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# A decade of Central and Eastern European Proteomic Conference (CEEPC): Credibility, cohesion and vision for the next decade

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ABSTRACT

The Central and Eastern European Proteomic Conference (CEEPC), has reached a special milestone as it celebrates its 10th anniversary. Today, an expansive network of proteomics in Central and Eastern Europe stands established to facilitate scientific interactions and collaborations in and around Central and Eastern Europe, as well as with international research institutions worldwide. Currently, when many conferences are struggling to attract participants, CEEPC is thriving in its status and stature as well as expanding by attracting newer member countries. CEEPC's success is driven by mutual respect between scientists sharing interest in proteomics and its applications in multidisciplinary research areas related to biological systems. This effort when interwoven with exciting ambience steeped with culture, and tradition is also a reason why participants enjoy it. CEEPC's careful balance between excellence and cohesion holds the key to its success. It is evident that CEEPC is ready for the next decade of excitement and expectations of multifaceted proteomics in Central and Eastern Europe. Additionally, in the era of emerging personalized medicine where treatment selection for each patient is becoming individualized, CEEPC and proteomics is expected to play a significant role moving forward for the benefit of mankind.



## 1. Significance

The manuscript reviews a decade of the Central and Eastern European Proteomic Conference (CEEPC) by highlighting key aspects that led to the advancement of proteomic in this region as well as points to its uniqueness and endeavours. The CEEPC has purported interactions in and around Central and Eastern Europe, as well as linked it to international institutions worldwide, making it a truly international conference of importance and one which is greatly enjoyed by many who attend it on a regular basis.

The manuscript is a key part of the 'Special Issue - Journal of Proteomics' denoting the 10th anniversary of the Central and Eastern European Proteomic Conference (CEEPC).

## 2. Genesis of Central and Eastern European Proteomic Conference

Up to the late 1980s, collapse of communist regimes and their replacement by democracy and market economies led to dramatic changes in scientific research in former Eastern Bloc countries. With some exceptions, scientific and medical research as a whole suffered from isolation and in particular protein science as many of these research institutions felt neglected and often without connectivity to other pioneering research laboratories or organizations. Around the same time, the concept of the proteome was introduced at the first Siena meeting in 1994 with subsequent publication in 1995 [1]. Since then, proteomics as the comprehensive study and characterization of proteins in living cells and tissues has expanded dramatically and revolutionised protein science and research, providing stunning insight into complexity of proteins compared to easily accessible genes.

The technologies such 2-D gel electrophoresis combined with sensitive silver staining, Edman's amino acid sequencing from separated protein spots, often followed by antibody production against such protein antigens with a view to easier identification by immunodetection proved highly successful. Establishment of bioinformatic tools for evaluation of protein maps as well as developments in 2-D liquid chromatography, changed the way of looking at protein diversity and functionalities in variety of biological samples. The commencement of an era of mass spectrometry approaches since the third millennium represented a quantum jump allowing quick and precise protein identification at peptide level, thus turning proteomics into an exciting biomedical research reality [2–4]. Currently, using modern instrumentation, we can explore up to five orders of magnitude in dynamic

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range of cell/tissue proteins, but some biological fluids including serum or cerebrospinal fluid encompass up to 10–12 orders of magnitude [5] and yet calling for other novel or more powerful technologies and tools.

