HUPO Brain Proteome Project
TOWARD A CODE OF CONDUCT

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The prevalence of neurodegenerative diseases in all societies increases steadily and so do the costs for comprehensive scientific proteomics studies. This is due to immense expenses for equipment and consumables as well as to a high number of repetitions to fulfill the statistical imperative. At the same time, techniques become even more complex, whereas suitable samples are scarce, especially when dealing with the valuable human brain. What is the consequence? What should be done to overcome this contradiction within the triangle validated protein analyses, time, and money?

The Human Brain Proteome Project (BPP)1 is one of the initial initiatives of the Human Proteome Organisation (HUPO). Operating since 2003, it gathers a critical mass of researchers from academia and industry aiming at advancing knowledge of neurodiseases and aging to elaborate new diagnostic approaches and medications. HUPO BPP wants to perform suitable quantitative proteomics on disease-related brain areas and bodily fluids to analyze the brain proteome of human as well as mouse models with healthy, neurodiseased, and aged statuses with a focus on Alzheimer and Parkinson disease. Recent work has shown that standards in proteomics and especially in bioinformatics are mandatory to allow comparable analyses. To address this challenge, the HUPO BPP is closely working together with the HUPO Proteome Standards Initiative (HUPO PSI). Two standardization pilot studies are already finished and documented in a special edition (Proteomics, Volume 6, Issue 18). Due to the combined effort of 18 laboratories worldwide a huge amount of data sets with current proteomics technologies were gained and analyzed. Only a very few of the identified differentially expressed proteins could be found by many or all of the participating groups, although each of the individual laboratories could show to have detected several dozens of reproducible differences. The yield of an individual protein is very dependent on the conditions for sample preparation, i.e. salt concentration, pH, detergents, temperature, etc., and every little change will result in a different sample composition and thus another result. Therefore it is important that experiments are repeated independently several times to show their reproducibility as it was already suggested by Wilkins et al. (1).

During the studies, participants agreed that the standards and standard operating procedures are essential for successful work. Annotations concerning sample handling, preparation, separation, and identification have to be considered and documented. Different approaches and search engines are complementary. The separation features of the different techniques do overlap and can be applied successively. Nevertheless every study has to show the reproducibility of its results. As the overlap of the identified proteins in regard to the different laboratories is not optimal, it is extremely important that their own data are handled very critically. The validation of the proteins identified is the next essential step. These and other considerations are also discussed in some of the latest publications of the HUPO BPP consortium (2–4).

To fix these maxims, the next workshops will be essential. The 9th HUPO BPP workshop will take place in Barbados from January 9 to 10, 2008. In this workshop, involved colleagues will discuss and lay down the HUPO BPP roadmap for the next years, stressing standard operating procedures, suitable models, and study designs. Funding and further integration into HUPO’s world also will be an important issue. The 10th HUPO BPP congress is scheduled for the HUPO World Congress in Amsterdam, August 2008. Interested colleagues are always welcome and may visit the HUPO Brain Proteome Project website for the latest news.

REFERENCES


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1 The abbreviations used are: BPP, Brain Proteome Project; HUPO, Human Proteome Organisation.