

REPORT

4th HUPO Brain Proteome Project Workshop in Munich, Germany

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More than 70 interested colleagues attended the 4th Workshop of HUPO's Brain Proteome Project. The project was presented within nine talks mainly focusing on two running pilot studies as well as on data re-processing. A bioinformatics jamboree in Hinxton, UK, and the 5th Workshop taking place in Dublin next February were announced.

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The 4th World Congress of the Human Proteome Organisation (HUPO) took place at the International Congress Center Munich from August 29 to September 01, 2005. Prior to this annual meeting, several HUPO initiatives came together in the Munich Dorint Sofitel Bayerpost Hotel on Saturday and Sunday, August 27 and 28. More than 70 active players and interested colleagues attended the 4th HUPO Brain Proteome Project (HUPO BPP) that focused on the pilot studies "mouse" and "human" and planned publications. In these studies, mouse brains of different age stages as well as human post-mortem brain tissue and tissue from an epileptic surgery, respectively, were compared by proteomic approaches.

Generated data has been collected in a central Data Collection Center (DCC, located at the Medizinisches Proteom-Center, Bochum) and will be analysed with special parameter sets. In nine talks the status and the next steps of the projects were introduced.

Helmut E. Meyer, the chair of the Brain initiative, gave a warm welcome and a short retrospective of the studies. Herbert Thiele (Bruker Daltonics, Bremen, Germany) referred to the concept of data management, data acquisition and data re-processing of the HUPO BPP. He focused on the advantages of the planned metascoring and the used software ProteinScape™ (Bruker Daltonics) as well as of distinct soft-

ware components such as *e.g.* ProteinExtractor and PTM-Explorer allowing to handle the reprocessing of approximately one million data sets.

The following three presentations exemplarily showed the diversity of used proteomic approaches: Johan Robben (Hasselt University, Belgium), Georg Arnold (Laboratory for Functional Genome Analysis, Munich, Germany) and Young Mok Park (Korean Basic Science Institute, Daejeon, South Korea) presented their analysis strategy ranging from 1D- and 2D-gel electrophoresis followed by MS or nanoLC-MS/MS and LC-gas phase fractionation-MS/MS to 2D-DIGE.

All MS-data sets were saved in a compatible data format via ProteinScape™ and were sent to the central DCC. In his talk "Data Reprocessing of the Pilot Studies" Christian Stephan (Medizinisches Proteom-Center, Bochum) pointed out how a standardized re-processing of data sets is carried out in detail. Due to the heterogeneity of the data (*e.g.* approximately half of the results originate from LC-MS/MS, approximately 30% from 1D-gels with subsequent MS and 20% from 2D-gels with subsequent MS) a so called decoy IPI data base has been implemented to allow an estimation of the false-positive rate (for more details see www.hbpp.org). Parameters for the used search engines Mascot (Matrix Science), Sequest (Thermo), Phenyx (GeneBio) and Protein-Solver (Bruker Daltonics) are adopted by using iterative search runs aiming at a false-positive rate below 5%. Protein lists will be generated from these identified peptides by using ProteinExtractor and analyzed in more detail by invited analysts during a jamboree that will take place at the EBI in Hinxton, UK, in early January 2006. Results of the studies will be published in a special issue of PROTEOMICS and will be available to the public.

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In addition to the analysis of mass spectrometric data, gel images of different groups were compared in order to generate a master gel. Andrew Dowsey (Imperial College, London, UK) is handling this task using the software ProteomeGRID. He reported that the comparison concerning conventional stained gels is ongoing while the 2D-DIGE gel images are rather difficult to compare. Lennart Martens from the University Ghent, Belgium, opposed the discussed approaches and similarities of the HUPO BPP and the HUPO Plasma Proteome Projects (HUPO PPP) in his talk “Lessons to be learned from the HUPO BPP and PPP Pilot Studies”. Both projects are large consortia, but differ in the way of data reprocessing. Martens stressed that both are doing pioneer work, elaborate standards and bring proteomics groups together. Moreover, the last years revealed that definition of a bioinformatics platform and supply of manpower are of highest importance.

Jens Wiltfang und Piotr Lewczuk (Universitaetsklinikum Erlangen, Germany) presented the subproject “Clinical

Neuroproteomics of Dementias: Identification of novel biomarkers for their early diagnosis and preventive therapy”, aiming at the study of very well characterized samples of human cerebrospinal fluids (CSF) from “mild cognitive impairment” (MCI) patients. Brain derived peptides will be identified in CSF which could serve as potential biomarkers for neurodegenerative diseases. A training course “Workshop of Early Neurochemical Diagnosis of Dementias” will be organized in Erlangen on December 16, 2005 for members of the National Genome Research Network (NGFN) as well as of the HUPO BPP.

The 4th HUPO BPP Workshop was closed with the announcement that the next meeting will take place in Dublin, Ireland, on February 15–16, 2006, kindly hosted by Mike Dunn and Stephen Pennington, both Conway Institute of Biomolecular and Biomedical Research. Here, the pilot studies will be finalized and new projects as well as strategies will be elaborated. More information is available at www.hbpp.org and www.hupo.org.