The political changes in Eastern Europe followed by inclusion of several former Eastern Bloc countries into the European Union did not bring any immediate support or advancement of research and development, which stayed well below the European level at that time. Established in 2003, the Czech Proteomics Society, section of the Czech Society for Biochemistry and Molecular Biology, was simultaneously debating the above mentioned inertia as well as ways to rectify the imbalance in proteomic research in Central and Eastern Europe. It all began with a vision to create a dynamic and integrated proteomics focused research community inclusive of all different countries and cultures. The term Central and Eastern European Proteomic Conference (CEEPC) was jointly coined in 2007 by Josef Chmelik [6], Suresh Jivan Gadher and Hana Kovarova [7] to address the apparent lack of visibility of advancing proteomics as well as sporadic meetings and infrequent international collaborations involving these countries. This effort reflected support given by members of Czech Proteomic Section as well as a group of friendly researchers from Russia, United Kingdom, Canada and the United States and led to the birth of the 1st CEEPC jointly organized with the 3rd Czech Proteomic Conference in 2007 in Prague [7]. Invitation to participate was sent to Austria, Hungary and Germany and the Scientific advisory board was established and included Hana Kovarova (Academy of Sciences of the Czech Republic, Prague, Czech Republic), Suresh Jivan Gadher (Oxford, United Kingdom and Thermo Fisher Scientific, Frederick, MD, USA), Ales Svatos (Max-Planck Institute of Ecology, Jena, Germany), Karoly Vekey and Laszlo Drahos (Hungarian Academy of Sciences, Budapest, Hungary), Günter Allmaier (University of Technology, Vienna, Austria). These board members represent the countries central to the CEEPC and these members together with others mentioned in the acknowledgement below, helped propagate the original vision. Success and expansion of the CEEPC board now also includes Romania represented by Felicia Antohe (Romanian Academy, Bucharest, Romania), Macedonia by Katarina Davalieva (Macedonian Academy of Sciences and Arts, Skopje, Republic of Macedonia) and Poland by Lukasz Marczak (Polish Academy of Sciences, Poznan, Poland). We now have countries waiting to join the CEEPC as their proteomic research and ambitions grow and their need for collaboration and interconnectivity increases. These countries will be incorporated into the CEEPC on their merit of proteomic progression and with a view to the betterment of the future of their young researchers.

## 3. Ethos and uniqueness of Central and Eastern European Proteomic Conference

Today, an expansive network of proteomics in Central and Eastern Europe stands established to facilitate expert scientific interaction and collaborations and thrives on mutual respect and friendship. An informative website at http://ceepc.eu/ not only distinguishes CEEPC from other proteomic organizations but also underlines the uniqueness and individuality of its ethos and ideology. The birth and birthplace of CEEPC together with advancing proteomics is captured by the CEEPC logo showing the ascending spires of the city of Prague outlined by the intensity of protein/peptide peaks of mass spectrometry depicting the pinnacles of excellence and cohesion of the CEEPC community (Fig. 1).

The initial vision of a forum for enthusiastic scientists and researchers to meet and discuss their work in a relaxed manner in middle sized meetings remains unchanged to this day. Rotation of the meeting's venue each year to cultural cities of the world such as Prague, Vienna, Budapest, Jena, Poznan and others to come adds to the intertwining of cutting edge research and the excitement that goes with it. CEEPC's documented success is not only due to different aspects of proteomics but also due to encompassed diverse proteomic topics as well as the added appreciation of the culture of the day [7–14; http://ceepc.eu/].


**Fig. 1.** LOGO of the Central and Eastern European Proteomic Conference (CEEPC). CEEPC logo depicting the peaks of intensity of modern day approaches intertwined with silhouette of the city spires - reaching the pinnacle of excellence and cohesion.

Today, CEEPC stands a well recognized community among the national and European proteomic societies, associations or their affiliations and appreciates support coming from such organizations as well as the academic institutions following the ethos and ideology of CEEPC (Czech Academy of Sciences, Hungarian Academy of Sciences, University of Technology in Vienna, Max-Planck Institute of Ecology, Romanian Academy, Macedonian Academy of Sciences and Arts, and Polish Academy of Sciences). As with all conferences, the funding remains a constant challenge and in the past organizations such as European Science Foundation or Deutsche Forschungsgemeinschaft have facilitated young scientists to attend as well as funded scientific leaders in the field to travel and present their research at these conferences. Interestingly, many of these invited speakers and participating researchers and scientists from all over the world are often returning for this intoxicating mixture of proteomics and informal atmosphere of the CEEPC. The expanding CEEPC stands to grow as neighboring mainly Eastern European countries come on-board to propagate CEEPC concept further. CEEPC provides a careful balance between excellence and cohesion and this holds the key to its success.

