Japan. J. Breed. 41 : 211～221 (1991)

Resistance and Its Inheritance to Bacterial Blight of IR8 Rice Cultivar Group

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In order to identify the bacterial blight resistance gene of rice cultivar IR8, one of the rice baceterial blight differentials, a research was carried out under a collaboration between Ministry of Agriculture, Forestry and Fisheries (MAFF), Japan and International Rice Research Institute (IRRI), Philippines. Inoculation test using Japanese and Indonesian races of bacterial blight pathogen, was first carried out with cultivars which are known to show the reaction pattern similar to that of IR8. The results indicated that cultivars of IR8 reaction pattern showed resistance to Japanese races IB, II, IIIA and V, and Indonesian races IV and V but susceptibility to Japanese races IA, IIIB and IV. It was found that Japanese race IV differs pathogenetically from Indonesian race IV. Moreover, there was no difference between the reaction pattern of Elwee and Heen Dikwee which were considered to belong to different reaction groups by YAMADA *et al.* (1979a). The results of gene identification by F_2 analysis showed that IR8, Elwee and RP9-3 have the same gene for resistance to Japanese races IB and IIIA. The allelic test between the resistance gene of IR8, Elwee, and RP9-3, and the resistance gene(s) of Peta and IR944-102-3-2 showed that Peta and IR944-102-3-2 also have the same gene with IR8 and have another dominant gene for resistance to Japanese races. This study showed that IR8, Elwee, RP9-3, Peta, and IR944-102-3-2 have the gene *Xa-11* for resistance originally identified by OGAWA and YAMAMOTO (1986).

KEY WORDS: *Oryza sativa, Xanthomonas campestris* pv. *oryzae,* disease resistance, resistance gene, bacterial blight.

Introduction

Rice cultivar, IR8 is used as the susceptible check in differential set to identify races of bacterial blight (BB) pathogen of rice at International Rice Research Institute (IRRI), Philippines. By the comparison study of two differential sets (IRRI and Japanese) for distinguishing races of BB pathogen, HORINO *et al.* (1981) indicated that IR8 was susceptible to Japanese races I and IV but resistant to races II, III and V. OGAWA (1983) also showed that IR8 was resistant to Japanese races IB, II, IIIA and V but susceptible to races IA, IIIB and IV, and proposed that IR8 is suitable to be added to Japanese differentials. YAMADA *et al.* (1979a) found the several cultivars which showed the reaction patterns of IR8 to Japanese races, and they grouped the six cultivars into Elwee and Heen Dikwee groups by the disease index to Japanese race V.

From the genetic analysis of two lines (IR1529-680-3-2 and IR944-102-2-3), OGAWA and YAMAMOTO (1986) reported that the reaction pattern similar to that of IR8 in the two lines is governed by one dominant gene, designated as *Xa-11* for resistance. Then, from the examination of pedigree records, it was estimated that the same dominant gene may have been incorporated into IR1529-680-3-2, IR944-102-2-3 and RP9-3 from Peta through IR8.

Received May 7, 1990.

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To confirm this hypothesis, the present study was carried out and we also discussed the grouping of cultivars of IR8 reaction type.

This research was conducted under a collaboration between IRRI and Ministry of Agriculture, Forestry and Fisheries (MAFF), Japan.

Materials and Methods

Thirteen cultivars showing reaction pattern similar to that of IR8 to Japanese BB races, together with Japanese BB differentials, were tested their reaction to seven standard Japanese races and two Indonesian races. The original seeds of IR8 used are taken from International Rice Germplasm Center (IRGC), IRRI. We purified IR8 for uniformity of maturity and morphology before inoculaion by growing ten single plant selection. As the data of Table 1 show, the lesion length of each selection when inoculated with four Philippine races, was quite similar. Only lines 1, 9 and 10 had slightly longer lesions. The leaves of lines 1, 8 and 10 were slightly longer. Lines 7～10 were somewhat later in maturity. We selected individual No. 6 for further experimental work. Seeds of the other cultivars used were taken from National Institute of Agrobiological Resources, Tsukuba, Japan.

The cultivars were inoculated with standard Japanese races, e.g. IA (isolate T7174), IB (isolate T7156), II (isolate T7147), IIIA (isolate T7133), IIIB (isolate Q6803), IV (isolate H75373) and V (isolate H75304) under field conditions at Chugoku National Agricultural Experiment Station (CHUGOKU) in 1979. These cultivars were also inoculated with Indonesian races IV (isolate Xo7435) and V (isolated Xo7306) in the isolation greenhouse at Tropical Agriculture Research Center (TARC), Tsukuba, Japan, in 1985. In the inoculation test with Indonesian races at TARC, plants of each cultivar were planted in pots (1/5000a, 3 plants per pot), and were inoculated at booting stage. In all inoculation tests, six tiller groups of three plants separated into two tiller groups of each cultivar were prepared and each group was inocu-

