

22. Molecular mapping of a blast resistance gene in an *indica* rice cultivar Yanxian No. 1

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Rice blast, caused by *Pyricularia grisea* Sacc., is one of the most destructive diseases of rice worldwide. Utilization of genetic resistance is the most effective and economical way of controlling blast disease. In the past few decades, more than 40 major blast resistance genes have been mapped through molecular marker technology (Zhou et al. 2004). Yanxian No.1, an elite *indica* rice cultivar from Jiangsu Province in China, shows resistance to all blast isolated from Japan and northern China (Lei et al. unpublished data). Identification and molecular mapping of the resistance gene(s) existing in cv. Yanxian No.1 will help in effective use of its broad-spectrum resistance in rice breeding programs.

F₂ population, derived from the cross between an universally susceptible variety Lijiangxintuanheigu (LTH, female) and the resistant cv. Yanxian No.1 (male), were used for gene mapping. Two blast isolates 97-27-2 (race 537.1) and Zhong10-8-14 (race 433.1) from northern China, both virulent to LTH and avirulent to Yanxian No.1, were used as differential isolates to identify resistance genes. The growing of seedlings, preparation of inoculum, inoculation and disease evaluation followed Zhou's procedure (Zhou et al. 2004).

The segregation of resistance and susceptibility in the F₂ population to both differential isolates 97-27-2 (1139R : 414S, $\chi^2 = 2.190$ for the ratio 3R:1S) and Zhong10-8-14 (1819R : 613S, $\chi^2 = 0.044$ for the ratio 3R : 1S) fitted the segregation ratio of 3R:1S, indicating that the resistance of Yanxian No.1 to these two isolates was controlled by a single dominant gene, designated tentatively as *Pi-y1(t)* and *Pi-y2(t)*, respectively. To determine their chromosome positions, bulked-segregating analysis (BSA) and recessive class analysis (RCA) were performed in F₂ populations, respectively. The results showed that three SSR markers RM166, RM3535 and RM3248 on chromosome 2 gave polymorphism between resistant and susceptible bulks. For linkage analysis, 328 F₂ plants extremely susceptible to 97-27-2 and 489 F₂ plants extremely susceptible to zhong10-8-14 were tested with the RCA approach. The results showed both the genes *Pi-y1(t)* and *Pi-y2(t)* were flanked by RM3248 and RM208. The distances of the two markers each to the gene *Pi-y1(t)* were both 0.8cM, while the distances to the gene *Pi-y2(t)* were 1.3 cM and 1.7cM (Fig. 1A, B). The results indicated that the two gene *Pi-y1(t)* and *Pi-y2(t)* could be one

same gene in that their positions is too close, designated tentatively as *Pi-y(t)*.

The region of chromosome 2 carrying *Pi-y(t)* also harbors the blast resistance genes, *Pi-x(t)* (Huang et al. personal correspondence), *Pi-g(t)*, *Pi-b*, *Pi-tq5(t)* and *Pi-25(t)* (Zhou et al. 2004). The allelism test indicated that *Pi-y(t)* could be non-allelic to either *Pi-x(t)* or *Pi-g(t)*. Since *Pi-y(t)* is relatively far from *Pi-b*, *Pi-tq5(t)* and *Pi-25(t)*, *Pi-y(t)* could be non-allelic to these genes (Fig. 1C).

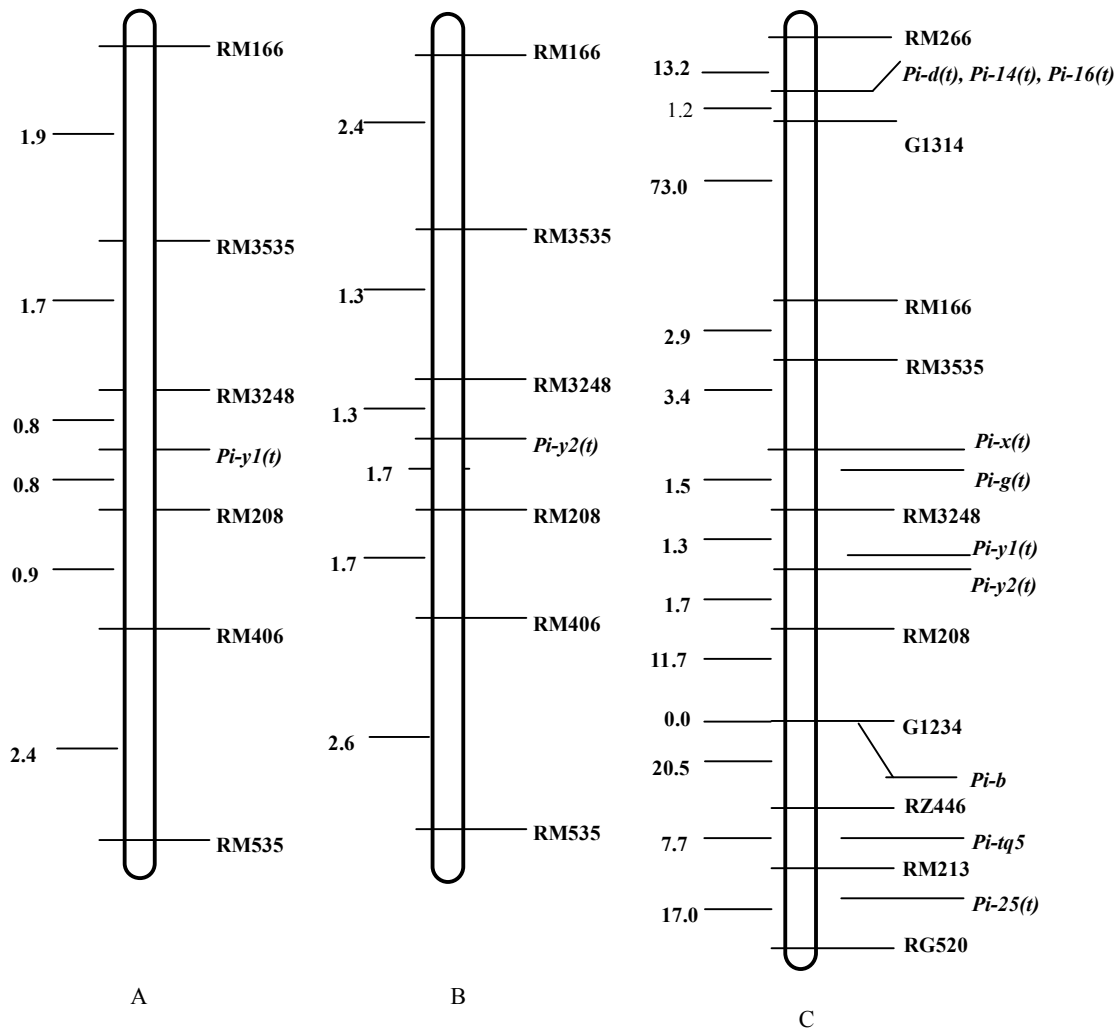


Fig. 1A, B: SSR map of *Pi-y1(t)* (A) and *Pi-y2(t)* (B) on rice chromosome 2. C: Location of known rice blast resistance gene on chromosome 2. Orders and map distance followed Zhou et al. (2004).

Reference

Zhou, J. H., J. L. Wang, J. C. Xu, C. L. Lei and Z. Z. Ling, 2004. Identification and mapping of a rice blast resistance gene *Pi-g(t)* in the cultivar Guangchangzhan. Plant Pathol. 53: 191-196.