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GENETICS OF RESISTANCE TO *XANTHOMONAS ORYZAE* PV. *ORYZAE* (ISHIYAMA) DYE IN *ORYZA SATIVA* L.

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ABSTRACT

The inheritance of resistance and allelic relationships in three lines of rice, i.e. B 76, Kogyoku and CNGS 20083, was studied against pathotype IX08 of *Xanthomonas oryzae* pv. *oryzae*, causing bacterial leaf blight (BLB). The resistance of line B 76 is governed by single dominant gene. The cultivar Kogyoku has two independently inherited dominant genes for resistance. A single recessive gene confers resistance in line CNGS 20083. Study of allelic relationships showed that genes for BLB resistance in the cultivars/lines B 76, Kogyoku and CNGS 20083 are different. Crosses of the line B 76 with other genotypes having already known resistance genes demonstrated that B 76 contains gene(s) which are different than Xa1, Xa3, Xa Kg (Xa12), Xa6, Xa7 and Xa11.

Key words: Pathotype, resistance, allelic relationship, bacterial leaf blight.

Bacterial leaf blight (BLB) of rice (*Oryza sativa* L.) caused by *Xanthomonas oryzae* pv. *oryzae* (Ishiyama) Dye, is one of the most widespread and destructive disease [1]. Recent reports on variation for virulence in the causal organism from several countries [2–5] suggest that consistent efforts to identify new and diverse genes for resistance are required to combat this disease. So far 14 genes have been identified from different cultivars/lines and designated as Xa1 through Xa14 [1, 6], but none of these genes is effective [2] in northwestern India. Resistance to the pathotypes of *X. oryzae* pv. *oryzae* prevalent in India have been identified [2, 7, 8], but the mode of inheritance and allelic relationship of genes conferring resistance in these stocks with known Xa genes is not known. The present paper reports inheritance and allelic relationship of genes for resistance from three lines, i.e. B 76, Kogyoku and CNGS 20083, against an Indian pathotype IX08. These lines were also subjected to tests against two other pathotypes, IX01 and IX05, to identify new gene(s) in these lines/cultivars.

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MATERIALS AND METHODS

Three pots each (size 25 x 30 cm) with two plants each of B 76, Kogyoku and CNGS 20083 and the lines with the known Xa gene(s) namely Kogyoku (Xa1, Xa3, Xa12), Java 14 (Xa1, Xa3, Xa12), IR 20 (Xa4), Malagkit Sungsong (Xa6), IR 1160-8-61-1 (Xa7), Khao-Lay-Nhay (Xa9), CAS 209 (Xa10) and IR 8 (Xa11) were maintained in open experimental area. The cultivar Taichung Native 1 (TN 1) was used as susceptible check. Five leaves of 70-day-old plants were inoculated by clipping off the tips with scissors dipped in aqueous suspension of 48 h old bacterial cultures adjusted to a concentration of 10^6–10^8 cells/ml, as suggested by Kauffman et al. [9]. Fourteen days after inoculation, lesion size was measured at the inoculated tips in cm. All cultivars/lines/plants with average lesion length less than 25% of that seen on susceptible cultivar TN 1 were classified as resistant (R), between 26 to 50% as moderately resistant (MR), and more than 51% as susceptible (S). The multipathotype tests were conducted first during 1988 and repeated during 1989.

Three stocks, namely, B 76, Kogyoku and CNGS 20083 were crossed with TN 1. The F_1, F_2 and F_3 generations were studied against the pathotype IX08 under field conditions. These three genotypes were also intercrossed among themselves to study the allelic relationships. The F_2 populations obtained from such crosses and from the crosses B 76 x Malgkit Sungsong (Xa6), B 76 x IR 1160-8-6-1 (Xa7) and B 76 x IR 8 (Xa11) were also tested against the pathotype IX08.

