

## **Label-free quantitative proteomics and abiotic stress-response in rice**

Paul A. Haynes

Department of Chemistry and Biomolecular Sciences, Macquarie University  
Australian Proteome Analysis Facility

Rice serves as the staple food source for a large percentage of the human population, and it is also an excellent model cereal crop. The rice genome sequence is complete yet nearly one-third of the genes encoded have no known function. Our aim is to examine changes in protein expression patterns in rice which occur in response to environmental stress, and then functionally characterise selected stress-response proteins using tagged gene expression and mass spectrometric techniques. The outcome will be potential candidates for use in selective breeding programs to enhance rice production and improve crop sustainability.

The first stage of this project is identification of rice proteins which show differential expression in response to abiotic stress, principally temperature and drought stress. We are using a variety of label-free quantitative proteomics approaches to identify these stress-response proteins in both cell culture and whole plant material. Our longer term project goal is that these proteins will then be expressed as TAP-tagged transformants in rice callus tissue, and we will use mass spectrometric techniques to identify the binding partners of each orphan in immunoprecipitation pull-down experiments. This data will be used to infer an initial protein function on the basis of protein-protein interactions identified.