Proteomic basics — quantification and post-translational modifications of proteins: The 3rd European Summer School in Kloster Neustift

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doi:10.1016/j.jprot.2009.11.007

The field of proteomics has gained importance in recent years. Proteomic and associated technologies have become indispensable tools in molecular, cellular and systems biology. These techniques allow the analysis of highly complex protein mixtures and can thus lead to an understanding of cellular processes and to the identification of disorders associated with various diseases. Although protein identification is performed on a routine basis in many laboratories, reproducible sample preparation, reliable quantification, detection of post-translational modifications, and detection of protein–protein and protein–ligand interactions are far from being routine issues. A profound understanding of principles and methods is required to successfully apply, optimise and develop methods for proteome studies. Therefore young scientists and newcomers in the field of proteomics should be well trained in the theoretical and practical basics of their research.

For these reasons, in 2004 a series of summer schools in "Proteomic Basics" (www.proteomic-basics.eu) were launched. At first (2004–2006) the summer school was held only for German students as an initiative within the programme framework "Modern Methods of Protein Analysis" supported by the German Federal Ministry for Education and Research (BMBF). In 2007, the summer school opened up for graduate students and post-docs from all European countries [1,2]. The German Volkswagen Foundation has provided a sound financial basis for a European summer school series for the past three years. Additionally, the European Summer School has received whole-hearted support from the European Proteome Association (EuPA), and almost all national proteome societies provided funding for stipends to the successful applicants to participate in the summer schools. Each summer school was designed to build on the previous ones, while at the same time retaining the "basics" character of the summer schools.
course. The focus of the three European summer schools was on “Sample Preparation and Separation” (2007), “Protein Identification — Mass Spectrometry” (2008), and “Quantification and Post-translational Modifications of Proteins” (2009).

The organisers — Katrin Marcus, from the Medizinisches Proteom-Center Bochum, of the Ruhr-Universität Bochum; Henning Urlaub, from the Max Planck Institute for Biophysical Chemistry, Göttingen; and the co-organiser Carla Schmidt from the same institute invited 65 master’s and graduate students, post-docs and technical assistants to this year’s summer school, which focussed on “Quantification and Post-translational Modifications of Proteins”. Since the number of applicants (about 110) greatly exceeded the number of places available, the number of participants was increased to 65 at short notice. In the end, 64 participants from all over Europe came to Kloster Neustift, Brixen/Bressanone, South Tyrol, Italy to attend the week-long course (Fig. 1). The course’s international character was enhanced by the participation of 12 outstanding speakers and company representatives from Austria, Denmark, England, France, Germany, Italy, the Netherlands, and Norway (Fig. 2).

Ole N. Jensen (University of Southern Denmark, Odense, Denmark) opened the Summer School with a plenary lecture about “Adventures in Proteomics”. He presented a survey of ongoing research projects in which advanced mass spectrometry was used to identify, quantify, and characterise proteins from several different organisms. The focus of his lecture was on the mapping and quantification of post-translational modifications of proteins [3] and thus provided an ideal start-up for the sessions that were to follow.

The first two lectures covered quantification by 2-D electrophoresis and the reduction of the most abundant proteins in a sample. Thierry Rabilloud (CEA, Grenoble, France) described and critically analysed the most widely used detection methods [4–6], and Pier Giorgio Righetti introduced the “ProteoMiner Technology” [7], an approach allowing the capture of all species present in a proteome, but at much reduced protein concentration differences.

In the following lectures the analysis of various post-translational modifications (PTMs) was discussed. Karl Mechtler (Research Institute of Molecular Pathology, Wien, Austria)
presented several enrichment methods and mass-spectrometry techniques for the analysis of phosphopeptides [8–10], Carolin Huhn and Renee Ruhaak (Leiden University Medical Center, Leiden, The Netherlands) gave a survey of the many analytical techniques applied to the analysis of glycosylated proteins [11,12], and Angela Bacchi (San Raffaele del Monte Tabor Foundation, Milan, Italy) focused on PTMs in redox proteomics, in particular state-of-the-art techniques for the analysis of nitric-oxide-induced S-nitrosylation [13,14]. Oliver Pötz (NMI, University of Tübingen, Reutlingen, Germany) completed this part of the programme with a lecture about targeted phosphorylation analysis by immunoaffinity-based proteomics [15].

