

Dissection of guard cell ABA signal transduction mechanisms using combined single cell-type functional genomics and cell biological approaches

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Guard cells have been developed for dissecting early signal transduction mechanisms. Relatively few signal transduction components have been identified from recessive ABA insensitive disruption mutants known to function during early ABA signal transduction upstream of transcription. The limited number of genetically identified positive ABA transducers is most likely due to redundancy in genes encoding ABA signaling components. To overcome this limitation and to dissect redundant signal transduction proteins, we have developed an alternative “single cell-type genomics” approach. This approach includes gene chip experiments performed with *Arabidopsis* guard cell RNA and degenerate oligo-based PCR screening of *Arabidopsis* guard cell cDNA libraries. Data obtained from detailed molecular genetic and cell biological analyses demonstrate that two NADPH oxidase catalytic subunit genes play central roles as positive signal transducers in guard cell ABA signal transduction. In addition, comprehensive analyses of microarray experiments with *Arabidopsis* guard cell and mesophyll cell RNA will be presented. From the microarray results, we identify a strongly ABA-induced protein phosphatase 2C gene in guard cells. A T-DNA disruption mutation in this gene confers ABA-hypersensitive regulation of stomatal closing and seed germination. The presented data provide a basis for cell-type specific genomic scale analyses of gene function.