Table 1. Heading date and lesion length at floweing stage of IR8 plant for uniformity check to inoculation with four Philippine BB races IRRI, 1983

Line No.	Heading date (June)	Reaction to Philippine race (lesion length in cm)[1]			
		1	2	3	4
1	27	12.3-19.3-25.0	10.0-17.2-30.0	11.4-21.1-30.5	13.5-23.7-28.5
2	25	11.0-21.6-30.9	8.0-14.4-21.8	8.2-23.8-27.0	5.2-13.2-19.1
3	26	10.0-18.5-28.2	7.5-13.8-19.5	11.6-21.9-30.6	7.5-15.4-31.2
4	25	11.6-21.5-26.2	6.5-13.8-21.1	15.0-19.9-26.2	7.9-14.1-21.3
5	25	7.5-19.0-30.4	—	8.0-21.3-30.2	6.1-13.9-20.5
6	25	7.6-18.4-25.0	6.0-14.6-20.5	12.5-21.7-31.1	7.0-14.7-20.7
7	29	13.2-19.0-26.1	6.6-14.3-20.9	7.5-22.2-30.1	9.4-16.5-25.4
8	30	10.0-18.1-26.3	6.2-13.9-20.6	13.8-22.8-33.0	9.5-15.6-30.0
9	30	8.7-19.1-30.0	6.4-16.0-23.0	17.6-25.0-34.6	7.7-20.8-33.5
10	30	11.0-19.4-28.0	7.5-15.6-25.0	13.6-22.5-32.0	16.5-23.0-28.9

1) Minimum-average-maximum.

lated with a single race.

The uppermost fully developed leaves of each plant were cut with scissors wetted with bacterial suspension about 5cm below the tip. The lesion length was measured 14 to 21 days after inoculation. However, the evaluation of resistance was done continuously for about one month after inoculation not only by lesion length but also by sympton of the lesion.

For genetic analysis, crosses and F_1 growing was made at IRRI. The growing of F_2 populations and inoculation tests were done at TARC. The F_2 populations of the crosses IR24/IR8, IR24/Elwee, Java 14/IR8, IR8/RP9-3, IR8/Elwee, Elwee/RP9-3, IR8/Peta, Peta/RP9-3, Elwee/Peta, IR8/IR944-102-3-2 and IR944-102-2-3/Elwee, were inoculated with Japanese races. IR24 was used as susceptible parent to all the used races.

Other experimental procedures followed were based on the standard methods of the previous one (OGAWA *et al.* 1990).

Results and Discussion

1. Reaction of IR8 and other cultivars to Japanese and Indonesian bacterial blight races

The reaction of differential cultivars to the BB races, and those of cultivars known to show similar reaction pattern to IR8 were shown in Table 2. The races were Japanese races IA, IB, II, IIIA, IIIB, IV and V, and Indonesian races IV and V. Among the races. Japanese races IA, IB, II and IIIA, and Indonesian races IV and V showed enough virulence to susceptible check Kinmaze of Japanese differentials which showed over 15cm lesion length at 20 DAI (days after inoculation). Japanese races IIIB and IV were lower virulent to Kinmaze the lesion length were 7.9cm to the race IIIB and were 9.2 to the race V compared with the above races. Japanese race V showed the lowest virulence to Kinmaze the lesion length was 3.4cm among the used races. The low virulence of Japanese race V, compared with the other standard races had also been reported by earlier studies (YAMADA *et al.* 1979a, 1979b, OGAWA and YAMAMOTO 1987a, 1987b). Therefore, there was a difficulty of evaluation of the resistance in each rice cultivar to Japanese race V. From this point, we used Indonesian race V, which was first designated as race V according to Japanese differential system of BB races (YAMAMOTO *et al.* 1977).

Each Japanese differential showed similar reaction to each standard race with earlier studies (YAMAMOTO *et al.* 1977, YAMADA *et al.* 1979a, OGAWA 1983, OGAWA and YAMAMOTO 1987b), except those of Chugoku 45 and Java 14 (evaluated to be moderate in this experiment) to Japanese race IV, which were caused by the low virulence of the race in this experiment. Cultivars of IR8 type showed over 8.3cm lesion length and longer or similar lesion length compared with that of susceptible check Kinmaze to Japanese races IA, IIIB and IV. On the other hand, these cultivars showed below 7cm lesion length, which was lower or similar degree in lesion length compared with those of resistance in differentials to Japanese races IB, IIIA and V, and Indonesian races IV and V. Based on these reactions, cultivars of IR8 type were evaluated to be resistant reaction to Japanese races IB, II, IIIA and V, and Indonesian races IV and V, but to be susceptible to Japanese races IA, IIIB, and IV.

