

## GENETIC ANALYSIS OF RESISTANCE TO BACTERIAL BLIGHT (*XANTHOMONAS ORYZAE* pv. *ORYZAE* ISHIYAMA) IN SOME RICE (*ORYZA SATIVA* L.) LINES

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### ABSTRACT

Genetics of resistance to a local isolate of *Xanthomonas oryzae* pv. *oryzae* causing bacterial blight was studied in four lines of rice (*Oryza sativa* L.) namely BR 285-5-6-6-2, BR 319-1-HR28, IET 8584 and IET 8585. Resistance of IET 8585 was controlled by two dominant independently inherited genes, while in the remaining two lines resistance was conferred by one dominant and one recessive gene each. Reaction of F<sub>2</sub> populations in intercrosses of resistant stocks showed that one of the dominant genes of IET 8585 is allelic to the dominant gene of BR 285-5-6-6-2, BR 319-1-HR28 and IET 8584. The resistance gene(s) of IET 8584 were nonallelic to the gene(s) of BR 285-5-6-6-2 and BR 319-1-HR28. In all, two dominant and two recessive genes were postulated to be conferring resistance in these four rice lines.

**Key words:** Rice, *Oryza sativa*, resistance, bacterial blight, *Xanthomonas oryzae* pv. *oryzae*.

Genetic characterization of new and diverse sources of resistance has immense importance in breeding rice varieties resistant to bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* Ishiyama. Inheritance of resistance to this disease has been studied in several rice lines [1–3]. However, new types of virulences resulting in the breakdown of resistance sources have been recorded frequently [4, 5]. Inheritance of bacterial blight resistance was studied in four rice strains namely BR 285-5-6-6-2, BR 319-1-HR28, IET 8584 and IET 8585 which are known to be resistant to a majority of *X. oryzae* pv. *oryzae* isolates from Punjab [6] and 33 other locations across Asia [7].

### MATERIALS AND METHODS

The bacterial blight resistant lines namely BR 285-5-6-6-2 (Biplab x Chandina), BR 319-1-HR28 (IR 5 (D) x Biplab), IET 8584 (IET 4141 x CR 98-7216) and IET 8585 (IET 4141 x

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CR 98-7216) were crossed with the susceptible cultivar Taichung Native 1 and amongst themselves. The F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> progenies of the resistant x susceptible crosses and F<sub>1</sub> and F<sub>2</sub> plants of the intercroses among resistant parents were analysed.

Seventy-day-old plants at maximum tillering stage to boot leaf stage were inoculated with aqueous cell suspension of a local isolate of *X. o. pv. oryzae*, by the leaf clipping technique [8]. The inoculum (10<sup>9</sup> cfu/ml) was prepared from 48h old growth of the bacterial culture on potato-sucrose-peptone-agar (2:1:1:2) medium at 25°C.

Reaction to bacterial blight was scored 21 days after inoculation, following the Standard Evaluation System of Rice [9]. Plants with score up to 5 on the 1-9 scale were classified resistant while those with higher scores were classified as susceptible and designated as R and S. The F<sub>1</sub> and F<sub>2</sub> plants were scored individually, while the F<sub>3</sub> families were only classified as homozygous resistant, segregating or homozygous susceptible. The observed segregation ratios in F<sub>2</sub> and F<sub>3</sub> generations were tested by using the  $\chi^2$  test to determine their goodness of fit.

## RESULTS AND DISCUSSION

The reaction of F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> populations obtained from crosses of the four resistant lines with TN 1 (Table 1) showed that F<sub>1</sub>s of all the crosses were resistant, indicating that resistance in all the four lines was dominant. The F<sub>2</sub> populations of the crosses BR 285-5-6-6-2 x Taichung Native 1, BR 319-1- HR28 x Taichung Native 1, and IET 8584 x Taichung Native 1 segregated in the 13 resistant : 3 susceptible ratio ( $p = 0.05$ ), indicating that resistance of each of these three resistant lines was due to one dominant and one recessive gene each. A good

Table 1. Reaction of F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> generations from the crosses of four resistant rice lines with cv. Taichung Native 1 to bacterial blight (*X. oryzae pv. oryzae*)

Cross	F <sub>1</sub> Pheno- type	No. of F <sub>2</sub> plants		$\chi^2$ at P = 0.05		No. of F <sub>3</sub> families			$\chi^2$ at P = 0.05 (7:8:1)
		R	S	(15:1)	(13:3)	R	seg.	S	
BR 285-5-6-6-2 x Taichung Native 1	R	193	47	—	0.11	58	64	11	0.98
BR 319-1-HR28 x Taichung Native 1	R	169	41	—	0.08	46	73	12	4.85
IET 8584 x Taichung Native 1	R	253	48	—	2.55	55	60	8	0.04
IET 8585 x Taichung Native 1	R	214	16	0.192	—	52	74	8	1.58

Reaction: R—resistant, S—susceptible, and seg.—segregating.

fit ( $p = 0.05$ ) for 7 homozygous resistant: 8 segregating: 1 homozygous susceptible ratio in F<sub>3</sub> generation from these three crosses confirmed this conclusion. The F<sub>2</sub> generation from the cross IET 8585 x Taichung Native 1 segregated in a ratio of 15R:1S ( $p = 0.05$ ) indicating that resistance in IET 8585 is controlled by two dominant genes segregating independently. These results were confirmed in the F<sub>3</sub> generation.

The results on reaction of F<sub>2</sub> plants obtained from the intercrosses among the four resistant rice lines are presented in Table 2.

All the F<sub>2</sub> plants of cross IET 8584 x IET 8585 were resistant, indicating that at least one gene in these two lines is common. This may be due to the common parentage of these two lines. IET 4141, one of the parents of these two sister lines has been reported to be resistant to bacterial blight and blast, *Piricularia oryzae* [10]. The resistant parents of IET 4141, which was selected from the derivatives of two crosses, i.e. Lacrose x Zenith and Nira x Zenith has been demonstrated to carry a single dominant gene for resistance to *X. oryzae* pv. *oryzae* [11]. The F<sub>2</sub> population of crosses BR 285-5-6-6-2 x BR 319-1-HR28 and BR 285-5-6-6-2 x IET 8585 also did not segregate for susceptible plants. BR 285-5-6-6-2 and BR 319-1-HR28 have Biplab as the common parent [7]. Biplab may be the source of resistance to bacterial blight in these two breeding lines. Since the F<sub>2</sub> population from the remaining two crosses among the resistant parents, i.e. BR 285-5-6-6-2 x IET 8584 and BR 319-1-HR28 x IET 8584, segregated for susceptible plants, the gene(s) in IET 8584 could not be allelic to those in BR 285-5-6-6-2 and BR 319-1-HR28. Two dominant and two recessive genes were proposed to confer resistance in these four rice lines.

One dominant gene Xa4 and two recessive genes, xa5 and xa8, are known to confer resistance against a majority of the virulences of *X. o. pv. oryzae* prevalent in Punjab [12]. The relationship of the genes controlling resistance in the rice lines studied here with the known resistance genes (*Xa* genes) needs to be investigated.

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**Table 2. Reaction of F<sub>2</sub> plants from intercrosses among four rice lines resistant to bacterial blight (*X. oryzae* pv. *oryzae*)**

Cross	Reaction
BR 285-5-6-6-2 x BR 319-1-HR28	Resistant
BR 285-5-6-6-2 x IET 8584	Segregating
BR 285-5-6-6-2 x IET 8585	Resistant
BR 319-1-HR28 x IET 8584	Segregating
BR 319-1-HR28 x IET 8585	Resistant
IET 8584 x IET 8585	Resistant

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