Additionally, one CEEPC's uniqueness is its ability to publicize the humanitarian needs or plight of the populations affected by various threats including poverty, lack of clean drinking water, or infectivity caused by unpredictable Ebola and Zika viruses with devastating effect. CEEPC raises awareness of these societal, medical and socio-humanitarian issues directly via its website at http://www.ceepc.eu/humanity. This will remain CEEPC's uniqueness in pointing out such humanitarian issues and challenges where scientific and medical research can help eradicate such viruses or related diseases.

## 4. Decade of Central and Eastern European Proteomic Conference

The annual CEEPC can now be considered as the bedrock of proteomics in Central and Eastern Europe and since its creation, has seen acceleration in proteomics and vast improvements in related multidisciplinary applications. Additionally, the CEEPC has provided a new momentum and a fresh outlook not only to the researchers from participating countries but also to the young generation of researchers fascinated by proteomics (Fig. 2).

These series of CEEP conferences have become a well-recognized proteomic event in the calendar with established traditions providing a special focus to the European regions where proteomics has not yet fully developed but with promising potential of progress and advancement. CEEPC has always managed to attract key speakers relevant to their theme of 'Proteomes, Proteomics and Biological Systems'. Intense scrutiny of the scientific program provides a solid backbone to the meeting and addition of diverse speakers selected on merit from submitted abstracts makes this conference even more representative and refreshing.

A look-back at a decade of CEEPC published meeting reports [7–14], it is evident that many if not all important aspects of proteomics were

**Fig. 2.** Mesmerizing and totally absorbing presentations.

covered over the years. Of these, the most frequently presented and discussed were disease and clinical proteomics, biomarker discovery, technological / analytical advancements, bioinformatics as well as quantification in proteomics and quantitative mass spectrometry. The scientific topics corresponding to the multidisciplinary character of proteomics including plant, insect, bacterial and ecosystems' proteomics were also regular parts of these conference series and created deeper interactions between scientists and researchers who benefited from each other's expertise to advance their own specialty. Additionally, the beauty or challenges of proteomics such as post-translational modifications, protein species / isoforms and their diversity in a variety of cells and tissues, structural proteomics, metabolomics and metabolic networks have been the subjects of interest. Recent focus on translational and personalized medicine, as well as stem cells and neuro-proteomics, reflects the challenges of today as well as the trajectory of proteomic research for the outcomes to improve the quality of life.

All in all, CEEPC has managed to achieve its aims of disseminating information, to help the formation of stronger bonds between researchers and to promote collaboration among various laboratories not only in Central and Eastern Europe but also globally. From 197 countries of the world, participants from 35 countries attended 1st – 9th CEEPC organized from 2007 to 2015. The number of participants for each annual meeting varied from 62 to 134 of registered scientists and reached up to 150 participants in total including representatives of the supporting companies or organizations (Table 1). The contribution of the TOP 15 countries over the period of 2007 to 2014 expressed as percentage of registered participants from each country of the total number of all participants is shown in Fig. 3. It shows significant contributions from Czech Republic (31.04% corresponding to the 235 participants over the period 2007–2014) and countries including Austria (17.85%; 136 participants), Germany (17.03%; 129 participants) and Hungary (12.64%; 96 participants). Additionally, contribution of the countries which joined CEEPC recently is evidenced by Romania, Macedonia and Poland and also worldwide. CEEPC managed to attract junior and senior scientists and especially young students mainly from the European region, together with an international list of excellent speakers from many different countries [7–14]. This combination with limitation on numbers created a low to medium size conference which was much more enjoyable, informative and allowed the possibility of interaction at all levels. Spiced with the local hospitality and tinged with anticipation, it is now a conference penciled on many calendars year after year.

