

EXPERT
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Tremendous progress in proteomics and metabolomics in Central and Eastern Europe

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The 8th Central and Eastern European Proteomic Conference (CEEPC) co-hosted with the 2nd International Metabolomics Austria

Vienna University of Technology, Vienna, Austria, 30 June–4 July 2014.

The ever expanding Central and Eastern European Proteomic Conference (CEEPC) hosted its 8th annual meeting in Vienna, Austria, in July 2014 with resounding success, highlights of which are shared in this report. Tremendous progress in proteomics over the past decade in Central and Eastern Europe continues to rapidly accelerate due to networking across borders as well as access to sophisticated technologies. As the popularity of targeted proteomics in pathogenesis grows to unravel the complexities, so does the use of advanced analytical instrumentation. In addition, development of more sensitive research methodologies and a massive integration of technologies now give optimism to gain better understanding of the structure, functions and isoforms of various proteins as well as their complex interactions in biological systems. This, together with the confidence to qualitatively and/or quantitatively interrogate proteins of interest has led to promising developments for the identification of potential new drug targets for the treatment of various diseases.

Following in the tradition after the 7th Central and Eastern European Proteomic Conference (CEEPC) in Jena, Germany [1], the 8th CEEPC was held at the Vienna University of Technology, Karlsplatz, Vienna, Austria from 30 June to 4 July 2014 [2]. These firmly established series of CEEPC [3–6] have helped strengthen collaboration between scientists and clinicians from all over the world. Participants attending the conference were privileged to listen to presentations on ‘cutting edge proteomics’ complimented not only by the warmth of the Austrian hospitality but also by the splendor of historical Vienna. Stepping outside after the day’s lectures was equally thrilling with buzz of summer evening excitement and throngs of Viennese drinking and chatting, imbibers enjoying the pleasures of wine, food and music in the open in Karlsplatz. The conference aimed to bring together ‘Proteomics’ and ‘Metabolomics’ over the 5 days and well-known invited speakers as well as young researchers with excellent ideas and latest results to share, gathered together once again at this prestigious conference.

The Conference commenced in the afternoon of the first day with a presentation from Erica Hartman (Institute of Environmental Biology and Biotechnology, CEA, Bagnols-sur-Cèze, France) on ‘Proteogenomics’, detailing studies where experimental proteomic data was used to verify or correct theoretical genome sequencing, assembly and annotation. It allowed recognition of anomalies in genome sequence databases and amelioration of the quality of data in public repositories with possible refinement of genome sequence data processing algorithms to reduce errors in assembly and coding sequence prediction. Corina Mayrhofer (Institute of Animal Breeding and Genetics, Vienna University of Veterinary Medicine, Tulln, Austria) followed by highlighting subcellular proteomics and insights into the communication between male gametes and the female reproductive tract, summarizing a powerful strategy for the identification of molecules in the oviduct related to mating and insemination. This presentation was followed by Aleš Svatoš (Research Group Mass Spectrometry, Max Planck Institute for

Chemical Ecology, Jena, Germany) who delivered an excellent talk on liquid chromatography–tandem mass spectrometry (LC–MS^E)-based quantification of heterologous expression of antimicrobial peptides from the leaf apoplast of *Nicotiana attenuata*, proposing a universal high-throughput screening protocol for confirming stable expression of antimicrobial peptides and their quantitative comparison between different transgenic plant lines.

The second day started with a presentation by Daniel Kolarich (Max Planck Institute of Colloids and Interfaces, Potsdam, Germany), who presented an interesting talk entitled, ‘Glycoproteomics and Glycomics: Challenges, Considerations and Solutions’. Despite tremendous recent advances in qualitative glycoproteomics, questions regarding the MS signal intensity relations between various forms of un-/de-/glycosylated peptides had remained unanswered until this study. Marek Sebel (Palacky University, Olomouc, Czech Republic) followed and it was a pleasure listening to this presentation. Marek discussed physiology and enzymology of amino aldehyde dehydrogenases, a superfamily of plant oxidoreductive enzymes catalyzing oxidation of ω-amino aldehydes to the corresponding amino acids using NAD(P)⁺ as a coenzyme. This presentation was followed by Károly Vékey (Hungarian Academy of Sciences, Budapest, Hungary) with a talk on semi-preparative protein isolation and enrichment using reversed phase HPLC whereby protein families, which when eluted in one band, may then be subsequently studied using proteomic methodologies. An exciting talk entitled, ‘Identification of serum proteome components associated with progression of non-small cell lung cancer’ was presented by Piotr Widlak (Maria Skłodowska-Curie Memorial Cancer Center and Institute of Oncology, Gliwice, Poland), who discussed comparative analysis of serum from patients with different stages of non-small cell lung cancer using three complementary proteomic approaches to identify proteome components associated with progression of cancer. Biomarker candidates with potential importance for molecular proteomic staging of non-small cell lung cancer were identified with potential use in early detection of lung cancer. Equally fascinating were presentations from Goran Mitulović (Medical University of Vienna, Vienna, Austria) on ‘HPLC for Proteomics’, Ingrid Miller (Vienna University of Veterinary Medicine, Vienna, Austria) on ‘Characterization of α 1-acid glycoprotein in pigs of different age’, and Sophie Fröhlich (Institute of Chemical Technologies and Analytics, Vienna, Austria) on ‘*In vivo* protein and lipid adsorption on vascular replacement systems studied by mass spectrometry imaging’. Andreas Rizzi (Institute of Analytical Chemistry, University of Vienna, Vienna, Austria) concluded the day’s proceedings with an excellent presentation focused on quantitative profiling of glycans released from glycoproteins using HPLC–ESI-MS with stable-isotope-coded glycan labeling.

