Proteomics is rapidly developing into a routine approach for protein analysis in many laboratories. The series of European-wide Summer Schools ‘Proteomics Basics’ (http://www.proteomic-basics.eu/) aims at teaching of comprehensive knowledge in proteomics research and applied technologies for master and graduate students and postdocs currently moving into the field of proteomic research. In the next 3 years the series will cover the theoretical basis of the fundamental topics in the various areas of proteomic analysis, i.e. sample preparation and handling, mass spectrometry, post-translational modifications and quantitation given by leading experts in the field. This summer school series embodies a unique advantage in comparison with conventional scientific meetings and university curricula: internationally renowned experts will give a detailed perspective view of the fundamentals of their particular proteome research area, something which is usually not encountered at conferences and congresses. Here, we give a report on the first European Summer School ‘Sample Preparation and Handling’ within the series ‘Proteomic Basics’ that was held at the monastery in Neustift close to Bressanone/Brixen, Italy from August 12 to 18, 2007.

Keywords:
Education / EuPA / Sample handling / Summer school

In recent years, proteomics and associated technologies for protein identification have become indispensable tools in molecular and cellular biology, and in the relatively new field of systems biology. These techniques make it possible to analyse the system wide regulation of cellular processes at the protein level and, in that context, to study disorders associated with various diseases at the protein level. Fundamentally new developments in new mass-spectrometric technologies (MS) for protein detection and analysis coupled with the continuing improvement in existing methods (e.g. liquid chromatography (LC) and gel electrophoresis), today allow the rapid and efficient determination of the composition of highly complex protein mixtures. Only a few years ago, this would have been considered unachievable. Although protein identification is performed worldwide on an almost routine level in the laboratories, reproducible sample preparation, localisation of post-translational protein modifications, reliability and workflow of these

Correspondence: Dr. Henning Urlaub, Bioanalytical Mass Spectrometry, Max-Planck-Institute for Biophysical Chemistry, Am Fassberg 11, 37077 Göttingen, Germany
E-mail: henning.urlaub@mpi-bpc.mpg.de
Fax: +49-551-2011197

Abbreviation: EuPA, European Proteome Association

* Additional corresponding author: Dr. Katrin Marcus, E-mail: katrin.marcus@rub.de

Received: October 5, 2007
Accepted: November 1, 2007
ble gel-based and MS quantification procedures of proteins, detection of protein–protein and protein–ligand interactions and, importantly, the identification of proteins that escape detection under standard conditions (e.g. protein isoforms and membrane proteins) are still far from being routine issues. Therefore, it requires a profound understanding of underlying principles to develop new methods and to improve on existing ones. Young scientists who enter the field of proteomics should therefore be well trained in both theoretical and practical basics of their research.

These were the considerations that lay behind the organisation of a Summer School in ‘Proteomic Basics’ (http://www.proteomic-basics.eu/ and links therein) which was started in 2004, continued in 2005 and 2006, and now took place in 2007 addressing a different audience. While in the past 3 years the summer school was dedicated for students from Germany, as an initiative within the program framework ‘Modern Methods of Protein Analysis’, supported by the German Federal Ministry for Education and Research (BMBF) this year’s Summer School saw an important new departure. For the first time, the Summer School has been open for students from all European countries (Fig. 1). The organisers, Katrin Marcus from Medizinisches Proteom-Center, Ruhr-Universität Bochum and Henning Urlaub from the Max Planck Institute for Biophysical Chemistry, Göttingen (and the co-organisers Eva Kuehn-Hoelsken, Carla Schmidt and Thomas Schu- lenborg) have initiated a European Summer School in Proteomic Basics (http://www.proteomic-basics.eu/2007/ index.html) for interested Master’s and doctoral students as well as junior postdoctoral workers with the deliberate aim of stimulating knowledge, experience and know-how transfer between students and young scientists that transcends national boundaries.

The organisers received whole-hearted support from the European Proteome Association (EuPA), which – as the roof organisation of the individual, national proteome societies – coordinated the announcement of the Summer School throughout the European states. In addition, almost all the national proteome societies provided funding for stipends to support the successful applicants to participate in the Summer School.

The particular idea of ‘going European’ convinced the German Volkswagen Foundation of the long term benefit of the project. The generous support received has made it possible to provide a found financial basis for a Summer School series for the following 3 years. Each consecutive Summer School will build on previous school(s) without disturbing the ‘Basics’ character of the courses. This years’ focus was on ‘Sample Preparation and Separation’; in the years to come it will be on ‘Mass Spectrometric Methods’ and ‘Post-Translational Modification and Protein Quantification’, respectively.

The number of applications for this years’ event was impressive. Even though it was possible to increase on short notice the number of places to 50, more than one-third of the applicants unfortunately had to be rejected because of space constrains. In selecting the participants, the organisers endeavoured to take into account the applicant’s scientific background, but, in addition, the country of origin was considered, so as to include participants from as many different European countries as possible. In the first event, participants came from Norway, Sweden, Finland, Denmark, the Netherlands, France, Spain, Portugal, Greece, Austria, Croatia, Slovenia, Hungary, the Czech Republic, Israel and Germany (Fig. 2).

