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Methods and Strategy for Monitoring Race Distribution and Identification of Resistance Genes to Bacterial Leaf Blight (*Xanthomonas campestris* pv. *oryzae*) in Rice

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Abstract

For controlling bacterial leaf blight of rice, caused by *Xanthomonas campestris* pv. *oryzae*, the use of resistant cultivars is the most economical and effective method due to the scarcity of effective bactericidal agents and to the need for preserving the environment. Against this background, the resistance genes to this disease so far identified will be reviewed. Under the collaboration between the Tropical Agriculture Research Center, Japan and the International Rice Research Institute, Philippines, the genes identified were rearranged from *Xa-1* to *Xa-12* based on the numbering system of rice gene symbols and them near-isogenic lines with single resistance genes were developed. By using these near-isogenic lines, the strategy for monitoring the race distribution and the methods of identification of new resistance genes are reviewed.

Discipline: Plan breeding
Additional key words: allelism test, differentials, near-isogenic line, plant disease

Introduction

Bacterial leaf blight caused by *Xanthomonas campestris* pv. *oryzae* is responsible for heavy damage to rice in the rice-growing countries. For controlling the disease, the use of resistant cultivars is the most economical and effective method due to the scarcity of effective bactericidal agents and to the need for preserving the environment.

Since the pathogenic specialization of the causal bacterium of rice bacterial leaf blight was first reported in Japan, a number of reports have been published on the variability of the pathogenicity of the bacterium and of the resistance of rice cultivars.

Since the rice cultivars and bacterial races used as differentials in each country were different, the respective groups of scientists found it difficult to distinguish the resistance gene(s). In order to control the disease, it was deemed important to set up a common base to define the relationship between the virulence of the bacterial races and the resistance of rice cultivars to the races. Recent research on bacterial leaf blight has been carried out mostly in Japan and at IRRI (International Rice Research Institute, Philippines) and in both locations different differential cultivars and bacterial groups were used.

Against this background, the collaborative studies on the resistance to rice bacterial leaf blight between Japan and IRRI were carried out for establishing a common base of research and for controlling the disease.

This paper deals with the results of the collaboration and the strategy for monitoring the race distribution and for the identification of resistance genes using the near-isogenic lines developed under the collaboration.

Resistance genes to bacterial leaf blight of rice

1) Genes identified in various countries

The identification of the resistance genes in each country, except for *Xa-kg*, was based on analyses using local bacterial isolates. As a result of the genetic studies on the resistance to the disease conducted

Table 1. Resistance genes to bacterial leaf blight originally identified in rice[1,3]

Gene identified	Cultivar analyzed	Isolate used	Note	Reference
		Japanese isolates		
X_1	Kogyoku	Giken 44		30)
X_2, X_3	Shimotsuki	Nara Himeji	Complementary gene for X_1	30)
Xa-1	Kogyoku Koganemaru Pi No. 1	X-17	Chromosome 11 (Nishimura 1961)	22)
Xa-2	Rantai Emas 2	X-17 X-14	Linked with *Xa-1* (2-16%)	22)
Xa-3	Wase Aikoku 3 Java 14 Koentoelan Nagomasari	Q6808 (I) Q7102 (I) T7174 (I) H5809 (II) T7147 (II) Q6809 (III) T7133 (III)	Adult resistance	1)
Xa-1^h	IR28 IR29 IR30	T7174 (I)		32)
Xa-kg^h	IR28 IR29 IR30	H75304 (V)	Linked with *Xa-1*^{h}: (2.0±0.65%)	32)
Xa-11	IR944-102-2-3- RP9-3	T7174 (I) T7147 (II) T7133 (IIIA) IVA7505 (IV)		9)
		Philippine isolates		
Xa-4	IR20 IR22 IR1529-680-3	PXO 25 (1)		21)
xa-5	IR1545-339 RP291-7	PXO 25 (1)		21)
Xa-4^a	IR22 Sigadis TKM6, etc.	PXO 61 (1)		4)
Xa-4^b	Semora Mangga	PXO 61 (1)	Adult resistance	4)
Xa-6	Malagkit Sungsong Zenith, etc.	PXO 61 (1)		23)
Xa-7	DZ78 DV85 DV86	PXO 61 (1)	Adult resistance	24)
xa-8	PI231129	PXO 61 (1)		24)
xa-9	Khao Lay Nhay Sateng	PXO 61 (1)	Linked with *Xa-6* (5.9%)	26)
Xa-10	Cas209	PXO 61 (1) PXO 86 (2) PXO 79 (3) PXO 71 (4)	Linked with *Xa-4* (27.6±0.2) Chromosome 5 (Shastry et al. 1960)	34)

(Table 1, continued)