Race IV of BB pathogen were named to the group of isolates which showed virulence to all Japanese differentials by YAMAMOTO *et al.* (1977) using Indonesian isolates, and the group-

Table 2. Reaction of rice cultivars of IR8 type to Japanese and Indonesian races at booting to flowering stages. CHUGOKU 1979, TARC 1985

Cultivar	Japanese Race							Indonesian Race	
	IA	IB	II	IIIA	IIIB	IV	V	IV	V
	T7174	T7156	T7147	T7133	Q6803	H75373	H75304	Xo7435	Xo7306
Japanese differentials									
Kinmaze	16.2	20.6	18.7	19.3	7.9	9.2	3.4	22.6	19.1
	S	S	S	S	S	S		S	S
Kogyoku	0.2	0.2	12.4	6.3	7.1	14.8	0.1	14.1	0.2
	R	R	S	S	S	S		S	R
Te-tep	4.9	3.6	1.7	20.8	23.8	7.3	0.1	5.5	1.6
	R	R	R	S	S	S		R	R
Chugoku 45	0.9	1.0	1.7	0.5	0.5	3.7	2.4	17.2	13.4
	R	R	R	R	R	M		S	S
Java 14	0.3	0.4	1.0	0.4	1.8	3.4	0.1	29.4	0.3
	R	R	R	R	R	M		S	R
IR8 reaction types[1)]									
IR2071-636-5-5(E)	10.2	0.6	0.9	1.3	9.3			1.0	1.5
	S	R	R	R	S			R	R
Elwee (E)	14.6	1.6	3.5	2.3	37.6	12.0	0.2	2.1	1.3
	S	R	R	R	S	S		R	R
RP5-12	21.2	2.6	2.2	1.5	18.9			1.7	1.4
	S	R	R	R	S			R	R
Java	21.4	3.0	1.0	1.7	22.1			1.1	1.8
	S	R	R	R	S			R	R
RP9-3	18.3	1.4	2.4	2.2	26.7	19.8	1.1	3.1	1.9
	S	R	R	R	S	S		R	R
IR8	26.4	1.8	1.7	2.2	19.2	12.9	0.2	1.2	1.3
	S	R	R	R	S	S		R	R
IR1414-67-3-2	23.2	1.7	1.3	4.4	17.8	8.3	0.4	2.6	2.1
	S	R	R	R	S	S		R	R
RP4-10	30.7	3.2	3.7	2.0	20.7			1.6	3.3
	S	R	R	R	S			R	R
Heen Dikwee (H)	30.0	2.9	5.8	4.9	23.3	17.9	1.1	2.9	4.2
	S	R	R	R	S	S		R	R
M304 (H)	15.0	2.9	1.7	3.3	12.5	15.0	1.7	6.8	4.3
	S	R	R	R	S	S		R	R
Yetlew	32.7	6.5	4.1	5.1	29.7			4.7	4.6
	S	R	R	R	S			R	R
Col. No. 8	32.7	6.5	4.1	5.1	29.7			4.1	4.9
	S	R	R	R	S			R	R
M104 (H)	18.5	2.1	2.4	3.0	20.1	23.3	0.4	5.4	5.7
	S	R	R	R	S	S		R	R

Upper row: Average lesion length (cm) of 9 leaves (3 leaves×3 plants).
Lower row: R-resistant, S-susceptible, and M-moderate.
1) E: Cultivar of Elwee group, H: Cultivar of Heen Dikwee group identified YAMADA *et al.* (1979a).

ing was followed by SATO *et al.* (1976) and HORINO (1978) using Japanese isolates. At that time, IR8 was not inoculated with their isolates. In this experiment, cultivars of IR8 type reaction showed more susceptibility to Japanese race IV than those of Te-tep, Chugoku 45, while these cultivars showed short lesion length, which was below 6.8cm, to Indonesian race IV. The Indonesian race IV was more virulent than Japanese race IV. These results indicated that Japanese race IV differs pathogenically from Indonesian race IV.

YAMADA *et al.* (1979a) set up two new cultivar groups, Elwee and Heen Dikwee in Japanese differential system for BB race. The cultivars belonged to Elwee and Heen Dikwee groups were reported to have similar reaction to Japanese races I, II, III and IV but different reaction to Japanese race V. They divided the resistance in the used cultivars to Japanese races V (H75304) by disese index 2 (the index: 0 to 7 by their criterion). A cultivar showed below the index 2 to Japanese race V was classified into Elwee group while a cultivar showed over the index 2 to the race was classified into Heen Dikwee group. The highest disease index in Heen Dikwee group was 2.3 in cultivar M304 to Japanese race V.

