



A decade of proteomics accomplished! Central and Eastern European Proteomic Conference (CEEPC) celebrates its 10th Anniversary in Budapest, Hungary

Suresh Jivan Gadher, László Drahos, Károly Vékey & Hana Kovarova

To cite this article: Suresh Jivan Gadher, László Drahos, Károly Vékey & Hana Kovarova (2017) A decade of proteomics accomplished! Central and Eastern European Proteomic Conference (CEEPC) celebrates its 10th Anniversary in Budapest, Hungary, Expert Review of Proteomics, 14:7, 567-569, DOI: [10.1080/14789450.2017.1339604](https://doi.org/10.1080/14789450.2017.1339604)

To link to this article: <http://dx.doi.org/10.1080/14789450.2017.1339604>



Accepted author version posted online: 06 Jun 2017.
Published online: 16 Jun 2017.



Submit your article to this journal [↗](#)



Article views: 7



View related articles [↗](#)



View Crossmark data [↗](#)

MEETING REPORT



A decade of proteomics accomplished! Central and Eastern European Proteomic Conference (CEEPC) celebrates its 10th Anniversary in Budapest, Hungary

Suresh Jivan Gadher^a, László Drahos^b, Károly Vékey^b and Hana Kovarova^{c,d}

^aThermo Fisher Scientific – Life Science Solutions, Frederick, MD, USA; ^bResearch Centre for Natural Sciences, Hungarian Academy of Sciences, MS Proteomics Research Group, Institute of Organic Chemistry, Budapest, Hungary; ^cAcademy of Sciences of the Czech Republic, Institute of Animal Physiology and Genetics, Libechev, Czech Republic; ^dResearch Center PIGMOD, Laboratory of Applied Proteome Analyses, Libechev, Czech Republic

ABSTRACT

The Central and Eastern European Proteomic Conference (CEEPC) proudly celebrated its 10th Anniversary with an exciting scientific program inclusive of proteome, proteomics and systems biology in Budapest, Hungary. Since 2007, CEEPC has represented 'state-of-the-art' proteomics in and around Central and Eastern Europe and these series of conferences have become a well-recognized event in the proteomic calendar. Fresher challenges and global healthcare issues such as ageing and chronic diseases are driving clinical and scientific research towards regenerative, reparative and personalized medicine. To this end, proteomics may enable diverse intertwining research fields to reach their end goals. CEEPC will endeavor to facilitate these goals.

ARTICLE HISTORY

Received 1 March 2017
Accepted 5 June 2017

KEYWORDS

Central and Eastern European Proteomic Conference (CEEPC); proteomics; neuroproteomics; mass spectrometry imaging; biomarkers; glycosylation; diseases; drug discovery; system biology

1. Introduction

It was befitting to celebrate the 10th Anniversary of Central and Eastern European Proteomic Conference (CEEPC) in a city such as Budapest steeped in history and culture. CEEPC too has a decade of history and culture and plays a positive role in promoting European proteomics [1]. It has purported interactions in and around Central and Eastern Europe, as well as internationally, making it a truly recognized conference of importance. More importantly, encouraging young researchers to present their findings and rotation of the meeting's venue annually to wonderful iconic locations with cultural diversity, gives these young investigators an air of excitement and reciprocation [2–8].

In a world where life expectancies are increasing, population is aging and need for disease treatments pressing, CEEPC stands to tackle societal challenges of the next decade with advanced understanding of protein functionality using newly developed, sophisticated proteomic approaches which may help unravel these diseases. CEEPC also raises awareness of socio-humanitarian issues directly via its website at <http://www.ceepc.eu/humanity>. This remains CEEPC's novel quality: pointing out dilemmas and injustices, and alerting individuals or organizations to intervene if possible.

2. Proteomics in Hungary

Proteomics commenced in Hungary approximately 15 years ago in Budapest and Szeged and later at Universities of Debrecen and Pécs where proteomic techniques (gel-based and gel-free; mass spectrometry (MS), electrophoresis and

chromatography) were utilized to progress research. Currently, diverse proteomics in Hungary includes studies on protein glycosylation (mostly MS based); brain research (in synapse); and extracellular vesicle proteomics (in embryonic development) as well as diverse disease proteomics is ongoing.

