

Advances and expansion of Central and Eastern European Proteomics

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Proteomes, Proteomics and Biological Systems: 5th Central and Eastern European Proteomic Conference Prague, Czech Republic, 19–22 September 2011

Prague, also known as the 'City of a Hundred Spires', which is situated on the bank of River Vltava and is a historical Bohemian capital rich in history and beauty, set the stage for an exciting meeting that brought together high-caliber experts to share their knowledge as well as propagate the central theme and focus on 'Proteomes, Proteomics and Biological Systems'. More than 120 delegates from all over the world attended in pursuit of excellence and enjoyed not only excellent science but also took back home fairy-tale memories of Prague and its offerings. The 5th Central and Eastern European Proteomic Conference was organized in Prague, Czech Republic, on 19–22 September 2011, with resounding success.

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The conference [101] commenced with opening lectures from Peter Jungblut (Max Planck Institute for Infection Biology, Berlin, Germany) and Javier Munoz (Bijvoet Centre for Biomolecular Research, Utrecht, The Netherlands). We listened to an excellent presentation from Peter Jungblut on 'The protein species concept and molecular basis of the search for biomarkers'. Jungblut introduced the concept of protein species where one protein may be subdivided into several species by modification, which may represent different functions; hence, the challenges for protein species proteomics suggested were: complete separation of all protein species of each protein; 100% sequence coverage identification; and correlation of function to each protein species. Javier Munoz presented a talk on 'Unravelling key molecular components in stem cell biology with mass spectrometry-based proteomics', describing how mass spectrometry-based proteomics can identify key molecular components in the biology of both embryonic and adult stem cells. Comparing the proteomes of human induced pluripotent stem cells, human embryonic stem cells and parental fibroblasts in depth, differential quantitative results indicated that human induced pluripotent stem cells are nearly indistinguishable from their embryonic

counterparts. On the second day, the session on proteomic diversity and related fields comprising of stem cell proteomics and proteomics for clinical applications, commenced with Katrin Marcus (Medizinisches Proteom-Center, Ruhr-University Bochum, Germany) who presented a talk on 'Biomarker discovery using proteomics – application in neurodegenerative diseases'. The advantages and challenges of comprehensive proteome analysis of human samples for biomarker discovery in Alzheimer's and Parkinson's disease were presented, highlighting the difficulties and complexities involved in finding suitable biomarkers.

The Central and Eastern European Proteomic Conference's (CEEPC) invitation to the Indian Proteomic Society was kindly accepted by Ravi Sirdeshmukh (Institute of Bioinformatics, ITPL, Bangalore, India) who presented a talk on 'Advances in glioma proteomics – new technologies and approaches'. In efforts towards the development of biomarkers for the diagnosis and treatment of gliomas, Ravi presented a study of differential membrane proteins of the clinical specimens of gliomas using quantitative proteomics. The session continued with Jirina Tyleckova (Institute of Animal Physiology and Genetics AS CR, v.v.i., Libechov, Czech

Republic), who presented a talk on 'The neural progenitor surfaceome'. To gain a comprehensive view of cell surface molecules (surfaceome) of neural progenitor cells, the cell surface-capturing (CSC) technology, in combination with label-free quantitative proteomic workflows, was utilized. Rita Hrabakova (Institute of Animal Physiology and Genetics) presented results on 'Cancer cell resistance to AURK-directed therapy: implications for anti-cancer strategies', illustrating the mechanisms contributing to development of drug resistance towards aurora kinase inhibitors in response of cancer cells. The theme was picked up by Tadashi Kondo (National Cancer Centre Research Institute, Tokyo, Japan) who presented a study on 'Cancer proteomics for biomarker development toward personalised medicine'. Tadashi showed the identification of proteins unique to important clinicopathological features and correlations between biomarker candidates and clinicopathological observations. Vojtech Tambor (University of Defence, Hradec Kralove, Czech Republic), who was voted the best young researcher, presented his findings. Vojtech's presentation on 'Deep proteome characterisation as a tool for identification of novel intra-amniotic infection and inflammation biomarkers in preterm birth patients' focused on the identification of biomarkers for predicting pregnancy-related complications due to intra-amniotic infection and inflammation.

The conference continued with a session entitled 'Proteomic diversity and related fields – protein post-translational modification and functions'. László Drahoš (Chemical Research Centre Hungarian Academy of Sciences, Budapest, Hungary) presented a talk entitled 'Glycosylation patterns and glycopeptide biomarkers' and showed a novel high-throughput approach for determining site-specific glycosylation patterns, including a method capable of studying not only a purified glycoprotein sample, but also glycoprotein mixtures like blood plasma. The session continued with a presentation from Jiri Suttner (Institute of Haematology and Blood Transfusion, Prague, Czech Republic) who talked about 'The estimation and proteomics of S-nitroso proteins'. Jiri described a method suitable for the measurement of total and low/high-molecular-weight S-nitroso compounds in plasma and platelets and concluded that the identification of S-nitrosylated proteins may substantially improve our knowledge and diagnosis of hemostasis disorders and cardiovascular diseases.