## 5. Outlook for the next decade of CEEPC and proteomics

### *5.1. Rapid advances of scientific technologies and their interconnectivity*

The field of proteomics has grown rapidly due to incredible advances in technologies that provide data necessary for the better understanding of biological processes. Mass spectrometry has been in use for several years but recently, its use has expanded rapidly to cover most of the research fields. Development of ionization techniques and mass analyzers together with bioinformatics to evaluate collected data has enabled the use of these tools to a greater and more sensitive extent to analyze peptides and proteins which may have crucial relevance to biological processes and importantly to diseases affecting mankind [15–16]. Importantly, many associated research areas including development of a variety of distinct technologies as well as novel directions in system biology and various biomedical applications such as biomedical engineering to design concepts to medicine and biology for healthcare purposes, remain topics of interest of the CEEPC. Whilst many of the currently applied proteomic technologies are still traditional, newer and emerging technologies will certainly have a significant role to play. Leveraging LC-MS-based multi-analyte proteomics with unprecedented depth and accuracy to interrogate cell proteins or using next generation immunoassay multiplexing capable of several orders of magnitude greater sensitivity than conventional single systems, would facilitate understanding of the biological processes and their dysfunctions which may result in disease development. One such example is the ultrasensitive detection of neurodegenerative biomarkers including amyloid and tau proteins and their phospho-form in blood. The measurement of tau protein in cerebrospinal fluid has been well documented, but the presence and measurement of tau in human blood components has been elusive and difficult due to inadequate sensitivity of available assay methods [17–18].

Proteomics significantly expands a foundation laid by relatively static genomics by providing a dynamic picture on molecular processes occurring in an organism. Biochemical pathways and signaling networks offer examples of the interrelation of genomic, transcriptomic and proteomic studies mainly in the area of biomedicine [19]. Leveraging genomic technologies such as next generation sequencing will definitely facilitate faster and accurate analysis of biological systems and importantly predictions of outcome of diseases. Since sequencing is not simply restricted to coding regions, whole genome sequencing allows discovery of mutations in regulatory regions such as promoters and enhancers,

**Table 1**
Overview of the series of the CEEP conferences over the period 2007–2014.

| | Date | Venue | Number of registered participants[a] | Meeting report |
|---|---|---|---|---|
| 1st CEEPC | October 29–31, 2007 | Prague | 133 | Proteomics 2008, 8, 927–929 |
| 2nd CEEPC | October 12–15, 2008 | Jena | 63 | – |
| 3rd CEEPC | October 6–9, 2009 | Budapest | 134 | Expert Rev. Proteomics 2010, 7, 15–17 |
| 4th CEEPC | August 29–September 3, 2010 | Vienna | 95 | Eupa bulletin, February 2011, 4, 9–12 |
| 5th CEEPC | September 19–22, 2011 | Prague | 91 | Expert Rev. Proteomics 2012, 9, 9–11 |
| 6th CEEPC | October 14–17, 2012 | Budapest | 105 | Expert Rev. Proteomics 2013, 10, 13–15 |
| 7th CEEPC | October 13–16, 2013 | Jena | 62 | Expert Rev. Proteomics 2014, 11, 255–257 |
| 8th CEEPC | June 30–July 4, 2014 | Vienna | 76 | Expert Rev. Proteomics 2015, 12, 9–11 |

Total number of registered participants excluding representatives of supporting companies and organizations over the period 2007–2014 was 759.
Average number of registered participants per conference over the period 2007–2014 was 95.
More detail information and pdf files of the meeting reports are available on website at http://ceepc.eu/.
[a] Number of registered participants excluding representatives of supporting companies and organizations.

