

Conference Report on the
Second International Conference of the Hellenic Proteomics Society
“From Discovery to Applications”

Kolimbari, Crete, Greece, May 23rd - 25th 2007.

This meeting organized by the Hellenic Proteomics Society took place at the Greek Orthodox Academy, a congress center located on the Aegean Sea side, close to the lovely village of Kolimbari. The chosen place, although deeply rooted in the religious traditions, provided the perfect conditions for an intense exchange about the latest developments of a fast evolving research area in life sciences.

Before the beginning of the conference, five workshops were planned as a first morning session. I would like to mention the great overview given by Axel Ducret from the Roche Center of Medical Genomics about the importance of sample preparation for mass spectrometry. Despite the huge improvements in the analytical tools we have nowadays in our hands, one should always think about the good old biochemical principles required to prepare samples that can generate useful data.

Along the same lines, Peter James from Lund University gave some practical hints and tricks for those who are interested in moving to membrane proteomics. Considered for a long time not to be manageable by proteomics strategies, the biological membranes, when intelligently processed, can be perfectly well investigated even by classical 2D gels.

The first session dealing with “*Proteome Analysis*” started with a fascinating talk by Pier Giorgio Righetti from the Polytechnic of Milano about the Protein Equalizer Technology. This revolutionary methodology based on combinatorial hexapeptides coupled to beads, allows the capture of virtually all the proteins present in a given proteome. The great advantage is that it gives access to the low abundant proteins usually “unseen” by proteomics tools in complex biological samples like blood or urine.

Of high interest was also the talk given by Dominic Desiderio from the University of Tennessee Health Science Center on the identification of 3-nitro-tyrosine proteins as biomarkers candidates for human pituitary adenomas.

The second day was entirely dedicated to “*Clinical Proteomics and Diagnostic Markers*”. Among the speakers of this session Helmut Meyer from the University of Bochum presented his work on the identification of 60 biomarkers for pancreatic carcinoma and liver cirrhosis. By applying laser microdissections to human clinical tissues, it is possible to precisely collect 1000 cells and to subsequently analyze this “sub-proteome” in a reproducible way with 2D DIGE gels. However the bottleneck for such an elegant approach remains the generation of good antibodies that are still required

in the validation phase of the biomarker candidates (Western blotting and immunohistochemistry). Out of the 60 candidates, only 7 useful antisera/antibodies could be raised.

Another highlight was the presentation by Jan van Oostrum from the Novartis Institute of Biomedical Research. He described a proteomics platform based on “reverse” protein arrays (RPA) to investigate signaling pathways associated to diseases. These arrays consist in spotting proteomes of interest (down to a single eukaryotic cell) in an array format. They are subsequently probed with selected fluorescent antibodies for analysis a multiplex manner. A very sensitive fluorescent detection system allows the acquisition of quantitative and kinetic expression profiles. The sensitivity of this technology restricts its use to proteins at least expressed in cells at 1000 copies.

The rest of the program gave a large opportunity to young scientists to present their work which brought some dynamics and enthusiasm. It was rather disappointing to see that instead of a fruitful discussion with the graduate students, the question parts turned into a systematic criticism by one or two senior scientists on the way the experiments were conducted (not enough 2D gels performed per condition, pooling of samples, and no solid statistical analysis of the results). In my opinion these judgments would have been legitimate if these scientists had presented final results, rather than "work in progress".

The last day was divided in two sessions. The morning program focused on “*Data Processing and Bioinformatics*”. Peter Bernd from the Roche Center of Medical Genomics reported on different statistical methods used by the industry to process large sets of data that proteomics generate. Efficient tools are of great help in the early stages of research programs to validate or abandon biomarker candidates. In agreement with the major criticisms that came up during the Thursday session, he also insisted on the necessity to generate independent and multiple data points for a given condition when one really wants to make quantitative proteomics. The only problem is that not so many university labs around the world can afford the high-throughput facilities of major pharmaceutical companies.

A provocative and rather appropriate answer to all these quite arrogant considerations was given by Paul Eilers from Utrecht University when he started his talk dedicated to pre-processing statistical methods of MALDI-TOF or SELDI-TOF spectra with the following statement: if one needs a large group of data points to see a differential expression for a given biomarker, you can play as long as you want with the statistical analysis, but you better forget about your candidate.

The meeting closed after several talks dedicated to “*Proteomics Technologies*”. Peter James gave another interesting talk about a new approach to selectively analyze, by MS/MS spectrometry, isotopically labeled peptides from digested proteins that change in expression levels or undergo post-translational modifications.

The abstract book will be published in *Cancer Genomics and Proteomics*, 2007, 4 (4): 255-294.