Our data on the reaction patterns of cultivars of IR8 type showed Elwee and Heen Dikwee were resistant to Indonesion race V, wihch was a original race used for inoculation test by YAMAMOTO *et al.* (1977) in Indonesia. Moreover, in our studies, cultivars of Heen Dikwee group did not show clear susceptibility to Japanese race V (Table 2). According to YAMADA *et al.* (1979a), the disease index of all cultivars classified Elwee and Heen Dikwee groups fall between 0.0 and 2.3 while Kinmaze was 4.0 and Wase Aikoku 3 was 3.6 the two cultivars are susceptible to the race V. From the results of our experiment and the data of YAMADA *et al.* (1979a), cultivars of IR8 reaction type (Elwee and Heen Dikwee groups) were considered to be resistant to Japanese and Indonesian race V, and not to be divided into two groups artificially, that is, M304 showed disease index 2.3 in YAMADA *et al.* (1979a) was considered to be resistant to race V.

Thus, we conclude that cultivars of Elwee and Heen Dikwee groups should be put in the same group. The little variation between susceptible and resistant cultivars to Japanese race V reported by YAMADA *et al.* (1979a) might be caused by the low virulence of the race while the relatively large difference between the disease index of cultivars of IR8 reaction type might be caused by the needle-prick inoculation method and the disease index scoring. Usually, the expansion of lesion after inoculation is faster in the needle-prick inoculation method than that in the clipping inocultion method for resistance to bacterial blight.

2. Genetic analysis of resistance to bacterial blight in IR8 type cultivars

In the previous paper (OGAWA and YAMAMOTO 1986), we reported genetic analysis of two breeding lines (IR1529-680-3-2 and IR944-102-2-3) and a cultivar RP9-3 which showed the reaction pattern similar to that of IR8. The result showed that IR1529-680-3-2 and IR944-102-2-3 have the same dominant gene as RP9-3. This gene was found to inherit independently of *Xa-1* and *Xa-3,* and was designated as *Xa-11.* From the examination of pedigree records, it was estimated that the same dominant gene may have been incorporated into IR944-102-2-3, IR1529-680-3-2, and RP9-3 from Peta through IR8.

To confirm this hypothesis, we analyzed F_2 populations from three hybrids, IR24/IR8,

IR24/Elwee and Java 14/IR8. Allelic tests were then carried out using seven hybrids, IR8/RP9-3, IR8/Peta, IR8/Elwee, Peta/RP9-3, Elwee/Peta, IR8/IR944-102-2-3, and IR944-102-2-3/Elwee.

In genetic analysis of F_2 population, the plant that stopped the expansion of lesion length between 18 to 21 DAI was evaluated resistant, while the plant continuing to develop the lesion beyond 21 DAI was evaluated susceptible. By this criterion, in the F_2 population of IR24/IR8, 260 plants were evaluated to be resistant to races IB and IIIA, and 88 plants were evaluated to be susceptible to the both races. This segregation agreed with a 3 : 1 ratio ($\chi^2 = 0.015$, P = 0.9-0.95). The frequency distribution of lesion length at 20 DAI to two BB races in the F_2 population of IR24/IR8 is shown in Fig. 1. Almost all of the plants evaluated to be resistant ranged the lesion length less than 6cm while almost all of plants evaluated to be susceptible ranged the lesion length over 10cm by races IB and IIIA. Few plants evaluated to be resistant or susceptible ranged the lesion length between 6 to 10cm. These plants were classified the susceptibility by the above mentioned criterion. The result of segregation in the F_2 population of IR24/IR8 indicated that IR8 has one dominant gene for

