

Development of New Sets of International Standard Differential Varieties for Blast Resistance in Rice (*Oryza sativa* L.)

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Abstract

The IRRI-Japan Collaborative Research Project has been developing new sets of differential varieties for resistance to blast disease (*Pyricularia grisea* Sacc.) in rice (*Oryza sativa* L.). The first international standard differential variety set composed of monogenic lines for 24 kinds of resistance genes (*Pia*, *Pib*, *Pii*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pit*, *Pita*, *Pita-2*, *Piz*, *Piz-5* (= *Pi2*), *Piz-t*, *Pi1*, *Pi3*, *Pi5(t)*, *Pi7*, *Pi9*, *Pi11(t)*, *Pi12(t)*, *Pi19(t)*, and *Pi20*) was released and has been widely used in various countries. Furthermore, the project has been developing near-isogenic lines (NILs) for blast resistance with three kinds of genetic backgrounds, a Japonica-type variety Lijiangxintuanheigu (LTH), an Indica-type variety CO39, and a newly developed ‘universal susceptible’ line US-2 which was derived from a cross between Indica and Japonica-type susceptible varieties. A total of 23 lines for 14 kinds of resistance genes, *Pia*, *Pib*, *Pik*, *Pik-h*, *Pik-s*, *Pita*, *Pita-2*, *Piz-5* (= *Pi2*), *Piz-t*, *Pi1*, *Pi3*, *Pi5(t)*, *Pi7*, and *Pi9*, have been developed by the recurrent backcross method using the monogenic lines with the LTH genetic background. Twenty lines for 14 kinds of resistance genes, *Pib*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pita*, *Pita-2*, *Piz-5* (= *Pi2*), *Piz-t*, *Pi1*, *Pi5(t)*, and *Pi7* have been developed with the CO39 genetic background. Moreover, a universal susceptible rice line, US-2, which has not been known to have any blast resistance genes in the genetic background, and can be cultivated easily under both tropical and temperate conditions, is also being used for the development of NILs as the next generation of differential varieties. These lines are offered as gene sources for breeding of blast resistance and as sets of international standard differential varieties used for the study of blast disease.

Discipline: Plant breeding

Additional key words: gene, International Rice Research Institute (IRRI), monogenic line, near-isogenic line

Introduction

Blast, caused by *Pyricularia grisea* Sacc., is one of the most destructive diseases of rice (*Oryza sativa* L.). The use of resistant varieties is an efficient method to control this disease. Differential varieties are important materials for improving blast resistance and for pathological studies. The relationship between the host plant

(resistance genes) and pathogen (avirulence genes) can be explained by the gene-for-gene theory¹. Therefore, virulence genotypes of pathotypes can be inferred when resistance genotypes are known for each differential variety and these can distinguish pathotypes (races) based on its reaction pattern or qualitative differences in reactions to different pathogen strains. In Japan, sets of 9 varieties⁹ and 12 varieties⁵ were selected and these have been used as blast differentials. However, these varieties were

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not readily available in other countries because several of these varieties had not only the target resistance genes but also harbored other gene(s) in the genetic backgrounds.

At the International Rice Research Institute (IRRI), near-isogenic lines (NILs) for blast resistance were developed for only four resistance genes, *Pi1*, *Pi3*, *Piz-5*, and *Pita*, with the genetic background of an Indica-type rice, CO39, and these were used as differential varieties⁷. To provide more useful materials than have ever been developed, the IRRI-Japan Collaborative Research Project released the monogenic lines for blast resistance as the first set of international standard differential varieties and the project has been developing NILs further^{2,8}. These monogenic lines and NILs were developed for targeting 24 kinds of resistance genes.

In the present paper, development of the set of differential varieties is reviewed and the perspective for further development under the IRRI-Japan Collaborative Research Project, and the utilization of differential varieties are discussed.

Materials and methods

The blast resistance genes were introduced by recurrent backcross breeding (Fig. 1). Three susceptible varieties, a Chinese Japonica-type, Lijiangxintanheigu (LTH),

an Indica-type, CO39, and a hybrid progeny line, US-2, derived from a cross between an Indonesian landrace, Kencana¹¹, and an Indica-type, Takanari⁴, were used as the recurrent parents. On the other hand, 25 varieties were used as donor parents of blast resistance genes (Table 1).