Gene identified	Cultivar analyzed	Isolate used	Note	Reference
		Sri Lankan isolates		
Xa-a, *Xa-k*	Wase Aikoku 3	CAR1	Multiple genes	31)
Xa-i	PI209938 Zenith RL Gopher		Multiple genes	31)
Xa-p	PI209938 Zenith		Multiple genes	31)
Xa-b	Bluebonnet/Rexark		Incomplete	31)
		Indonesian isolates		
Xa-kg	Kogyoku Java 14	Xo-7306 (V)	Linked with *Xa-1* (2%)	8)
		Indian isolates		
X_1	BJ1	H14		2)
X_2		H89		
X_3		H146		
I-X_1	IR8	H14, H89, H146	Inhibitor to X_1, X_2 and X_3	2)
A	Malagkit, Sungsong	X010		5)
B		X032		
P_1	Lacrosse/Zenith-Nira			
R	IRRI 69/469 IRRI 70/470			
I_p	IR8		Inhibitor to P_1	
		Chinese isolates		
Xa-a	IR28			36)
Xa-h		Linked with *Xa-a* (17%)		35)

mainly in Japan and at IRRI, *Xa-1*, *Xa-2*, and *Xa-3* were identified using Japanese isolates in Japan[1,22], while *Xa-kg* was identified using an Indonesian isolate in Japan[8]. Furthermore, two alleles of *Xa-1* and *Xa-kg* were recognized using Japanese isolates in Japan and they were designated as *Xa-1*^{h} and *Xa-kg*^{h}, respectively[32]. On the other hand, *Xa-4*, *xa-5*, *Xa-6*, *Xa-7*, *xa-8*, *xa-9*, and *Xa-10* were identified using Philippine isolates at IRRI[4,20,21,23,24,26,34]. *Xa-4*^{b} was recognized as an allele of *Xa-4*[4,25].

Genetic studies on the resistance to the disease have also been conducted in Sri Lanka, India and China using isolates obtained in the respective countries. *Xa-a* and *Xa-k* in Wase Aikoku 3, and *Xa-p* and *Xa-i* in PI209938 were identified using Sri Lankan isolates[31]. The incompletely dominant gene, *Xa-b* was also identified in Bluebonnet/Rexark using Sri Lankan isolates[31]. The three complementary genes, Xa_1, Xa_2, and Xa_3, and the inhibitor of Xa_1, I-X_1, were detected in IR8 using Indian isolates[2]. The presence of two complementary dominant genes, A and B, in Malagkit Sungsong, one dominant gene, R, in IRRI69/469 and one dominant gene, P_1, in Lacrosse/Zenith-Nira, was suggested using two Indian isolates[5]. Furthermore, two dominant genes, *Xa-a* (different from the *Xa-a* described earlier) and *Xa-h*, were identified using Chinese strains[35,36]. Genetic studies on the resistance of rice cultivars to the disease have also been carried out in Korea, Bangladesh, and Indonesia. However, the genes have not been designated. The identified resistance genes

to bacterial leaf blight are summarized in Table 1.

2) Rearrangement of identified genes

The results of identification of resistance genes to the disease obtained from each country can not be compared because each researcher used isolates collected in the respective countries. However, the genes identified in Japan and at IRRI were compared with each other using Japanese and Philippine isolates during the collaborative studies. As a result, the resistance genes, *Xa-1*, *Xa-2*, *Xa-3*, *Xa-4*, *xa-5*, *Xa-7*, *xa-8*, *Xa-10*, and *Xa-kg* were confirmed to be different from each other[13,14]. In addition, a new resistance gene to the Japanese isolates, *Xa-11* was identified in IR8, the susceptible differential to Philippine isolates[9,18]. However, *Xa-6*, *xa-9* and *Xa-4*^{b} identified at IRRI were allelic to *Xa-3* identified in Japan[15-17]. Based on these results, gene symbols for the resistance genes to bacterial leaf blight were rearranged following the numbering system of the rice gene symbols indicated in Table 2[10]. Therefore, the *Xa-kg* symbol was rearranged as *Xa-12*[10].

