

Characterization of genes regulating tillers and identification of markers for the development of new plant type in rice

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Optimization of shoot branching is important for the establishment of plant architecture to attain the potential yield in cereals. As tillering is one of the major components determining rice yield, there is a long history of studies on tillering. Recently, *OsTB1* was identified based on its sequence similarity with maize *TB1* (*TEOSINTE BRANCHED 1*), which acts as a repressor of axillary bud growth and an inducer of female inflorescence. Transgenic rice plants overexpressing *OsTB1* exhibited reduced lateral branching and *fine culm1* (*fc1*) containing the loss-of-function mutation of *OsTB1* exhibited enhanced lateral branching. In order to identify marker genes that are related to rice tillering, we characterized *OsTB1* in rice varieties with different tiller numbers. To investigate correlation between the tiller numbers and amount of *OsTB1*, 22 rice varieties were selected according to degree of the tiller numbers and its expression was examined by Northern blot analysis. In addition, to investigate the function of the maize *TB1* in rice, the chimeric construction to deliver maize *TB1* based on pCAMBIA were transferred into the embryogenic rice callus using *Agrobacterium* system. Phenotyping of tiller number for QTL identification is in progress using RILs derived from Dasan/TR22183 cross and the molecular map based on SSR markers. We have therefore tried to isolate downstream marker genes that are controlled by *OsTB1* to understand regulatory mechanism of lateral branching. To do this, we have produced recombinant *OsTB1* in *E. coli* and raised antibody against it. We are now doing CHIP (Chromatin Immunoprecipitation) assay and random oligomer selection assay to identify the specific *cis*-acting elements of promoters which bind with *OsTB1*. In addition, we are examining the localization pattern and stability of *OsTB1* using *XVE-GFP-OsTB1* or *XVE-CFP-OsTB1* transgenic plants that their expressions are induced by inducer, β -estradiol and *35S-OsTB1* transgenic plants after treatment of auxin.

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