EXPERT REVIEWS

Proteomics without boundaries across Central and Eastern Europe

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The 7th Central and Eastern European Proteomic Conference (CEEPC), considered as the bedrock of proteomics

Central and Eastern Europe, Jena, Germany, 13–16 October 2013

The 7th Central and Eastern European Proteomic Conference (CEEPC), considered as the bedrock of proteomics in Central and Eastern Europe, was held on 13–16 October 2013 at the Max Planck Institute for Chemical Ecology in Jena, Germany. Established in 2007, CEEPC now represents a cradle of proteomic interactions in and around Central and Eastern Europe, without limitations of borders and linking it to international institutions worldwide. Its mission remains to contribute to all approaches of proteomics including clinical, quantitative and structural proteomics and with a view to identifying potential targets for therapeutic interventions. The 7th CEEPC excelled at stimulating exchange of proteomic knowledge and imbibing local hospitality offered by Jena with its limestone hills and exotic charm.

The biggest conceptual challenge inherent in proteomics lies not only in the proteome's high degree of complexity, but also with proteomic organizations of today. Often, many such organizations, despite excellent intentions, may or may not be able to nurture or encourage free flow of ideas, knowledge and technological expertise due to the burden of administration often accompanied by bickering and commercial secrecy or affiliation to pharmaceutical and other industries. We hear of several proteomic conferences every year and while attendance may number in hundreds if not a thousand and parallel sessions galore, a sense of overburdening with limitless number of posters and conflict of which presentations or session to attend, often leaves the participant perplexed and questioning. This together with the increasing registration fees and conference participation costs overwhelms the enthusiasm of the participant *per se*.

The Central and Eastern European Proteomic Conference (CEEPC) ethos strives to prevent such complexities from crossing the boundaries pertinent to 'Proteomics' as reflected in its genesis [1–4]. It evolved from a need for collaboration and a forum for open interaction where novel ideas could be nurtured. Utilization of incredible friendship between scientists from all over the world was the solution and it all began with invitations to such researchers and friends to participate in CEEPC. Subsequent intense work over the years by its founder members has sculptured the organization to its present day status and stature, which continues to grow, bringing together the best researchers from all over the world without pressures and conflicts as mentioned before.

While participation of Russian and Indian proteomics in the previous CEEPCs was greeted with anticipation [2], recent inclusion of Poland and Romania to the Board has been exciting and expansive. Today, a stronger network of proteomics in Central and Eastern Europe stands established together with the initial vision of a forum for enthusiastic scientists and researchers to meet and discuss their findings in a friendly and relaxed manner [1]. The CEEPC offers a refreshing alternative to larger meetings and is congenial to all researchers, regardless of their country origin, status or research speciality and yet remains steeped in tradition and tinged with pride. Additionally, young researchers are encouraged to present their findings. Rotation of the meeting's venue each year to wonderful iconic locations of the Europe, such as Prague, Vienna,

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Budapest, Jena, Krakow and Bucharest and the sharing of diverse cultures, histories, fine haute cuisine, wines and music, adds to the intertwining of 'cutting edge' research and cultural excitement. To this day, CEEPCs' outstanding success is due to the undiminished enthusiasm of this unique group of friends, their academic institutional researchers and participating scientists from all over the world, returning each year for this intoxicating mixture of proteomics and camaraderie. This is an ever-expanding conference that stands to grow as neighboring countries with proteomic interest or excellence come onboard to propagate this concept further.

Report

The 7th CEEPC was organized in Jena, Germany from the 13th–16th October 2013 with resounding success and followed on from the 6th CEEPC in Budapest, Hungary the year before. High-caliber expert speakers and enthusiastic participants from various countries attended this meeting. Cutting-edge proteomics relevant to clinical medicine, plant, insect, bacteria and imaging of biomarkers were extensively discussed and debated. The Organizing Committee under the auspices of Ales Svatos put together a fascinating scientific and cultural program for all to enjoy. Located among limestone hills, Jena offered participants both the excitement of novel proteomics as well as the rich and fascinating historical charm of Goethe, Schiller, Hegel and Fichte, who left their mark on intellectual life while Abbe, Schott and Carl Zeiss – the inventor of microscope, laid the foundations to its economic prosperity.