The rearrangement of the genes has created problems which should be solved in future. It is generally recognized that *Xa-1*, *Xa-2*, and *Xa-12* are very closely linked. It is also possible that *Xa-1*, *Xa-2* and *Xa-12* are alleles at the same locus. In

Table 2. Rearranged genes for resistance to bacterial leaf blight

Rearranged gene	Dominance	Original designation	Representative cultivar
Xa-1	Dominant	*Xa-1*	Kogyoku
Xa-1^{h}	Dominant	*Xa-1*^{h}	IR28, IR29, IR30
Xa-2	Dominant	*Xa-2*	Rantai Emas 2, Te-tep
Xa-3	Dominant	*Xa-w*	Wase Aikoku 3
		Xa-4^{b}	Semora Mangga
		Xa-6	Zenith
		xa-9	Sateng
Xa-4	Dominant	*Xa-4*	TKM6, IR20, IR22
		Xa-4^{a}	
xa-5	Recessive	*xa-5*	DZI92, IR1545-339
Xa-7	Dominant	*Xa-7*	DV85
xa-8	Recessive	*xa-8*	PI231129
Xa-10	Dominant	*Xa-10*	Cas209
Xa-11	Dominant	*Xa-11*	RP9-3, IR8
Xa-12	Dominant	*Xa-kg*	Kogyoku, Java 14
Xa-12^{h}	Dominant	*Xa-kg*^{h}	IR28, IR29, IR30

Table 3. New genes for resistance to bacterial leaf blight recently identified

Identified gene	Dominance	Original donor	Representative cultivar
xa-13	Recessive		BJ1, Chinsurah Boro II
Xa-14	Dominant		Taichung Native 1
*xa-15**	Recessive	Harebare	M41
Xa-16	Dominant		Te-tep
Xa-17	Dominant		Asominori
Xa-18	Dominant		IR24, Milyang 23, Toyonishiki
xa-19	Recessive	IR24	XM5
xa-20	Recessive	IR24	XM6
Xa-21	Dominant	*O. longistaminata*	IR-BB 21

* Not approved yet.

Table 4. Near-isogenic lines for resistance to bacterial leaf blight of rice developed under TARC-IRRI collaboration[19)]

R-gene designation	Generation	Line no.	Cross
Xa-1 (*Xa-12*)[a)]			
IR-BB 1	BC_4F_4	IS630	IR24 * 5/Kogyoku
IR-BB 101	BC_4F_4	IS638	Toyonishiki * 5/Kogyoku
IR-BB 201	BC_4F_4	IS634	Milyang 23 * 5/Kogyoku
Xa-2 (*Xa-1*)[a)]			
IR-BB 2	BC_4F_5	B174	IR24 * 5/Te-tep
IR-BB 102	BC_4F_5	B205	Toyonishiki * 5/Te-tep
IR-BB 202	BG_4F_5	B221	Milyang 23 * 5/Te-tep
Xa-3			
IR-BB 3	BC_4F_6	IS 22	IR24 * 5/Chugoku 45
IR-BB 103	BC_4F_6	IS103	Toyonishiki * 5/Chugoku 45
IR-BB 203	BC_4F_6	IS 13	Milyang 23 * 5/Chugoku 45
IR-BB 3J	BC_4F_6	IS 40	IR24 * 5/Java 14
IR-BB 103J	BC_4F_6	IS 27	Toyonishiki * 5/Java 14
IR-BB 203J	BC_4F_6	IS 37	Milyang 23 * 5/Java 14
IR-BB 3Z	BC_4F_6	IS 74	IR24 * 5/Zenith
IR-BB 103Z	BC_4F_6	IS283	Toyonishiki * 5/Zenith
IR-BB 203Z	BC_4F_6	IS 68	Milyang 23 * 5/Zenith
IR-BB 3S	BC_4F_6	IS 91	IR24 * 5/Sateng
IR-BB 103S	BC_4F_6	IS 79	Toyonishiki * 5/Sateng
IR-BB 203S	BC_4F_6	IS341	Milyang 23 * 5/Sateng
Xa-4			
IR-BB 4	BC_4F_6	IS110	IR24 * 5/IR20
IR-BB 104	BC_4F_6	IS 98	Toyonishiki * 5/IR20
IR-BB 204	BC_4F_6	IS104	Milyang 23 * 5/IR20
xa-5			
IR-BB 5	BC_4F_5	IS133	IR24 * 5/IR1545-339
IR-BB 105	BC_4F_4	IS118	Toyonishiki * 5/FIR1545-339
IR-BB 205	BC_4F_5	IS299	Milyang 23 * 5/IR1545-339
Xa-7			
IR-BB 7	BC_4F_7	IS165	IR24 * 5/DV85
IR-BB 107	BC_4F_4	IS499	Toyonishiki * 5/DV85
IR-BB 207	BC_4F_5	IS491	Milyang 23 * 5/DV85
xa-8			
IR-BB 8	BC_4F_5	IS513	IR24 * 5/PI231129
IR-BB 108	BC_4F_5	IS831	Toyonishiki * 5/PI231129
IR-BB 208	BC_4F_5	IS818	Milyang 23 * 5/PI231129
Xa-10			
IR-BB 10	BC_4F_6	IS154	IR24 * 5/Cas209
IR-BB 110	BC_4F_5	IS140	Toyonishiki * 5/Cas209
IR-BB 210	BC_4F_6	IS150	Milyang 23 * 5/Cas209
Xa-11			
IR-BB 11	BC_4F_4	IS618	IR24 * 5/IR8
IR-BB 111	BC_4F_4	IS627	Toyonishiki * 5/IR8
IR-BB 211	BC_4F_4	IS624	Milyang 23 * 5/IR8

a): Not segregated.