3. Meeting details

The 10th CEEPC was held from 11 to 14 October, 2016 at the Research Centre for Natural Sciences, Hungarian Academy of Sciences, Budapest, Hungary, where more than 175 participants from worldwide assembled. The Organizing Committee under the auspices of László Drahos and Károly Vékey melded a scientific program focused on Neuroproteomics and Protein Glycosylation.

4. Report of proceedings – Day 1

The Conference commenced on the 11th of October with a lecture from Ka Wan Li (Department of Molecular and Cellular Neurobiology, Center for Neurogenomics and Cognitive Research, VU University, Amsterdam, The Netherlands) who discussed metabotropic glutamate receptors 5 (mGluR5) that has been implicated in mechanisms of synaptic plasticity and which may serve as potential therapeutic targets in many psychological disorders including autism. His findings implicated the absence of mGluR5 signaling for changes of specific synaptic pathways. Roman A. Zubarev (Department of Medical Biochemistry and

Biophysics, Karolinska Institute, Stockholm, Sweden) presented on characterization of novel potent anticancer agents using proteomics tools to determine their protein target, site of binding, and mechanism of action. Various approaches were outlined for development of novel anticancer agents.

This presentation was followed by a joint presentation by Suresh Jivan Gadher and Hana Kovarova (Institute of Animal Physiology and Genetics and Research Center PIGMOD, Academy of Sciences of the Czech Republic, Libečov, Czech Republic) on investigational proteomic approaches in transplantation research into devastating neurodegenerative disorders. Their findings underlined the roles of IFN α , IL-10, IL-1, and IL-8 in central nervous system inflammation and immune imbalance in novel transgenic Huntington's disease model. While pluripotent cells are an attractive option to treat neurodegenerative diseases, neuronal differentiation of neural precursor cells showed significant quantitative changes in cytokines, chemokines, and growth factors including VEGF, which could have implications on treatment.

An afternoon session devoted to brain proteomics commenced with a plenary lecture by Maciej Lalowski (University of Helsinki, Medicum, Meilahti Clinical Proteomics Core Facility, Helsinki, Finland) on assessing brain dynamics using mass spectrometry imaging (MSI) in Alzheimer's disease, where the intramyloid beta (A β) Arctic mutation [p.E693G] leads to early onset of Alzheimer's disease. Their findings raised the possibility that soluble oligomeric A β assemblies in the human brain act as potent A β -seeders and are also present in plasma, cerebrospinal fluid, and brain parenchymal space. Katalin Völgyi (MTA-ELTE NAP B Laboratory of Molecular and Systems Neurobiology, Laboratory of Proteomics Hungarian Academy of Sciences and Eötvös Loránd University, Budapest, Hungary) continued with Alzheimer's theme with a talk on 'Mitochondrial processes underlying Alzheimer's disease', showing early β -amyloid effect on mitochondrial and mitochondria-associated endoplasmic reticulum membrane proteome, describing new features of early Alzheimer's disease.

This was followed by two presentations on a similar topic – 'Synaptic brain receptors, transporters and channels (RTCs)' by Fernando Sialana (Department of Pharmaceutical Chemistry, University of Vienna, Austria and CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria) on benchmarking of RTCs for interrogation of synaptic connectivity and 'Proteomic profiling of synapses' by Balázs Györfy (MTA-ELTE NAP B, Neuroimmunology Research Group and Laboratory of Proteomics, Institute of Biology, Eötvös Loránd University, H-1117, Budapest, Hungary), showing synaptic apoptosis and involvement of neuronal pentraxin 1.

There were 75 poster presentations at the conference, organized into two 2-h sessions. Topics of the posters covered a vast number of proteomic fields as well a wide range of proteomic methodologies including gel-based, gel-free, capillary electrophoresis; MALDI imaging; and diverse clinical, biomedical, scientific, and research applications in human, animal, and plants. Participants were often seen viewing posters while enjoying a glass of wine or a cup of coffee.