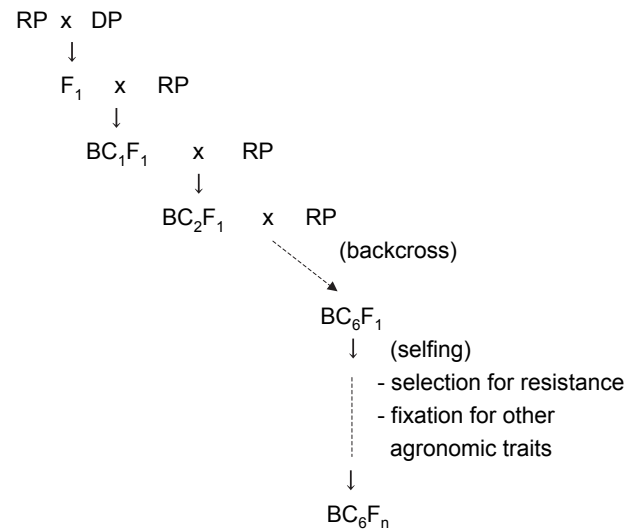


Fig. 1. Breeding scheme of near-isogenic lines for blast resistance gene

RP: Recurrent parent (LTH, CO39 and US2),
 DP: Donor parent of blast resistance gene (see Table 1).

Table 1. Generation of near isogenic line (NIL) series with blast resistance genes developed at IRRI in 2005 dry season

Targeted resistance gene	Donor (Original variety)	Recurrent backcross parents			
		Monogenic line	Near isogenic line		
		LTH	LTH	CO39	US-2
<i>Pia</i>	Aichi Asahi	BC ₁ F ₂₀	BC ₆ F ₁₅	—	—
	ML: IRBLa-A (Aichi Asahi)	—	—	—	BC ₆ F ₇
	CO39	BC ₁ F ₂₀	BC ₆ F ₁₅	—	—
	ML: IRBLa-C (CO39)	—	—	—	BC ₆ F ₇
	Zenith	—	BC ₆ F ₁₄	—	—
<i>Pib</i>	BL1	BC ₁ F ₁₅	BC ₆ F ₁₄	—	—
	ML: IRBLb-B (BL1)	—	BC ₃ F ₁	BC ₄ F ₁	—
	IRAT13	—	—	BC ₆ F ₁₄	—
	WHD-1S-175-1-127	—	—	BC ₆ F ₁₄	—
<i>Pii</i>	Fujisaka5	BC ₁ F ₂₀	—	—	—
	IRBLi-F5 (Fujisaka5)	—	BC ₃ F ₁	BC ₄ F ₁	BC ₃ F ₁
<i>Pik</i>	Kanto51	BC ₁ F ₂₀	BC ₆ F ₁₄	BC ₆ F ₁₄	—
	ML: IRBLk-Ka (Kanto51)	—	—	—	BC ₆ F ₈
	Kusabue	—	—	BC ₆ F ₁₄	—
<i>Pik-h</i>	K3	BC ₁ F ₁₅	BC ₆ F ₁₄	BC ₆ F ₁₄	—
	ML: IRBLkh-K3 (K3)	—	—	—	BC ₆ F ₇
<i>Pik-m</i>	Tsuyuake	BC ₁ F ₁₆	—	BC ₆ F ₁₄	—
	ML: IRBLkm-T (Tsuyuake)	—	BC ₂ F ₁	—	BC ₄ F ₁

Table 1. Generation of near isogenic line (NIL) series with blast resistance genes developed at IRRI in 2005 dry season (continued)