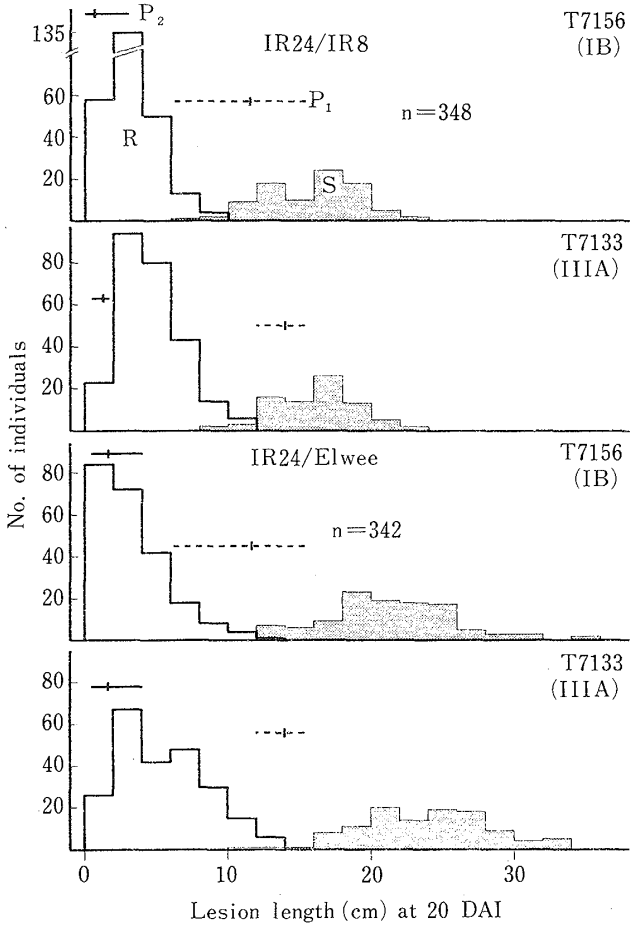

Fig. 1. Frequency distribution of F_2 plants according to lesion length from the crosses IR24 (P_1)/IR8 (P_2) and IR24 (P_1)/Elwee (P_2) at maximum tillering to flowering stages. TARC, 1985.

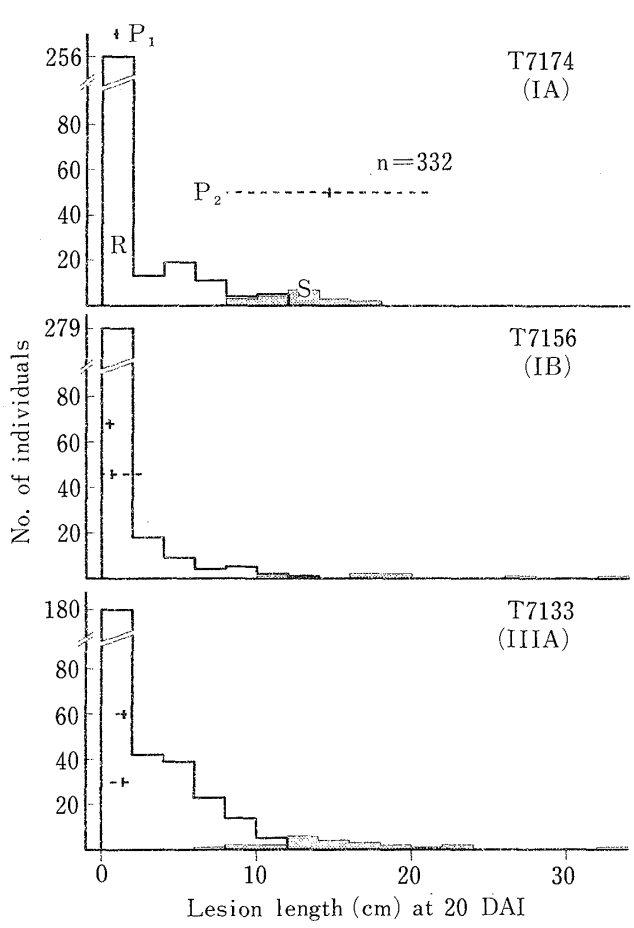

Fig. 2. Frequency distribution of F_2 plants according to lesion length from the cross Java 14 (P_1)/IR8 (P_2) at booting to flowering stages. TARC, 1985.

resistance to races IB and IIIA.

In the F_2 population of IR24/Elwee, 235 plants were evaluated to be resistant to races IB and IIIA but susceptible to race IA, and 107 plants showed susceptibility to the three races, that is, 235 plants showed the reaction type of SRP while 107 plants showed the reaction type of SSS to races IA, IB and IIIA (R: resistant, S: susceptible). These segregation data indicated that Elwee also has one dominant gene for resistance to races IB and IIIA, although the number of the resistant plants was lower than expected for ratio of 3 : 1 ($\chi^2=7.209$, $P=0.001$-0.01). Elwee does not head under natural condition in Japan, so that, plants of the F_2 population varied widely the growing stage at the inoculation, which was done at the one time. Therefore, there was a possibility that some resistant plants were evaluated to be susceptible becouse of rapid development of lesion in the young growing stage plant.

The frequency distribution of lesion length in the F_2 population of IR24/Elwee is shown in Fig. 1. The plants evaluated to be resistant from visual observation, ranged the lesion length below 14cm to races IB and IIIA at 20 DAI. The plants evaluated to be susceptible ranged the lesion length over 10cm at 20 DAI. The susceptibility of each plant ranged the lesion length from 10cm to 14cm was evaluated by visual observation according to the above mentioned criterion described already.

In the F_2 population of Java 14/IR8, 295 plants were resistant to three races IA, IB and IIIA (RRR), 11 plants were susceptible to race IA but resistant to races IB and IIIA (SRR), 19 plants were resistant to races IA and IB but susceptible to race IIIA (RRS), and 7 plants were susceptible to the three races (SSS). Java 14 carries two dominant genes, *Xa-1* and *Xa-3*, to Japanese races I and IIIA (Ogawa *et al.* 1978). *Xa-1* conveys resistance to races IA and IB but susceptibility to IIIA (RRS) while *Xa-3* conveys resistance to all the races (RRR). From the analysis of F_2 population of IR24/IR8, the dominant gene of IR8 is considered to convey resistance to race IB and IIIA but susceptibility to race IA (SRR). The above segregation agreed well with the ratio of 57RRR : 3SRR : 3RRS : 1SSS (capital letters from left to right are to races IA, IB and IIIA, R: resistant, S: susceptible) ($\chi^2=2.772$, $P=03$-05), showing segregation of the above mentioned three dominant genes in the population.

