

**P017** Transcriptomic analyses to identify guard cell signalling genes

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The number of stomata that develop on leaf surfaces is affected by environmental variables, regulated by (unknown) long-distance signals. Isolation of RNA from stomatal guard cells has proved difficult because of toughened cell walls, and contamination from other cell types. We used a blender-and-filter method to enrich for *Arabidopsis thaliana* guard cells. Enriched extracts were disrupted by bead-beating, followed by RNA extraction and transcriptomic analysis. ATH1 genechips were probed with either guard cell enriched or whole leaf cDNAs in triplicated experiments. Known guard cell transcripts, e.g. *KAT1*, *SDD1*, showed higher expression levels in guard cell enriched samples than whole leaf samples. Initial GeneSpring analysis, identified several potentially guard cell expressed genes that could be involved in extracellular signalling. Three selected upstream promoter regions were fused to the GUS gene and expressed in transgenic plants. GUS staining indicated that these genes were expressed in trichomes or vascular cells but not in guard cells. Reanalysis of the transcriptomic data using gMOS (gamma Model for Oligonucleotide Signal) to identify transcripts present at particularly low levels identified an additional set of potentially guard cell expressed genes. Promoter-reporter experiments with two of these genes indicated guard cell-specific expression patterns. One of these apparently guard cell-specific genes encodes a short peptide, a putative intercellular signalling molecule.