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IDENTIFICATION OF ALLELIC GENES CONFERRING RESISTANCE TO *XANTHOMONAS CAMPESTRIS* PV. *ORYZAE* IN EIGHT CULTIVARS OF RICE

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ABSTRACT

Rice cultivars Ruchi, RM 1, R 435-107, R 435-756, IR 54, RP 2151-40-1, BG 400-1 and DV 85 were genetically analysed against the Indian pathotype group I of bacterial blight. The varieties were crossed with the susceptible T(N)1 and amongst themselves. The F_1 and F_2 analyses clarified that the cultivars possessed one recessive gene for resistance. These genes for resistance can be grouped in to three allelic groups. Group 1-Ruchi and BG 400-1, Group-2 RP 2151-40-1, DV 85 and RM 1 and Group-3 IR 54, R 435-107, R 435-756.

Key words: *Oryza sativa, Xanthomonas campestris* pv. *oryzae*, recessive, allelism.

Bacterial blight of rice (*Oryza sativa* L.) caused by *Xanthomonas campestris* pv. *Oryza* (Ishiyama) Dye, is one of the most widespread diseases of rice in Asia, Africa, Australia and South America [1]. Genetic investigations aimed at identifying diverse genes for resistance to bacterial blight have been carried out at the International Rice Research Institute (IRRI), in India, Japan and several other countries. Fifteen major genes for resistance have been identified [2, 3]. Although large number of varieties, resistant to bacterial blight have been reported from India, less emphasis has been given to allelic genes. This study was undertaken to identify the genes for resistance in eight rice cultivars against pathotype [4].

MATERIALS AND METHODS

For inheritance studies, eight resistant varieties, i.e. Ruchi, RM 1, R 435-107, R 435-756, IR 54, RP 2151-40-1, BG 400-1 and DV 85, were crossed with the susceptible variety Taichung (Native) 1 (TN 1). The resistant varieties were also crossed amongst themselves for the allelic test. The bacterial blight strain pathotype 1 was used to inoculate the hybrid populations. The F_1 and F_2 progenies were inoculated following the modified clip inoculation method of Kauffman et al. [5] at the maximum tillering stage. The disease score was taken 18 days after inoculation for resistance, moderately resistance, moderately susceptible or susceptible grades based on the following criteria: resistant—infected leaf area less than 1%, moderately resistant—infected leaf area 1-5%, moderately susceptible—infected leaf area of 6–25%, and susceptible—infected leaf area 26–50%. For genetic analysis, the resistant and moderately resistant plants were grouped together as resistant, and moderately susceptible and susceptible plants were considered to be susceptible. The χ^2 test was used to determine the goodness of fit to the expected genetic ratios.

RESULTS AND DISCUSSION

The disease scores of the F_1 and F_2 populations from the crosses of TN 1 with the eight cultivars are presented in Table 1. All the F_1 progenies from the crosses between the resistant cultivars and susceptible TN 1 were susceptible, indicating that the resistance in these cultivars is caused by recessive genes. The F_2 populations in these crosses segregated for disease reaction in the ratio of 3S : 1R. So nature of resistance was also reported earlier [6–9], but many other studies [7, 8, 10–12] revealed one dominant gene for bacterial blight resistance. Similarly, the present study does not agree with the reported complex nature of resistance as digenic, trigenic, tetragenic, complementary or maternal inheritance [12–14].

Table 1. Reaction of F_1 and F_2 populations from the crosses of T(N)1 with resistant cultivars of rice to bacterial blight

Cross	F_1 reaction	F_2 reaction			χ^2 (3S : 1R)	P value
		total	R	S		
TN 1 x (R 269-12-1-1) Ruchi	Susceptible	532	121	411	1.422	0.3–0.2
TN 1 x RM 1	Susceptible	532	117	415	2.565	0.2–0.1
TN 1 x R 435-107	Susceptible	535	115	420	3.504	0.1–0.05
TN 1 x R 435-756	Susceptible	540	120	420	2.221	0.2–0.1
TN 1 x IR 54	Susceptible	540	116	418	3.565	0.1–0.05
TN 1 x RP 2151-40-1	Susceptible	532	114	418	3.618	0.1–0.05
TN 1 x BG 400-1	Susceptible	550	118	432	3.686	0.1–0.05
TN 1 x DV 85	Susceptible	535	115	420	3.496	0.1–0.05

R—resistant, S—susceptible.