The frequency distribution of lesion length to each race in the F_2 population of Java14/IR8 is shown in Fig. 2. As shown in Fig. 2, plants evaluated to be resistant ranged the lesion length from 0cm to 14cm while plants evaluated to be susceptible showed the lesion length over 6cm. Plants showed the lesion length between 6cm to 14cm, were evaluated the criterion mentioned already. The F_2 population segregated 314 resistant and 18 susceptible plants to race IA, and 325 resistant and 7 susceptible plants to race IB, and 306 resistant and 26 susceptible plants to race IIIA, respectively. This segregation ratio fitted well to ratio of 15 : 1, 63 : 1 and 15 : 1 to races IA, IB and IIIA, respectively. Therefore, from this segregation, it was confirmed that two dominant genes control for resistance to races IA and IIIA while three dominant genes control for resistance to race IB in the F_2 population of Java 14/IR8.

Table 3 shows the results of allelic tests within cultivars of IR8 type. In all the F_2 popu-

Table 3. Genetic segregation of reaction pattern to Japanese BB races in F_2 population from crosses between cultivars grouped in IR8 type reaction

Cross ( )[2]	Number of plants for each reaction pattern[1]		Total	Expected ratio	χ^2	P
	SRR	SSS				
IR8 (SRR) / RP9-3 (SRR)	362	0	362	1 : 0	0	1
IR8 (SRR) / Elwee (SRR)	366	0	366	1 : 0	0	1
Elwee (SRR) / RP9-3 (SRR)	355	0	355	1 : 0	0	1
	RRR	SRR				
IR8 (SRR) / Peta (RRR)	279	96	375	3 : 1	0.072	0.7-0.8
Peta (RRR) / RP9-3 (SRR)	276	100	376	3 : 1	0.511	0.3-0.5
Elwee (SRR) / Peta (RSS)	258	95	353	3 : 1	0.688	0.3-0.5
IR8 (SRR) / IR944-102-2-3 (RRR)	280	95	375	3 : 1	0.022	0.8-0.9
IR944-102-2-3 (RRR) / Elwee (SRR)	289	86	375	3 : 1	0.854	0.3-0.5

1) R: resistant, and S: susceptible; SRR, SSS, RRR, SRR show the susceptibility to Japanese races IA, IB and IIIA from left to right in each capital combinations.
2) Reaction pattern of each parent.
Note: Susceptibility was evauated by visual observation and lesion length measurement after inoculation at booting stage at TARC, 1985-1988.

lations of the corsses, IR8/RP9-3, IR8/Elwee, and Elwee/RP9-3, all plants showed resistance to races IB and IIIA but were susceptible to race IA from visual observation. The lesion length of each plant of F_2 population of IR8/Elwee was measured at 20 DAI in addition to visual evaluation for the susceptibility. As shown in Fig. 3, plants evaluated resistant distributed the lesion length below 4cm while plants evaluated susceptible distributed the lesion length over 4cm. The results indicate that the cultivars, IR8, Elwee and RP9-3 carry the same gene for resistance to race IB and IIIA.

In the F_2 populations of IR8/Peta, Peta/RP9-3, Elwee/Peta, IR8/IR944-102-3-2 and IR944-102-2-3/Elwee, the segregations agreed with a ratio of 3RRR : 1SRR (races IA, IB, and IIIA from left to right) (Table 3, Fig. 4). There was no other reaction type, such as SSS and SSR. The reaction type of RRR indicates that Peta and IR944-102-3-2 have an additional gene to the above races (at least to race I) while the reaction type of SRR indicates that of IR8. These results show that Peta and IR944-102-3-2 have the same dominant gene for resistance to races IB and IIIA as that was identified in IR8, RP9-3 and Elwee and ad-

