Indian J. Genet., 58(4): 427-431 (1998)

INHERITANCE AND ALLELIC RELATIONSHIPS BETWEEN GENES CONFERRING RESISTANCE TO *XANTHOMONAS CAMPESTRIS* PV. *ORYZAE* (ISHIYAMA) DYE IN RICE (*ORYZA SATIVA* L.)

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(Received: August 14, 1996; accepted: November 16, 1998)

ABSTRACT

The inheritance of resistance to a pathotype IX05 collected from north western India was studied in three lines of rice B 76, ARC 10464 and CNGS 20083. These lines were crossed to a susceptible cultivar Taichung Native 1 to generate F_1, F_2 and F_3 generations. The reaction of F_1 and segregation pattern in F_2 and F_3 generations suggest that the resistance of B 76 and CNGS 20083 was conditioned by a dominant and a recessive gene respectively. Breeding lines ARC 10464 carried two independently inherited dominant genes. Since the F_2 generations obtained from intercrosses of these three lines segregated for susceptible plants it is concluded that B 76, ARC 10464 and CNGS 20083 have different genes conferring resistance to pathotype IXC5 of *X. c.* pv. *oryzae*.

Key words: *X. c. pv. oryzae*, resistance, pathotype

Bacterial leaf blight (BLB) caused by *Xanthomonas campestris* pv.*Oryza* (Ishiyama) Dye is one of the most important disease of rice (*Oryza sativa* L.). This disease causes serious yield losses when it occurs in epidemic form [1]. In addition to environmental factors, the inherent susceptibility of rice cultivars is primarily responsible for outbreak of the epidemics [2-5]. Since effective chemical control of this disease is not available, use of resistant cultivars has been suggested by several workers to combat the disease. Several cultivars resistant to bacterial leaf blight have been identified and are being extensively grown in different parts of the world, however, evolution of new pathotypes have rendered many of these cultivars susceptible. Therefore, for long lasting, allelic relationships of the resistance genes from different cultivars and their expression against prevalent pathotypes is essential [6]. So far, fourteen genes for resistance to *X.c.*pv. *oryzae* have been identified from different rice cultivars/lines and designated from *Xa1* through *Xa14* [4, 7-13]. Sidhu *et al.* [14] reported that none

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of the genes from *Xa1* to *Xa11* is effective in Punjab and the resistance to BLB in many rices appear to be due to new and as yet undescribed genes. The present study is therefore, aimed to study the inheritance and allelic relationships between Xa genes from three resistant lines namely, B76, ARC 10464 and CNGS 20083 against an Indian bacterial blight pathotype IX05.

MATERIALS AND METHODS

Lines B76, ARC 10464 and CNGS 20083 were crossed to a susceptible parent Taichung Native 1 (TN 1) to obtain F_1, F_2 and F_3 generations. Lines were also crossed among themselves in all possible combinations to study the allelic relationships. Three metre long single row of the F_1, fifteen rows of F_2 and one row each from every F_2 plant were planted simultaneously under field conditions. All standard agronomic practices were followed during the cultivation of crop. For inoculations 48 hrs old culture of pathotype IX05 was multiplied on Potato-Sucroce-Peptone-Agar (PSPA) and seventy day old plants were artificially inoculated using leaf clipping method [15]. The culture concentration was maintained at 10^6-10^8 Cells/ml. The level of resistance was measured by using two systems. For parents, F_1 and F_2 plants, the actual lesion length was measured in cm and a plant was classified as resistant (R) when its mean lesion length was below 25% of that observed on TN1, as moderately resistant (MR) when its mean lesion length was 26-50% of that observed on TN1 and it was classified as susceptible (S), when its mean lesion length was 51-100% of that seen on TN 1. For fitting genetic ratios, both R and MR plants were grouped together and considered as resistant. Standard evaluation system (SES) developed by International Rice Research Institute, Philippines was used to evaluate the F_2 plant progenies (F_3 families). According to this system a plant with a score as 0-5 was considered as resistant and the plants with scores between 6-9 were considered as susceptible. Simple X^2 test was applied to test the goodness of fit of different genetic ratios.

