

3rd EuPA Congress 2009

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The third EuPA Congress in clinical proteomics took place in Stockholm from the 14th to the 17th of June. With its fourteen islands rich in history and art, Stockholm offered to the participant to the meeting a wonderful scenario, that was appreciate above all during the Welcome Reception that took place at the Stockholm City Hall, building of the Municipal Council and venue of the Nobel Prize banquet.

After a very interesting opening day of congress with oral presentations (Sessions: MALD&Imaging and Biomarkers), plenary lectures and the first poster session (98 scientific works exposed) the second day started under a wonderful sun. The session I'm going to summarize was entitled "Mass Spectrometry & Pathways", and I found it very interesting for the innovative aspects concerning MS introduced by the speakers.

With my great pleasure, the first speaker was Dr. Alexander Makarov, the inventor of the Orbitrap mass spectrometer, whose work changed the perspective of many proteomic researchers. During his talk "*Orbitrap Mass Spectrometry for Proteomics*" Dr. Makarov presented a brief history of the development of this mass analyzer, starting from the idea conception till the final commercial instrument production and concluding with examples of application in the pharmaceutical and proteomic field.

The second talk, entitled "*MRM MS-based assays to identify biomarkers for lung carcinoma of large-cell neuroendocrine (LCNEC)*" and presented by Prof. Toshihide Nishimura from the Tokyo Medical University, dealt with a more clinical application of mass spectrometry. Prof. Nishimura and

colleagues, in fact, showed the potential of MRM MS-approaches as a tool for biomarkers discovery and verification, particularly applied to the different subtypes of lung carcinoma (LCNEC, NSCLC and SCLC).

Prof. Peter Bergsten from the Department of Medical Cell Biology at Uppsala University presented a talk on *“Altered signaling in islets from individuals with type 2 diabetes mellitus”* where the theme of pathways was introduced. With the intent of assessing the label free LC FT-ICR MS system to get islets protein profile and to analyze the pathways in which identified proteins are involved using bioinformatics tools, they identified a new potential involvement of the pathways of islets regeneration and proliferation in T2DM progression.

The second part of the Mass Spectrometry & Pathways session started with the brilliant presentation of Prof. Roman Zubarev from the Department of Medical Biochemistry and Biophysics of the Karolinska Institutet in Stockholm *“Pathway Analysis via Protein Expression Measurements - ‘Why’s and ‘How’s”*. Prof. Zubarev presented a very interesting and innovative approach based on the application of MS techniques to identified proteins, and on bioinformatics and statistical tools to design a robust procedure to identify activated signaling pathways.

The combination of proteomic and transcriptomic approaches was introduced by the presentation of Cecilia Gelfi, from the University of Milan L.I.T.A., *“Respiratory complex I inhibition in muscles overexpressing mutant SDO1 regulates onset and disease progression in a mouse model of familial ALS”*. This work was a clear example of how the combined investigation of gene and proteins can contribute to understand disease phenotypes.

This parallel approach was applied also by Domitille Schvartz, from the University of Geneva, the only PhD student participating to the session. In her presentation *“Proteomic and transcriptomic modification of rat INS-1E pancreatic β -cells induced by chronic hyperglycemia”* she showed the presence and the expression modulation of new proteins connected to high glucose exposure in rat β -cells, linking glucotoxicity to other fundamental cellular processes.

Dr. Kathleen Carroll from the Manchester Centre for Integrative System Biology (University of Manchester) closed the session with the talk *“Towards an automated SRM approach to quantitation using a triple quadrupole mass spectrometer (TSQ Vantage)”*. This very technical presentation was focused on a new way of quantification of low abundant proteins through the use of TSQ Vantage machine and SRM approach.

In conclusion these very interesting presentations showed how mass spectrometry can find application in different research field, from very technical development to clinical applications. In addition, mass spectrometry can be used as a tool to obtain protein identification that can subsequently be analyzed by bioinformatics and statistical tools to better understand the pathways they are involved in. In these talks, in fact, the importance of pathways as connection to understand proteins function and interaction was well highlighted.

Personally, I found the 3rd EuPA congress very stimulating and instructive, above all for the different clinical aspects handled during all the meeting. This is just a little summery of one of the session; all full abstracts are collected in the 3rd EuPA Congress book.