The second part of the programme covered various labelling and quantification techniques, mainly for the MS-based quantification of proteins. In this part, Bernd Thiede (University of Oslo, Norway) started with an overview of different principles of labelling and quantification techniques by MS [16–23]. Out of these, metabolic labelling [16,24] was explained in more detail by Jeroen Krijgsveld (EMBL Heidelberg, Germany). Bernhard Küster discussed the pros and cons of the more widely used chemical labelling strategies (for review see ref. [25]), and Bettina Warscheid (Medizinisches Proteom-Center Bochum, Ruhr-Universität Bochum, Germany) introduced alternative methods for MS-based quantification (e.g. refs. [26–29]).

Matthias Selbach (MDC, Berlin, Germany) presented the MaxQuant software for data analysis of SILAC-based proteome studies [30,31]. His lecture about “MaxQuant and statistical analysis of large scale datasets” included a preview of the next Summer School, which will focus on statistics and data analysis.

In addition to the above-mentioned scientific lectures, company representatives from Applied Biosystems, Bruker Daltonics, Thermo Fisher Scientific, and Waters gave in-depth lectures on technical applications and latest developments. With lectures about “relative and absolute quantification of proteins by multiple reaction monitoring” (Christof Lenz, Applied Biosystems, Germany), “electron transfer dissociation (ETD) versus CID for the analysis of post-translational modifications” (Marcus Macht, Bruker Daltonics, Germany), “the LTQ Orbitrap — instrument basics, new developments and selected proteomics applications” (Kai Scheffler, Thermo Fisher Scientific, Germany), and “a high definition quantitative LC/MS strategy for unbiased discovery and targeted proteomics” (Mark A. McDowell, Waters, United Kingdom) the scientific programme of the Summer School was perfectly complemented.

The more interactive parts of the summer school were the two workshops. Every participant could choose two workshops of his or her interest. In total, five different workshops were available: (i) gel-based quantification and detection of PTMs, (ii) MS-based detection of PTMs, (iii) MS-based quantification, (iv) MaxQuant workshop, and (v) spectra interpretation and annotation. The workshops were supervised by the speakers and were designed differently — exercises, presentations and “question time” are only some examples. All the workshops offered enjoyed great popularity reflecting the strong motivation of the participants.

The scientific programme also included two poster sessions, which provided the participants with the possibility of discussing their own research projects with experts and other young scientists. The high quality of the presented posters and the persistence in discussing scientific questions were remarkable. For that reason, the number of poster prizes was increased at short notice from two to four. This year, the poster prizes were awarded to Violet Gautier (IPBS-CNRS, Toulouse, France), Riewert Hoppes (Netherlands Cancer Institute, Amsterdam, Netherlands), Mari Terweij (Netherlands Cancer Institute, Amsterdam, Netherlands), and Sonja Volk (NMI, Reutlingen, Germany). All poster prize-winners received a one-year subscription to the journal Nature.

It remains to be observed that, in addition to the scientific programme, diverse social activities were scheduled. A hiking tour, wine-tasting, the traditional soccer game, and rafting, mountain biking, climbing and sight-seeing in town added to the very open and communicative atmosphere (Fig. 3). All in all, the summer school was a very intensive scientific exchange of views and experiences. All participants returned home highly motivated to turn the ideas they had heard of during the week into reality.

Although the financial support of the German VW Foundation ended with the third European Summer School, the organisers are highly encouraged to organise a fourth European Summer School. It will focus on data analysis and statistics and will be held from August 1 to 7, 2010, again in Kloster Neustift. The organisers look forward to meeting next year’s participants!

Acknowledgment

The EU Summer School “Proteomic Basics” is largely supported by a grant from the German VW Foundation to K.M. and H.U.

REFERENCES


