

Meeting abstract

Analysis of proteins involved in programmed cell death in *Hemerocallis* petals

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Discovery of characteristic proteins expressed by a given cell type and how these proteins change during development or pathology, has only been feasible very recently. Powerful separation techniques coupled with the sensitivity and selectivity of mass spectrometry, are used to identify these proteins. Computer-based, bioinformatics techniques are used to match unique peptides to the genome.

We recently received a Major Research Instrumentation award from the National Science Foundation (USA) to obtain new state-of-the-art protein analysis equipment. Specifically, we have acquired a research grade hybrid quadrupole ESI-MS/MS mass spectrometer interfaced with a capillary liquid chromatograph (cap-LC). This system (Micromass V-QTM) is a sensitive (femtomole), high resolution, time of flight mass spectrometer (Tof) with electrospray ionization (ESI) sample introduction interface for the capLC.

Tandem quadrupole mass spectrometric capabilities and high resolution permits the determination of amino acid sequence of peptides. Software associated with the spectrometer is used to unsort multiple charged versions of the same peptides and proteins, drive the LC separations, and handle other, expected complications in data analysis.

As part of this proposal, we received funds to develop an education and outreach module for educators. The proposed module involves proteomics-based experiments conducted for the study of cell death in plants. The daylily flower (*Hemerocallis* spp.) provides an ideal model system for the study of non-stress related programmed cell death in plants. The entire genetic program/cascade occurs over

a compact 24-h period and can be studied in a series of specific sequential steps. We are currently analyzing changes in the daylily petal proteome during the various stages of cell death beginning at 12 h prior to flower opening and ending at the final stages of cell death 12 h after opening. A shotgun proteomics approach is currently being utilized. Data derived from this study will not only provide valuable insight in programmed cell death in plants, but also be used to teach proteomics and the study of biological processes to educators involved in biological instruction.