Gene Tagging Using the Rice Active Transposon, *nDart1*, and Analyses of Gene Functions

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We employ an active DNA transposon named *nDart1* (*non-autonomous DNA-based active rice transposon one*), belonging to the *hAT* superfamily, as gene tagging tools to identify useful rice genes and subsequently performed the mutant analyses by molecular techniques.

(1) Analysis of albino mutant, *al101*

al101 was isolated from the *nDart1* promoted mutants pool as an albino phenotype mutant and subsequently identified the gene by transposon display (TD) method, based on AFLP method. To unveil *AL101* gene function, we characterized the expression profile in various tissues by RT-PCR. It suggested that *AL101* was expressed not only in leaves, but also in roots. Transient assay using a GFP-fused *AL101* gene indicated that it was localized in chloroplast in a cell. Electron microscopy analysis demonstrated abnormal shape chloroplasts and undeveloped thylakoid membrane in *al101*. Moreover, we attempt to generate next generation of heterogeneous *AL101* transformant lines to obtain the homogeneous for complementation test.

(2) Analysis of elongated culm mutant

A mutant with excessively elongated culms was isolated from *nDart* tagging lines. By performing rough mapping and a subsequent modified TD method, it was revealed that the mutant was caused by a large (~103 kb) genomic deletion. On the basis of rice genomic annotation using RAP-DB, the large deleted region was predicted to contain 87 transposons and 11 genes including negative regulator of gibberellin (GA) signaling. The genomic deletion cleaved LTR transposon, *Houba*. We surveyed truncated sites of 119 *Houba* copies extracted from the rice genomic sequence data to evaluate the truncated site. It indicated that the cleavages were occurred in this site with high frequency.