Meeting Report on the 7th World Congress of the Human Proteome Organization (HUPO) in Amsterdam

PROTEOME BIOLOGY

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The 7th World Congress of the Human Proteome Organization HUPO was held in Amsterdam, the Netherlands, from August 16 to 20, 2008. The event offered a very dense 5-day agenda consisting of an exciting scientific program documenting the tremendous progress, the current challenges, and the major recent accomplishments of proteomics, an exhibition in which all the major vendors in the field of proteomics from around the globe showcased their products, technologies, and services, educational and training events in which new proteomic technologies were introduced and taught, and a series of workshops and discussion forums of all HUPO sanctioned initiatives, including a potential Human Proteome project. Around 1200 scientific abstracts were received, 80 companies signed up for and supported the exhibition, and the total number of registrations was just above 1700, with close to 700 also present for the weekend’s Pre-Program. More than 60 nationalities were represented at the meeting. Molecular & Cellular Proteomics 7:2288–2291, 2008.

The chairs had chosen “Proteome Biology” as the central theme of the meeting. In their view this theme indicates that despite the amazing complexity of the proteome, the field of proteomics has matured to a degree where significant progress in biology and medicine can be realized. This expectation is based on rapid progress in the development of powerful proteomics technologies that increasingly contribute to the editing of comprehensive maps of the proteomes of various cells and move forward the boundaries of the “terra incognita”. The title of the meeting also indicates the need for proteomics to progress beyond identifying the building blocks of the proteome toward understanding of how the complex biological functions of a cell are orchestrated via intricate networks of proteins interacting with themselves and other types of biomolecules. The “Proteome Biology” theme resonated well with the proteomics community as it attracted most of the top scientists in the field to Amsterdam. There they cumulatively presented, in the poster and oral contributions, a showcase for how indeed the field of proteomics has matured and is rapidly invading into mainstream biology and medicine. Around 1200 scientific abstracts were received, 80 companies signed up for and supported the exhibition, and the total number of registrations was just above 1700, with close to 700 also present for the weekend’s Pre-Program. More than 60 nationalities were represented at the meeting. An overview of the whole program of the meeting and all submitted abstracts are available via the web site of the publisher of Proteomics, which can be reached via the homepage of HUPO and the conference web site.

The scientific main part of the program ran from Monday till Wednesday and was preceded by a weekend program, for which already close to 700 attendees showed registered. The weekend workshops consisted of reports, discussions, and planning sessions for the several initiatives that fall under the HUPO umbrella, notably the HUPO Human Antibody Initiative, the HUPO Proteome Biology of Stem Cells Initiative, the HUPO Liver Proteome Project, the HUPO Brain Proteome Project, the HUPO Human Kidney and Urine Proteome Project, the HUPO Glycomics Initiative, the HUPO Cardiovascular Proteomics Initiative, and the HUPO Proteomics Standards Initiative. Besides these established initiatives new workshops were held on “Model Organisms” and “Proteomics Validation”. Collectively, these forums determine to a significant extent the direction of proteomics research for the immediate future. Of special interest were the well-attended sessions focused on a possible Human Proteome Project. On the Saturday morning a first workshop was held, for a packed room audience, chaired by John Bergeron and Mathias Uhlen, whereby proteomics leaders addressed several considerations around a Human Proteome Project. Lively discussions centered around the question whether such a project is feasible, timely, and “fundable”, what its primary focus should be, and what the role of HUPO would be in such a large undertaking. Views were still somewhat scattered ranging

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from gene-centric or chromosome-centric approaches to technology centered focusing on the analyses of complete proteomes, taking protein variants and post-translational modifications into account. The role of resource of human antibodies was seen as vital, but not as an end point. Experts presented the enormous progress made in technology in the last few years, which enable the community to set aims and expectations very high. In general the consensus was that the time is right for a Human Proteome Project. HUPO should not take the lead in directing but rather in coordinating the research. This session was followed by a session on the Saturday evening in which representatives from several national (Wellcome Trust, Netherlands Genomics Initiative, Genome Canada) as well as European (EU), American (DOE, NIH), and Asian funding bodies presented their activities, plans, and perspectives in the field of genomics and proteomics. The audience was left with the view that proteomics is high on the priority list of these funding agencies, and that a possible cooperative effort such as a Human Proteome Project could be established, provided it was given good leadership.

