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# The third Central and Eastern European Proteomic conference

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Suresh Jivan Gadher, Jirina Martinkova, László Drahos, Károly Vékey, Guenter Allmaier and Hana Kovarova†

*†Author for correspondence*
*IInstitute of Animal Physiology and Genetics, Academy of Sciences of Czech Republic, v.v.i., Rumburska 89, 27721 Libechov, Czech Republic*
*Tel.: +420 315 639 582*
*Fax: +420 315 639 510*
*kovarova@iapg.cas.cz*

## The third Central and Eastern European Proteomic conference

### *Budapest, Hungary, 6–9 October 2009*

The third Central and Eastern European Proteomic Conference was held at Hotel Benzcur, Budapest, Hungary, from the 6–9 October 2009. The meeting was the third in a series of proteomic conferences to be held in this region of Europe, with the key aim of strengthening the links with scientists from Central and Eastern Europe, as well as international groups worldwide. It was attended by more than 150 delegates from various countries and many proteomic topics, including biomarker discovery, post-translational modifications, clinical proteomics, as well as new proteomic technologies, which may facilitate future progress, were discussed over the 3 days.

**Keywords:** biomarkers • Central and Eastern Europe • mass spectrometry • proteomics • proteomics applications

The third Central and Eastern European Proteomics Conference (CEEPC) was held in conjunction with the 3rd Annual Meeting of the Hungarian Proteomics Society, the 4th Czech Proteomic Conference and the 7th Austrian Proteomic Association (AuPA) Proteome Research Symposium. The meeting was the third conference in the CEEPC series, which were previously held in Prague, Czech Republic [1,101] and Jena, Germany [102]. The aim of this conference is to bring together researchers, not only from countries of Eastern and Central Europe, but from all over the world, to discuss and debate all aspects of proteomics, as well as new perspectives moving forward [2]. More than 150 delegates from Hungary, the Czech Republic, Austria, Germany, Poland, Russia, Switzerland, the UK, Ireland, Denmark, Finland, Sweden, Italy and Turkey, as well as international participants from more distant countries, such as the USA, Iran, Pakistan and Peru, were privileged attendees to this ‘cutting-edge science’ conference presented by excellent speakers from diverse institutions, and this was complimented not only by the warmth of the Magyar autumn but also by great Hungarian hospitality. Budapest was undoubtedly an ideal and splendid venue, offering excellent historical sites, such as the Castle District, medieval and baroque splendor and spectacular views of Buda, Pest and the Parliament buildings, with the majestic Danube flowing by. More than 30 talks and 70 posters were presented over the 3 days. The program included well-known invited speakers, as well as young researchers with excellent ideas and results, whose attendance to the conference was facilitated by bursaries from the European Science Foundation (ESF), thus enabling more than 20 such participants (all MSc or PhD students) to attend. Interest focus ranged from biomarker discovery, separation techniques, advances in mass spectrometry and various proteomic technologies for the quantification of proteins and examination of post-translational modifications.

The conference commenced with a presentation by Helmut E Meyer (Ruhr-University Bochum, Germany) with a lecture entitled ‘High Performance Proteomics – a Successful Way to Biomarkers’, which discussed how high-performance proteomics can lead to reliable and far-reaching results in discovering new biomarker candidates for liver cirrhosis. Stephen R Pennington (University College Dublin Conway Institute, Ireland) also focused on biomarker discovery and developments in psoriatic arthritis and prostate cancer, emphasizing the potential of multiplexed quantitative protein measurements using multiple-reaction

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monitoring. Silvia Surinova (ETH Zurich, Switzerland), a young PhD student, delivered an excellent talk on detection of potential colorectal cancer markers in patients' plasma using an interesting but complex strategy for such marker detection. First, N-linked glycosylated proteins from epithelial tumor cells together with the patient's internal control epithelia were analyzed to characterize differences. These biomarker candidate glycoproteins were further monitored in two types of patients' plasma, peripheral plasma versus plasma from veins draining the tumor, to see if they are detectable in blood in order to assign significance of regulation due to cancer progression. Finally, as a verification phase, the discovered candidate biomarkers were screened across plasma using selected reaction monitoring.

Roman A Zubarev (Karolinska Institute, Sweden) discussed the developments in Pathway Search Engine for expression proteomics and its applications in tissue samples. He was followed by Agata Malinowska (IBB PAS, Warsaw, Poland) who presented a high-throughput liquid chromotography-MS approach for analyses of synaptosomes from mouse models of Alzheimer's disease. John Amster (University of Georgia, GA, USA) followed with a very interesting talk on the development of new tools for proteomic analysis of prokaryotes based more on accurate mass measurement. He explained the use of accurate mass measurement as a method for protein identification. Irena Selicharova (AS CR, Prague, Czech Republic) focused on the difficulties involved in a search for changes in proteomes of breast epithelial cells of women inheriting germline mutation in *BRCA1* compared with normal breast tissue of women without this mutation. This study was aimed at discovering possible preneoplastic changes in protein levels that may be related to a predisposition to breast cancer.

