T-DNA Insertional Mutagenesis for Rice Grain Quality

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Rice is the major crop for more than a half of the world population. Due to its small genome size, rice has been selected as the model crop plant. Recently, the genome sequence of the plant has been completed and identified more than 40,000 genes. To identify the gene function, we have developed a T-DNA tagging vector pGA2715, which can be used for both trapping and activation tagging of rice genes. The binary vector pGA2715 contains the promoterless *glucuronidase (GUS)* reporter gene next to the right border and the multimerized transcriptional enhancers from the cauliflower mosaic virus (CaMV) 35S promoter next to the left border. A total of 50,000 activation tagginglines were generated using the binary vector pGA2715. Histochemical GUS assay revealed that the GUS staining frequency from the pGA2715 lines was about two times higher than that from the lines transformed with abinary vector pGA2707, which lacks the enhancer element. This result suggests that the enhancer sequence present in the T-DNA enhanced GUS tagging efficiency. RT-PCR analysis of a subset of randomly selected pGA2715 lines has shown that expression of the genes immediately adjacent to the inserted enhancer was increased significantly. These results indicated that the large population of T-DNA-tagged lines transformed with pGA2715 could be used for trapping a gene using the *gus* reporter as well as for isolation of gain-of-function mutants. We have generated the sequence database for the T-DNA insertion site. The database (www.postech.ac.kr/ilfe/pfg) is open to public for *in silico* search for knockout and activation tagging mutants. Seeds are available upon request (genean@postech.ac.kr). Our goal is to identify the mutant lines that are altered in seed metabolites and to utilize them for development of a new variety.