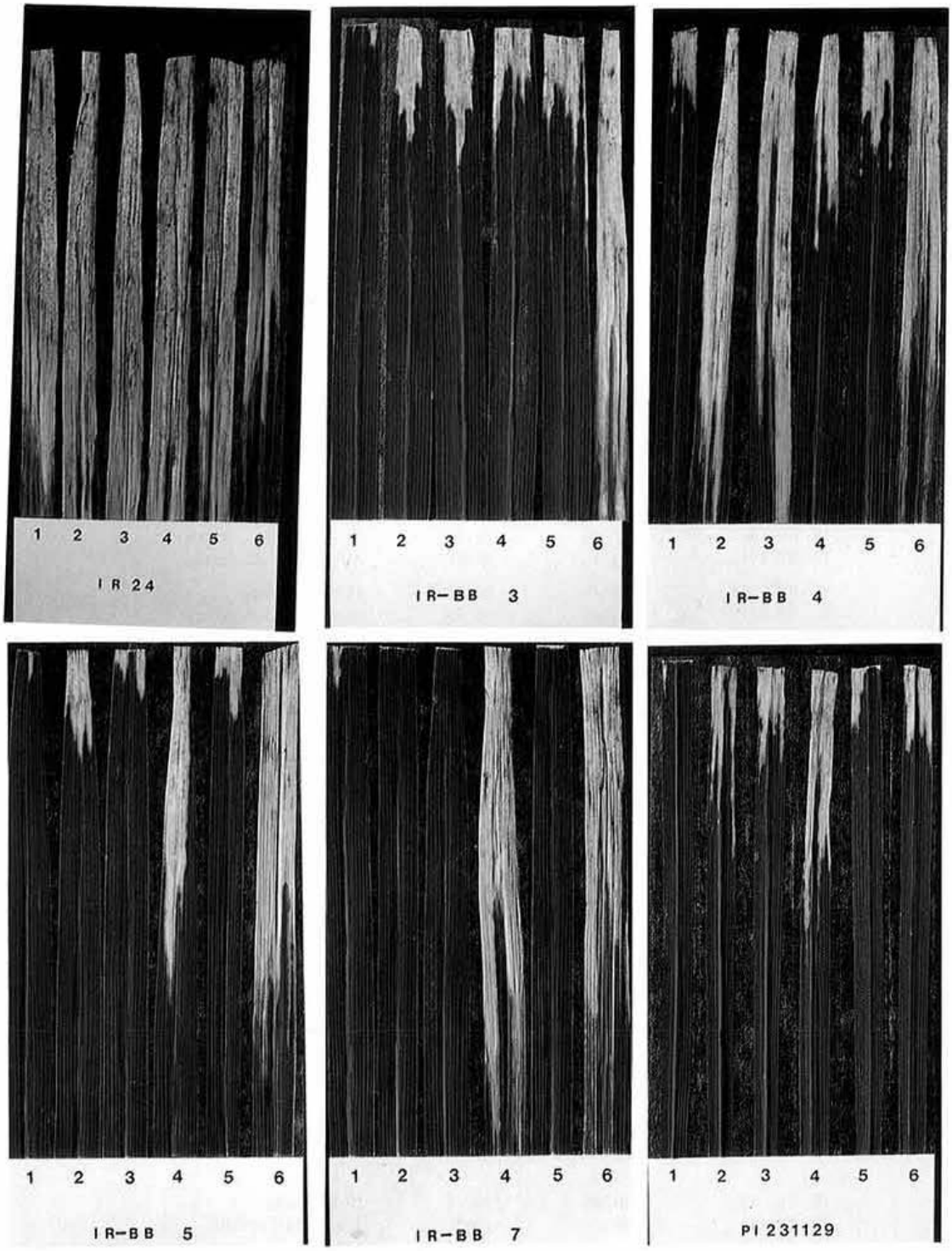
