

3rd EuPA Congress 2009

Stockholm Sweden | June 14 - 17 2009



DAPSOC
Danish Proteomics Society

FinnProt
Finnish Proteomic Society



Domitille Schvartz, PhD student, Biomedical Proteomic Research Group, Geneva

General introduction

The 3rd Eupa Congress took place in Stockholm, Sweden, from June 14th to June 17th, 2009. It was organized in the City Conference Center by Dr. G. Marko Varga and Prof. T. Laurell, and the topic area was “Clinical Proteomics – Protein Expression Research within Diseases”.

The Tissue Imaging Workshop happens before the beginning of the congress, in Uppsala (Sweden), on June 13th and 14th, mixing lectures and experimental work. Also, a pre-congress course at the Swedish academy of pharmaceutical science occurred on Sunday, 14th.

More than 400 participants from Europe and worldwide were presents to appreciate the variety of oral and poster presentations. The congress was organized with plenary lectures in the morning and oral sessions in the afternoon (two sessions in parallel), punctuated by poster sessions and vendor seminars. After the registration on Sunday afternoon, a nice welcome aperitif was offered by the organizers. The conference started the next day, by an opening lecture provided by G. Marko Varga, and M. Dunn, the EuPA president. Next, four noteworthy plenary lectures provided us key strategies combining proteomics tools and complementary techniques, to decipher interaction partners and induction of modifications (M. Mann, Max-Plank Institute for Biochemistry, Martinsried, Germany) or to understand T-cell activation and modifications (R. Lahesmaa, Turku Centre for Biotechnology, Turku, Finland). Also, T. Fehniger (Lund University, Lund, Sweden) and T. Ørntoft (Aarhus University Hospital, Skejby, Denmark) presented thought-worthy interventions on the needs of clinical biomarkers, and the progresses on this field.

The “Biomarkers” session

I focused especially my attention on the Biomarkers session. In fact, 7 attractive talks were given in this part, each giving prominence to the necessity of confident and specific biomarkers for new diagnostic tools and treatments.

The session began with a nice talk of M. Dunn, from UCD Conway Institute in Dublin (Ireland), entitled “*Proteomics of heart failure: the cardiac hydrophobic sub-proteome*”. He outlined a method, based on Triton X-114 phase extraction, to analyze hydrophobic and membrane-associated sub-proteome of the human heart. He could so point up protein unique to dilated cardiomyopathy or ischemic heart disease which highlighted defect of Ca²⁺-handling in heart failure.

Then, T. Kondo, from the National Cancer Research Institute in Tokyo (Japan), displayed his methods for the development of prognostic markers for cancer, in his presentation “*Cancer proteomics for personalized medicine: predictive biomarker for better treatment*”. Using a complete approach combining 2D-DIGE and mass spectrometry, his team detects an indicator of metastasis progression

after surgery in the case of gastrointestinal stromal tumors. He concludes by explaining that his strategy is on the way to be applied to 6 other cancers.

Also, M. De Wit, from the Tumor Profiling unit in Amsterdam (Netherlands), gave an instructive presentation about "*Identification of new biomarkers for colon cancer using genomics and proteomics*". His team use a powerful combination of genomics (microarray) and proteomics approaches (LC-MS/MS) on colon cancer cell lines, in order to find progression markers of colon cancer. They actually focused on cell surface proteins, which would be potentially targeted for treatments. Thanks to their approach, they identified promising candidates for high risk adenomas and colorectal cancers.

This talk closed the first part of the biomarkers session and made way for the first poster session of the congress. A hundred of posters were presented, related with tissue imaging, biomarkers proteomics and applications, and cancer proteomics. Animated and passionate discussions took place in the poster hall for about 1h30.

The rest of the biomarker session began with the rich talk of J. Calvete, from the Instituto de biomedicine de Valencia (Spain), entitled "*Snake venomomics and antivenomics: from ophidian evolution to biomedicine*". This group has a specific interest in the analysis of toxin composition from different snake's species. Their venomomics approach aims to find toxin specific antibody treatment after a bite. They also performed a comparative analysis of B.atrox population for different and targeted treatment.

This talk was followed by a presentation of J. Banha (Instituto Nacional de Saude Dr. Ricardo Jorge, Lisboa, Portugal) which dealt with "*biomarkers for Behçet's disease: in quest for the holy grail using proteomic tools*". He presented an interesting research based on serum analysis in order to detect specific biomarkers for Behçet's disease as there are no diagnosis tools available. They could so identified potential biomarkers able to discriminate significantly samples from Behçet's disease patients, related to defense mechanisms or also interestingly with lipid metabolism.

The session ended with two great talks, the first one on "PSA quantification of 80 plasma samples from the clinical routine using antibody microarray", presented by K. Järås (Lund University, Malmö, Sweden). She performed the development of a quantitative microarray approach using reduced amount of patient sample, and show a practical application to PSA concentration measurements. This technique will particularly be suitable for multiplex analysis, for instance for several biomarkers of prostate cancer.

The last talk of this session was given by D. Gibson, from Queen's university in Belfast (Ireland), entitled "*Temporal synovial proteome profiles of inflammation in juvenile arthritis patients*". They tried, by a proteomic approach based on 2D-DIGE analysis, to find biomarkers able to discriminate juvenile idiopathic arthritis subgroups. The aim is to improve the clinical management of this patients and their study leads to the identification of several proteins which could have a role in spread of joint inflammation. Further validations are ongoing.

This session provided a large view of different project on biomarker discovery and was really appropriated regarding to the essential role of

biomarkers into drug discovery and development. In parallel, an entire session was dedicated to Maldi & imaging.

Other sessions

A welcome reception happened at the City Hall, to close the first day. The rest of the congress was dedicated to eight other rewarding plenary lectures on Tuesday and Wednesday morning, followed by high-quality sessions about Organelle Proteomics & Expression Profiling, Mass Spectrometry & Pathways, Funding, Teaching & Collaborations, Drug Discovery & Chemical Proteomics, and also the so-awaited session of Senior and Young Scientists Awards. The Tuesday ended with the Congress Diner, in the nice Pillar Hall of the Norra Latin building, with a fantastic and funny music band for our great pleasure. This dinner was also the time for prizegiving, to P. Roepstorff (University of Southern Denmark, Odense, Denmark) for the EuPA Senior Scientific Award, and to A. Nilsson (Uppsala University, Uppsala, Sweden), for the Young Scientist award.

My participation to the congress

I had the great opportunity for this congress to present a part of my PhD project. Indeed, my abstract was selected for an oral presentation in the session “Mass Spectrometry & Pathways”, chaired by P. James and P. Juhasz, on Tuesday afternoon. Therefore I presented my work on the understanding of β -cells dysfunction by glucotoxicity, using both transcriptomics and proteomics approaches.

Conclusions

My participation to this congress provides me a large overview of the latest technologies used and the researches performed in the field of proteomics. These 4 days were the time for interesting meetings with others people invested in the same interests, and to share some questions and remarks, especially through poster sessions. Presentations displayed instructive applications of a wide-range of techniques, in proteomics as well as in transcriptomics or bioinformatics. This experience was greatly rewarding for me.