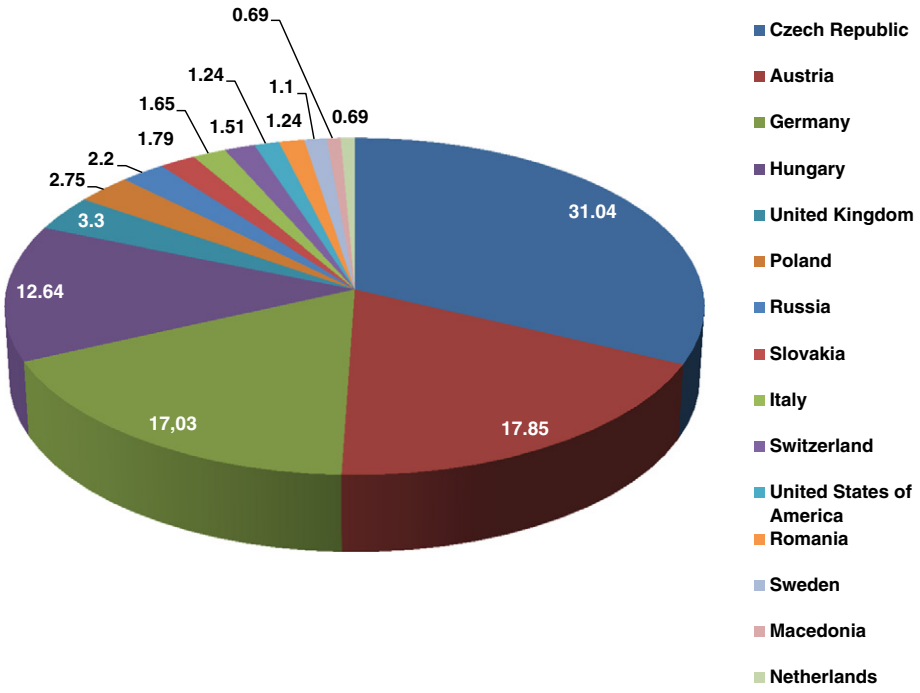


**Fig. 3.** Top 15 countries contributing to the Central and Eastern European Proteomic Conference and their global interactions from 2007 to 2014 expressed as percentage of registered participants from each country of the total number of registered scientists and researchers over this period.

and other non-coding regions including microRNA. Moving forward, next generation sequencing with powerful capabilities such as characterization of methylation, histone packaging and regulatory protein binding positions, should play a major role in evaluation of diverse disease models. Advances in flow cytometry together with high speed cell-sorting and live cell imaging are also fast becoming ideal tools for interrogating micro particles and cellular subsets in multiple formats.

The journey to gene edit embryos has already started in China, and whilst only a few years ago editing one gene was a major challenge, today researchers can quickly manipulate many tens of genes at a time. Gene-editing technologies, CRISPR, TALENs and zinc-finger nucleases, all have potential to correct gene defects [20–22] and the big question is when should they be deployed? The science is not quite yet ready, but undoubtedly will be in the next five to ten years judging by the accelerating rate of progress in gene editing. There is a growing debate on gene editing in human eggs, sperm and embryos, which have the power to change the DNA of unborn, however, it also has the power to prevent diseases by removing the faulty genes from the population gene pool, but could have the potential to do a life-time of harm if things were to go badly wrong.

Whilst genomics, proteomics and cellular science have come of age with exciting results to follow, cross collaboration of researchers from these specialties needs active fostering if we are to fully benefit from each other's expertise. Additionally, with ever increasing data, bioinformatics will be critical to understanding the real outcome for diverse biological systems. All technologies which generate data, now present a major challenge in the provision of computational infrastructure as well as the ability to interpret the wealth of data in order to build an accurate picture of scenario for possible intervention. Proteomics, like other "omics", depends heavily on advanced technologies. Instrumentation is very expensive and needs substantial resources from individual countries and international programs. This is one of the prime reasons why the proteomics in former Eastern European countries even currently lags behind the US and Western Europe despite recent large investments from mainly EU programs. Such programs have helped build new facilities equipped with modern sophisticated technologies but also with high expectations of outcome including publications, patents, and sustainability at a high level moving forward. It is evident that reaching many of these milestones and time points demand scientific and expert collaborations. To this end, CEEPC has provided connectivity to many of such countries for joint approaches and cross collaboration in order to justify such funding as well as achieve the required outcome.