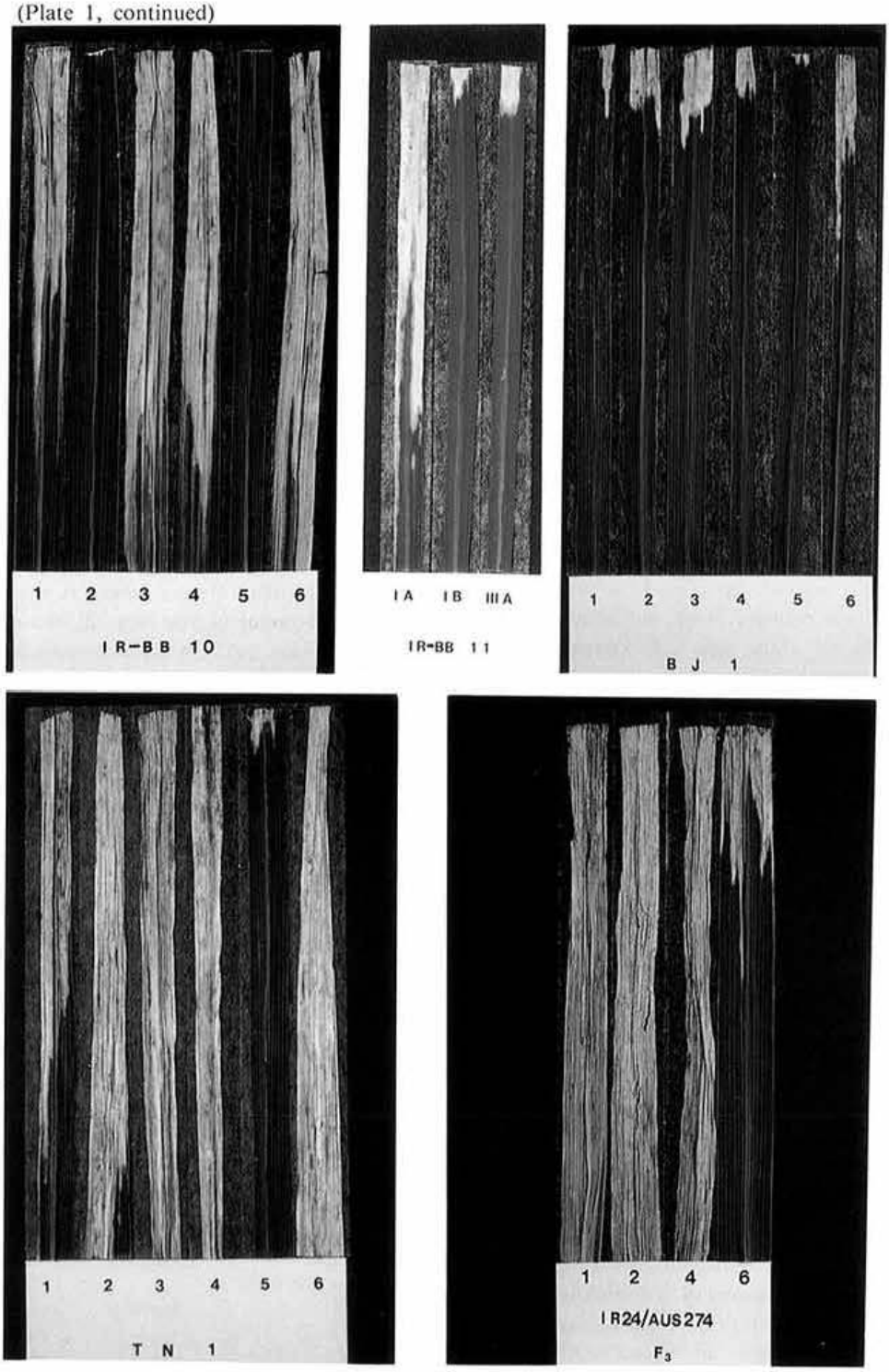


