

Novel blast resistance genes from a landrace rice variety in Myanmar

The use of broad-spectrum resistance genes is an effective way to achieve durable resistance against rice blast (*Pyricularia oryzae* Cavara) in rice (*Oryza sativa* L.).

We previously surveyed the diversity of blast resistance in 948 rice varieties and found Haoru (International Rice Research Institute genebank acc. no. IRGC33090), a Myanmar rice landrace with broad-spectrum resistance against blast.

We examined the genetic basis of Haoru's broad-spectrum resistance using the standard blast differential system consisting of the standard isolates and differential varieties.

For genetic analysis, we used the BC₁F₁ population and BC₁F₂ lines derived from crosses of Haoru with a susceptible variety, US-2. Co-segregation analysis of the reaction pattern in the BC₁F₁ population against the 20 standard isolates suggested that Haoru harbors three resistance genes.

Using bulk-segregant and linkage analysis, we mapped two of the three resistance genes on chromosomes 12 and 6, and designated them as *Pi58(t)* and *Pi59(t)*, respectively.

Pi58(t) and *Pi59(t)* were differentiated from other reported resistance genes using the standard differential system. The estimated resistance spectrum of *Pi58(t)* corresponded with that of Haoru, suggesting that *Pi58(t)* is primarily responsible for Haoru's broad-spectrum resistance.

In addition, *Pi59(t)* and the third gene were also proven to be new and useful genetic resources for studying and improving blast resistance in rice.

(Y. Fukuta [TARF, JIRCAS])

Table 1. Reaction patterns of Haoru and segregation lines harboring new resistance genes to standard differential blast isolates

Line	Resistance gene	Chr.	Reaction patterns																			
			Standard differential blast isolates from the Philippines																			
			PO6-6	CA89	43	CA41	M64-1-3-9-1	M39-1-3-8-1	M39-1-2-21-2	M36-1-3-10-1	JMB8401	IK81-25	IK81-3	BN111	V850256	V850196	V86010	JMB840610	BN209	M101-1-2-9-1	B90002	C923-49
Haoru	-	-	R	R	S	R	R	R	R	R	R	S	S	R	R	R	R	R	R	R	R	R
US-2	-	-	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
BC ₁ F ₂ line (US-2/Haoru/US-2)	<i>Pi58(t)</i>	12	R	R	S	R	R	R	R	R	R	S	S	R	R	R	R	R	R	R	R	R
IRBL12-M	<i>Pi12(t)</i>	12	S	S	S	S	S	S	S	S	S	S	S	S	S	M	M	R	R	R	R	R
IRBL19-A	<i>Pi19(t)</i>	12	S	S	S	M	S	S	S	M	M	S	S	S	S	S	S	S	S	S	S	S
IRBLta-CP1	<i>Pita</i>	12	S	S	S	R	M	M	S	M	R	R	S	R	R	S	S	S	S	S	M	S
IRBLta2-Pi	<i>Pita-2</i>	12	S	S	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S
IRBL20-IR24	<i>Pi20(t)</i>	12	S	S	S	S	S	S	S	S	S	M	M	R	S	S	R	S	S	S	R	R
BC ₁ F ₂ line (US2/Haoru/US2)	<i>Pi59(t)</i>	6	S	S	S	S	S	S	S	S	S	S	S	S	S	S	R	R	S	S	R	R
IRBLz-Fu	<i>Piz</i>	6	R	M	R	M	R	R	R	R	R	R	S	M	R	R	M	R	R	M	R	M
IRBLz5-CA-1	<i>Piz-5</i>	6	R	M	M	R	M	R	R	R	R	R	R	R	R	M	R	M	S	M	M	M
IRBLzt-T	<i>Piz-t</i>	6	S	S	S	R	R	S	S	S	S	S	S	S	S	S	R	R	S	S	R	R
IRBL9-W	<i>Pi9</i>	6	R	R	R	R	R	M	R	R	R	R	R	R	R	R	S	R	R	R	R	R

R: Resistant, M: Moderately resistant, S: Susceptible

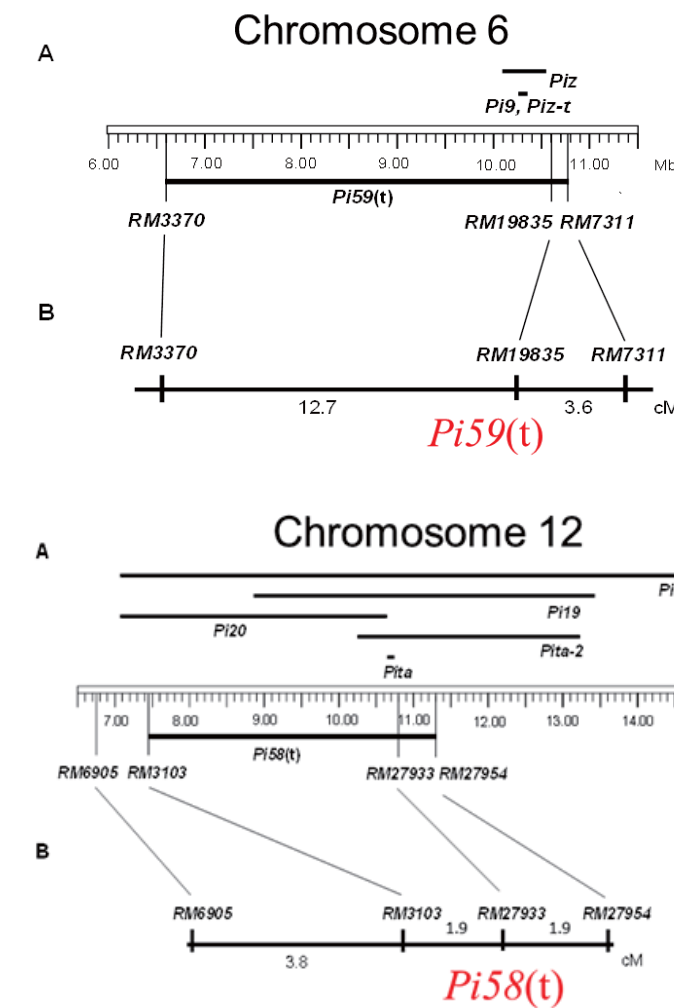


Fig. 1a. Position of resistance gene, *Pi59(t)*, on chromosome 6. A: Physical map. Position based on the Nipponabare's genome sequence. B: Genetic map. Genetic distances between the gene and markers were estimated using the BC₁F₂ lines of US-2/Haoru/US-2 (n=55).

Fig. 1b. Position of resistance gene, *Pi58(t)*, on chromosome 12. A: Physical map. Position based on the Nipponabare's genome sequence. B: Genetic map. Genetic distances between the gene and markers were estimated using the BC₁F₂ lines of US-2/Haoru/US-2 (n=106).