diagnostic biomarker and candidate for drug discovery.
- iii. Biomarker discovery:** Biomarkers play an important role in the pharmaceutical industry and are assuming an important role in drug discovery and development. Session dedicate to biomarker related topics were chaired by Dr. Martin Kussman

(Nestle Research center, Lausanne). Dr. Jacques Cornuz illustrated how better understanding of epidemiology, diagnostic tests procedures and medical economics has changed the concept of check-up over time to the present status. Dr. Hanno Langen's lecture was focused on issues related to validation of biomarker discovery. He discussed possibilities and limitations of MS based proteomics in search for novel biomarkers.

- iv. **Membrane proteomics related with mitochondria and platelets:** A method was described by Dr. Albert Sickmann from Wurzburg University to discover novel mitochondrial and platelet proteins including membranous proteins. He showed that his method was able to yield the most comprehensive catalogue of plasma membrane proteins. This catalogue also includes N-glycosylation and phosphorylation sites in human platelets.
- v. **Bioinformatics in proteomics:** Different bioinformatics research group develop algorithms, software and database tools to acquire and analyze MS data. These are valuable support towards application of MS in biomedical research. The major focus was on bioinformatics resources that enable MS based approaches in basic and clinical research. Dr. J. Colinge gave a very comprehensive and descriptive talk about *in silico* approach of proteomics. He described how mass spectrometry can be combined with different techniques to discover new drug targets. Besides this 'Human Proteome Initiative' of Swiss Institute of Bioinformatics was also explained.

Panel Discussions

On 2nd and 3rd day two very open, informal and unrestricted panel discussions were also held. Everyone was free to air his/her views. The first panel discussion was more of a generalized type of dialogue during which challenges and difficulties of proteomics was discussed. The second panel discussion was concentrated mainly on biomarker discovery and its real life validation. It was a unanimous opinion that sample collection and its subsequent handling is the main bottleneck in rapid discovery and validation of biomarkers.

Participations from Congress Sponsors

Two major companies involved in proteomics based instrument manufacturing had also showcased their state of art technology. The presentation by ‘*Platinum sponsor*’ Water Corporation about use of its cutting edge technology in human proteome was very useful and informative. The presentations by Dr. Sonya Scherman (Max Planck Institute in Martinsried, Germany) and Dr. Thérèse McKenna, (Technical Manager Proteomics, Waters Corporation) were also remarkable. Besides Water Corporation, Agilent technologies have also introduced their HPLC-Chip LC/MS workstation. The presentation of Dr. C. Gerner (Institute of Cancer Research, Vienna, Austria) regarding ‘*Human proteome database for clinical research*’ was especially very illustrative and educative.

My Participation

I presented a poster entitled “**Mitpred 2.0: An Improved Method of Mitochondrial Protein Prediction**”. The work was carried by the Bioinformatics group at Institute of Microbial Technology (IMTech), a leading bioinformatics research group in India. I described an improved method for mitochondrial protein prediction named as Mitpred (Ver 2.0) (<http://www.imtech.res.in/raghava/mitpred/>). The proposed method was an improvement of our previous method. Mitpred (Ver 2.0) was developed using combination of hidden Markov Model based Pfam domain searching and Support Vector Machines. Benchmarking with other subcellular localization prediction methods has shown that it has better prediction accuracy. Thus currently it is the best method for mitochondrial protein prediction. The discussions stemming with different scientists at my work were extremely exciting and fruitful in generating new ideas for further research.

Conclusions

Participation in this conference provided me the opportunity to represent India and IMTech at an international forum. I also reaped the benefits of seeing the current research in our field from close and the latest technologies that are being used and developed to enhance the capabilities of high throughput protein annotation. Such an experience would help me in shaping my future research career and the contacts established at this conference would be useful at to establish mutually beneficial collaborations.