Plate 1. Reaction of near-isogenic lines and representative cultivars to Philippine and Japanese races

(Plate 1, continued)



Note: The numbers on top indicate the respective races from the Philippines (except for Japanese race IR-BB 11).
IR24/AUS274 F_3 indicates the reaction of the segregant from the cross between IR24 (susceptible) and AUS274 (*xa-5*, *xa-13*). The plant carries only the *xa-13* gene.

addition, *Xa-1*^{h} and *Xa-12*^{h} were reported to be allelic genes of *Xa-1* and *Xa-12*. Analysis using IR28, IR29, and IR30 showed that these cultivars harbor *Xa-4*, which is also effective against the Japanese isolates. Therefore, *Xa-1*^{h} and *Xa-12*^{h} should be compared with *Xa-1* and *Xa-12* based on the resistance gene *Xa-4* of IR28, IR29, and IR30 to Japanese isolates.

3) Resistance genes recently identified

During the research collaboration between Japan and IRRI, two new genes, *xa-13* and *Xa-14*, were identified using Philippine races[11,29]. *xa-13* in BJ1, AC19-1-1, AUS274, Chinsurah Boro II, and Kalimakri77-5 is resistant only to race 6 of the Philippines[11]. *Xa-14* in Taichung Native 1 is resistant only to race 5 of the Philippines[29]. However, it has not been determined whether the two genes are resistant to the Japanese isolates. Although the presence of a recessive gene, *xa-15* (a mutant from Harebare), was reported, it has not been confirmed yet because no allelic test with known recessive genes[6] was conducted.

Xa-16 in Te-tep, and *Xa-17* in Asominori were identified using Japanese isolates[7,12], while *Xa-18* in Toyonishiki, Milyang 23, and IR24 was identified using a Myanmar isolate[33].

Two recessive genes, *xa-19* and *xa-20*, were induced in IR24 by N-methyl-N-nitroso-urea (MNU)[27,28]. The two genes were resistant to all the Philippine races.

The latest resistance gene identified is *Xa-21*, which was introduced into IR24 by backcrossing from a wild rice variety, *O. longistaminata*[3]. The resistance genes to bacterial leaf blight recently identified are summarized in Table 3.

Breeding of near-isogenic lines

Near-isogenic lines with various genes for resistance to major diseases and insects can be useful for identifying races and biotypes of diseases and insects as well as new genes for resistance. Moreover, isogenic lines can serve as donors of resistance in breeding programs and be excellent materials for studying the mechanism of resistance. In the case of rice diseases and insects, no near-isogenic lines can be used as common differentials internationally due to the difficulty in exchanging materials among rice-growing countries.

To establish a common basis of research on resistance to bacterial leaf blight, attempts were made to develop near-isogenic lines with diverse genes for the resistance to the disease under the above collaboration. As a result, the initial set of near-isogenic lines (more advanced generation than BC_4F_4) was developed using IR24, Milyang 23, and Toyonishiki as recurrent parents (Table 4)[19].

Strategy for monitoring race distribution and identification of new genes

1) Proposed international differentials for bacterial leaf blight pathogen.

The near-isogenic lines were developed with IR24 for use as international differentials to the bacterial leaf blight pathogen and as testers to identify new resistance genes to the disease. However, the genes recently identified are not related to these lines because the breeding of near-isogenic lines carrying the new resistance genes is currently underway.

Therefore, it is recommended to use the lines and

Table 5. Proposed international differentials for monitoring the race distribution of the bacterial leaf blight pathogen

Differentials	Ecotype	Resistance gene
Proposed international differentials:		
Toyonishiki	Japonica	*Xa-18*
IR24	Indica	*Xa-16*
IR-BB 1	Indica	*Xa-1*, *Xa-12*
IR-BB 2	Indica	*Xa-2*
IR-BB 3	Indica	*Xa-3*
IR-BB 4	Indica	*Xa-4*
IR-BB 5	Indica	*xa-5*
IR-BB 7	Indica	*Xa-7*
IR-BB 8	Indica	*xa-8*
IR-BB 10	Indica	*Xa-10*
IR-BB 11	Indica	*Xa-11*
IR-BB 21[a]	Indica	*Xa-21*
BJ1	Indica	*xa-5*, *xa-13*
Taichung Native 1	Indica	*Xa-14*
Asominori	Japonica	*Xa-17*
Optional differentials:		
M41[b]	Japonica	(*xa-15*)
XM5[c]		*xa-19*
XM6[c]		*xa-20*

a): Newly developed[3].
b): Mutant from Harebare.
c): Mutant from IR24.

cultivars shown in Table 5 for monitoring the race distribution of the bacterial leaf blight pathogen.

By using the 18 cultivars listed above, it is likely that most races could be identified and effective resistance genes could be recognized in each country.

2) Methods for identification of a new resistance gene

For the identification of a new resistance gene to bacterial leaf blight, the following steps are recommended:

Step 1: Comparison of reaction pattern; the above 18 differentials should be subjected to inoculation tests together with the resistant cultivar where the resistance gene is expected to be identified. If the reaction of the resistant cultivar is clearly different from that of the differentials and if it is confirmed that the resistant cultivar carries only one resistance gene in **Step 3**, the resistant cultivar can be considered to carry a new resistance gene.

Step 2: Hybridization; it is always necessary to obtain the F_1 hybrids between resistant and susceptible cultivars.

Step 3: Determination of the number of resistance genes; by breeding the F_2 population between susceptible and resistant cultivars, the number of resistance genes in the resistant cultivar should be estimated from the ratio of segregation in the population.

Step 4: Allelic test with dominant genes; when the F_1 hybrids obtained in **Step 2** are resistant to the isolates, it is necessary to develop F_2 hybrids between the resistant cultivar and the above differentials which carry dominant genes and show a similar reaction to that of the tested resistant cultivar. If susceptible plants are detected in every F_2 population, the resistant cultivar can be considered to carry a new resistance gene.