For inheritance studies, the parents, F_1, F_2 and F_3 populations were sown in nursery, and 40-day-old plants were transplanted to the field. Five leaves from each parent, F_1, F_2 plants and about 20 plants in each F_3 family were inoculated at booting stage with the pathotype IX08 as described above. The level of resistance was expressed as lesion length on each plant 14 days after inoculation. Plants showing resistant and moderately resistant reaction were grouped together for testing genetic ratios. As it was difficult to measure lesion length on the large number of F_3 plants individually, the 0–9 scale, as per the Standard Evaluation Systems (SES) of the International Rice Research Institute, Philippines, was used to evaluate the level of resistance of F_3 plants. Plants with a 0 to 5 score were considered as resistant and those with scores between 7 to 9 were classified as susceptible. Simple χ^2 test was used to test the fitness of genetic ratios in the segregating generations.

RESULTS AND DISCUSSION

The data on the overall response of the cultivars/lines B 76, Kogyoku and CNGS 20083 and other cultivars/lines with known gene(s) to the pathotypes IX01, IX05 and IX08 are given in Table 1. B 76, CNGS 20083 and Kogyoku were resistant to IX01, IX05 and OX08. Malagkit Sungsong was resistant to IX01 and moderately resistant to pathotypes IX05 and IX08. IR8 was moderately resistant to all three pathotypes. Khao-Lay-Nhay was also

Table 1. Rice genotypes, their Xa genes and reaction to three pathotypes of *X. oryzae pv. oryzae*

Cultivar/line		Reaction to different pathotypes		
		IX01	IX05	IX08
A) Cultivar/line with unknown genes:				
B 76		R	R	R
CNGS 20083		R	R	R
B) Cultivars/lines with known Xa gene(s):				
Kogyoku	Xa1, Xa3, Xa12	R	R	R
Java 14	Xa1, Xa3, Xa12	S	S	S
IR 20	Xa4	S	S	S
Malagkit Sungsong	Xa6	R	MR	MR
IR 1160-8-6-1	Xa7	V	MR	MR
Khao-Lay-Nhay	Xa9	MR	S	S
CAS 209	Xa10	S	S	S
IR 8	Xa11	MR	MR	MR
C) Susceptible check:				
Taichung Native 1	Xa14	10.2*	13.1*	14.0*

V—reaction variable over seasons.

*Average lesion length in cm.

moderately resistant to pathotype IX01 but susceptible to pathotypes IX05 and IX08. Java 14, IR 20 and CAS 209 were susceptible to all three pathotypes. The reaction of line IR 1160-8-6-1 was variable in the 1988 and 1989 crop seasons.

The genotypes of Kogyoku and Java 14 (Xa1, Xa3, Xa12) are reported to be similar [10] in respect of their reaction against Japanese races. However, Kogyoku is resistant while Java 14 is susceptible to the pathotypes from northwestern India. These observations suggest that Kogyoku has new and undescribed Xa genes in addition to Xa1, Xa3 and Xa12. Ogawa et al. [6, 10], however, suggested that Kogyoku has some additional gene(s) which are different from Xa1, Xa3 and Xa12. Similar results were reported by Gupta et al. [2].

The F_1s from the crosses of B 76 and Kogyoku with TN 1 were moderately resistant to pathotype IX08, whereas the F_1 of the cross CNGS 20083 x TN 1 was susceptible. The plants with moderately resistant and resistant reaction were combined in the resistant group to calculate segregation ratios. The segregation data from F_2 and F_3 generations of the crosses between the resistant genotypes B 76, Kogyoku, CNGS 20083 and the susceptible parent TN 1 as well as the F_2 populations of the crosses among the resistant genotypes and the crosses of B 76 with Malagkit Sungsong (Xa6), IR 1160-8-6-1 (Xa7), and IR 8 (Xa11) against the pathotype IX08 are presented in Table 2. The F_2 population of the cross B 76 x TN 1

