

## **A Large Scale Identification of Functional Genes through Proteomic Analysis of Promoter Trap Lines in *Arabidopsis***

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Phenotypic manifestation of a genome largely depends on the function of the encoded proteins and the regulatory elements including the promoter. An effective way to get information on both of the function and the regulation of a gene is to analyze promoter trap lines. As a part of the Crop Functional Genomics Program of Korea, we have initiated generation of promoter-trap line resources in *Arabidopsis* in association with proteomic profiling. On one hand, we are generating promoter-trap lines with a single T-DNA insertion along with the expression patterns of the reporter gene and the flanking sequences. On the other hand, we plan to generate proteomic profiling of the promoter-trap lines. The proteomic profiles will be used as molecular phenotypes of the promoter trap lines. As an initial step, we have generated reference proteomic maps using wild type and known mutant lines. In many, if not all, cases, a gene functions in an interactive network with other genes and it may be hard or even misleading to understand *in vivo* function of a gene by assaying function of a gene alone. Our long-term goal is to predict functions of genes in a combinatorial fashion by analysis of the proteomic profiles of mutant lines including the promoter trap lines to establish "Combinatorial Functional Genomics" in *Arabidopsis*. We will present our plan and progress toward our final goal.