Step 5: Allelic test with recessive genes; when the F_1 hybrids obtained in **Step 2** are susceptible, the resistant cultivar should be crossed with differentials, which carry a recessive gene and show a similar reaction to that of the resistant cultivar, to obtain the F_1 hybrids. If every F_1 hybrid is susceptible to the isolates, it is assumed that the resistant cultivar carries new resistance gene.

If there is more than one resistance gene in the tested resistant cultivar in **Step 3**, a similar procedure should be adopted from **Step 1** onward except for **Step 3** after obtaining segregants carrying only one resistance gene from the hybridization between susceptible and resistant cultivars.

Resistance reactions of cultivars

There are various kinds of resistance reactions to the bacterial leaf blight pathogen in rice cultivars. Usually, it is recommended to observe rice plants during 2 to 4 weeks after inoculation by applying the clipping method. Suitable concentration of bacteria for inoculation may be 10^8 cells/m*l*. The resistant plants show a lesion length below about 6 cm at 3 weeks after inoculation. However, the reactions vary depending on the virulence of the inoculum, weather conditions, plant age, etc.

The resistance reactions of cultivars can be classified into the following categories.

1. Highly resistant; no or minimal lesion development after inoculation (reaction of cultivar with *Xa-10* gene to Philippine race 2).
2. Resistant; lesion length below about 6 cm at 3 weeks after inoculation (reaction of cultivar with *Xa-4* gene to Philippine race 1).
3. Resistant with lesions showing a brown margin; lesions are less than about 6 cm long at 3 weeks after inoculation and they are characterized by a brown margin or spots around the lesions (reaction of cultivar with *Xa-3* gene to Philippine races 1 to 4).
4. Moderately resistant or susceptible, i.e. variable; lesions continue to develop after inoculation, but more slowly than in the case of the susceptible cultivars (reaction of cultivars with *Xa-4* and *xa-5* genes to Philippine race 4).
5. Susceptible; lesions continue to develop after inoculation. These reactions are illustrated in Plate 1.

References

1) Ezuka, A. et al. (1975): Inheritance of resistance of rice variety Wase Aikoku 3 to *Xanthomonas oryzae*. *Bull. Tokai-Kinki Nat. Agr. Exp. Sta.*, **28**, 124-130.
2) Jayaraj, D. et al. (1972): Genetics of resistance to bacterial leaf blight in rice. *Indian J. Genet. Plant Breed.*, **32**, 77-89.
3) Khush, G. S. et al. (1990): A new gene for resistance to bacterial blight from *O. longistaminata*. *Rice Genet. Newsl.*, **7**, 121-122.
4) Librojo, V. et al. (1976): Genetic analysis of bacterial blight resistance in four varieties of rice. *SABRAO J.*, **8**, 105-110.

