

Although transposons occupying a large portion of the genome in various plants were once thought to be junk DNA, they play an important role in genome reorganization and evolution. Active DNA transposons are important tools for gene functional analysis. The endogenous non-autonomous transposon, *nDart1-0*, in rice (*Oryza sativa* L.) is expected to generate various transposon-insertion mutants because *nDart1-0* elements tend to insert into genic regions under natural growth conditions. The transpositions of *nDart1-0* were promoted by an active autonomous element, *aDart1-27*, on chromosome 6. By using the endogenous *nDart1/aDart1-27* system in rice, a large-scale *nDart*-inserted mutant population was easily generated under normal field conditions, and the resulting tagged lines were free of somaclonal variation. The *nDart1/aDart1-27* system was introduced into a rice variety, Koshihikari, named MK-1. 3000 MK-1 plants were grown in field conditions (IPSR, Okayama Univ.). The genome of all plants were isolated for identifying insertion sites of *nDart1*.

I. Dominant mutation in rice

Seed size and number were controlled by various genes in the plants. It was reported that expression changes of high contribution genes for seed size, number and panicle shape resulted in decrease of total yield. A strategy for boosting rice yield based on molecular biology is to stack the finely tuned gene expressions. The *Lgg* mutant bore slightly large grains (Figure 1) as a dominant inheritance. Transposon-display identified the insertion site of the *Lgg* mutant.

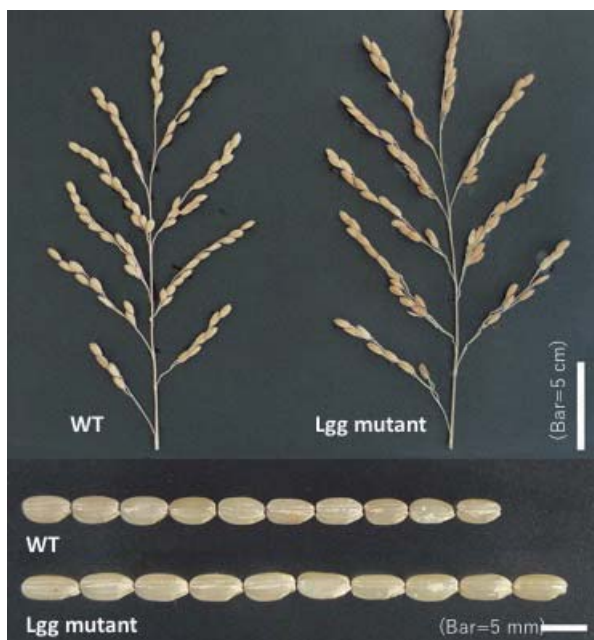


Figure 1. Phenotype of Large gain (*Lgg*). Harvested panicle and seeds.

II. Semidominant mutation in rice

The semidominant mutations produce the intermediate phenotype in individuals heterozygous for the gene concerned. The semidominant mutations were occasionally isolated from the MK-1, it was unclear what causes dominant mutations. Efficient selection and analysis of dominant mutants to analyze the gene functions in rice is very useful. Newly isolated, *Bushy dwarf tiller2* (*Bdt2*), which has the valuable agronomic traits of multiple tillering and dwarfism, was obtained from the MK-1 (Figure 2). Genetic analysis revealed the *Bdt2* mutation was controlled by two genetic elements. One *Bdt2* element, *Bdt2a* showed weak dwarf phenotype, another element, *Bdt2b* strengthened the effect of *Bdt2a*. A wild plant produces only 10 spikes or less, while *Bdt2a* produced 3 times as many, *Bdt2* produced 10 times the ears.



Figure 2. Phenotype of *Bushy dwarf tillers2* (*Bdt2*). (A) Two-month-old plants in the field (B) Segregants of *Bdt2* mutants. *Wild type* (left), *Bdt2a* (middle), *Bdt2* (right). (C) Abnormal bract of *Bdt2*.