

Application of activation tagging screen in plant developmental biology

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After the completion of the genome sequence of Arabidopsis, the paradigm of genomics has been shifted to the investigation of gene function to unlock the potential of individual genes. The most critical way to assess the role(s) of a gene is from a phenotype(s) of its loss-of-function mutant, although there are still some technical glitches to generate the mutants and to interpret their phenotypes in plants, including limited use of targeted mutagenesis, functional redundancy, and embryo lethality. Activation tagging screen has been developed to overcome the drawbacks of the loss-of-function screen, and the methodology allows us to screen both gain-of-function and loss-of-function mutants. The system takes advantage of 35S enhancer sequences, which lead to transcriptional activation of a gene near a T-DNA insertion, thereby giving rise to a gain-of-function phenotype. If a T-DNA is inserted into a coding region of a gene, however, the loss-of-function phenotype will be observed in the next generation.

It has been shown activation tagging is very useful to identify a gene(s) involved in a developmental process; for instance, FT, a floral inducer. FT shows similarity to human Raf kinase inhibitor and its transcriptional activation causes early flowering. FT controls timing of phase transition by regulating relative levels between FT and TFL1, a homologous gene of FT. Further analyses have shown a small region in the 4th exon of them distinguishes very between FT-like and TFL1-like activity in the chimeric genes. Application of the activation tagging screen in plant developmental biology will be further discussed.