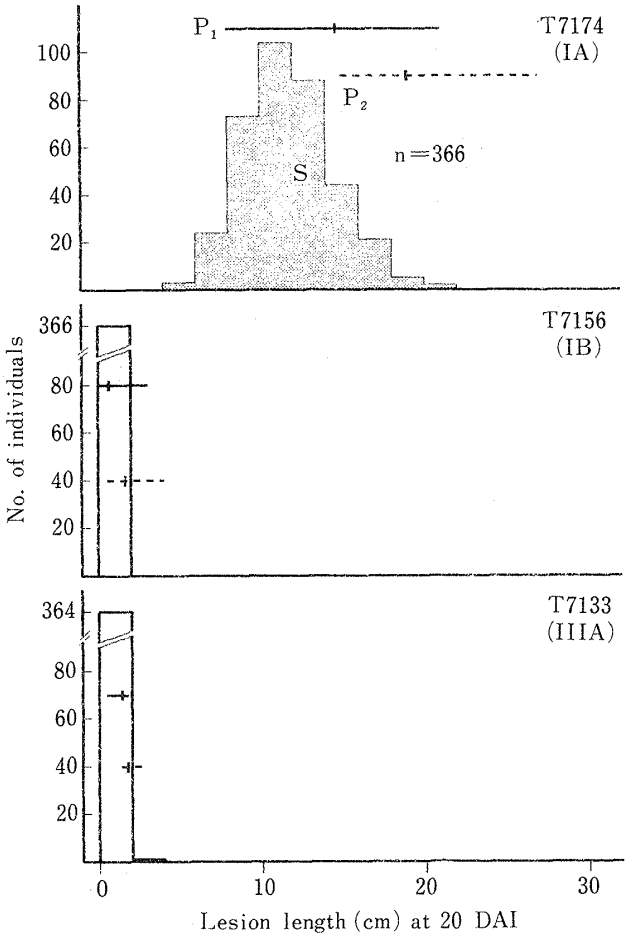

Fig. 3. Frequency distribution of F_2 plants according to lesion length from the cross IR8 (P_1)/Elwee (P_2) at maximum tillering to flowering stages. TARC, 1987.

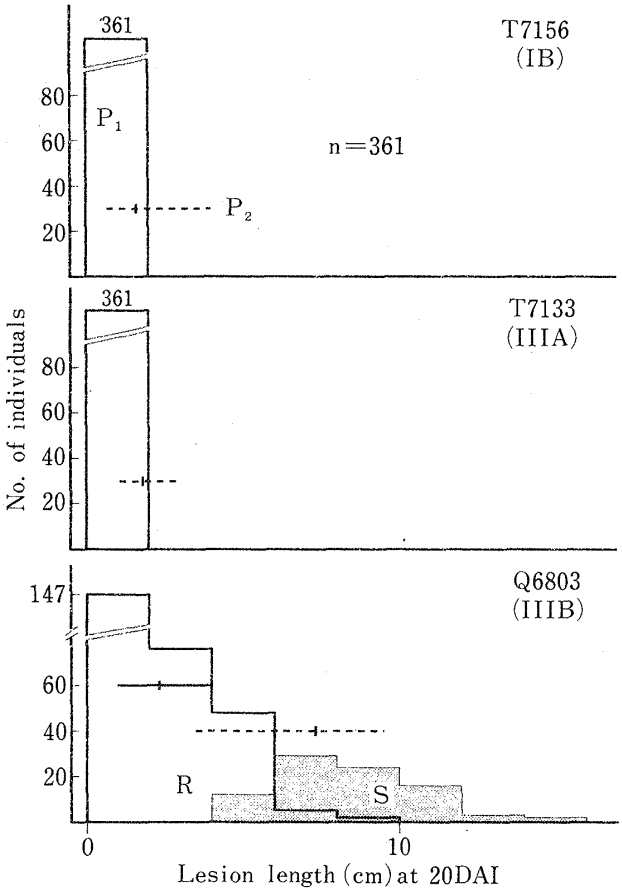

Fig. 4. Frequency distribution of F_2 plants according to lesion length from the cross of IR944-102-3-2 (P_1)/Elwee (P_2) at maximum tillering to flowering stages. TARC, 1987.

ditional gene for resistance to the race(s). Thus, we can conclude that IR8, Elwee and RP9-3 have *Xa-11* reported by OGAWA and YAMAMOTO (1986). Peta has *Xa-11* and another dominant gene, which needs to be identified for resistance to Japanese race IA, IB and IIIA.

Acknowledgment

The authors wish to express their sincere thanks to Messrs. G. A. Busto, Jr. and R. E. Tabien, Research Assistants at IRRI, for their kind help.

Literature Cited

HORINO, O. 1978. Distribution of pathogenic strains of *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson in Japan in 1973 and 1975. Ann Phytopathol. Soc. Japan. **44**: 297~301.

———, T. W. MEW, G. S. KHUSH and A. EZUKA 1981. Comparison of two differential systems for distinguishing pathogenic groups of *Xanthomonas campestris* pv. *oryzae*. Ann. Phytopath. Soc. Japan. **47**: 1~14.

OGAWA, T. 1983. Pathogenic specialization in bacterial groups I and III of *Xanthomonas campestris* pv. *oryzae* in Japan. Ann. Phytopath. Soc. Japan. **49**: 69~72.