Targeted resistance gene	Donor (Original variety)	Recurrent backcross parents			
		Monogenic line	Near isogenic line		
		LTH	LTH	CO39	US-2
<i>Pik-p</i>	K60	BC ₁ F ₂₀	—	BC ₆ F ₁₄	—
	ML: IRBLkp-K60 (K60)	—	BC ₃ F ₁	—	BC ₆ F ₇
<i>Pik-s</i>	Shin2	BC ₁ F ₂₀	BC ₆ F ₁₄	—	—
	ML: IRBLks-S (Shin2)	—	—	—	BC ₆ F ₇
	ML: IRBLks-F5 (Fujisaka5)	—	—	—	BC ₆ F ₇
	Caloro	—	—	BC ₆ F ₁₄	—
	B40	—	BC ₆ F ₁₄	—	—
	Zhaiyeqing8	—	BC ₆ F ₁₁	—	—
<i>Pish</i>	Shin2	BC ₁ F ₂₀	—	BC ₆ F ₁₄	—
	ML: IRBLsh-S (Shin2)	—	BC ₃ F ₁	BC ₄ F ₁	BC ₃ F ₁
	BL1	BC ₁ F ₁₈	—	BC ₆ F ₁₄	—
	ML: IRBLsh-B (BL1)	—	BC ₃ F ₁	—	—
	Kusabue	—	—	BC ₆ F ₁₄	—
<i>Pit</i>	K59	BC ₁ F ₆	—	—	—
<i>Pita</i>	C101PKT	BC ₅ F ₁₆	BC ₂ F ₁	—	—
	ML: IRBLta-CP1 (C101PKT)	—	BC ₂ F ₁	—	BC ₆ F ₈
	K1	BC ₂ F ₁₈	BC ₆ F ₁₄	—	—
	ML: IRBLta-K1 (K1)	—	—	—	BC ₆ F ₈
	C105TTP2L9	BC ₃ F ₁₈	BC ₆ F ₁₆	—	—
	ML: IRBLta-CT2 (C105TTP2L9)	—	—	—	BC ₆ F ₈
	Zhaiyeqing8	—	BC ₆ F ₁₄	—	—
Yashiromochi	—	—	BC ₆ F ₁₄	—	
<i>Pita-2</i>	Reiho	BC ₁ F ₁₆	—	BC ₆ F ₁₄	—
	ML: IRBLta2-Re (Reiho)	—	—	—	BC ₃ F ₁
	Pi No. 4	BC ₁ F ₁₄	BC ₆ F ₁₁	BC ₆ F ₁₄	—
	ML: IRBLta2-Pi (Pi.No.4)	—	—	—	BC ₄ F ₁
	IR64	—	—	BC ₆ F ₁₂	—
	Fukunishiki	—	BC ₆ F ₁₅	—	—
<i>Piz</i>	Fukunishiki	BC ₁ F ₂₀	BC ₃ F ₁	—	—
	ML: IRBLz-Fu (Fukunishiki)	—	—	—	BC ₄ F ₁
<i>Piz-5</i>	C101A51	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	—
	ML: IRBLz-CA (C101A51)	—	—	—	BC ₄ F ₁
	K60	—	BC ₆ F ₁₄	—	—
	Tadukan	—	BC ₆ F ₁₄	—	—
<i>Piz-t</i>	Toride1	BC ₆ F ₁	BC ₆ F ₁₅	—	—
	ML: IRBLzt-T (Toride1)	—	—	—	BC ₆ F ₈
	IR56	—	—	BC ₆ F ₁₂	—
<i>Pil</i>	C101LAC	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	—
	ML: IRBL1-CL (C101LAC)	—	—	—	BC ₆ F ₇
<i>Pi3</i>	C104PKT	BC ₂ F ₁₈	BC ₆ F ₁₆	—	—
	ML: IRBL3-CP4 (C104PKT)	—	—	BC ₄ F ₁	BC ₄ F ₁
	Taebaeg	—	BC ₆ F ₁₅	—	—

Table 1. Generation of near isogenic line (NIL) series with blast resistance genes developed at IRRI in 2005 dry season (continued)

Targeted resistance gene	Donor (Original variety)	Recurrent backcross parents			
		Monogenic line	Near isogenic line		
		LTH	LTH	CO39	US-2
<i>Pi5</i> (t)	RIL249 (Moroberekan)	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	–
	ML: IRBL5-M (RIL249)	–	–	–	BC ₆ F ₈
<i>Pi7</i> (t)	RIL29 (Moroberekan)	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	–
	ML: IRBL7-M (RIL29)	–	–	–	BC ₆ F ₇
<i>Pi9</i> (t)	WHD-IS-75-1-127	BC ₃ F ₁₈	BC ₆ F ₁₆	–	–
	ML: IRBL9-W (WHD-1S-75-1-127)	–	–	BC ₃ F ₁	BC ₆ F ₇
<i>Pi11</i>	Zhaiyeqing8	BC ₂ F ₁₈	–	–	–
	ML: IRBL11-Zh (Zhaiyeqing8)	–	–	BC ₄ F ₁	–
<i>Pi12</i> (t)	RIL10 (Moroberekan)	BC ₂ F ₁₈	–	–	–
	ML: IRBL12-M (RIL10)	–	BC ₃ F ₁	BC ₄ F ₁	BC ₆ F ₇
<i>Pi19</i>	Aichi Asahi	BC ₁ F ₁₇	–	–	–
	ML: IRBL19-A (Aichi Asahi)	–	BC ₁ F ₁	BC ₁ F ₁	BC ₁ F ₁
<i>Pi20</i> (t)	IR24	BC ₁ F ₁₆	–	–	–
	ML: IRBL20-IR24 (IR24)	–	BC ₂ F ₁	BC ₃ F ₁	BC ₃ F ₁

