

12. Genetic analysis and molecular mapping of a rolled leaf gene, *rl 11(t)*, in EMS-induced IR64 mutant

Y. -F. SHI^{1,2)}, J. CHEN¹⁾, W. -Q. LIU¹⁾, Q. -N. HUANG^{1,2)}, B. SHEN²⁾, H. LEUNG³⁾ and J. -I. WU¹⁾

1) China National Rice Research Institute, Hangzhou 310006 China

2) Hangzhou Normal University, Hangzhou, 310036 China

3) International Rice Research Institute, DAPO Box 7777, Metro Manila Philippines

Leaf structure is an important trait affecting grain yield through the changes of photo-synthesis in crops such as rice. We identified a EMS-induced IR64 mutant, W32, with rolled leaf in the whole duration of rice growth. The mutant shows almost complete rolled leaf from the first leaf at seedling stage to the flag leaf at reproductive stage. By crossing the mutant to IR24 and PA64, the F₁ plants from both crosses showed flat leaves indicating the recessive manner of genetic control for the trait. Genetic analysis of both the F₂ populations derived from W32/IR24 and W32/PA64 showed that the rolled leaf was controlled by a single gene (Table 1).

To map the gene that tentatively termed *rl 11(t)*, an extended F₂ population consisting of 1846 mutant type individuals was developed by crossing W32 to PA64, a flat leaf variety. Bulk analysis was carried out using a mutant DNA pool consisting of 10 rolled leaf individuals and a wild type DNA pool consisting of 10 flat leaf individuals. 188 SSR markers covering the whole genome were screened for polymorphism between W32 and PA64. 68 out of 188 SSR markers were polymorphic, and subsequently were used for screening the two DNA pools. Two SSR markers, RM6697 and RM6574, were found polymorphism between the two DNA pools, and both of them are located near the telomere on the short-arm of chromosome 7. There were 9 and 22 recombinants were identified after genotyping of 43 rolled leaf F₂ individuals indicating the gene was more close to RM6697 that is closer to the end of telomere on chromosome 7. Therefore, more SSR markers from RM6697 upwards to the telomere were synthesized for further analysis. The rolled leaf gene *rl 11(t)* was finally narrowed down to a 79 kb region near the telomere of the short arm of chromosome 7 between RM20783 and RM20794 (Fig. 1). Further fine mapping and cloning of *rl 11(t)* is currently underway.

Up to now, there are 10 rolled leaf genes have been reported (Nagato et al., 1998). There first six genes, *rl 1* to *rl 6*, were identified by classical genetic analysis, and located on chromosome 1, 4, 12, 1, 3 and 7, respectively. The other four genes *rl 7*, *rl 8*, *rl 9(t)* and *rl 10(t)* were mapped by DNA marker analysis and located on chromosome 5, 5, 9 and 3, respectively (Li et al., 1998 Shao et al., 2005 Yan et al., 2006 Yi et al., 2007). Except *rl 6*, *rl 11(t)* reported in present study was also located on chromosome 7, however, the allelic relationship between *rl 6* and *rl 11(t)* needs to be further studied.

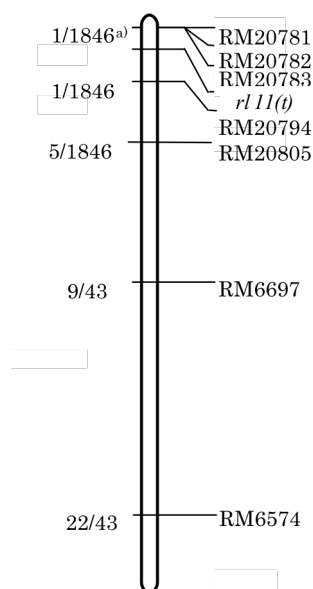


Fig. 1 The location of *rl 11(t)* on Chromosome 7.

a) The numbers on the left of chromosome indicate the number of recombinant/number of F₂ individuals tested for the corresponding marker.

Table 1 Genetic analysis of rolled leaf mutant W32

<u>Cross</u>	<u>F₁</u>	<u>Number of F₂ plants</u>			<u>P_(3:1)</u>
		<u>Total</u>	<u>Flat leaf</u>	<u>Rolled leaf</u>	
<u>W32 / IR24</u>	<u>Flat leaf</u>	<u>1613</u>	<u>1207</u>	<u>406</u>	<u>0.874</u>
<u>W32 / PA64</u>	<u>Flat leaf</u>	<u>771</u>	<u>560</u>	<u>211</u>	<u>0.129</u>

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