



Conference report on the
6th Annual World Congress of HUPO
« Proteomics : From Technology development to
Biomarker Application. »

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Priscille Giron,
Department of Structural Biology and Bioinformatics, K.Rose's Group
University Medical Center (CMU)
Geneva, Switzerland

The 6th world annual world congress of Human Proteomics Organisation was held in the “Ultra-modern” city of Seoul, South Korea, at the COEX center in the hearth of the business district. With over ten million people, Seoul is South Korea's largest city and one of the largest cities in the world by population as well as by density. Thus in addition with an intense scientific program this meeting was also a great opportunity to discover a fascinating contemporary city mixed with ancient history and traditional culture.

Before the official start of the congress, pre-congress activities were organized. Two days of HUPO initiatives and workshops on current development, progresses and “standards initiatives” were planed. In parallel, young scientists and non expert public had the opportunity to follow an Educational day and a Clinical day was organized.

The Educational day chaired by A. Görk started with a good overview of proteomic Technologies, 2D electrophoresis and MudPIT. Other approaches were discussed like the use of antibodies for targeted proteomics. Thus the presentation of M. Uhlen of the PrEST strategy, for Protein Epitope Signature Tag, and its use for systematic generation of specific antibodies was convincing (Agaton et al (2003) Molecular and Cellular Proteomics. 2, 405-416). An

overview of MS technologies and Bioinformatics tools for protein identification was also nicely presented.

The Clinical day was interesting in the open remarks. Thus the session given on biofluids led to interesting questions, thanks to S. Hanash: "Pooling or not pooling? Depletion or no depletion? Isotopic or label free labelling? Gel or LC?" Issues that one cannot have unique answers, all depend on what aim to achieve.

The congress itself was organized on plenary sessions that started and ended days, on parallel sessions where the wide variety of proteomics technologies and applications were presented and on posters sessions.

The plenary sessions gave us the opportunity to cover the diversity of proteomics applications.

S. Hanash gave a great presentation on the importance to organise biomarker discovery in collaborative efforts. He thus presented the collaborative work on colon cancer where ten proteomic laboratories worked in parallel on the same colon cancer cases but with their preferred proteome platforms. Thus, 2343 proteins were identified and 65 with differential expression with 11 proteins found in different laboratories. It thus permitted to maximize the comparison of results obtained and the evaluation of potential biomarkers.

S.H. Kim gave a very interesting and comprehensive talk on structural proteomics. His team tried to map the protein universe in a structural point of view. With comparing structures similarities of proteins, they defined motifs and link these motifs with similarity distances. They also integrated organisms' information and protein function when known. Thus they developed a computational method to map the protein structure space. This mapping could be very interesting in terms of evolution of protein structure and function, and why not on predicting a protein function through its structure? (Hou & al, PNAS 2005)

To the Mass Spectrometry point of view, J.Yates presented an overview of the use of MS technologies and strategies in identifying proteins. R.Aebershold emphasized the importance of obtaining complete and quantitative accurate MS data sets in its presentation on systems biology.

To his part, R.D. Smith gave a great overview on the problems and solutions to which MS technology is confronted. Throughput increases, sensitivity... can lead to limitation of existing platforms. He presented the several developments made in high-speed nanoscale separation, electrospray ionization (multi nanoemitter electrospray arrays) and some illustrations.

At the end of the proteomics workflow is the Bioinformatics field that was nicely represented by R. Apweiler, one of the Congress Co organisers. He pointed out the problem of dilution of the information through the number of different data resources. Proteomics studies have led to an enormous amount of data that however is scattered over many resources. There is a need of creating public, if possible unique, databases domain to manage and compile these information. There is also a need of data standards to make it comprehensible for everyone.

All scientists had the opportunity to present their work in the parallel sessions (symposiums) and with the posters sessions (more than 1300 posters!)

I won't be able to give you an exhaustive report on every work presented how much dense and diverse were the sessions. To who would feel frustrated by this report, an abstract book has been published in Molecular & Cellular Proteomics (www.mpconline.org).

Symposiums and Posters were covering many different fields. A big part was dedicated to Biomarkers proteomics and applications, Mass spectrometry advances and Disease proteomics. Another part was on targeted proteomics: chemical, structural, glyco-, phospho-proteomics, as well as metabolomics, plants, model animal and microbial proteomics. And a last part was turned around other omics technologies: biochips, nanotechnology, protein separation technologies and Bioinformatics.

The Congress closed with the election of HUPO Nominations Committee (see http://www.hupo.org/communications/Annual_special_meetings/Council/2007/2007-Council_Election-Results.pdf) and with the introduction of the 7th Annual World Congress of HUPO, which will be held next year in Amsterdam, Netherlands. (<http://hupo2008.nl/>)