——— and T. YAMAMOTO 1986. Inheritance of resistance of bacterial blight in rice. Rice Genet-

ics : 471～480. International Rice Research Institute, Philippines.
——— and ——— 1987a. Selection of recurrent parents to develop near-isogenic lines resistant to bacterial blight of rice. JARQ **21** : 65～69.
——— and ——— 1987b. Reaction of rice cultivars resistant to Japanese and Philippine races of *Xanthomonas campestris* pv. *oryzae*. JARQ **21** : 138～145.
———, T. MORINAKA, K. FUJII and T. KIMURA 1978. Inheritance of resistance of rice varieties of Kogyoku and Java 14 to bacterial group V of *Xanthomonas oryzae*. Ann. Phytopathol. Soc. Japan **44** : 137～141.
———, T. YAMAMOTO, G. S. KHUSH and T. W. MEW 1990. Genetics of resistance in rice cultivars, Chugoku 45 and Java 14 to Philippine and Japanese races of bacterial blight pathogen. Japan. J. Breed. **40** : 77～90.
SATO, T., Y. S. CHOI, M. IWASAKI and B. WATANABE 1976. Distribution of races of *Xanthomonas oryzae* in Kyushu. Ann. Phytopathol. Soc. Japan **42** : 357.
YAMADA, T., O. HORINO and S. SAMOTO 1979a. Studies on genetics and breeding of resistance of bacterial leaf blight in rice. I. Discovery of new varietal groups on the basis of reaction patterns to five different pathotypes of *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson in Japan. Ann. Phytopath. Soc. Japan **45** : 240～246.
———, ——— and ——— 1979b. ———. II. Newly-discovered Wase Aikoku group varieties native to Japan. Japan. J. Breed. **29** : 191～196.
YAMAMOTO, T., R. H. HARTINI, M. MUHAMMAD, T, NISHIZAWA and D. M. TANTERA 1977. Variation in pathogenicity of *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson and resistance of rice varieties to the pathogen. Contr. Centr. Res. Inst. Agric. Exp. Stn. **9** : 5～9.

イネ白葉枯病菌に対するIR 8 品種群の抵抗性とその遺伝

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イネ白葉枯病菌レースの国際判別品種を設定するため，抵抗性遺伝子を一つずつもつ準同質遺伝子系統を育成する前提として，日本とIRRIの判別品種の抵抗性遺伝子の同定を行っている．本報では，IR 8についての分析結果を報告する．

イネ品種IR 8はIRRIの判別品種の一つで，全てのフィリピン産白葉枯病菌レースに対して感受性を示す(Table 1)．一方，日本産白葉枯病菌レースIB，II，IIIA，Vに対して抵抗性を示すが，レースIA，IIIB，IVに対しては感受性を示す（OGAWA 1983，OGAWA and YAMAMOTO 1987 b)．本研究ではまず，このIR 8と同様な反応型を示す品種に，日本産白葉枯病菌レースIA，IB，II，IIIA，IIB，IV，V及びインドネシア産白葉枯病菌レースIV，Vを接種して反応型を比較した．しかし，日本産白葉枯病菌レースV（H 75373）は他の研究者の結果（YAMADA *et al*. 1979 a，1979 b，OGAWA and YAMAMOTO 1987 a，1987 b）と同様に他のレースと比較して病原力が弱く，このレースに対する品種の抵抗性の判定は困難であった．一方，インドネシア産白葉枯病菌レースVは，病原力が強かったが，IR 8型の反応を示す品種は，全て明らかな抵抗性を示した（Table 2)．また，これらの品種は，日本産白葉枯病菌レースIVに対しては感受性を示すが，インドネシア産レースIVに対しては抵抗性を示した．従って，日本産白葉枯病菌レースIVは，インドネシア産レースIVと同じレースとはいえず，両レースには病原性の分化があると結論した．

さらに，YAMADA *et al*.（1979 a）の報告したElwee群及びHeen Dikwee群の品種も，このIR 8型品種群に含まれた．YAMADA *et al*.（1979 a）は日本産白葉枯病菌レースVに対する反応から，この品種群を二つの品種群に分けたが，本研究結果ではその根拠は見出されなかった．これらの品種群は日本産及びインドネシア産白葉枯病菌レースVに対して抵抗性を示した．

IR 8型品種の抵抗性の遺伝分析の結果（Table 3，Figs 1-4)，IR 8，Elwee及びRP 9-3は同じ優性遺伝子を，また，Peta及びIR 944-102-3-2はこれら3品種と同じ優性遺伝子ともう一つの別の優性遺伝子を持つと結論した．既にOGAWA and YAMAMOTO（1986）によってRP 9-3のこの優性遺伝子は *Xa-11* と同定された．従って，これらの品種のIR 8型の反応は *Xa-11* によって支配されていると結論できた．結果として，IRRIの判別品種IR 8は一つの優性遺伝子 *Xa-11* を持つことを明らかにした．