On the Saturday of the pre-program Ole Jensen and Thierry Rabilloud organized the “Educational Day”, a series of master-classes on different aspects of proteomics technologies, with many excellent contributions on topics like 2D gel analysis, mass spectrometry, protein quantification, analysis of post-translational modifications, data base searches, and bioinformatics.

On the Sunday of the pre-program Dennis Hochstrasser and Helmut Meyer organized the well-attended “Clinical Day” around the theme “Biomarkers from Discovery to Clinical Application”, whereby the presenters gave views from both industry as well as academia. This session has become a strong tradition in the HUPO meeting, attracting interest from both clinicians, industry as well as proteomics experts discussing diagnostics as well as proteomics standards.

The main scientific program started on Monday, ostensibly chaotically with an opening session for which the chairs apparently did not show up. When the president of HUPO, Rolf Apweiler, started to act as a substitute session chair and presented an opening address, he was interrupted by a real-life exhibition of Rembrandts Nightwatch (Fig. 1), in which the meeting chairs acted as well. The chairs took subsequently the stage whereby Albert Heck opened the meeting (Fig. 2). The dense scientific program consisted of two times five parallel sessions per day, and two poster session. Topics of these sessions covered both technology as well as applications, with title ranging from “Innovation in Mass Spectrometry”, “Bionformatics”, “Peptide Separation”, “Biomarkers”, “Standards For Clinical Proteomics” to “Proteome Biology of Stem Cells” and “Proteome Biology of Infectious Diseases”. All session were of very high quality. An overview of the whole program of the meeting and all submitted abstracts are available via the web site of the publisher of Proteomics, which can be reached via the homepage of HUPO. An impression of the crowded exhibition and poster room is shown in Fig. 3.

In total 10 plenary lectures were given. In line with the theme of Proteome Biology, a few leading biomedical researchers from outside the mainstream core of proteomics had been invited, discussing their latest work related to hot topics such as stem cell biology, cancer and cellular signaling, all areas where the rapidly expanding role of proteomics is readily apparent.

The state-of-the art “hard-core” mass spectrometry-based proteomics was elegantly and comprehensively addressed in plenary lectures by Ruedi Aebersold (ETH, Zurich and ISB, Seattle) (Fig. 4), John Yates (Scripps, La Jolla), and Matthias Mann (MPI Martinsried). Using the ever increasing power of mass spectrometry hand-in-hand with dedicated sophisticated bioinformatic software tools they showed that for model organisms such as yeast and drosophila mass spectrometry-based proteomics is close to enabling the coverage of a whole proteome in a single experiment, detecting unique peptides for each gene/protein. In a direct comparison it was shown that the sensitivity of MS-based

\[\text{MS-based}^1\] proteomics could

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1 The abbreviation used is: MS, mass spectrometry.
rival at present any other technique, thus tackling the dynamic range problem allowing also the identification of proteins present at low copy numbers. Furthermore, these three MS-based proteomics musketeers pointed out very well that proteomics does not stop at the identification stage, displaying the expansion in abilities to probe protein interaction networks and protein modifications, linking proteomics also to epigenetics. Protein quantification, using stable isotope labeling was a major contribution to the conference. It was shown that stable isotope labeling has rapidly moved up the evolutionary ladder, with experiments reported on both a stable isotope-labeled rat as well as a stable isotope labeling with amino acids in cell culture (SILAC) mouse. Mathias Uhlen (Royal Institute of Technology, Sweden) presented the latest update of his Human Protein Atlas, generated with more than 6,000 validated antibodies corresponding to 5,000 human genes. The atlas now also contains more than 4 million high-resolution images generated by immunohistochemistry and confocal microscopy. Uhlen was confident that it should be possible to extend the protein atlas to a majority of all human proteins.

