

2009 Report: Proteomics

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A MASC subcommittee for *Arabidopsis thaliana* proteomics was established to consolidate databases, technique standards and experimentally validated candidate genes and functions. Since that time many new approaches and databases were developed. Altogether the resources of the MASC Proteomics (MASCP) subcommittee provide the largest collection of proteomics data for this higher model plant. This common effort of MASCP is comparable with the HUPO organization (human proteome project) and has identical potential with respect to advanced proteomic techniques (such as Mass Western and collections of thousands of proteotypic peptides) and a large collection of proteomic databases (contacts with HUPO are established by members of MASCP).

Recent activities:

- MASCP published a joint report: “The Multinational Arabidopsis Steering Subcommittee for Proteomics Assembles the Largest Proteome Database Resource for Plant Systems Biology” (Journal of Proteome Research 2008, 7 (10), pp 4209–4210) that provides a series of resources for plant proteome researchers.
- Meetings and the organization of proteomics workshops are established on a regular basis at the International Conference on Arabidopsis Research. A well attended workshop was held in 2008 in Montreal, and another is planned for Edinburgh in 2009. The workshop included research presentations by MASCP members and others, including students and postdocs who submitted proteomics-related abstracts and were selected for oral presentation, followed by group discussion.
- A common webpage “MASC proteomics” was established including standards for different proteomic techniques, databases, procedures; meetings, proteome labs, etc. (see <http://www.masc-proteomics.org/>). This webpage will also host discussion platforms and database-crosslinks in the future.
- The last couple of years have seen significant advance in our understanding of the peroxisome proteome in Arabidopsis, thanks to a number of MASCP members (Plant Cell October 2007 19:3170-93; Plant Physiology, December 2008 148(4):1809-29; Plant Physiology, March 2009 10.1104/pp.109.137703)
- The major databases associated with MASCP, AtProteome (www.AtProteome.ethz.ch), Plant Proteome Database (PPDB) (<http://ppdb.tc.cornell.edu>), SUBA (www.plantenergy.uwa.edu.au/suba2), ProMEX (<http://promex.mpimp-golm.mpg.de/home.shtml>) and PhosPhAT (see <http://phosphat.mpimp-golm.mpg.de/>) have continued to be updated and expanded in 2008-2009.
- A special issue of the Journal of Proteomics was initiated and edited by Dr Jesús Jorrín-Novo, titled “Plant Proteomics”, Volume 72, Issue 3, Pages 283-574 (13 April 2009). This contained research articles and reviews by a wide range of plant proteome researchers including a number of MASCP members. This shows the increasing breadth of proteome research in both Arabidopsis and other plants. Examples of articles in the issue include: Abiotic environmental stress induced changes in the *Arabidopsis thaliana* chloroplast, mitochondria and peroxisome proteomes; Hydroponics on a chip: Analysis of the Fe-deficient Arabidopsis thylakoid membrane proteome; Phosphoproteomic analysis of nuclei-enriched fractions from *Arabidopsis thaliana*; Blue native DIGE as a tool for comparative analyses of protein complexes, and Validation of gel-free, label-free quantitative proteomics approaches: Applications for seed allergen profiling.
- The increased use of large protein interaction databases being developed by various agencies for plant protein data and their cross-linking to MASC proteomics resources is the main goal of the next years.