The international character of the meeting was enhanced by the participation of 15 outstanding speakers from England, Denmark, Belgium, France, Spain, Austria, Italy, Germany, Canada and the USA, who held lectures and seminars on the fundamentals of sample preparation and sample separation in proteome research.

Matthias Mann (MPI of Biochemistry, Martinsried, Germany) opened the Summer School with a survey of his current research topics revolving around mass spectrometric-based protein quantitation using stable isotope labels in cell culture (SILAC) (for review see ref. [1]). This gave participants a memorable insight into the methodological complexity of modern proteome research and provided the ‘appetiser’ for the scientific content of the Summer School.

The first 2 days were dedicated entirely to fundamental aspects of sample preparation and separation: Helmut E. Meyer (Medizinisches Proteom-Center, Ruhr-Universität Bochum, Germany) presented a critical comparison of the planning and in particular the reproducibility of proteome studies per se [2], and Thomas P. Conrads (Cancer Institute, University of Pittsburgh, USA) gave the participants an introduction to clinical proteomics with in depth descriptions on the handling of samples from the pathology departments (e.g. [3]).

Pier Giorgio Righetti (Politecnico di Milano, Milan, Italy) and Christian Huber (Saarland University, Saarbrücken, Germany) taught the basic aspects of the separation techniques used routinely in proteome analyses – 2-DE [4, 5] and LC [6]. Kris Gevaert (University of Gent, Belgium) went more
into the details and gave an impressive demonstration of the analytical potential of LC by using COFRADIC, applied for example to the analysis of noncanonical N termini of hydrolysed proteins [7].

To preserve the original character of the Summer School – the provision of a general and comprehensive perspective of all the principles in proteomics – a number of general topics were covered in the second part of the summer school. These included (i) MS the key technology in proteomics (Bernhard Küster, Technical University of Munich, Germany) [8]; (ii) MS data evaluation and the stochastic considerations of putative hits derived from MS search engines (John Cottrell, Matrix Science, London, England) [9]; (iii) the identification of PTMs with special consideration of phosphorylated proteins (Karl Mechtler, IMP, Vienna, Austria) [10]; the fundamentals of mass spectrometric quantification of proteins (Ole Jensen, University of Southern Denmark, Odense, Denmark) [11].

In the final part of the Summer School, the topics of sample preparation and separation were taken up again, both by Thierry Rabilloud (CEA, Grenoble, France) in a lecture on the intensive work-up and the – technically challenging – separation of membrane proteins [12], and by Daniel Figeys (Ottawa Institute of Systems Biology, University of Ottawa, Canada) [13], who gave the participants a survey of the various technologies available for processing protein complexes and investigating protein–protein interactions.

To end the Summer School, lectures with a more general scope were held by Roland Kellner (Merck Serono, Darmstadt, Germany), who outlined the steps in the development of a substance into a commercial product at Merck [14], and by Concha Gil (Universidad Complutense, Madrid, Spain), who gave a detailed presentation of EuPA’s training activities for students within the European network [15]. Last but not least, Friedrich Lottspeich (MPI of Biochemistry, Martinsried, Germany) addressed the question of directions that proteome research may be expected to take in the future.

In addition to the above intensive scientific lecture programme, representatives of the firms Agilent Technologies, Applied Biosystems, BD Biosciences, Bruker Daltonics, Dionex, Ludesi, Qiagen, Serva and Waters gave in depth lectures on a wide variety of technical applications, and presented the latest developments in their respective fields.

Apart from the scientific programme, the participants profited from the intensive discussions that took place during two long poster evenings, and from the ‘interactive seminars’ on the various scientific topics that were chaired by the speakers. As in earlier years, poster prizes were awarded. This year they went to Stephanie Kaspar of the Leibniz Institute of Plant genetics and Crop Plant Research (Gatersleben, Germany) for her poster on ‘Proteome analysis of the effect of UV irradiation on barley leaf tissue using a 2-D approach and LC-based separation techniques’, and to Jurjen van Bolhuis of the Erasmus University (Rotterdam, The Netherlands) for his poster on ‘Characterisation of signal transduction complexes associated with c-Kit, the receptor for stem cell factor’.

It remains to be recorded that the diverse social activities – hiking, rafting, sight-seeing in town, a wine-tasting – added to the very open and communicative atmosphere. However, these were not the only reasons for the participant’s enthusiastic response to this Summer School. Above all, it was the intensive scientific exchange of views and experiences that sent them home highly motivated to turn the ideas they heard of during the week, in discussions with speakers and colleagues, as fast as possible into reality.

The next Summer School – the second European one – will be held from July 13 to 19, 2008, again in the Kloster Neustift. Its focal theme will be the mass spectrometric identification of proteins.

The organisers look forward to meeting next year’s participants!

The EU Summer School ‘Proteomic Basics’ is largely supported by a grant of the German VW Foundation to K. M. and H. U.

The authors have declared no conflict of interest.
References