The complex nature of the proteome and the intricate networks of interactions as revealed also by large scale proteomics projects was further addressed by Anne Claude Gavin (EMBL), who compared the networks of proteins to social network, pinpointing at stronger and more transient interactions, not only between proteins, but also in between proteins and metabolites and other small molecules. Sung-Hou Kim (Berkeley) addressed the proteome in a three-dimensional context, focusing on protein structure and folding, in the context of available folding space. Furthermore, he notified the audience that the genome entails a lot of information, not encoding proteins, but large amounts of functional RNAs. Their function especially in relation to the proteome is still largely terra incognita. Tony Pawson (University of Toronto) provided dazzling examples of how quantitative proteomics can go hand-in-hand with signaling cell biology, linking temporal and spatial proteomics. Intracellular cell-cell signaling was investigated by his group using a combination of microscopy and quantitative SILAC-based proteomics, using co-cultures of cells. Hans Clevers (Hubrecht Laboratory, Utrecht) introduced the audience to the intestinal epithelium, which is the most rapidly self-renewing tissue in adult mammals. Using elegant molecular biology approaches his laboratory defined the stem cells of the small intestine and colon and showed how they can be used in the laboratory to build up these tissues. Moreover, Lgr5 was revealed to be unique biomarker for stem cells in a plethora or multiple adult tissues and cancers. Peter Andrews (University of Sheffield, UK) gave an overview of the current state of research on embryonic stem cells, embryonal carcinoma cells, and induced pluripotent cells. The common features in between embryonic stem cells and embryonal carcinoma cells is striking, and one of the hypothesis is that disruption of genes that regulate stem cell behavior may affect tumor progression, particularly in tumors, in which enhanced self renewal capacity is linked to a more aggressive tumor phenotype. Erin O’Shea (Harvard University) provided the audience with a beautiful biological puzzle, which her group solved, centered around the role of the little known compound myo-D-inositol heptakisphosphate (IP7), which is produced in response to phosphate limitation and is shown to regulate the activity of a protein kinase complex that coordinates downstream cellular responses.

The meeting ended with a plenary Awards session in which the European Proteomics Association (Eupa) awarded a Senior Scientist Award in Proteomic Sciences to Stellan Hjerten, for his broad and pioneering contributions to the bioanalytical separation sciences. Moreover, Eupa awarded European PhD Young Investigator Prize to Tine Tingham (University of Southern Denmark). She was selected out of five candidates, all of whom had given oral presentations at the HUPO 2008 conference, in a dedicated session that was described as one of the highlights of the meeting. HUPO itself awarded the HUPO Young Investigator Prizes, for junior scientists at the start of their career to Jesper Olsen (Max Planck Institute, Martinsried), Shabaz Mohammed (Utrecht University), and
Adriana Paes Leme (Instituto Butantan, Brasil). Following presentations by these three candidates, Shabaz Mohammed was selected to also receive the "Nieuw Amsterdams Peil" award of 5000 euro, a prize given by the local government to promote science. Senior HUPO awards were presented to Catherine Costello (the HUPO Discovery in Proteomic Sciences award), Richard Simpson (the HUPO Distinguished Service Award), and to Matthias Mann and Dennis Hochstrasser (the HUPO Distinguished Achievement Award). These latter awards were sponsored by the ACS Journal of Proteome Research. Hochstrasser accepted his award with a presentation in which he clearly showed his optimism for the future of proteomics, but warned the audience to not take too much a gene-centric view, telling the audience that the proteome is more beautiful and diverse than that. Mann’s award was accepted with a lecture in which he described from a personal perspective the enormous progress made in proteomics from the early days of electrospray ionization to the complex analyses of whole proteomes at present. Finally, the organizers of the 8th HUPO World Congress in Toronto presented their plans, and HUPO announced its next president, namely Young-Ki Paik, from South Korea and other changes in the governing board of HUPO. The meeting ended with a conference dinner, hosted in the City Council “City Hall-Opera”, to which the attendees were transported the "Amsterdam-way", i.e. the canal boat.