The next session was on proteomic diversity and related fields – microbial proteomics and bioprocessing, and Martina Marchetti-Deschmann (Vienna University of Technology, Austria) discussed 'Monitoring the fermentation process of *Penicillium chrysogenum* by combining a gel-based proteomics approach and intact cell mass spectrometry'. Martina's study focused on the filamentous fungus *Penicillium chrysogenum*, which belongs to the group of ascomycota and is the source of several important β -lactam antibiotics. Martin Hajduch (Institute of Plant Genetics and Biotechnology, Slovak Academy of Sciences, Nitra, Slovakia) concluded this session with a presentation entitled 'Flax seed proteome in remediated, formerly radioactive, Chernobyl area'. His study showed recovery of the formerly radioactive area.

The keynote speaker for the plant proteomics sessions, Wolfram Weckwerth (University of Vienna, Austria), presented a talk on

'Green systems biology – from genotype to phenotype in eco-systems research and biotechnological applications'. A systems biology approach combining molecular data, genetic evolution, environmental cues and species interactions with modeling and prediction of active biochemical networks was proposed. Plant proteomics continued with the presentation by Marek Sebel (Faculty of Science, Palacky University, Olomouc, Czech Republic) on 'Identification and biotyping of phytopathogens using MALDI-TOF mass spectrometry', discussing mass spectrometry of phytopathogens belonging to the group of downy mildews or powdery mildews. The talk entitled, 'Pharmaco-proteomic analysis of phosphatidylinositol 3/4-kinase inhibitor wortmannin in *Arabidopsis*' was by Tomas Takac (Faculty of Science, Palacky University, Olomouc, Czech Republic). Tomas emphasized the application of pharmaco-proteomic analysis to discover regulatory proteins involved in vacuolar sorting and endocytosis. The session continued with several other presentations focused on *Arabidopsis thaliana*.

The session on structural and functional proteomics, focusing on protein interactions and functions, resumed with Javier De Las Rivas (University of Salamanca, Salamanca, Spain) on 'Exploring protein–protein interaction networks integrated with pathways to identify hub proteins and critical interactions'. Javier discussed the complete map of protein interactions that can occur in a living organism and referred to it as the 'interactome'. This session continued with a presentation entitled: 'The three bottlenecks in HPP implementation' by Alexander Archakov (Institute of Biomedical Chemistry RAMS, Moscow, Russia). Professor Archakov discussed the international Human Proteome Project and greater complexity of the proteome compared with the genome was discussed as the reason for the existence of these three bottlenecks.

Novel mass spectrometry and the methodologies that go with it have contributed significantly to proteomic research, and Bernd Wollscheid (Institute of Molecular Systems Biology, Zürich, Switzerland) opened this session with a presentation entitled, 'Caught in the act: ligand-based receptor capturing (LRC) on living cells'. Bernd discussed the ligand-based receptor capturing approach for the highly specific and sensitive detection of ligand interactions with their corresponding receptors under near-physiological conditions and the 'surfaceome' as a cellular information gateway and a 'chemoproteomic technology' for the unbiased detection of ligand–receptor interactions on living cells. The session concluded with a presentation by Ales Svatos from Max Planck Institute for Chemical Ecology (Jena, Germany) with a talk on 'Simultaneous determination of ^{15}N -incorporation levels in plant proteins and their absolute quantitation to study nitrogen flux and protein turnover'. Svatos presented specific approaches for ecologically relevant quantitative proteomics.

The final session on structural and functional proteomics and incorporating proteome mining and biomarkers commenced with Michael Taussig (Babraham Bioscience Technologies, Cambridge, UK) who discussed 'Affinity reagents and protein arrays for proteome analysis', including an Affinomics program that aims to extend affinity proteomics research by generating a large-scale resource of validated protein-binding molecules

for characterization of the human proteome. Chris Turck (Max Planck Institute of Psychiatry, Munich, Germany) continued with an excellent presentation on 'From proteomes to pathways to bio-signatures – progress towards understanding psychiatric disorder etiology'. He discussed biomarker detection efforts, ranging from quantitative mass spectrometry of brain tissue and body fluid proteins to *in silico* analyses of public data. Jiri Petrak (First Faculty of Medicine, Charles University, Prague, Czech Republic) presented an interesting presentation on 'Beauty hidden in lipids – proteomics of membrane proteins based on their trans-membrane domains'. Petrak introduced an improved method for proteomic analysis of trans-membrane proteins based on single-step enrichment of membrane fraction, opening of membrane vesicles at low pH and enzymatic digestion of all non-transmembrane proteins.

The meeting concluded with the closing lecture given by Vladimir Havlicek (Institute of Microbiology, Academy of Sciences of the Czech Republic, Prague, Czech Republic) entitled 'Mass spectrometry... *quo vadis?*', illustrating emerging technologies, particularly tandem ion mobility spectrometry and accurate mass spectrometry imaging.

It was evident from this conference that proteomics has promising and exciting potential across scientific, medical and biomarker

research for the benefit of mankind. Fresher challenges and a greater level of urgency to deal with healthcare issues, whether it be regenerative and reparative medicine or clinical studies, are bringing diverse researchers closer. To this end, proteomics may enable diverse fields such as stem cell research, metabolomics or diseases research to reach the end goal of new therapies [1]. Additionally, the recent inclusion of countries such as India and Russia in the CEEPC board, has provided new momentum and a fresh outlook, not only for the participating countries but also for the young generation of researchers fascinated by proteomics. In keeping with tradition, the next (6th) CEEPC will be held in Budapest, Hungary in 2012, where once again 'exciting advances in proteomics' will be discussed for the benefit of mankind.

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