RESULTS AND DISCUSSION

A. *Inheritance Studies*

The observations on disease reaction on F_1 and the segregation pattern in F_2 and F_3 generations obtained from different resistant × susceptible crosses against pathotype IX05 are given in Table 1. The F_1 plants obtained from cross B76/TN1 were resistant. In the F_2 generation 130 resistant (R) and 54 susceptible (S) plant were observed. The F_3 generation contained fifteen homozygous resistant, 35 segregating and twenty homozygous susceptible (HS) F_2 plant progenies. These observations indicate that F_2 and F_3 generations segregate in a 3R:1S and 1HR:2Seg:1HS ratios, respectively suggesting the presence of single dominant gene in B76. Likewise all F_1 plants obtained from the cross ARC 10464/TN1 were resistant indicating the dominant nature of resistance. The F_2 generation segregated into 178 resistant and 15 susceptible plants while F_3 generation contained 32 homoxygous resistant, 35 segregating and three homozygous susceptible F_2 plant progenies. The observations suggest that the F_2 and F_3 generations segregated in a 15R : 1S and 7HR : 8 Seg: 1HS ratio indicating the presence of two dominant independently inherited genes in ATC 10464 to pathotype IX05. The F_1 plants obtained from cross CNGS 20083/TN1 were susceptible indicating the recessive nature of resistance in this line. The F_2 generation contained 63 resistant and 161 susceptible plants which is very close to 1R:3S ratio and the F_3 generation contained 14 homozygous resistant, 40 segregating and 14 homozygous susceptible F_2 plant progenies and the F_3 generations segregated in 1HR: 2 Seg: 1HS ratio. It is concluded from these observations that resistance of CNGS 20083 to pathotype IX05 is governed by single recessive gene.

Table 1. Segregation for reaction to Xanthomonas campestris pv. oryzae pathotype IX05 in three crosses

S.No.	Cross	F_1 Reaction	No. of F_2 plants		Ratio	χ^2 value	No. of F_3 families*			Ratio	$\chi 2$ value
			R	S			HR	Seg	HS		
1.	B76/TN1	R	130	54	3:1	1.984	15	35	20	1:2:1	0.714
2.	ARC 10464/TN1	R	178	15	15:1	0.763	32	35	3	7:8:1	3.272
3.	CNGS 20083/TN1	S	63	161	1:3	1.167	14	40	14	1:2:1	2.118

*HR = Homozygous resistance; Seg = Segregating; HS = Homozygous susceptible,
R = Resistant, S = Susceptible

B. *Allelic tests*

The observations on disease reaction on F_1 and F_2 plants obtained from different resistant × resistant cross against pathotype IX05 are given in Table 2. The F_1 plants from the three crosses B76/ARC 10464, B76/CNGS 20083 and ATC 10464/CNGS 20083 were resistant. The F_2 population from crosses B76/ARC 10464, B76/CNGS 20083 and ARC 10464/CNGS 20084 segregated in 63R: 1S, 13R: 3S and 61R: 3S ratio. Thus confirming the presence of single dominant gene in B76, two dominant genes in ARC 10464 and a recessive gene in CNGS 20083. These observations also suggest that the *Xa* genes in these lines used for the present work are non-allelic.

Table 2. Allelic relationships between the Xa genes from three resistant lines

Cross	F_1 reaction	No. of F_2 plants		Total	Ratio	χ^2 value
		R	S			
B76/ARC 10464	R	115	1	116	63:1	0.0214
B76/CNGS 20083	R	75	12	87	13:3	1.4030
ARC 10464/CNGS 20083	R	85	5	90	61:3	0.1517

R = Resistance; S = Susceptible

Pathotypes prevalent in India are reported to be different than those prevalent elsewhere in the world [4, 16] and there is an evidence to support that some Indian pathotypes like IX05 are able to detect new genes. Moreover, studies on inheritance of resistance to different pathogens are relevant to the breeding programmes only if such work is done in relation to the prevalent pathotypes. Although ARC 10464 and B76 have shown differential reaction to many Indian pathotypes, the land race CNGS 20083 has shown consistent resistance to all the pathotypes of X. *c.* pv. *oryzae* used by Gupta *et al.* [16]. Simple nature of inheritance and the diversity of *Xa* genes identified from the three cultivars/lines used for the present work suggest that such material can be successfully exploited in breeding cultivar resistant to bacterial leaf blight of rice.

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