### *5.2. The quest for disease biomarkers using proteomics*

There is an immense interest in identifying disease biomarkers and such an approach is highly suited because of the need for reduced sample requirements and high throughput possibilities. Some of such interests include comparative analysis of protein expression in normal and disease cells and/or tissues to identify aberrantly expressed proteins that may represent new targets, analysis of secreted proteins in cell lines and primary cultures, as well as direct biological fluid protein profiling. Until now, too many studies took the easy and more manageable route of looking at one or a limited number of factor(s) at a time and often leading to incomplete or a poor understanding of the disease. Now with combination of sophisticated technologies with sensitivity, specificity and speed, multiple parameters can be studied to gain a much better understanding of the on-going processes such as cell-cell, cell-matrix and cell signaling interactions. There are now limitless possibilities to fully understand biomarker intricacies and functionalities in a disease scenario. Biological fluids such as serum, plasma and cerebrospinal fluid are ideal samples that contain an archive of information due to the presence of a variety of proteins released by the diseased tissue. Preference for 'non-invasive' sampling and sophisticated technologies needing only a few microliters of the patient's sample is greatly facilitating research on exotic biological fluids such as tears, mucus, saliva, vaginal and specific stem cell lysates from sorted cell populations. The possibility to quantitate low abundant target analytes and the availability of monoclonal, polyclonal and super-clonal antibodies allow an amenable approach to investigating many diseases. Whilst antibody unreliability has taken its toll across very many studies, a drive to validate antibodies as well as parallel and novel antibody-less approaches will stand complex proteomic research in good stead [23–24].

### 5.3. Challenges and urgencies to deal with healthcare issues of today

It is evident from a decade of CEEP conferences that proteomics has promising and exciting potential across a variety of research areas with common aim for the benefit of mankind. Fresher challenges and greater urgencies to deal with healthcare issues, may it be ageing or chronic diseases, is driving research and proteomics towards regenerative medicine and personalized approaches of medicine. To this end, proteomics may enable diverse fields such as stem cell research [25–26], metabolomics [13], drug discovery and disease research [7–14] to reach the end goal of new therapies. In the era where medicine is increasingly underpinned by understanding of disease and an evolving evidence base for best practice, the concept of personalized medicine together with patient-centricity, where treatment selection for each patient becomes individualized, has gained momentum. If there are topics that need long-term foresight and planning in research in particular, ageing is certainly one of them. Europe currently is the fastest ageing continent and researchers with vision and creative thinking can become the leading force in the world contributing to the interpretation of, and solutions to, the problems stemming from ageing population. The ability to individualize a patient's care has become a pressing issue in the field of dementia and neurodegenerative diseases as there is a growing recognition that both the global incidence of dementia and other serious neurological diseases are still rife [25]. Recent President Obama's $100 M BRAIN (*Brain Research through Advancing Innovative Neurotechnologies*) initiative highlights this and is therefore a step in the right direction.

One may recall the days of debates on '*Scientific Uncertainties and Ethical Dilemmas*' of stem cell research. Since then there have been many significant advances in the field of stem cell research, although progress has perhaps been slower than was originally predicted [27]. During this time, we have witnessed the emergence of regenerative medicine, which promises to be one of the most fascinating and controversial scientific developments of the 21st century. The possibility of repairing or replacing tissue or organ function lost due to age, disease, damage or congenital defects, using human stem cells, raises deep ethical issues often evoking strong emotions and this field must be undertaken with a simultaneous consideration of the ethical issues involved. Human induced pluripotent stem cells (iPSC) have had an unprecedented impact on similar parameters in disease research. In addition to circumventing ethical and moral disputes associated with the use of blastocyst-derived embryonic stem cells, iPSCs provide new perspectives for personalized medicine in the future.

## 6. Conclusion

Tremendous progress has been made in understanding the functions of proteins using newly developed, sophisticated proteomic-wide approaches. Whilst opportunities and approaches have been discussed in detail, other challenges remain. One such challenge is for proteomics community to work hand in hand for better and deeper understanding of the proteomic data outcome. It is evident from all the CEEP conferences to date that the spirit and the quality of the CEEP Conferences is a privilege to be repeated and offering hospitality to be savored with newer challenges and greater excitement of proteomics. Looking forward to the next decade, CEEPC stands to champion these challenges in order to make the world better and safer.

## Conflict of interest statement

There are no conflicts of interest to report. No writing assistance was utilized in the production of this manuscript.

## Authors' contributions

S.J.G. was responsible for the conception and design of this manuscript. Both authors contributed to the drafting of the article, and reviewed and revised the finally submitted manuscript. Both authors contributed to the final approval of the manuscript for publication.

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