A total of 20 Philippines strains¹⁰ that were clarified by the pathogenicity and selected as the differential blast isolates, were used to estimate the resistance genes by the reaction pattern (Table 2). Avirulent isolates to the resistance genes were inoculated to confirm the presence and homozygosity of the corresponding genes in each developing progeny. Ten seedlings per line raised in plastic trays were inoculated at the 4th or 5th leaf stage by spraying with a spore suspension. Six or seven days after inoculation, each line was evaluated by their susceptibility based on the degree of infection of each seedling. The reaction was classified into a scale of 0 to 5 with slight modifications as described previously by Mackill and Bonman⁶. Scale 3 was further divided into two ratings depending on the breadth of the lesion. Where the biggest lesion was elongated less than or more than 3 mm, the plant was rated as 3⁻ or 3⁺, respectively. The reactions of differential varieties were categorized and summarized into three reaction classes wherein 0–2 were resistant (R), 3⁻ was moderately resistant (M), 3⁺ was moderately susceptible (MS), and 4–5 were considered susceptible (S). LTH and CO39 were used as susceptible check varieties.

During the development, lines targeting *Pi19* or *Pit* were susceptible to all Philippine blast isolated and used for selection. Lines with *Pik*, *Pik-m*, *Pik-h*, *Pik-p*, *Pi1*, or *Pi7* showed the same reaction pattern to the isolate of each other. Varieties with *Piz*, *Piz-5* (*Pi2*) or *Pish* showed a wide spectrum of resistance to the Philippine isolates. For these genes, selection was done at the National Institute

of Crop Science (NICS) in Japan under the IRRI-Japan shuttle research program, because of difficulty in selection by using the Philippine blast isolates.

Agronomical traits including heading date and several morphological characteristics of the developed lines were evaluated to confirm the genetic uniformity and similarity to the corresponding recurrent parent.

Results

1. Monogenic lines as a new set of international standard differential varieties

Thirty-one monogenic lines for targeting 24 kinds of resistance genes, *Pia*, *Pib*, *Pii*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pit*, *Pita*, *Pita-2*, *Piz*, *Piz-5* (*Pi2*), *Piz-t*, *Pi1*, *Pi3*, *Pi5*(t), *Pi7*, *Pi9*(t), *Pi11*(t), *Pi12*(t), *Pi19*(t), and *Pi20*, were developed⁷. Twenty-five blast resistant varieties were used as donor parents of the resistance genes. Monogenic lines were bred by the backcross method to transfer the single gene into the recurrent parent, LTH, which was not identified to have any major resistance gene in the genetic background.

These monogenic lines were fixed with the resistance genes and showed clear reactions to blast isolates from the Philippines, however, they also had diverse agronomic traits among them. As a result of an evaluation of culm length, panicle length, days to heading, 100-grain weight, panicle number, spikelet fertility, leaf length, and leaf width over 4 cropping seasons, significant differences

Table 2. Reaction patterns of monogenic lines to blast isolates from the Philippines

