

P014 Comparison of transcript and protein profiles in salt stressed *Arabidopsis* cells.

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Despite many years of intensive research, the mechanisms that confer salinity tolerance on some plants are still poorly understood. In part, this situation has arisen due to the understandable desire to work with intact tissues, but the plethora of different cell types, and their commensurate division of labour, has confounded progress. To circumvent this problem we have developed a cell suspension culture of *Arabidopsis thaliana* that survives in over 350 mM NaCl (non-habituated cultures do not survive >80 mM). To survive all cells must be expressing salt tolerance traits and the associated genes and proteins involved in halotolerance are, therefore, enriched in these cultures. Although not a good model for the intact plant, such resources are better suited for identifying cellular processes that maintain ionic balance in saline media. Non-habituated and salt-habituated (HHS) cultures have been characterized at the physiological level including a profile of their ion content. Light- and electron microscopy has suggested vesicle trafficking may have a role to play in salt tolerance; the HHS cells appear to be aneuploid. We have completed a parallel study on the transcript and protein profiles of the HHS cell exposed to high salinity using Affymetrix microarray chips and DiGE 2-D gel electrophoresis / mass spectrometry. Several sequences were found to be differentially abundant at both the transcript and protein level; we will provide a more complete description of these studies.