Ecology and Epidemiology

Variation in Pathogenicity of Some Indian Isolates of Xanthomonas campestris pv. oryzae

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The authors express their appreciation to M. S. Swaminathan, Director-General, International Rice Research Institute, Manila, Philippines, for his inspiration and encouragement.

Accepted for publication 18 February 1986.

ABSTRACT

Gupta, A. K., Sharma, S. C., and Saini, R. G. 1986. Variation in pathogenicity of some Indian isolates of Xanthomonas campestris pv. oryzae. Phytopathology 76:881-883.

Pathogenicity of 13 isolates of X anthomonas x campestris x pv. or y zae was tested using 13 rice cultivars and lines. All the isolates were virulent on two International Rice Research Institute (IRRI) differentials, IR 20 (X a-4) and IR 1545-339 (X a-5), and two Japanese differentials, Tetep (X a-1, X a-2) and Java 14 (X a-1, X a-3, X a-Kg), showing that these six resistance genes are of little practical value in resistance breeding in northwestern India. Based on the reactions on a set of nine cultivars and lines, DV 85 (X a-5),

Xa-7), CAS 209 (Xa-10), and IR 1160-8-6-1 from IRRI; Kinmaze, Kogyoku (Xa-1, Xa-3, Xa-Kg), and Wase Aikoku 3 (Xa-3) from Japan; and three Indian breeding lines, B76, ARC 10464, and CNGS 20083, 11 different pathotypes were identified. These pathotypes have different virulences as compared to those reported from Japan and Philippines. Additional unidentified resistance genes were observed in seven differentials including Kogyoku, Kinmaze, and Wase Aikoku 3.

Additional key words: avirulence, bacterial blight.

Bacterial leaf blight of rice, caused by Xanthomonas campestris pv. oryzae (X. c. pv. oryzae), has posed a serious threat to rice cultivation in India in recent years. Sources of resistance to this disease have been identified (1,10) and are being used in breeding blight-resistant rice cultivars. It is, however, essential to assess variation in pathogenicity of the bacterial populations in order to develop cultivars with a long-lasting resistance. Variation in

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pathogenicity of X. c. pv. oryzae from India has not been evaluated fully for lack of a suitable set of differentials. We report here the presence of 11 pathotypes of X. c. pv. oryzae in northwestern India using a set of nine differentials selected from sets used in Japan, the International Rice Research Institute (IRRI), Philippines, and some local rices. We also observed some new and as yet unidentified Xa genes present in seven differentials including Kogyoku, Kinmaze, and Wase Aikoku 3, which were used in this study.

MATERIALS AND METHODS

Rice plants infected with X. c. pv. oryzae were collected during

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1980 to 1982 from eight different districts of Punjab and Haryana, two major rice growing states in northwestern India. Thirteen single-cell colonies of bacteria isolated from these infected plants were cultured on potato sucrose peptone agar medium at 25 C. Individual isolates were transferred to fresh PSPA medium every 2 mo and reinoculated on a susceptible host, Taichung Native-1 (TN-1), every year to maintain virulence of the isolates. Thirteen rice cultivars and lines were used for studying pathogenic variation. These consisted of four IRRI differentials, IR 20, IR 1545-339 (henceforth referred to as IR 1545), DV 85, and CAS 209; five Japanese differentials, Tetep, Java 14, Kinmaze, Wase Aikoku 3, and Kogyoku, obtained from G. S. Khush, IRRI; three Indian breeding lines, ARC 10464, B76, and CNGS 20083; and one IRRI breeding line, IR-1160-8-6-1 (IR-1160). These were grown in an open field area in earthen pots (30 × 45 cm) with two plants per pot and two pots per cultivar. All the tests were conducted in 1983 and repeated in 1984. TN-1 was used as a susceptible check. Ten leaves per pot of 70-day-old plants were inoculated by clipping off the tips with scissors dipped in aqueous bacterial suspension from 2-dayold cultures and adjusted to a concentration of 10°-10° cells per milliliter, as suggested by Kauffman et al (4). Fourteen days after inoculation, basipetal lesion development from the inoculated leaf tips was recorded in centimeters. Cultivars and lines with average lesion lengths less than 25% of that recorded on the susceptible check cultivar (TN-1) inoculated with the same isolate were classified as resistant (R). Those with lesion lengths varying between 25 and 50% of that reached on TN-1 were classified as moderately resistant (MR). Others with lesion lengths greater than 50% of that recorded on TN-1 were classified as susceptible (S). Line and isolate combinations that gave inconsistent results over the years 1983 and 1984 were classified as variable (V).

RESULTS

The reactions of the rice cultivars and lines to different isolates of X. c. pv. oryzae are given in Table 1. Based on these reactions, the isolates were classified as 11 pathotypes and named IXO-1 through 11. All the isolates were virulent on IRRI differentials IR 20 and IR 1545. The remaining two differentials, DV 85 and CAS 209 from IRRI, classified these isolates into three pathotypes. Japanese differentials Tetep and Java 14 were susceptible to all the isolates. Using the remaining three Japanese differentials, the 13 isolates were classified into five distinct pathotypes. Rices ARC 10464, B 76, and CNGS 20083 from India and IR 1160 from IRRI also classified these isolates as five pathotypes that showed different

reaction patterns from the five pathotypes identified using Japanese differentials. IR 1160 was resistant to IXO-7 in 1983 but ranked as moderately resistant in the tests conducted during 1984; however, this did not affect the differentiation of the isolates. The five pathotypes, differentiated on the basis of their reaction to ARC 10464, B 76, CNGS 20083, and IR 1160, could be further subdivided into 11 pathotypes using cultivars DV 85, CAS 209, Kogyoku, and Wase Aikoku 3. Cultivar DV 85 differentiated pathotype IXO-4 from IXO-8, and CAS 209 differentiated IXO-2 from IXO-5. Kogyoku and Wase Aikoku 3 differentiated pathotype IXO-2 from IXO-7 and IXO-3 from IXO-11.