Table 2. Segregation for reaction to pathotype IX08 in different crosses of rice

Cross	No. of F_2 plants		Ratio	χ^2 value	No. of F_3 families			Ratio	χ^2 value
	res	sus	R:S		HR	Segr	HS	HR:Segr:HS	
A. Resistant x Susceptible:									
B 76 x TN 1	74	26	3:1	0.053	18	43	24	1:2:1	0.854
Kogyoku x TN 1	156	12	15:1	2.229	29	44	8	7:8:1	3.176
CNGS 20083 x TN 1	22	59	1:3	0.202	15	45	21	1:2:1	1.889
B. Intercrosses:									
B 76 x Kogyoku	104	2	63:1	0.072	—	—	—	—	—
B 76 x CNGS 20083	129	24	13:3	0.947	—	—	—	—	—
Kogyoku x CNGS 20083	82	2	61:3	0.995	—	—	—	—	—
C. Crosses with known Xa genes:									
B 76 x Malagkit Sungsong (Xa6)	90	2	63:1	0.221	—	—	—	—	—
B 76 x IR 160-8-6-1 (Xa7)	118	1	63:1	0.404	—	—	—	—	—
B 76 x IR 8 (Xa11)	156	3	63:1	0.111	—	—	—	—	—

*HR—homozygous resistant; Segr—segregating; HS—homozygous susceptible; Res—resistant; Sus—susceptible.

segregated in 3 resistant : 1 susceptible ratio, while the F_3 families from this cross segregated in the ratio of 1 homozygous resistant : 2 segregating : 1 homozygous susceptible. The F_2 generation of the cross Kogyoku x TN 1 segregated in the 15 resistant : 1 susceptible ratio, and its F_3 families segregated in the 7 homozygous resistant : 8 segregating : 1 homozygous susceptible ratio.

The F_2 population from the cross CNGS 20083 x TN 1 segregated in 1 resistant : 3 susceptible ratio, while the F_3 generation segregated in the 1 homozygous resistant : 2 segregating : 1 homozygous susceptible ratio. It is, thus, concluded that B 76 has a dominant gene, Kogyoku has two independently inherited dominant genes, and a single recessive gene confers resistance against the pathotype IX08 in CNGS 20083.

The F_2 populations obtained from the crosses among B 76, Kogyoku and CNGS 20083 (the resistant genotypes) segregated into susceptible and resistant plants when tested against the pathotype IX08, suggesting that the gene(s) in these three cultivars/lines are different from each other. The F_2 generations from the crosses B 76 x Kogyoku, B 76 x CNGS 20083 and Kogyoku x CNGS 20083 segregated in 63:1, 13:3 and 61:3 ratio, respectively. This observation confirms the presence of a dominant resistance gene in B 76, two different dominant genes in Kogyoku, and one recessive gene in CNGS 20083. This means that the four genes causing resistance to bacterial leaf blight in B 76, Kogyoku and CNGS 20083 are different. The F_2 generations from the crosses B 76 x Malagkit Sungsong (Xa6), B 76 x IR 1160-8-6-1 (Xa7), and B 76 x IR 8 (Xa11) segregated in 63 resistant : 1 susceptible ratio against the pathotype IX08, which suggests that the Xa gene in B 76 is non allelic to the gene(s) for resistance against this pathotype in Malagkit Sungsong, IR 1160-8-6-1 and IR 8. It is also evident that each tester for the genes Xa6, Xa7 and Xa11 used in this study carries an unknown additional resistance gene against the Indian pathotype IX08. Similar observations for some other cultivars have been reported earlier [2].

The present investigation suggests that resistance to *Xanthomonas oryzae pv. oryzae* in rice is a simple qualitatively inherited trait. Pyramiding of additional diverse genes from the three cultivars/lines B 76, Kogyoku and CNGS 20083 and complete assessment of the pathogenic potential of the local populations of X. *oryzae* pv. *oryzae* may prove useful in evolving cultivars resistant to leaf blight through simple breeding methods.

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