PBIII-2

Rice *Cell Cycle Switch* Genes play an Essential Role in Overall Development through Regulation of Mitotic Cell Cycle Rather than Endoreduplication

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Plant growth and development rely on precise concert of cell division and cell expansion. For a possible role in endoreduplication during endosperm development, tagging lines of *Cell Cycle Switch* genes, *Osccs1* and *Osccs2*, were reverse-genetically isolated from a population of about 100,000 T-DNA tagging lines. The knockout mutants exhibited similar prominent phenotypes, including semi-dwarfism, small kernels, and reduced fertility. Different from the *Osccs1*, panicles of *Osccs2* were hardly emerged from flag leaf sheath, due to greatly reduced elongation of the first internode. Extensive microscopy on *Osccs1* kernels and *Osccs2* leaves revealed that reduced sizes of the mutant plant organs were resulted from reduced cell number rather than reduced cell size. Although *Medicago CCS52* was reported to be involved in positive regulation of endoreduplication, no difference in nuclear size between the knockouts and WT was detected. Among three examined cyclin genes, transcript level of *OsCyclinB2* was substantially increased in both knockout mutants. Furthermore, ectopic expression of *OsCCS1* in *Saccharomyces cerevisiae* resulted in enhanced cell division that was determined by optical density of the cell culture. These results suggest that OsCCS may be involved in timely degradation of M-phase cyclins (i.e., B-type cyclins), possibly through association with and activation of anaphase-promoting complex. Therefore, slower exit from M-phase or slower transition from G1 to S-phase may be responsible for reduced cell number in the knockout mutants. Because OsCCS1 and OsCCS2 have five and four WD-40 repeats, respectively, that are commonly known to form multi-protein assemblies, we performed yeast two-hybrid screening of proteins interacting with OsCCS. In addition to the yeast two-hybrid data, results from the analyses of *OsCCS1* overexpression and antisense transgenic plants will be presented. This work was supported in part by a grant from the Biogreen 21 Program, Rural Development Administration of Korea and Crop Functional Genomics Center (21st Century Frontier Program).