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To cite this article: Suresh Gadher, Mangesh Bhide & Hana Kovarova (2018): Pursuit of proteomic excellence and the excitement in Košice, Slovakia, at the 11th Central and Eastern European Proteomic Conference (CEEPC), *Expert Review of Proteomics*, DOI: [10.1080/14789450.2018.1469983](https://doi.org/10.1080/14789450.2018.1469983)

To link to this article: <https://doi.org/10.1080/14789450.2018.1469983>



Published online: 04 May 2018.



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MEETING REPORT

Pursuit of proteomic excellence and the excitement in Košice, Slovakia, at the 11th Central and Eastern European Proteomic Conference (CEEPC)

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ABSTRACT

The Central and Eastern European Proteomic Conference (CEEPC) successfully launched its second decade of proteomics in Košice, Slovakia with a program of systems biology, cellular, clinical, veterinary and sports proteomics. Whilst many conferences are struggling to attract participants, CEEPC with its outstanding track record and unique ‘family – feel’ packaged with excellent ambiance is thriving and bringing together proteomics experts from academia, industry, scientific specialties, clinics and precision medicine communities interested in resolving mysteries about protein functionalities in health and disease. CEEPC is also renowned for addressing humanitarian global healthcare issues, may it be ageing, chronic diseases or global epidemics. This year CEEPC intertwined with Košice Peace Marathon’s pursuit of excellence in sports and initiatives including sports medicine and global peace.

ARTICLE HISTORY

Received 22 February 2018
Accepted 24 April 2018

KEYWORDS

Central and Eastern European Proteomic Conference (CEEPC); proteomics; neuroproteomics; clinical proteomics; mass spectrometry imaging; biomarkers; sports medicine; systems biology; veterinary proteomics; ‘Košice International Peace Marathon’

Košice with its academic heritage set the scene for the 11th Central and Eastern European Proteomic Conference (CEEPC) and infused a sense of pursuit of excellence by extending a warm welcome to researchers and scientists not only from Central and Eastern Europe but from all over the world.

CEEPC excels at raising awareness of medical and socio-humanitarian issues via its website [1] and this year added ‘global peace’ to its list of initiatives. This is CEEPC’s uniqueness in pointing out humanitarian challenges while focusing on scientific, medical, and proteomic priorities of *understanding biological processes and diverse diseases* [2]. Additionally, encouraging young researchers to present their findings and offering a rich mix of historical and humanitarian excitement differentiates CEEPC from other societies [3–10].

The 11th CEEPC was held from 27 to 29 September 2017 at the Hilton Hotel Košice where more than 120 worldwide participants gathered. The Organizing Committee under the auspices of Mangesh Bhide put together a fascinating program with a focus on diverse proteomic topics [11]. The meeting was a great success. The 3-day meeting with its social program was thoroughly enjoyed by all and many participants stayed over the weekend to enjoy Košice and its International Peace Marathon culminating in the releasing of ‘white doves’ for world peace.

With major focus on ‘societal and medical challenges’, the conference commenced on 27 September 2017 with a plenary lecture from Chris Turck (Max Planck Institute of Psychiatry, Munich, Germany) entitled, ‘Pathway illumination for disease research – from Omics to Biosignatures’. Identification of biosignatures for psychiatric disorders and antidepressant drug response using sensitive high-throughput proteomics and

metabolomics platforms were discussed. Molecular pathways in mouse models that represent defined endophenotypes characteristic for human psychiatric disorders including anxiety, posttraumatic stress disorder, and schizophrenia were examined together with drugs that target the monoaminergic and glutamatergic systems to delineate mechanisms relevant for therapeutic response and novel drug targets. The ultimate goal remains to complement imprecise clinical parameters with molecular biosignatures to improve patient diagnosis, stratification, and treatment.

Suresh Jivan Gadher (Thermo Fisher Scientific, Carlsbad, CA, USA) followed with a presentation on, ‘The power of tears’ and a novel proteo-genomic high sensitivity assay which could revolutionize precision medicine in clinic. Human tears with their biomolecule repertoire serve as a good source for biomarkers and offer an excellent opportunity for patient stratification in precision medicine. ProQuantum™ Immunoassays incorporating analyte specificity of high affinity antibody–antigen binding with the signal detection and amplification of real-time PCR were shown to offer multidimensional analyses of DNA, RNA, and now biological proteins.

Morning continued with Alon Savidor (The Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science, Rehovot, Israel) who gave an insight into full-length de novo protein sequence determination by Database-Independent Protein Sequencing. To date, there is no available method for full-length protein sequencing, independent of a reference database, in high throughput. Alon discussed unambiguous, rapid, database-independent, full-length protein sequencing approach.

Afternoon commenced with Mario Cindrić (Department of Molecular Medicine, Rudjer Boskovic Institute, Zagreb, Croatia) discussing automated sample preparation in proteomics, multidimensional chromatography, and biotypization. A simple peptide derivatization procedure with 5-formylbenzene-1, 3-disulfonic acid (CAF-/+ reagent) results in that the positive ion mode peptide fragmentation data can be confirmed by negative ion mode fragmentation data and *vice versa*. In doing so, validity of the protein sequence coverage is significantly improved and complex posttranslational modifications can be deduced in a single experiment.

