

MASC Proteomics- 2006 Subcommittee Report

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Proteomics using *Arabidopsis thaliana* as a model system has made great progress in recent years¹. The throughput and accuracy of protein identification techniques such as shotgun proteomics based on liquid chromatography coupled to mass spectrometry (LC/MS) or two-dimensional gel-electrophoresis (2DE) relies strongly on the availability of whole genome sequences. In light of the enormous complexity of a dynamic proteome, sample throughput presents a bottleneck for future research. The availability of both a complete genome sequence and high quality genome annotation makes *Arabidopsis thaliana* an ideal system to develop new technologies and identify candidate genes. Furthermore, *Arabidopsis thaliana* proteomics research will give direction to future plant proteomics developments and can serve as a unique database resource, especially when coordinated with the metabolomics and bioinformatics initiatives. It is an opportune moment to establish a working group devoted to *Arabidopsis* proteomics, and combine the efforts of different research groups to develop programs which will consolidate databases, technique standards and experimentally validated candidate genes and functions.

Subcommittee goals and priorities:

- Organization of a common webpage including standards for different proteomic techniques, databases, procedures, meetings, proteome labs, etc.
- Meet at Arabidopsis International Conference each year.
- Discuss international network grant proposals for plant proteomics.
- Develop standards for two-dimensional gel-electrophoresis, shotgun proteomics, and quantitative proteomics.
- Write guidelines for minimal requirements for different types of proteomic studies and distribute these to plant journals (especially: Plant Molecular Biology, Plant Physiology, Plant Cell, and the Plant Journal) for their consideration of publication standards – issues include experiments, data analysis and call of identifications. These activities will be coordinated with the MASC metabolomics subcommittee chaired by Ian Graham, the subcommittee for bioinformatics and the Proteomics Standard Initiative (PSI).
- Hold a workshop each year at the International *Arabidopsis* Conference on the methods/practice of proteomics to inform the community, make new contacts, and to develop initiatives for proposals.
- Develop a master list of the *Arabidopsis* gene loci that have been identified at the proteomic level by mass spectrometry.
- Work towards a central international database of MS/MS spectra derived from *Arabidopsis* samples.
- Collaborate with TAIR and other interested parties on *Arabidopsis* proteomic data storage.

(1) Glinski, M.; Weckwerth, W. *Mass Spectrom Rev* **2005**.