5) Moses, C. J. et al. (1974): Inheritance of resistance to bacterial blight in rice. *Indian J. Genet. Plant Breed.*, **34**, 271–279.
6) Nakai, H. et al. (1988): Studies on mutation breeding of rice for bacterial leaf blight resistance. 6. Determination of gene of the resistant M41 mutant to the multiple races. *Jpn. J. Breed.*, **35** (suppl. 1), 290–291 [In Japanese].
7) Noda, T. & Ohuchi, A. (1989): A new pathogenic race of *Xanthomonas campestris* pv. *oryzae* and inheritance of resistance to it. *Ann. Phytopath. Soc. Jpn.*, **55**, 201–207.
8) Ogawa, T. et al. (1978): Inheritance of resistance to rice varieties Kogyoku and Java 14 to bacterial group V of *Xanthomonas oryzae*. *Ann. Phytopath. Soc. Jpn.*, **44**, 137–141.
9) Ogawa, T. & Yamamoto, T. (1986): Inheritance of resistance of bacterial blight in rice. *In* Rice genetics. IRRI, Manila, 471–479.
10) Ogawa, T. (1987): Gene symbols for resistance to bacterial leaf blight. *Rice Genet. Newsl.*, **4**, 41–43.
11) Ogawa, T. et al. (1987): A new recessive gene for resistance to bacterial blight of rice. *Rice Genet. Newsl.*, **4**, 98–100.
12) Ogawa, T. et al. (1989): Resistance gene of rice cultivar, Asominori to bacterial blight of rice. *Jpn. J. Breed.*, **39** (suppl. 1), 196–197 [In Japanese].
13) Ogawa, T. & Khush, G. S. (1989): Major genes for resistance to bacterial blight in rice. *In* Bacterial blight of rice. IRRI, Manila, 177–192.
14) Ogawa, T. et al. (1990): Genetics of resistance in rice cultivars, Chugoku 45 and Java 14 to Philippine and Japanese races of bacterial blight pathogen. *Jpn. J. Breed.*, **40**, 77–90.
15) Ogawa, T. et al. (1990): Genetics of resistance in rice cultivars, Zenith and Cempo Selak to Philippine and Japanese races of bacterial blight pathogen. *Jpn. J. Breed.*, **40**, 183–192.
16) Ogawa, T. et al. (1990): Genetics of resistance in rice cultivars Sateng to Philippine and Japanese races of bacterial blight pathogen. *Jpn. J. Breed.*, **40**, 329–338.
17) Ogawa, T. et al. (1990): Genetics of resistance in rice cultivars, IR20 and Semora Mannga to Philippine and Japanese races of bacterial blight pathogen. *Jpn. J. Breed.*, **40**, 435–447.
18) Ogawa, T. et al. (1991): Resistance and its inheritance to bacterial blight of IR8 rice cultivar group. *Jpn. J. Breed.*, **41**, 211–221.
19) Ogawa, T. et al. (1991): Breeding near-isogenic lines of rice with single genes for resistance to bacterial blight pathogen (*Xanthomonas campestris* pv. *oryzae*). *Jpn. J. Breed.*, **41**, 523–529.
20) Olufowote, J. O. et al. (1977): Inheritance of bacterial blight resistance in rice. *Phytopathology*, **67**, 772–775.
21) Petpisit, V. et al. (1977): Inheritance of resistance of bacterial blight in rice. *Crop Sci.*, **17**, 551–554.
22) Sakaguchi, S. (1967): Linkage studies on the resistance to bacterial leaf blight, *Xanthomonas oryzae*. *Bull. Nat. Inst. Agr. Sci., Jpn.*, Ser. D**16**, 1–18 [In Japanese with English summary].
23) Sidhu, G. S. & Khush, G. D. (1978): Dominance reversal for a bacterial blight resistance gene in some rice cultivars. *Phytopathology*, **68**, 461–463.
24) Sidhu, G. S. et al. (1978): Genetics analysis of bacterial blight resistance in seventy-four cultivars of rice, *Oryza sativa* L. *Theor. Appl. Genet.*, **53**, 105–111.
25) Sidhu, G. S. et al. (1979): Genetics analysis of bacterial blight in seventy cultivars of rice, *Oryza sativa* L., from Indonesia. *Crop. Improv.*, **6**, 19–25.
26) Singh, R. J. et al. (1983): A new gene for resistance to bacterial blight in rice. *Crop Sci.*, **23**, 558–560.
27) Taura, S. et al. (1991): Identification of a recessive gene in induced mutant line XM5 of rice to bacterial blight. *Jpn. J. Breed.*, **41**, 427–432.
28) Taura, S. et al. (1992): Identification of a recessive gene to rice bacterial blight of mutant line XM6, *Oryza sativa* L. *Jpn. J. Breed.*, **42**, 7–13.
29) Taura, S. et al. (1992): Resistance gene of rice cultivar, Taichung Native 1 to Philippine races of bacterial blight pathogens. *Jpn. J. Breed.*, **42**, 195–201.
30) Washio, O. et al. (1966): Studies on breeding rice varieties for resistance to bacterial leaf blight. *Bull. Chugoku Agr. Exp. Sta.* Ser. A**13**, 55–85 [In Japanese with English summary].
31) Watanabe, S. (1976): Studies on the breeding of rice varieties resistant to bacterial leaf blight in Sri Lanka. *Tohoku Nat. Agr. Exp. Sta.*, **54** [In Japanese with English summary].
32) Yamada, T. (1984): Multiple alleles at the *Xa-1* and *Xa-kg* loci for resistance to bacterial leaf blight. *Rice Genet. Newsl.*, **1**, 97–98.
33) Yamamoto, T. & Ogawa, T. (1990): Inheritance of resistance in rice cultivars, Toyonishiki, Milyang 23 and IR24 to Myanmar isolates of bacterial leaf blight pathogen. *JARQ*, **24**, 74–77.
34) Yoshimura, A. et al. (1983): Inheritance of resistance to bacterial blight in rice cultivar Cas209. *Phytopathology*, **73**, 1409–1412.
35) Yu, G. X. et al. (1986): Location of genes for resistance to Chinese strains of bacterial blight, *Xanthomonas campestris* pv. *oryzae* in IR28. *Rice Genet. Newsl.*, **3**, 86–87.
36) Zhao, X. P. et al. (1985): Studies on the inheritance of rice to bacterial blight. *J. Huazhong Agr. Coll.*, **3**, 11–22 [In Chinese with English summary].

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