Katarina Davalieva (Research Centre for Genetic Engineering and Biotechnology 'Georgi D Efremov', Macedonian Academy of Sciences and Arts, Skopje, Republic of Macedonia) focused on schizophrenia, and structural and biochemical abnormalities of white matter. The cellular specificity of isolated proteins and their involvement in canonical pathways and complex neuropsychiatric disorders were discussed. The final presentation of the day was by Giselle Knudsen (Mass Spectrometry Facility, Department of Pharmaceutical Chemistry, University of California, San Francisco, CA, USA) who presented an exciting talk on 'Tau post-translational modification in wild-type and human amyloid precursor protein transgenic mice', refuting the hypothesis of extensive O-GlcNAc modification of endogenous tau and suggesting that posttranslational modification of physiological tau was regulated by diverse mechanisms.

5. Report of proceedings – Day 2

Conference resumed on Day 2 with a plenary lecture from Lilla Turiák (MS Proteomics Research Group, Research Centre for Natural Sciences, Hungarian Academy of Science, Budapest, and Center for Biomedical Mass Spectrometry, Department of Biochemistry, Boston University School of Medicine, Boston, MA, USA), entitled, 'Integrating GAGomics and proteomics for tissue analysis', focusing on analysis of glycosaminoglycans (GAGs) to better understand biochemical and pathological processes in amyloidosis and schizophrenia. Lilla concluded that GAGs are linear polysaccharides containing repeating disaccharide units of uronic acid or galactose and an amino sugar (HexA/Gal-HexNAc) and play essential roles through protein binding.

Xaveer Van Ostade (University of Antwerp, Wilrijk, Belgium) discussed the detection of cervical (pre)cancer on the basis of cervicovaginal fluid and the need for glycoprotein biomarkers for optimization of accuracy using protein abundance combined with differential posttranslational modifications to increase the accuracy of the assay. Tomáš Takáč (Centre of the Region Haná for Biotechnological and Agricultural Research, Faculty of Science, Palacký University, Olomouc, Czech Republic) discussed the power of shotgun proteomics coupled with cell biology to study vesicular trafficking and cytoskeleton, revealing cytoskeletal protein profilin 1 as a regulatory protein participating in the formation of vesicular brefeldin A compartments and small RabA1d as a new marker for early endosomes.

Matthias Holzlechner (Institute of Chemical Technologies and Analytics (CTA), Technische Universität Wien, Vienna, Austria) brought Day 2 to as close with a presentation on Immune cell characterization and *in situ* localization by intact cell MS and MSI. Matthias demonstrated that MSI was suitable for characterization and *in situ* localization of immune cell accumulations without using antibodies.

The evening was a highlight, with Hungarian hospitality at the Gala Conference dinner to celebrate the 10th Anniversary of the CEEPC [8].

6. Report of proceedings – Day 3

The third and final day commenced with a lecture from Tadashi Kondo (Division of Rare Cancer Research, National Cancer Center Research Institute, Tokyo, Japan) on

'Proteomic approach to sarcoma research toward clinical application', showing that integrated proteomic approaches are powerful tools in identifying prognostic or predictive biomarkers in sarcomas. Felicia Antohe (Institute of Cellular Biology and Pathology 'Nicolae Simionescu', Bucharest, Romania) presented a fascinating talk on alarmins in chronic noncommunicable diseases including atherosclerosis, diabetes, and cancer, highlighting the role of heat shock proteins, high-mobility group box 1 protein, and S100 proteins as main alarmins involved in maintaining and amplifying inflammation in these diseases. The morning session was concluded by Mangesh Bhide (Laboratory of Biomedical Microbiology and Immunology, University of Veterinary Medicine and Pharmacy, Komenského, Kosice, Slovakia) with a presentation on, 'From PCR to protein: protein synthesis pipelines'. Mangesh covered novel and rapid protein production strategies (PCR to protein) utilizing rapid ligation, vivid fluorescent tags, and cost-effective prokaryotic and eukaryotic expression hosts.

György Marko-Varga (Clinical Protein Science & Imaging Group, BioMedical Center, University of Lund, Lund, Sweden, and Department of Surgery, Tokyo Medical University, Tokyo, Japan) discussed issues facing global healthcare and need for personalized medicine strategies of matching specific disease genotypes and phenotypes with specific pharmaceutical drug treatment that had shown efficacy in important diseases. The rest of the afternoon appeared to be an all-Austrian affair with Corina Mayrhofer, Ingrid Miller, and Guenter Allmaier presenting. Corina discussed the identification of spermatozoa associated oviduct derived molecules by fluorescence labeling, whereas Ingrid outlined the ability of 2D-DIGE to distinguish gender-specific impact of a flame retardant on the rat liver proteome, both presentations highlighting the importance of proteomic methodologies as well as gender-specific difference in proteins of interest.

