7. A novel semi-dwarf mutant mutagenized with ion beam irradiation controlled by a dominant gene, *SD-d(t)*

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Plant height is an important agronomic trait in rice. So far, many studies have been made on the height of rice plants. This trait has shown genetic models of a major gene and polygenes in different genetic backgrounds of rice. In a major gene model, the dwarfism and semi-dwarfism are generally inherited with a recessive gene, rarely with a dominant gene (Saeda and Kitano, 1992). To date, more than 70 semi-dwarf and dwarf mutants have been reported, but only *D53*, *D-h* and *Ssi1* are the dominant mutations among them (Iwata et al., 1977 Koh et al., 1993 Wu et al., 1997). Here we report a new semi-dwarf mutant controlled by a dominant gene.

Many mutant genes had been cloned and characterized at molecular and biochemical levels (Ashikari et al., 1999 Sasaki et al., 2002, Hong et al., 2003 Itoh et al., 2004). Exploring novel rice mutant genes can be applied not only in breeding programs but also in scientific research. As a new resource of mutagens, low-energy ion beam irradiation is characterized as less physiological damage, wider mutation spectrum, and higher mutation frequency in comparison with the mutations from other inducing methods (Yu et al., 1991 Wei et al., 1995). By nitrogen ion irradiation, we had screened a semi-dwarf mutant in a *japonica* rice cultivar Y98148, designated as Y98149(Fig. 1). They had been identified as NILs(near isogenic lines)(Tong et al., 2001 Liu et al., 2004).

Fig.1 Phenotype of the *SD-d(t)* mutant. Wild type (Y98148; left) and mutant (Y98149; right)

To determine the genetic mode of the mutation, the dominant semi-dwarf mutant was crossed to two normal cultivars, Y98148 and Wan3(*indica*), respectively. Both the F_2 populations derived from the two crosses, Mutant/Y98148 and Mutant/Wan3, showed the same segregation ratio of three mutant to one wild-type phenotype (Table 1), which was consistent with the previous result (Tong et al., 2003). It was revealed that the mutation was controlled by a single dominant nuclear gene, henceforth tentatively symbolized as *SD-d(t)*. Then we used 91 recessive homozygous tall plants from cross of Mutant/Wan3 for mapping of *SD-d(t)*. Among the 506 pairs of SSR (simple sequence repeat) primers throughout all the chromosomes 126 pairs showed polymorphism between the two parents. The linkage between the *SD-d(t)* locus and SSR markers were investigated by BSA (Bulked Segregation Analysis) method with minor

modification. Linkage analysis indicated that the *SD-d(t)* locus was linked with some SSR markers located on the short arm of chromosome 6 and *SD-d(t)* gene was successfully mapped between the two SSR markers RM253 and RM7023 with map distances of 7.1 cM and 4.8 cM, respectively (Fig. 2). Fine mapping of *SD-d(t)* by using more genetic markers and more recombinants in this region are under progression.

Table 1 F_2 segregation of mutant characters in rice crosses

Cross	Total plants	Semi-dwarf plants	Tall plants	Expect ratio	χ^2	*P*
Y98148/Y9149	704	531	173	3:1	0.05	0.75-0.90
Wan3/Y98149	419	311	98	3:1	0.18	0.50-0.75

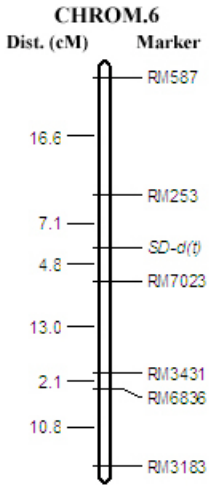

Fig. 2 The linkage map of *SD-d(t)* with molecular markers on chromosome 6.

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