

HUPO 5th Annual World Congress October 28th-November 1st, 2006 Long Beach, CA

Translating Proteomics from Bench to Bedside

The 5th annual HUPO World congress situated this year in Long Beach, started by welcome address of the organisers Profs. Peipei Ping, John R. Yates III and by the President of HUPO, John Bergeron.

Then, the first plenary lecture was done by Dr. Anna D. Barker (Deputy director, National Cancer Institute) on the future directions in Advanced Technologies for Molecular-based diagnostics and Therapeutics. During the lecture, she explained why the NCI is interesting on accelerating Biomarker discovery. Indeed, it was shown that almost 600 thousands Americans died from cancer in 2005, and that almost 1.5 million will be diagnosed with cancer this year. If it goes at this speed, in 2025 the number of cancer cases will approach 2 millions.

Furthermore, if we look at the FDA statistic, we could see that since 1988 less than 1 biomarker per year was approved by them. This means that before finding good biomarkers, which might be available to diagnose diseases, will require a long process.

Nevertheless, the NCI thinks that early detection is a really good hope and a major possibility to extend life of people. For this they encourage research on biomarker discovery. The message was that we have to go on putting a lot of effort to reach our goal.

Then, several lectures on biomarkers discovery were done. During all of these talks we could learn a lot of things. First of all, new tools were mentioned in this field of research. They are available and apparently useful. For example, the use of protein chips seem to be performed as good as Elisa assays. The laboratory of Prof. Michael P. Snyder made comparisons between, protein Chips, Elisa and IFA. The results below tend to prove it.

	Number of Sera	Accuracy	Sensitivity	Specificity
ELISA	396	91 %	87 %	97 %
Chip	399	92 %		
IFA	399	97 %		

Then, they used this protein Chip to see Phosphorylation on Yeast proteins and also to diagnose SARS. On the SARS test, they managed to give 55 positive tests over 56.

Second of all, Prof. Mathius Uhlen showed us a new tool which will be really helpful in the Proteomics field. A protein Atlas is available on internet (www.proteinatlas.org). There will

be a link from Uniprot to it. A strategy involving the systematic generation of protein specific affinity reagents and tissue micro-array has been followed and recently they published the first version of the Protein Atlas containing expression profiles of 660 proteins in 48 normal human tissues and 20 different cancers. A new publicly available version will be released containing more than one million images corresponding to more than 1500 antibodies. This new version will contain also a Cell Atlas containing 46 human cell lines and 12 clinical cell samples. All the validated antibodies used in the Atlas will be available to the scientific community. A new search function will be released to allow queries about protein profiles in normal and disease tissues to allow in silico biomarker discovery.

A other new tool was shown during this congress, it is the FFE technology (Free Flow Electrophoresis). It is commercialized by BD.

It is matrix-free electrophoresis technique in which no solid matrix, such as acrylamide gel electrophoresis or separation phases in chromatography, is used. Instead, the analytes are separated according to their charge and electrophoretic mobility in a continuous laminar flow of buffer solutions in an electric field applied at right angles to the flow direction.

The laminar flow is collected in 96 capillaries at the end of the separation chamber, thus enabling continuous fractionation in a collection plate. Depending on the composition of the separation media three completely different separation principles can be used: Isoelectric focusing (IEF), Zone electrophoresis (ZE), and Isotachopheresis (ITP).

Then, the fractions obtained can be used to do 2D PAGE and chromatography. If you want to trace one particular protein that you know its activity, you can do it with this technique. The buffer does not denature proteins.

This congress was well turned on biomarkers discovery. It was well shown and proved that this specific research takes time and is going through two different parts: first on the biomarker discovery then the validation. Both are important and need a long précised investigation. There are actually two ways of doing it. Either you do “brut force method” (screening process by using LC/MS-MS techniques) or using “clever tricks” (looking for one particular marker at a time, using different protein properties). These two ways are complementary.

It was also shown that we have new tools at our disposal to go further on biomarkers discovery. They are more and more accurate, sensitive and specific but they need to be analyzed and combined to other results obtained with other approaches (genomics, metabolomics, transcriptomics). All together, we will have a clear sensitive and specific answer.

Next year, the HUPO Congress will take place in Seoul. It will be turned on Technology development to Biomarker Applications.