DISCUSSION

Observations summarized in Table 1 show that differential cultivars from IRRI (Philippines) or Japan alone cannot be used for assessing pathogenic variation in X. c. pv. oryzae from India. Some workers reported two pathotypes of X. c. pv. oryzae based only on the differential reactions of DV 85 and Cempo Selak (5,11). According to these reports, pathotype-I, which was avirulent on DV 85, was prevalent all over India, and pathotype-II, virulent on DV 85, was restricted only to West Bengal and Orissa in eastern India. Out of the 11 pathotypes reported here only IXO-8 can be classified as pathotype-I because of its virulence on DV 85. The other 10 isolates that are similar to pathotype-II could be distinguished using additional differentials proposed here. Our observations showed that nine cultivars and lines, namely DV 85, CAS 209, Kogyoku, Wase Aikoku 3, Kinmaze, IR 1160, ARC 10464, B 76, and CNGS 20083, can constitute a useful differential set for monitoring pathogenic variation of X. c. pv. oryzae in this region. Although Kinmaze is not necessary to differentiate any of the pathotypes reported here, it may be useful in identifying new pathotypes from India.

Horino et al (3) reported DV 85 to be resistant and Kinmaze to be susceptible to all pathotypes from Japan and the Philippines. Wase Aikoku 3 was reported to be resistant to all pathotypes so far tested from the Philippines as well as to most of the pathotypes from Japan. In our tests Kinmaze showed resistance to pathotype IXO-2 and IXO-7. DV 85 and Wase Aikoku 3 were susceptible to 10 and nine of our pathotypes, respectively. Two Japanese differentials, Tetep and Java 14, and two IRRI differentials, IR 20 and IR 1545, were susceptible to all 11 pathotypes. These observations show that the pathotypes prevalent in the Philippines, Japan, and India represent very different virulence combinations.

TABLE 1. Reaction of 15 rice lines to 11 pathotypes of Xanthomonas campestris pv. oryzae collected in the Indian states of Punjab and Haryana in 1980-1982

Differential line	Known - Xa-gene(s)	IXO-Race										
		1	2	3	4	5	6	7	8	9	10	11
IRRI ^a differentials												
IR 20	Xa-4	S^b	S	S	S	S	S	S	S	S	S	S
IR 1545-339	xa-5	S	S S	S	S S S	S S S	S	S	S	S	S	S
DV 85	xa-5, Xa-7	S	S	S		S	S	S	R	S	S	S
CAS 209	Xa-10	S	R	S	R	S	R	R	S	R	R	S
Japanese differentials												
Tetep	Xa-1, $Xa-2$	S	S	S	S	S S	S	S	S	S	S	S
Java 14	Xa-1, Xa-3, Xa-Kg	S S	S	S	S S	S	S	S	S	S	S S	S S R
Kogyoku	Xa-1, Xa-3, Xa-Kg	R	R	S	R	R	R	S	R	R		
Wase Aikoku 3	Xa-3	R S	R R	S	S	S	S S	S	S S	S	S	MR
Kinmaze	¢	S	R	S	S	S	S	R	S	S	S	S
New differentials												
IR 1160-8-6-1		S	R	S	R	R	S	V	MR	MR	S S	S
ARC 10464		R	R R	S S	R	R	MR	R	R	MR	S	
B 76	***	R	R	S	R	R	R	R	R	S	MR	S
CNGS 20083	***	R	R	R	R	R	R	R	R	R	MR	MR
Susceptible check												
Taichung Native-1	None	16.4d	15.8	16.9	15.4	18.2	14.9	18.0	16.7	18.9	21.2	14.7

a IRRI, International Rice Research Institute.

Ratings are based on lesion length compared to that on Taichung Native-1, the susceptible check: R (resistant) = lesion length 25% of that on TN-1; MR (moderately resistant) = 25-50%; S (susceptible) = 50%; V = varied among tests. Determinations were based on means of 40 ratings.

Unidentified resistance genes.

Mean lesion length (cm) for 40 inoculated leaves.

Four resistance genes have been reported from the IRRI differentials used in this study: Xa-4 in IR 20 (8); xa-5 in IR 1545 (7); xa-5 and Xa-7 in DV 85 (12); and Xa-10 in CAS 209 (13). Two genes, Xa-1 and Xa-2, are reported in Tetep (9). Java 14 and Kogyoku are known to carry Xa-1, Xa-3, and Xa-Kg (6). Ezuka et al (2) reported that Wase Aikoku 3 also has Xa-3. Susceptibility of IR 20, IR 1545, Tetep, and Java 14 to all the pathotypes reported here indicated that genes Xa-1, Xa-2, Xa-3, Xa-4, xa-5, and Xa-Kg do not provide effective resistance against bacterial blight in northwestern India. That the reactions of ARC 10464, B 76, CNGS 20083, and IR 1160 to the 11 pathotypes differed from the reactions of the cultivars with genes Xa-1, Xa-2, Xa-3, Xa-4, xa-5, Xa-7, Xa-10, and Xa-Kg, indicates that these four lines have a different resistance gene or genes. The resistance of Kogyoku and Wase Aikoku 3 to the pathotypes that are virulent on Java 14 indicates the presence of an additional unidentified resistance gene or genes in these two cultivars. Cultivar Kinmaze, which is susceptible to all the pathotypes from the Philippines and Japan (3) but resistant to Indian pathotypes IXO-2 and IXO-7, also must have some as yet unidentified resistance gene(s). These seven cultivars and lines need to be characterized through multi-isolate tests and genetic analysis.

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