13. Characterization and mapping of *tillering dwarf rice 2*, *tdr2*

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Variation in branching pattern is one of the typical morphologies distinguishable between monocotyledonous and dicotyledonous plants, and also its regulation is an important agricultural target for crop breeding. Cloning of genes regulating the shoot branching is essential for understanding the mechanism of branching pattern. Mutants defected in shoot branching genes show low or high tillering phenotype. Based on such unique phenotypes, we have screened mutants as a first step to isolate and characterize genes related to the branching mechanism. We succeeded to isolate some mutants showing abnormal branching and focused on a mutant called *tillering dwarf rice 2* (*tdr2*). *tdr2* was isolated from the *Tos17* mutants pools (Hirochika 2001), and showed about 5 times higher tiller number than the wild-type plant (Fig. 1). So far, a few genes, such as *D3, MOC1, OsTB1* and *HTD1,* which are associated with branching mechanism, has been isolated (Ishikawa et al. 2005, Li et al. 2003, Takeda et al. 2003, Zou et al. 2005). However, *tdr2* was located at a different position of the rice genome and therefore it should encode a novel factor involved in the branching mechanism. As an initial step of positional cloning of *tdr2,* we constructed the linkage map of *tdr2*.

An F_2 population, which was produced crossing between recessive homozygote *tdr2* (*joponica* cultivar) and Kasalath (*indica* cultivar), was used for linkage analysis. Twenty-four recessive homozygote *tdr2* plants were selected from the F_2 population and 65 molecular markers covering the whole rice genome were applied for mapping *tdr2*. As the result of linkage analysis of *tdr2* and 65 molecular markers, *tdr2* is located between molecular markers RM237 and R30008 within 29.5cM on the long arm of chromosome 1 (Fig. 2). This information is useful to start cloning the *tdr2* and now we are conducting the high resolution mapping *tdr2*.

References

Hirochika, H., 2001. Contribution of the *Tos17* retrotransposon to rice functional genomics. Curr. Opin. Plant Biol. 4: 118-122.

Ishikawa, S., M. Maekawa, T. Arite, K. Onishi, I. Takemura and J. Kyozuka, 2005. Supression of tiller

bud activity in tillering dwarf mutants of rice. Plant Cell Physiol. 46: 79-86.

Li, X., Q. Qian, Z. Fu, Y. Wang, G. Xiong, D. Zeng, X. Wang, X. Liu, S. Teng, H. Fujimoto, M. Yuan, D. Luo, B. Han and J. Li, 2003. Control of tillering in rice. Nature 422: 618-621.

Takeda, T., Y. Suwa, M. Suzuki, H. Kitano, M. Ueguchi-Tanaka, M. Ashikari, M. Matsuoka and C. Ueguchi, 2003. The *OsTB1* gene negatively regulates lateral branching in rice. Plant J. 33: 513-520.

Zou J., Z. Chen, S. Zheng, W. Zhang, G. Jiang, X. Zhao, W. Zhai, X. Pan and L. Zhu, 2005. Chracterizations and fine mapping of a mutant gene for high tillering and dwarf in rice (*Oryza sativa* L.). Planta 222: 604-612.

Fig. 1. Gross morphology of the *tdr2* mutant. Wild type (cv. Nipponbare; left) and *tdr2* mutant (right).

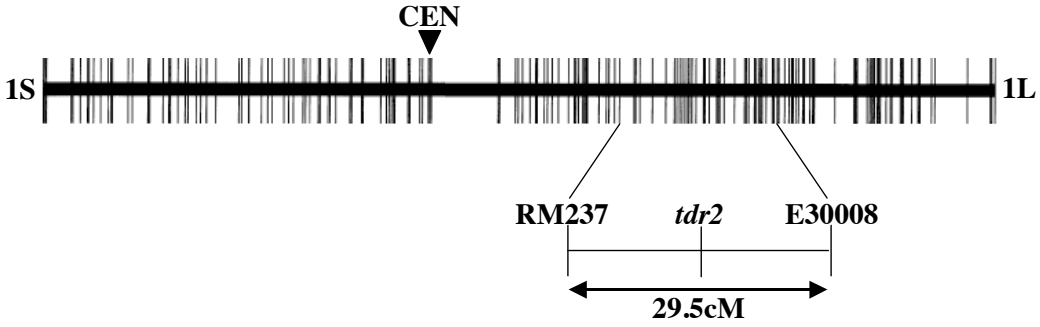

Fig. 2. The linkage map of *tdr2*. *Tdr2* is located between molecular marker RM 237 and E30008 on the long arm of chromosome1.