

# Identification of an *nDart1* tagged *bushy dwarf tillers1 (bdt1)* mutant

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Rice (*Oryza sativa* L.), one of the most important staple foods has had its 383-Mb genome sequenced. Although the map-based genome sequence and subsequent gene annotation that followed predicted the presence of 32,000 genes in rice, the function of these genes remains mostly unknown. A rice mutant line was developed using the active endogenous DNA transposon, *nDart1* to obtain mutants effectively. A semidominant mutant with multiple tillering and dwarfism was isolated from the *nDart1* promoted tagging line MK1 (Figure 1). By employing *nDart1*-transposon display method, which is a powerful technique for the detection of integration sites of *nDart1* elements on the genome, it was elucidated that the mutant was accompanied by insertion of *nDart1-3* into 43-bp upstream of a non-protein coding transcript region, a precursor of microRNA referred to as *OsmiR156d*. In the mutant, the major transcript initiation site of the precursor was altered and the expression level was slightly increased. Moreover, the *nDart1*-tagged mutant exhibits similar phenotypes to *OsmiR156-b* or *-h* overexpressed transgenic plants. It suggested that insertion of *nDart1-3* resulted in overexpression of *OsmicroRNA156d*.



Figure 1. Phenotypes of wild-type and *bdt1* mutants. Three-month-old wild-type plant (left) and *bdt1* homozygous mutant (right).