Crosses made for allelic test among the resistant cultivars and their F_1 and F_2 reactions (Table 2) revealed the F_1 Ruchi x BG 400-1, RM 1 x RP 2151-40-1, RM 1 x DV 85, R 435-107 x R 435-756, R 435-107 x IR 54, R 435-756 x IR 54, and RP 2151- 40-1 x DV 85 were resistant and the F_2 progenies of these crosses did not segregate for susceptibility. The remaining crosses

Table 2. Reaction of F_1 and F_2 populations from the crosses among resistant rice cultivars to bacterial blight

Cross	F_1	F_2 reaction			Ratio tested	χ^2	P value
		total	R	S	S : R	(9 : 7)	
Ruchi (R 269-12-1-1) x RM 1	S	525	235	290	9 : 7	0.225	0.7–0.5
Ruchi (R 269-12-1-1) x R 435-107	S	535	239	296	9 : 7	0.189	0.7–0.5
Ruchi (R 269-12-1-1) x R 435-756	S	538	240	298	9 : 7	0.160	0.7–0.5
Ruchi (R 269-12-1-1) x IR 54	S	540	235	305	9 : 7	0.011	0.9–0.8
Ruchi (R 269-12-1-1) x RP 2151-40-1	S	542	225	317	9 : 7	1.102	0.3–0.2
Ruchi (R 269-12-1-1) x BG 400-1	R	540	540	0	0 : 1	—	—
Ruchi (R 269-12-1-1) x DV 85	S	530	235	295	9 : 7	0.074	0.8–0.7
RM 1 x R 435-107	S	540	225	315	9 : 7	0.951	0.5–0.3
RM 1 x R 435-756	S	545	220	325	9 : 7	2.524	0.2–0.1
RM 1 x IR 54	S	540	214	326	9 : 7	3.724	0.1–0.05
RM 1 x RP 2151-40-1	R	542	542	0	0 : 1	—	—
RM 1 x BG 400-1	S	545	215	330	9 : 7	3.955	0.05–0.02
RM 1 x DV 85	R	538	538	0	0 : 1	—	—
R 435-107 x R 435-756	R	540	540	0	0 : 1	—	—
R 435-107 x IR 54	R	544	544	0	0 : 1	—	—
R 435-107 x RP 2151-40-1	S	545	218	327	9 : 7	3.102	0.1–0.05
R 435-107 x BG 400-1	S	540	215	325	9 : 7	3.397	0.1–0.05
R 435-107 x DV 85	S	545	217	328	9 : 7	3.413	0.1–0.05
R 435-756 x IR 54	R	548	548	0	0 : 1	—	—
R 435-756 x RP 2151-40-1	S	545	216	329	9 : 7	3.740	0.1–0.05
R 435-756 x BG 400-1	S	540	217	323	9 : 7	2.787	0.1–0.05
R 435-756 x DV 85	S	544	220	320	9 : 7	2.419	0.2–0.1
IR 54 x RP 2151-40-1	S	542	222	320	9 : 7	1.706	0.2–0.1
IR 54 x BG 400-1	S	540	220	320	9 : 7	1.986	0.2–0.1
IR 54 x DV 85	S	545	217	328	9 : 7	3.413	0.1–0.05
RP 2151-40-1 x BG 400-1	S	545	220	328	9 : 7	2.524	0.2–0.1
RP 2151-40-1 x DV 85	R	530	530	0	0 : 1	—	—
BG 400-1 x DV 85	S	548	225	323	9 : 7	1.601	0.3–0.2

R—resistant, S—susceptible.

showed susceptible reaction in F_1 and their F_2 progenies segregated in the ratio of 9 S : 7 R. The genetic analysis thus showed that the eight resistant cultivars showing resistance for bacterial blight can be grouped into three nonallelic classes. The resistance genes in each group are nonallelic to other groups. These are allelic gene group I with Ruchi and BG 400-1; Group II with RP 2151-40-1, DV 85 and RM 1; and group III with IR 54, R 435-107 and R 435-756. Among these varieties, RM 1 is a purple leaf mutant derived from the susceptible purple strain R 2270, and R 435-107 and R 435-756 were derived from the crosses of IR 54 x Surekha. The remaining cultures were derived from other sources.

Earlier genetical study at IRRI [15] indicated a dominant gene in IR 54 allelic to Xa4 gene. However, with the exception of cv. IR 54 other IRRI varieties like IR 22, IR 36, IR 64, which also possess Xa4 gene, are susceptible to the Indian isolates of Xanthomonas. The recessive nature of IR 54 allelic group seems to be a new source of resistance. The IRRI differential IR 1545-339, a tester for xa5 recessive gene, is also susceptible to the Indian isolates and, therefore, the recessive gene xa5 identified earlier in DV 85 [7] must be some other gene nonallelic to the present recessive gene in DV 85, RP 2151-40-1 or in RM 1.

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