Target gene	Designation ^{a)}	Generation	Blast Isolates ^{b)}																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<i>Pit</i>	IRBLt-K59	BC ₂ F ₁₁	MS-S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	
<i>Pi19</i> (t)	IRBL19-A	BC ₁ F ₁₃	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
<i>Pia</i>	IRBLa-A	BC ₁ F ₁₆	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
	IRBLa-C	BC ₁ F ₁₆	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
<i>Pib</i>	IRBLb-B	BC ₁ F ₁₁	S	S	S	S	S	S	S	S	S	S	S	S	S	R-M	R	R-M	R	R	R	R	M
<i>Piks-s</i>	IRBLks-F5	BC ₁ F ₁₆	S	S	S	S	S	S	S	S	S	S	S	S	S	R	R	S	S	S	S	S	S
	IRBLks-S	BC ₁ F ₁₆	M	S	S	S	S	S	S	S	S	S	S	S	S	R	R	S	S	S	S	S	S
<i>Pik</i>	IRBLk-Ka	BC ₁ F ₁₅	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pik-p</i>	IRBLkp-K60	BC ₁ F ₁₄	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pik-h</i>	IRBLkh-K3	BC ₁ F ₁₄	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pik-m</i>	IRBLkm-Ts	BC ₁ F ₁₂	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pi1</i>	IRBL1-CL	BC ₃ F ₁₄	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pi7</i> (t)	IRBL7-M	BC ₃ F ₁₄	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Piz-t</i>	IRBLzt-T	BC ₁ F ₁₆	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
<i>Pita</i>	IRBLta-K1	BC ₂ F ₁₄	MS	S	R	R	R	R-M	S	M	R	R	S	R	R	S	S	S	S	S	S	R-M	M
	IRBLta-CT2	BC ₃ F ₁₄	S	S	R	R	R	R	S	S	MS	R	R	R	R	S	S	S	S	S	S	R	MS
	IRBLta-CP1	BC ₃ F ₁₂	S	S	R	R-M	M	M	S	S	S	R	R	R	R	S	S	S	S	S	S	S	S
<i>Pii</i>	IRBLi-F5	BC ₁ F ₁₆	R	S	R-M	S	S	M	S	R	R	R-M	R	S	R-M	S	S	S	S	S	S	S	S
<i>Pi3</i>	IRBL3-CP4	BC ₃ F ₁₄	R	S	R	S	S	M	R	S	R	M	R-M	S	R	S	MS	S	S	S	S	S	S
<i>Pi5</i> (t)	IRBL5-M	BC ₃ F ₁₄	R	S	R	S	S	M	R	S	R	R-M	R-M	S	R	S	S	S	S	S	S	S	S
<i>Pi12</i> (t)	IRBL12-M	BC ₂ F ₁₄	S	S	S	S	S	S	S	S	S	S	S	S	M	M	R	R	R	R	R	R	R
<i>Pi20</i> (t)	IRBL20-IR24	BC ₁ F ₁₂	S	S	S	S	S	S	S	S	S	S	R	S	S	R	S	S	S	S	S	S	R
<i>Pi11</i> (t)	IRBL11-Zh	BC ₂ F ₁₄	S	S	S	S	S	S	S	S	MS	S	MS-S	M	S	S	R-M	R	R	R	R	R-M	R-M
<i>Pita-2</i>	IRBLta2-Pi	BC ₁ F ₁₀	S	S	R	R	R	R-M	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S
	IRBLta2-Re	BC ₁ F ₁₂	S	S	R	R	R	R-M	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S
<i>Pi9</i> (t)	IRBL9-W	BC ₃ F ₁₄	R	R	R	R	R	R-M	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
<i>Pish</i>	IRBLsh-S	BC ₁ F ₁₆	R-M	M	R-M	R-M	M	M	R-M	R-M	R-M	M	M	M	M	M	R-M	M	M	M	M	R-M	MS
	IRBLsh-B	BC ₁ F ₁₆	R-M	M	M	M	M	MS	M	M	M	R-M	MS	M	M	M	R-M	M	M	M	M	M	MS
<i>Piz</i>	IRBLz-Fu	BC ₁ F ₁₆	R-M	M	R	R-M	R-M	M	R-M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
<i>Piz-5</i>	IRBLz5-CA	BC ₃ F ₁₄	R	R-M	M	R	R-M	M	R-M	R	R	R-M	M	M	M	M	M	M	M	M	M	M	M
	IRBLz5-CA(R)	BC ₃ F ₁₂	R	R-M	R-M	R	R-M	R-M	R	R	R	R-M	R	R-M	R-M	M	M	M	M	M	M	M	R-M

a): Monogenic lines are designated as IRBL followed by the resistance gene then the abbreviation of the resistant donor variety.

b): 1: PO6-6, 2: CA89, 3: 43, 4: CA41, 5: M64-1-3-9-1, 6: M39-1-3-8-1, 7: M39-1-2-21-2, 8: M36-1-3-10-1, 9: JMB8401, 10: IK81-25, 11: IK81-3, 12: BNI11, 13: V850256, 14: V850196, 15: V86010, 16: JMB840610, 17: BN209, 18: M101-1-2-9-1, 19: B90002, 20: C923-49.

R: resistant, M: moderately resistant, MS: moderately susceptible, S: susceptible, R-M: varied from moderately resistant to resistant.

between the monogenic lines and the recurrent parent, LTH were observed (data not presented).

These monogenic lines were designated as 'IRBL' lines (IRRI bred blast resistance lines) followed by the resistance gene, and then the abbreviation of the resistant donor variety. For example, IRBLa-A is a line with a resistance gene *Pia* originating from Aichi Asahi as a donor parent. These lines have been distributed to more than 30 institutes around the world through the International Network for Genetic Evaluation of Rice (INGER) and the IRRI-Japan Collaborative Research Project, IRRI.