The second day started with the talk from Helena Skalnikova (AS CR, Libechov, Czech Republic), who introduced an exciting piece of work on neural stem cells and related cell-based therapy in spinal cord injury. The presentation was in two parts; the first focused on studies in the rat model of spinal cord transection. The signaling protein and phosphoprotein changes from motor neurons and sensor neurons were identified using Kinexus antibody microarrays at different time intervals after injury. The second part of the presentation focused on the characterization of molecular mechanisms governing neural stem cell differentiation in a porcine model. The neural stem cells were found to exhibit high levels of GRK2, several members of the FAS pathway and phosphorylations of αβ-crystallin (S45). Enhanced levels of integrin, PDGF and MAPK signaling and heme-oxygenase 2 were also observed, in keeping with characteristics of differentiated neural cells. Tamas Janaky (University of Szeged, Hungary) presented an interesting talk on chemical frames as references for protein quantification in proteomics. His results, based on the distinction between chemical and physical properties of the proteins, were correlated to quantification of proteins. William J Griffith's (Swansea University, UK) presentation, entitled 'Brain Proteomics', discussed a large study with interdisciplinary approaches in studying expression of enzymes involved in cholesterol metabolism. The effects on the proteome after treatment of neurons with 24S-hydroxycholesterol and 24S,25-epoxycholesterol were monitored using iTRAQ and SILAC methodologies. Rudolf Oehler (Medical University of Vienna, Austria) discussed the identification of antibodies against non-HLA antigens in chronic kidney rejection. These antigens were identified as tubulin β chain, vimentin, lamin-B1 and Rho GDP-dissociation inhibitor 2. Further detailed analysis of vimentin expression revealed that anti-non-HLA antibodies are directed against a small number of specific protein isoforms.

Joszef Tozser (University of Debrecen, Hungary) presented a fascinating talk on the proteome analysis of human tears. He presented human tears as an unusual and difficult but non-invasive starting material from patients with diabetic retinopathy. Progression of the disease was monitored by looking at tear proteins at specific time points. Among several interesting presentations, one of particular interest was from another student – Daniela Schmid (Max Planck Institute for Chemical Ecology, Jena, Germany). Schmidt's focus was on the characterization of sex-related proteins in *Scytosiphon lomentaria*, a species of brown algae. She was able to compare cytosolic proteins from male and female gametes with more than 500 proteins being separated by 2DE and sequenced subsequently, with approximately 80% of the proteins being identified. In spite of this degree of identification, the overall conclusion showed a low variability between the protein patterns of male and female gametes.

Among many fascinating talks on the last day of the meeting was a presentation from Guenter Allmaier (Vienna University of Technology, Austria), who presented the peptidome and proteome analysis of snake venoms. Lyophilized samples from South American *Bothrops* species venoms showed complex mixtures comprising of small peptides, glycoproteins and phosphoproteins. The importance of understanding these biological fluids is essential as there are possible applications of these new lead compounds in pharmaceutical applications, development of alexipharmic agents and/or in evolution of allergenicity. Karel Bezouska (AS CR Prague, Czech Republic) delivered an entertaining talk on the identification of surface oligosaccharide profiles responsible for the sensitivity of tumor cells for natural killing, as well as for the ability of tumors to eliminate the killer lymphocytes – better elaborated as 'how to kill the killer'. Veronika Suni (Turku Centre for Biotechnology, Finland), another ESF-supported student speaker, introduced a 'spectral library searching method' based on synthetic phosphopeptides to assist analysis and validation of phosphopeptides using SpectraST. This tool is a part of the 'Trans-Proteomic Pipeline' used by some researchers in their studies.

The conference concluded with a closing lecture from Ron MA Heeren (FOM – Institute for Atomic and Molecular Physics, The Netherlands) who presented developments in imaging MS. Closing remarks were delivered by the organizers from the Hungarian Academy of Sciences, Hungarian Chemical Society, and Hungarian Proteomic Society together with the Austrian Proteomics Association and the Czech Proteomic Society. The meeting was a great success and established precedence for such meetings on a regular basis. Additionally, time was set aside to elect permanent members and welcome new members to the Advisory

Board and Organizing Committee. The venue for the next meeting will be the University of Vienna, Austria from the 29th August to the 2nd September 2010, where, all interested in proteomics and proteomic-related topics will gather together to savor the Austrian hospitality and share the fascination of proteomes and metabolomes. It is envisaged that inclusion of a 1-day session with a focus on metabolomics may add to the excitement.

For more details on the third Central and Eastern European Proteomics Conference visit the conference website [103].

## Financial & competing interests disclosure

*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.*

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101 The Czech Proteomic Society, section of CSBMB http://2007.czproteo.cz

102 2nd Central and Eastern European Proteomics Conference (CEEPC) on Proteomics Driven Discovery and Applications www.ceepc.eu

103 The 3rd CEEPC host also the 3rd Annual Meeting of the Hungarian Proteomics Society, the 4th Czech Proteomic conference and the 7th AuPA (Austrian Proteomic Association) Proteome Research Symposium www.chemres.hu/ms/3rdceepc/index.html

## Affiliations

- Suresh Jivan Gadher
  Millipore Bioscience, St Charles, MO, USA
  and
  Institute of Animal Physiology and Genetics, Academy of Sciences of Czech Republic, v.v.i., Rumburska 89, 27721 Libechov, Czech Republic
- Jirina Martinkova
  Institute of Animal Physiology and Genetics, Academy of Sciences of Czech Republic, v.v.i., Rumburska 89, 27721 Libechov, Czech Republic
- László Drahos
  Hungarian Academy of Sciences Chemical Research Center, Pusztaszeri ut 59-67, Budapest, Hungary
- Károly Vékey
  Hungarian Academy of Sciences Chemical Research Center, Pusztaszeri ut 59-67, Budapest, Hungary
- Guenter Allmaier
  Institute of Chemical Technologies and Analytics, Vienna University of Technology, Vienna, Austria
- Hana Kovarova
  Institute of Animal Physiology and Genetics, Academy of Sciences of Czech Republic, v.v.i., Rumburska 89, 27721 Libechov, Czech Republic
  Tel.: +420 315 639 582
  Fax: +420 315 639 510
  kovarova@iapg.cas.cz