11. Characterization and mapping of *tillering dwarf rice 1*, *tdr1*

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Molecular cloning and functional analysis of genes associate with tillering will help us understanding for rice branching mechanism. So far, a few genes, *D3, MOC1, OsTB1* and *HTD1* associated with tillering has been isolated (Ishiwata et al. 2005, Li et al. 2003, Takeda et al. 2003, Zou et al. 2005). However, cloning of these genes is not enough to illustrate the model of branching mechanism. To further study on the tillering mechanism in rice, we have screened some rice tillering mutants. A *tillering dwarf rice 1* (*tdr1*) mutant, which was isolated from the *Tos17* mutants pools (Hirochika 2001), shows high tillering phenotype (Fig. 1). In this study, as an initial step of positional cloning and functional analysis of *tdr1,* we characterized and mapped *tdr1*.

tdr1 shoots were shorter than wild type Nipponbare, by reduction of the culm length (Table 1). The tiller number of *tdr1* is about three times larger than that in Nipponbare (Table 1). Panicle length and number of primary panicle branches of *tdr1* are about half of those in Nipponbare (Table 1). These phenotypes indicate that the mutation of *Tdr1* increases the growth of vegetative axillary bud, and consequently, it is a useful candidate for analysis of branching mechanism.

For mapping, F_2 population from the crosses between recessive homozygote *tdr1* (*joponica* cultivar) and Kasalath (*indica* cultivar), were produced. Ninety-four recessive homozygote *tdr1* plants were selected from F_2 population and used for mapping. As the result of linkage analysis of 65 molecular markers covering the whole rice genome, *tdr1* is located between a CAPS marker C1232 and the end of short arm of chromosome 9 (Fig. 2). According to the linkage map of RGP (Rice Genome Project) map (Harushima et al. 1998), the genetic distance from a CAPS marker C1232 to the end of short arm of chromosome 9 is 0.8 cM. Fine mapping of *tdr1* by using more genetic markers and more recombinants in this region are under progression. The positional cloning of *tdr1* and learning the function of *TDR1* in tillering is our next objective.

Fig. 1. Phenotype of the *tdr1* mutant. Wild type (cv. Nipponbare; left) and *tdr1* mutant (right).

Table 1. Growth of *tdr1* and Nipponbare shoot

Line	n	Culm length (cm)	No. of tiller	Panicle length (cm)	No. of primary panicle branches
tdr1	5	28.6±3.0	60.6±5.0	12.1±1.1	5.8±0.4
Nipponbare	5	83.3±3.0	21.4±0.5	24.1±0.9	11.8±0.8

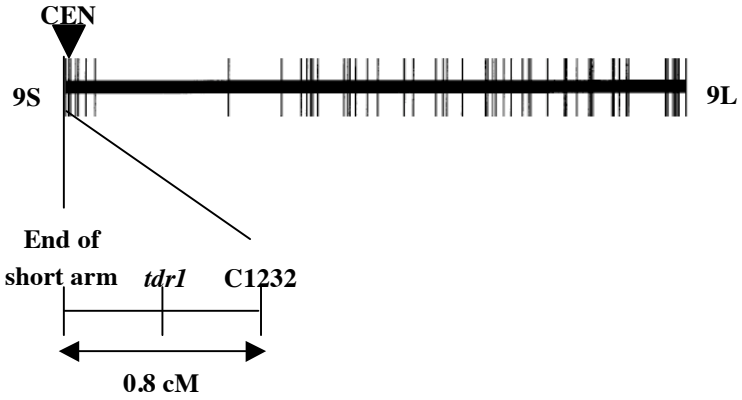

Fig. 2. The linkage map of *tdr1* with molecular markers on chromosome 9. The recessive mutant gene, *tdr1*, is located between marker C1232 and end of short arm of chromosome 9.

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