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Study of endoreduplication in rice development by using reverse genetic approach

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Objectives

We aimed to determine the role of endoreduplication in rice development by using T-DNA tagging lines.

Materials and Methods

1. Material

Plant - *Oryza sativa* cv. Dong-Jin T-DNA tagging lines.

2. Methods

T-DNA tagging lines for genes involved in endoreduplication were isolated from the T-DNA end sequence database. Genotyping PCRs and various cell biology methods were used to identify homozygous T_2 sublines and to characterize phenotypes of the homozygous lines, respectively.

Results and Discussion

Endoreduplication as a modified cell cycle duplicates the whole genome without subsequent M-phase and cytokinesis. A round of endoreduplication is common in most of differentiated cells of plant vegetative tissues, whereas it occurs extensively up to 5 times in cereal endosperm cells. During endosperm development, the period of active endoreduplication is concomitant with cell enlargement and active biosyntheses of starch and storage proteins. To date, however, the function of endoreduplication in endosperm development was not elucidated. In this study, we isolated T-DNA tagging rice mutants for the genes that have been reported for involvement in endoreduplication and examined their functions in development of endosperm as well as vegetative tissues. Among several candidate genes including *Cell Cycle Switch 52 (CCS52)*, *Constitutive Pathogen Response 5(CPR5)*, *Kip-Related Protein 2 (KRP2)*, *Wee1*, and *Retinoblastoma (Rb)* homolog, we have isolated T-DNA tagging lines for each gene, except *Rb* homolog. As the first available for T_2 sublines, *OsCCS52* T-DNA tagging homozygous lines have been further characterized. Their distinct phenotypes include poor vegetative growth, reduced kernel size, and reduced number of fertile kernels per panicle, compared to the corresponding wild type. Furthermore, expression level of *OsCCS52* in developing kernels of the WT was higher than in vegetative tissues such as roots and leaves. Characterization of T-DNA tagging lines for the other candidate genes and comparison of DNA contents in vegetative cells and endosperm cells between the *OsCCS52* T-DNA tagging homozygous lines and the WT are in progress.

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