PLAN AND ENVIRONMENTAL PROTEOMICS

Research in our laboratory focusses on plant and environmental proteomics. We aim to understand what happens at the molecular level when an organism is exposed to changes in its external environment. We work in different systems, including plants and animals. We use mass spectrometry to identify and quantify proteins present inside cells, and we are constantly refining the analysis approaches we use, in terms of both protein chemistry and bioinformatics. In recent years we have published a number of studies on the effects of temperature stress on rice cells and seedlings, drought stress on rice plants, temperature stress on grape cells, and drought stress and changes in day length on grape vines. We also work on marine organisms, and have published numerous studies on the effects of heavy metal contamination and disease outbreaks in Sydney rock Oysters. The latter work is performed in collaboration with Professor David Raftos in Biological Sciences at MQ and is supported by funding from the Australian Research Council.

ANALYSIS OF TEMPERATURE AND DROUGHT STRESS IN PLANTS

Drought stress affects plants severely and is a real problem facing our society in the face of future climate change.

The figure to the right (above) shows rice plants from a previous study in our laboratory involving analysis of drought signalling. We were able to show using split-rooted pots that the molecular signal for drought stress is communicated from droughted roots to well-watered roots, but not the other way around.

The figure to the right (below) is a heat map generated from label-free quantitative shotgun proteomic analysis of rice cells exposed to five different temperatures. The cluster on the right corresponds to cells subjected to 3 days at 44°C, and is clearly the most different to the others. This is a summary of the identification and quantification of more than 2500 proteins, generated from more than two million spectra of raw mass spectrometric data. We also developed our own software to enable quantification of those proteins which are differentially expressed between different environmental conditions.

We have recently begun working on a project involving reengineering of rice root architecture, to enable plants to grow steeper and deeper roots and hence become more efficient at water usage. We are also following up on some of our previous work and screening a range of different rice varieties and species for the presence and amount of several proteins we have previously identified as being strongly correlated with enhanced drought tolerance.
This work is being performed in collaboration with Professor Brian Atwell in Biological Sciences at MQ and Professor Hosseini Salekdeh at ABRII in Iran.

The picture below shows grapevines growing in a controlled greenhouse, which were part of our recently published study on bud break and daylength in different varieties of grapevines and how this changes in response to changes in day length. We found that even one hour less of sunlight can cause some varieties to remain dormant while other varieties begin vegetative growth.

ARCHAEOLOGICAL PROTEOMICS

We have recently begun a series of studies aimed at identifying proteins from ancient materials recovered from archaeological sites. This has included the analysis of ancient skin samples recovered from 4000-year-old Egyptian mummies, where we were able to provide evidence of acute inflammation and suggest a possible cause of death. We are continuing to expand on this work, as we have access to a large number of archaeological samples from various collaborators in ancient history departments at MQ and elsewhere. This is difficult and exacting work, but represents exciting interdisciplinary research using cutting edge molecular technologies to reveal biological information which is highly valuable in the archaeological context.

Selected Publications
