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Poster Abstract – C.08

GENE-TRAP LINES IDENTIFY GUARD CELL-SPECIFIC GENES IN ARABIDOPSIS

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Drought is a major environmental issue contributing to crop losses. Plant breeders are facing the challenge of designing new crops that are more efficient at water use and engineering plants that are resistant to drought. Land plants lose over 95% of their water via transpiration through stomatal pores, distributed on the surface of leaves and stems. The opening and closing of the pore is mediated by turgor-driven volume changes of two surrounding guard cells. These highly specialized cells integrate internal signals and environmental stimuli to modulate stomatal aperture for plant survival under diverse conditions. Engineering of stomatal responses in mutant or transgenic plants represents a promising tool to design new crops with a more sustainable water use and opens new possibilities to improve plant survival and productivity during drought. Genetic manipulation of stomatal activity relies on the availability of guard cell-specific mutations and promoters to avoid undesired effects on plant growth and development. Gene trap insertion lines, in which endogenous proteins are fused to reporter proteins, are particularly suitable for identification of genes whose expression is restricted to specific domains (i.e. guard cells). Gene trap lines also provide a powerful tool for functional studies, since gene trap insertions often disrupt the tagged genes and give rise to mutant phenotypes. We employed a large scale gene trap screen to identify genes expressed in guard cells and the promoters that drive their specific expression. In collaboration with the other members of the Exon Trapping Insert Consortium (EXOTIC), we established the expression pattern of the GUS reporter gene in approximately 20,000 *Arabidopsis* gene trap lines. Among the 1153 lines showing GUS activity in leaf tissues, we identified 5 lines in which the reporter gene was exclusively or preferentially expressed in guard cells. Here we report the results of *i)* the detailed analysis of the spatial and developmental profiles of GUS expression in the gene trap lines, *ii)* the identification of the genomic insertion sites of the gene trap element *iii)* the analysis of the expression pattern of the tagged gene under standard and stress conditions, and *iv)* the bioinformatics analysis of the promoter regions of the guard cell-specific genes. All together, our results indicate that the gene trap lines isolated in the screen provide valuable marker lines to study pathways that are unique to guard cells, a powerful tool for reverse genetics analyses of guard cell-specific genes, and a precious source of guard cell-specific regulatory regions.