

P002 Low molecular weight proteomics in *Arabidopsis thaliana* and *Oryza sativa*
Jon Griffin, Johnathan Napier and Peter Shewry
Crop Performance and Improvement Division, Rothamsted Research, Harpenden, Herts AL5 2JQ

The number of predicted genes in the genome of *Arabidopsis thaliana* is 25,498 and analysis of these sequences revealed that 18% were low molecular weight (<20 kDa) proteins. Most current proteomic studies have been biased to proteins greater than 15 kDa. Using an adapted proteomic approach we aim to identify proteins and peptides that have either not been previously characterised or studied, or have not been identified by the use of bioinformatic algorithms when the *Arabidopsis thaliana* genome was analysed. Two different separation approaches have been undertaken. The first based on 2-Dimensional Electrophoresis using high percentage Tris-Tricine gels and the second using 2-Dimensional Chromatography with size exclusion and reverse phase chromatography. Identification of proteins was using MALDI-TOF MS and ESI-MS/MS following trypsin digestion. It is anticipated that some of the components identified will have biological activities (e.g. anti-microbial) or physical properties (e.g. surface activity), which will allow their exploitation. This poster details our findings so far.