Jean M. H. van den Elsen (University of Bath, Bath, UK) opened the third day’s proceedings with a presentation on ‘Protein glycation analysis using boronic acid-based gel electrophoresis methods’. Using such methods, glycated proteins in

complex biological samples were detected, confirming this approach as a powerful and much needed proteomics tool. This was followed by a thought provoking presentation by Günter Allmaier (Institute of Chemical Technologies and Analytics, Vienna University of Technology, Vienna, Austria). Günter discussed human rhinovirus and the proteomics of charged species in the gas phase, where size and molecular mass determination of these particles was facilitated with high accuracy in the gas phase at atmospheric and high vacuum by nano-ESI combined with a differential mobility analyzer and quadrupole-reflectron TOF analyzer. This technique was also used to dissociate the ionized virus particles into the protein subunits to generate a protein pattern similar to a gel electrophoretic pattern but with exact molecular mass of the individual components. An interesting talk on complex proteomics platform for functional genomics and systems biology was presented by Wolfram Weckwerth (Department of Ecogenomics and Systems Biology, University of Vienna, Vienna, Austria). It included mass accuracy precursor alignment (MAPA) as a rapid exploratory analysis step, Mass Western for targeted proteomics, covariance inverse (COVAIN) for multivariate statistical analysis, and PROMEX as a database module. Martina Marchetti-Deschmann (Institute of Chemical Technologies and Analytics, Vienna University of Technology, Vienna, Austria) presented an exciting talk on tumor micro-heterogeneities and the study of differentiation of primary tumor and metastatic cells in tissue by MS imaging, MS profiling and intact cell MS. MS imaging allowed detailed investigation of metastasis and primary tumor comparison.

The forth day commenced with a presentation by Juan Calvete (Instituto de Biomedicina de Valencia, Valencia, Spain). Juan focused on the concepts and technologies utilized for venom research and their possible therapeutic use. Robert D. Hall (Wageningen University, Wageningen, The Netherlands) discussed metabolomics approaches for improving food crops where use of combined non-targeted metabolomics and transcriptomics approaches combined with advanced statistical analysis could identify candidate gene/metabolite correlations. A final set of presentations by Yvonne Schindlegger (University of Natural Resources and Life Sciences, Vienna, Austria) on non-targeted MS-based ligand screening of bacterial secondary metabolites associated with heavy metal mobilization in soil, and Łukasz Boguszewicz (Maria Skłodowska-Curie Memorial Cancer Center and Institute of Oncology, Gliwice, Poland) on ¹HRMS *in vivo*-based metabolomics in the evaluation of regional variations in the human brain concluded the day.

The final day, focused on metabolomics, commenced with a presentation by Dirk Walther (Max Planck Institute for Molecular Plant Physiology, Potsdam-Golm, Germany) entitled, ‘The metabolic interplay between plants and phytopathogens’. Dirk outlined various theoretical approaches for studying interaction of plants and phytopathogens on a biochemical level, demonstrating the potential of investigating pathogen–host interactions from the perspective of interacting metabolic networks. Rainer Schuhmacher (Institute of Agrobiolgy, University of Natural Resources and Life Sciences, Tulln, Austria) presented

an overview of a novel ^{13}C stable isotope labeling-assisted workflow for improved untargeted LC–HRMS-based plant metabolomics developed and applied to assess the wheat metabolome. This approach also enabled the detection of seven novel deoxynivalenol derivatives. Harald Köfeler (Medical University of Graz, Graz, Austria) discussed the application of an integrated ultrahigh resolution lipidomic platform on hepatic lipid droplets under genetic and nutritional stress, showing that phospholipid and diacylglycerol lipid classes remained largely untouched, whereas molecular triacylglycerol species were enriched in fasting and high fat diet conditions, with a distinctive shift towards long chain polyunsaturated fatty acids. The afternoon sessions included Thomas Nägele (Institute of Institute of Ecogenomics and Systems Biology, University of Vienna, Vienna, Austria) discussing the merits of metabolomics coupled to comprehensive genome-wide metabolic network reconstruction as a predictive tool in systems biology, and Hannes Doerfler (Institute of Ecogenomics and Systems Biology, University of Vienna, Vienna, Austria) applying mzGroupAnalyzer to LC–MS raw data, to prove the existence and relation of known molecules, proposing novel compounds and pathways in molecules arising during oxidative stress within the secondary metabolism of *Arabidopsis thaliana*.

Final presentations by Christoph Bueschl (University of Natural Resources and Life Sciences, Vienna, Austria) on the study of heat-induced flavonoid degradation in grapes using stable isotope labeling-assisted metabolomics resulting in detection of 63 phenylalanine derived grape metabolites, and Maria Doppler (Institute of Agrobiotechnology, University of Natural Resources and Life Sciences, Tulln, Austria) on establishment of a metabolite database and LC–HRMS/MS library for metabolomics of wheat, brought this successful session on plant system biology with integration of metabolomics and proteomic ideologies to a close.

The conference concluded with closing remarks by the organizers from the Austrian Proteomics Association and associated Proteomic Societies. The meeting was a great success giving credence and precedence to CEEPC. The venue for 9th CEEPC in 15th – 18th June 2015 on Poznan, Poland [7], where once again, all proteomes, proteomics and biological systems related topics will be discussed.

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