

1st HUPO HBPP Workshop at Castle Mickeln, September 5th/6th 2003

Deciphering the human genome was one of the main challenges of this century as well as one of the biggest hopes to overcome aging and diseases. Recently, it is more apparent that genetic information alone is not sufficient to understand cell processes. The protein complement, the proteome, remains unknown since one can not deduce which mRNA is translated into protein. Additionally, alternative splicing and posttranslational modifications increase the number of putative protein species. In consequence, diagnosis and therapies concerning, e.g. most neurodegenerative pathologies and aging processes – severe social and financial burdens of society - still do not exist. The most promising approach therefore is the analysis of the whole proteome of a cell or tissues hopefully leading to the evaluation of early onset biomarkers and new diagnostic tools as well as to medication.

The Human Brain Proteome Project (HBPP) is an international initiative under the patronage of the Human Proteome Organisation (HUPO) aiming at the analysis of the brain proteome in health, aging and neurodegeneration. In order to discuss essential details and to start practical work, 45 scientists from Germany, the US, France, Great Britain, Finland, Austria, China, the Czech Republic and Hungary met at Castle Mickeln, Duesseldorf, Germany for two days. At the outset, five committees were formed: Executive Committee, Specimen Collection and Handling Committee, Technology Platforms and Standardization Committee, Database and Bioinformatics and Training and Education Committee. Participants decided within these committees basic strategies, e.g. focusing on Aging, Alzheimer's disease, and Parkinson's disease, corresponding brain areas and in addition cerebrospinal fluid. Standardization guidelines concerning specimen handling, methods and data formats have been set up with regard to the international standardization programmes, e.g. of the Brain-Net Europe and the HUPO standardisation initiative. The integration of companies has been extensively discussed offering multiple possibilities of interaction and participation. Analysis of human brain proteomes will start immediately after this 1st HUPO HBPP Workshop with the acquisition and distribution of specimen tissues and the identification of brain proteins.

Participants agreed to initiate two pilot studies:

- 1) Quantitative proteome analysis of normal mice brain for the purpose of
 - a) Assessment of the quality of 2D- and non 2D-gel based quantitative proteome analysis
 - b) Feeding the brain proteome database with reliable data
 - c) Comparing proteome and transcriptome by performing mRNA profiling

Analysis will include different developmental stages. Whole dry-ice frozen brain of female C57/Bl6 mice of embryonic day 16 (E16), postnatal day 7 (P7) and of 8 weeks will be provided. Analyses should be done with 5 to 10 different samples of each stage using suitable techniques for quantitative proteome analysis.

- 2) Quantitative proteome analysis of human brain from biopsies and autopsies for the purpose of
 - a) Assessment of protein stability in post mortem tissue
 - b) Feeding the brain proteome database with reliable data

The study will begin in January 2004 and will end within a year yielding the first results in early summer 2004.

Participants agreed to present the HBPP at the 2nd HUPO World Congress in Montreal in early October and to get together for a 2nd HUPO HBPP Workshop in Paris in the beginning of 2004. Further information will be available at www.hbpp.org.

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