2. Near-isogenic lines (NILs)

Two sets of NILs for blast resistance with different genetic backgrounds, LTH and CO39, were completed for several resistance genes, and the series of US-2 NILs and the remaining combinations in the LTH and CO39 genetic background of differential varieties were also developed for targeting 24 kinds of resistance genes.

(1) LTH genetic background

The monogenic lines have been further backcrossed with LTH to generate NILs. A total of 23 lines for 14 kinds of resistance genes, *Pia*, *Pib*, *Pik*, *Pik-h*, *Pik-s*, *Pita*, *Pita-2*, *Piz-5* (*Pi2*), *Piz-t*, *Pi1*, *Pi3*, *Pi5*(t), *Pi7*, and *Pi9*, have been generated to advanced generations (more than BC₆F₁₀) by 2005 (Table 1). Six agronomic traits (culm length, panicle length, panicle number per plant, days to heading, spikelet fertility, and 100-seeds weight) of these lines were almost fixed and similar to that of LTH (data not presented).

(2) CO39 genetic background

As a representative variety of Indica-type rice, CO39 was used to develop NILs for blast resistance. This variety is susceptible to blast fungus, but it is reported to harbor a resistance gene *Pia*³. NILs for 23 kinds of resistance genes have been developed (Table 1). Among them, 20 lines have been developed to more than the BC₆F₁₀ generation for 14 kinds of resistance genes, *Pib*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pita*, *Pita-2*, *Piz-5* (*Pi2*), *Piz-t*, *Pi1*, *Pi5*(t), and *Pi7*, and can be used as differential varieties. This is because *Pia* showed resistance to a small number of blast isolates and had a narrow spectrum. This is the first Indica-type background differential variety set for a large number of resistance genes.

(3) US-2 genetic background

LTH and CO39 were good susceptible checks and have the genetic backgrounds as differential varieties. However, seeds of these two lines are difficult to obtain in sufficient amounts because they lodge easily after head-

ing under tropical conditions. US-2 was developed as a 'universal susceptible' rice line, which is not known to have any blast resistance genes in the genetic background. Unlike LTH and CO39, it can be cultivated easily under both tropical and temperate conditions (Ando and Hayashi, unpublished). US-2 is a suitable variety for the genetic background of international differential varieties for blast resistance. NILs with the US-2 genetic background are also being developed for targeting 21 resistance genes, *Pia*, *Pii*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pita*, *Pita-2*, *Piz*, *Piz-5*, *Piz-t*, *Pi1*, *Pi3*, *Pi5*, *Pi7*, *Pi9*, *Pi12*(t), *Pi19*, and *Pi20* (Table 1).

Discussion

Monogenic lines are used in the first set of international differential varieties which targeted a large number of resistance genes while harboring only a single one in each genetic background. These differential varieties that were developed are useful tools to clarify the pathogenesis of blast races and to identify the resistance genes in rice varieties based on the gene-for-gene theory¹. Without using expensive facilities, a set of these varieties can provide useful information for breeding programs to improve blast resistance. These lines are also offered as useful materials for genetic and molecular biological studies of blast resistance in rice. Furthermore, these lines can be important breeding materials to improve blast resistance of a rice variety.

The monogenic lines had been distributed to plant pathologists and breeders in 30 institutes in 14 countries world wide by 2004. These materials will allow a comprehensive study to be made of blast at a global level. These can be used as standard varieties in international collaborative research. The information on blast research will be exchanged among breeders, pathologists and other scientists through the collaboration. For example, these distributions and the geographical relationships between resistance genes in rice varieties and blast races might be clarified under the collaboration. In addition, the information will be very useful to understand the characters of blast disease and make plans for rice breeding of a durable resistance system.

We have been continuously developing the blast resistant NILs, even after releasing the monogenic lines. Newly developed NILs will be released replacing the monogenic lines shortly. A set of NILs is the most suitable material for race differentiation. NILs with the LTH and CO39 backgrounds can be used as gene sources in breeding programs for Japonica and Indica-type rice varieties, respectively. Although NILs with the US-2 genetic background will be more efficient tools, they are still

under development and take time to be established. In addition to the 24 targeted genes, lines for other resistance genes including QTL, field resistance and panicle blast resistance will be developed with this genetic background, to clarify the effect of each gene and QTL or for analysis of these abilities in more advanced studies such as gene pyramiding.

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