Guenter Allmaier (Institute of Chemical Technologies and Analytics, Vienna University of Technology, Vienna, Austria) rounded off the meeting with a presentation entitled, 'Virus proteomics in the liquid and gas phase', where proteomic-based strategies to evaluate vaccine preparations of different viruses were discussed. Classic approaches based on gel electrophoresis, *in-gel* digestion, peptide mass fingerprinting, and tandem MS by means of MALDI TOF/RTOF mass were discussed.

The Conference concluded with closing remarks from the Organizing Committee. In keeping with the CEEPC tradition, prizes were awarded for the best three posters, recipients of which were as follows: *Kata Badics, Katalin Völgyi et al.* for 'Early mitochondria associated membrane (MAM) protein changes in APP/PS1 mice'; *Jana Vaclavkova, Marián Hajdúch et al.* for 'Application of DARTS (drug affinity responsive target stability) for identification of the ligand-binding part of the protein'; and *Gabor Jarvas, Andras Guttman et al.* for 'Investigation of the ultra-low ESI-MS flow rate in proteomics applications'.

The meeting was a success and an important milestone in the history of CEEPC continuity. The venue for the 11th CEEPC is Kosice, Slovakia (27–29 September, 2017), where once again, all proteomes-, proteomics-, and systems biology-related topics will be debated [9,10].

Tribute

This meeting report is dedicated to Dr. Hana Kovarova - founder member of CEEPC for her vision, dedication and efforts in making this 10th Anniversary milestone a possibility. Today, an expansive network of proteomics stands established in Central and Eastern Europe with links internationally, thanks to her intense efforts.

Funding

This work was supported by the Institutional Research Concept RVO67985904 (IAPG, AS CR, v.v.i) and by the National Sustainability Program LO1609 (Czech Ministry of Education, Youth and Sports).

Declaration of interest

The authors have no relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript. This includes employment, consultancies, honoraria, stock ownership or options, expert testimony, grants or patents received or pending, or royalties.

References

1. Central and Eastern European Proteomic Conference (CEEPC) <http://ceepc.eu>
2. Gadher SJ, Marczak Ł, Łuczak M, et al. Proteomic landscape in Central and Eastern Europe: the 9th Central and Eastern European Proteomic Conference, Poznan, Poland. *Exp Rev Proteom.* 2016;13(1):5–7.
3. Gadher SJ, Marchetti-Deschmann M, Allmaier G, et al. Tremendous progress in proteomics and metabolomics in Central and Eastern Europe. *Exp Rev Proteom.* 2015 Feb;12(1):9–11.
4. Gadher SJ, Kovářova H. Proteomics without boundaries across Central and Eastern Europe. *Exp Rev Proteom.* 2014 Jun;11(3):255–257.
5. Gadher SJ, Kovarova H. Advances and expansion of Central and Eastern European proteomics. *Exp Rev Proteom.* 2012;9(1):9–11.
6. Gadher SJ, Martinkova J, Drahos L, et al. The third Central and Eastern European Proteomic conference. *Exp Rev Proteom.* 2010 Feb;7(1):15–17.
7. Gadher SJ, Bezouska K, Kovářová H. 1(st) Central and Eastern European Proteomic Conference & 3(rd) Czech Proteomic Conference 29-31 October 2007, Prague, Czech Republic. *Proteomics.* 2008 Mar;8(5):927–929.
8. Gadher SJ, Kovarova H. A decade of Central and Eastern European Proteomic Conference (CEEPC): credibility, cohesion and vision for the next decade. *J Proteom.* 2017;153:2–7.
9. 11th Central and Eastern European Proteomic Conference (CEEPC) [Internet]; [2017 Feb 2]. Available from: <http://lbmi.uvm.sk/ceepc2017/Kosice/Welcome.html>
10. Central and Eastern European Proteomic Conference – news and views [Internet]; [cited 2017 Feb 2]. Available from: http://www.ceepc.eu/news_views