Gustavo Makert (Clinic for Birds and Reptiles, Faculty of Veterinary Medicine and Department of Immunology, Vaccine Technologies Unit, Fraunhofer Institute for Cell Therapy and Immunology, Leipzig, Germany) presented an interesting talk on vaccine development for the control of the ectoparasite *Dermanyssus gallinae*: a potential vector of pathogenic agents. *Dermanyssus gallinae* causes devastation in poultry farming worldwide and several strategies to control this parasite have failed. Gustavo discussed a solution where mite protein extracts could be used to immunize hens with two different adjuvants followed by IgY isolation from eggs to test for mite mortality in an *in vitro* feeding assay. Complete protein sequences can then be deduced from genomic and transcriptomic assemblies derived from high-throughput sequencing of total DNA and RNA. The results showed that such a strategy could help develop a vaccine against *Dermanyssus gallinae*.

Lucia Borszukova Pulzova (Laboratory of Biomedical Microbiology and Immunology, University of Veterinary Medicine and Pharmacy, Kosice, Slovakia) addressed the challenges of serodiagnosis of Lyme borreliosis – a tick-borne zoonosis. Lucia alluded to numerous antigens of *Borrelia* outer surface proteins OspA to OspG as key proteins for development of a reliable immunodiagnostic assay. The combination of specific B-cell epitopes from OspA and OspC proteins could address diagnostic accuracy of serologic assays in future.

Day 2 of the conference brought numerous exciting presentations. Dasa Cizkova (Institute of Neuroimmunology, Slovak Academy of Sciences, Bratislava, Slovakia and University of Veterinary Medicine and Pharmacy, Kosice, Slovakia) focused on spinal cord injury and utilization of proteomics and smart scaffolds for effective regeneration and functional recovery. Adriana Murgoci (Institute of Neuroimmunology, Slovak Academy of Sciences, Bratislava, Slovakia) alluded to the role played by microglia in both development and neurological disease as well as their influence depending on their origin on exosome content, which in turn can influence numerous functional and pathological aspects.

Vladimir Havlíček (Institute of Microbiology of the CAS, Prague, Czech Republic) and Gabriel Mazzucchelli (Mass Spectrometry Laboratory, University of Liège, Belgium) emphasized the advantages of mass spectrometry in proteomic research. Vladimir introduced the rapid evaporative ionization mass spectrometry as a molecular classification and biomarker discovery tool useful for spectral feature definition prior to mass spectrometry imaging. Gabriel elaborated the merits of multienzymatic limited digestion proteolysis for maximum sequence coverage.

László Drahos (MTA-TTK NAP B MS Neuroproteomics Group and Proteomics Laboratory, Hungarian Academy of Sciences, Budapest, Hungary) showed that in sleep deprivation, phosphorylation-based signaling activates the thyroid hormone synthesis and insulin secretion as a whole-body response. Altered proteins and protein signaling pathways using bioinformatics tools correlated this to sleep-related synaptogenesis and molecular maintenance.

Afternoon session commenced with Katrin Marcus (Medizinisches Proteom-Center, Ruhr-Universität, Bochum, Germany) eloquently presenting 'tissue-based clinical proteomics in neurological/neuromuscular diseases' where combination of powerful omics could lead to insights into pathomechanisms. Katrin also reminded the audience why proteomics was pursued in clinical research by quoting Carl Sagan, 'Somewhere something incredible is waiting to be known!'

László Prókai (Institute for Healthy Aging, Center for Neuroscience Discovery, University of North Texas Health Science Center, Fort Worth, TX, USA) alerted the audience about drug abuse in society including opioids and methamphetamine. LC-MS/MS analyses in combination with powerful bioinformatics was able to not only reveal novel protein associations but also potential neurobiological indicators or consequences of methamphetamine abuse.

Katarína Bíliková (Laboratory of Molecular Apidology, Institute of Forest Ecology, Slovak Academy of Sciences, Bratislava, Slovakia) discussed the honeybee proteins and their use in medicine and pharmacy. Proteins both floral and from honeybee origin were shown to have broad range of therapeutic properties including anticancer, antioxidant, antibacterial, antifungal, and antiviral. Of the proteins, apalubmins were shown to be active compounds with healing properties.

Final day focused on veterinary proteomics which is only now being developed with a great potential for further insight into disease processes that cross species barriers. David Eckersall and Nicolas Guillemin (ERA Chair Laboratory, Faculty of Veterinary Medicine, University of Zagreb, Zagreb, Croatia) presented a scenario each. David showed that proteome of bovine nasal secretion contained IgA, glutathione S-transferase, lactoferrin, and odorant binding protein, all with potential for host protection against infection. Bioinformatics, Gene Ontology analysis, disease modeling, and proteomics together can help elucidate molecular pathways involved in infectivity and/or diseases and can be useful in predicting potential biomarkers. Nicolas too used such approaches to visualize interactions and pathways to better understand babesiosis in dog. Eva Klement (Laboratory of Proteomics Research, Biological Research Centre, Hungarian Academy of Sciences, Szeged, Hungary) presented the final talk of the meeting, 'Beyond the cell wall – extracellular phosphorylation' which suggested that additional kinases and certain proteins may be controlled by an interplay between glycosylation and phosphorylation.

The conference concluded with closing remarks by the organizers; however, the Slovak hospitality and warmth continued as many participants prepared to participate in the Košice International Peace Marathon or sample the delights of Košice or both. The venue and dates for the 12th CEEPC, 2018 is Bucharest, Romania, from 24 to 26 October 2018,



where once again all proteomes, proteomics, and biological systems-related topics will be discussed [12,13].

Funding

This paper was not funded.

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 apart from those disclosed. Peer reviewers on this manuscript have no relevant financial or other relationships to disclose.

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