With major focus on 'Clinical proteomics and Interactomics', the conference commenced on the 14th of October with Corinna Henkel (Bochum, Germany) presenting matrix-assisted laser desorption/ ionization (MALDI) imaging as a powerful tool in the context of biomarker detection. H. Alexander Ebhardt (Zurich, Switzerland) followed with analysis of perturbed protein network in human diseases where accurate peptide quantification of subtle changes is critical. Additionally, SWATH-MS approach was also discussed. Piotr Widlak (Gliwice, Poland) presented an interesting talk on 'Radiotherapy-related changes in serum proteome patterns of head and neck cancer patients; the evidence for effects of low radiation doses', concluding that the observed effects reflected the patient's whole body response to irradiation. This was followed by a presentation by Andrea Sinz (Wittenberg, Germany) exploring the incorporation of unnatural photoreactive amino acids into the proteins of interest followed by UV-induced cross-linking and MS analysis that can be employed to derive 3D structural information of proteins. Karl Mechtler (Vienna, Austria) questioned the audience with the presentation entitled, 'Which biomarker would you like to discover today?' with reference to Acute Kidney Injury. Karl discussed iTRAQ labeling method for the quantification of proteins in patients' urine samples and emphasized that the method should be simple, reliable and rapid. Gili Ben-Nissan (Rehovot, Israel) followed with a presentation on the COP9-signalosome as a model of large heterogeneous protein complexes, demonstrating importance of the integration of various mass spectrometry, biochemical and imaging techniques. Suresh Jivan Gadher (Frederick, MD, USA) debated the epithelial–mesenchymal cross-talk with reference to contractile and cytoskeletal protein involvement in transition toward myofibroblasts and cancer-associated fibroblasts in wound healing and tumorigenesis. The study of the proteomic response of the human pathogenic fungus *Aspergillus fumigatus* to hypoxia by Olaf Kniemeyer (Jena, Germany) focused on characterization of candidate genes for their role in hypoxia by generating deletion mutants. Hana Kovářova (Libechov, Czech Republic) presented an interesting talk on possible key proteins in spinal cord injury-induced spasticity. Several proteins were exclusively changed in the spinal lumbar ventral horns; hence, potential new treatment strategies should primarily target dermatome muscle-specific spinal segments to prevent spasticity development. G. Kalló (Debrecen, Hungary) introduced an LC-coupled multiple reaction monitoring mass spectrometry method for the identification and quantification of defensins where multiplex feature has advantage over classical ELISA. Laszlo Drahos (Budapest, Hungary) rounded off the day's proceedings with a presentation on glycoprofiling of human plasma proteins, discussing the development of a method for studying not only a purified glycoprotein, but also dealing with glycoprotein mixtures like blood plasma.

Day 2 of the conference brought numerous exciting presentations focused on plant, insect and bacterial proteomics. Waltraud Schulze (Stuttgart, Germany) took us "Into the unknown: Systems biology approaches in exploring novel protein functions in plant signaling pathways", proposing that SIRK1 is involved in regulation of sucrose-specific osmotic responses by direct interaction with an aquaporin via phosphorylation, which is controlled by phosphorylation-dependent receptor internalization. Joy Michal Johnson (Jena, Germany) presented the model plant *Arabidopsis thaliana*, expressing the bioluminescent $Ca2^{+}$ reporter apoaequorin in the cytosol to elucidate the role of cytosolic $Ca2^{+}$ signaling in beneficial and pathogenic interactions.

The 'Quantitative proteomic session' saw several excellent presentations from Heidrun Rhode (Jena, Germany), Claudia Michael (Vienna, Austria) and Rudolf Kupcik (Pardubice, Czech Republic). Heidrun discussed automated native sample preparation for biomarker search, highlighting several advantages including high proteome coverage, flexible dynamic range with respect to molecular weight and sample amount, optional enzymatic and immunological analytics additional to mass spectrometry. Claudia addressed the advantages of quantitative N-Glycan analysis using μLC–PGC–ESI–qTOF–MS, while Rudolf discussed Phosvitin as a standard protein for optimization of enrichment of multiply phosphorylated proteins with success.

The final day focused on 'Spatially-resolved proteomics – imaging of biomarkers' with presentations from Marc Baumann (Helsinki, Finland), Isabelle Fournier (Lille, France), Andreas Römpp (Giessen, Germany) and Ferdinand von Eggeling (Jena, Germany), all addressing diverse aspects of spatiotemporal proteomics. Marc discussed 'imaging mass spectrometry as a new tool

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for searching for the invisible and addressed the potential of MALDI-profiling/imaging technologies in disease proteomics, drug action and studies of cellular processes. Andreas addressed 'Accurate mass MALDI imaging' at 25 μm pixel size for proteins after on-tissue digestion. Ferdinand concluded this session with a talk on a new concept of multimodal registration for 3D image reconstruction. Such fusion of modality-dependent information was shown to facilitate the correlation of anatomical and spectral features.

Andrej Shevchenko (Dresden, Germany) brought the proceedings of the conference to a close with a presentation describing proteolipidomics by high-resolution mass spectrometry. Andrej discussed the technological implications of merging both 'proteo-centric' and 'lipido-centric' approaches by adopting a more systematic view on the collective behavior of proteins and lipids within biological membrane using instruments of the Orbitrap family.

Conclusion

It was evident from 7th CEEPC that proteomics has excelled and encompasses many biological and clinical research areas. Judging by the high quality of presentations of young generation of researchers fascinated by proteomics, giant leaps in proteomics can enable diverse fields such as stem cell biology, drug discovery and disease research to reach the end goal of new therapies. The spirit and the quality of the conference in Jena in 2013 is a privilege to be repeated. Hence, in keeping with tradition, the next 8th CEEPC will be held in Vienna, Austria from 30th June to 4th July, 2014, where once again exciting advances in proteomes, proteomics and biological systems-related topics will be discussed in this vibrant city, offering excellent hospitality to be savored with newer challenges and even deeper fascination of proteomics.

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