Pathogenic Variability in Xanthomonas oryzae

O. R. Reddy and S. H. Ou

Former Research Fellow and Plant Pathologist, respectively, of The International Rice Research Institute (IRRI), Los Baños, The Philippines. Present address of senior author: All-India Coordinated Rice Improvement Project, Rajendranagar, Hyderabad-500 030, India.

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ABSTRACT

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Inoculations with 51 isolates of Xanthomonas oryzae (the causal organism of bacterial blight of rice) from 11 countries of Asia on 32 rice cultivars revealed wide difference in virulence of the pathogen and susceptibility of cultivars tested. Tall cultivars like BJ 1, Semora Mangga, Chinsurah Boro II, Hashikalmi, UCP-28, and semidwarf cultivars, such as Ratna and IR20, showed a broad spectrum of resistance to

the isolates of the pathogen. The spectrum of resistance of breeding lines RP291-7-1 (A), RP633 (C), IR1545-339, and IR1514A-E666 was superior to that of their parents. Among the resistant group of rice cultivars and virulent strains of the pathogen differential reaction patterns were observed. The significantly different cultivar-isolate interaction suggested that a vertical pathotype exists in X. oryzae.

Additional key words: bacterial blight of rice, virulence, cultivar resistance.

Bacterial blight of rice, caused by Xanthomonas oryzae (Uyeda & Ishiyama) Dowson, is an important disease in tropical Asia (15). A knowledge of the pathogenic variability of this bacterium is necessary to exploit genetic pools for developing a rice with stable resistance to this pathogen.

Several Japanese workers classified X. oryzae into strains, but the criteria they used for classification varied widely which makes interpretation difficult (7, 13). In tropical Asia, wide variation in pathogenicity was reported from India (3, 5, 6, 10, 12) and The Philippines (4, 9, 14). Recent studies with a large number of isolates from Asia and Australia revealed that tropical isolates were more virulent than those from Japan and Australia, but that no distinct races were evident (2, 11, 16). Buddenhagen and Reddy (2) reported a horizontal relationship between the pathogen and host, with the exception of a few of the Indian isolates and all of the Australian isolates that were studied. Subsequently, Australian isolates were considered to be distinct pathotypes that had evolved on indigenous wild rice species (1). In The Philippines, a strain named the "Isabela strain" broke down the dominant gene which conferred resistant to some rice cultivars (14).

The present study used widely different isolates of X. oryzae and many rice cultivars to investigate further the host-pathogen relationship, with special reference to the relationship between virulent strains of the pathogen and resistant groups of rice cultivars.

MATERIALS AND METHODS

Fifty-one isolates of X. oryzae from 11 Asian countries, were selected from cultures at the Plant Pathology

Department of the International Rice Research Institute (IRRI), The Philippines, and were tested against 32 rice cultivars. The reaction of 20 selected strains on 11 rice cultivars was further studied in a replicated strip plot design.

Rice seedlings were grown in the greenhouse in 15-cm diameter circular clay pots filled with 1 kg of Banlic clay soil to which fertilizer was added (40 g triphosphate, 100 g ammonium sulfate, and 40 g potash/50 kg of air-dried soil). Five seedlings were maintained in each pot and one pot was used for each bacterial isolate and rice cultivar combination. The two youngest expanded leaves of each 30-day-old seedling were clipped at about 8 cm from the tip with scissors dipped in a bacterial suspension of 10^8 cells/ml (O.D.620 nm = 0.4) of 24-hour-old cultures grown on Wakimoto agar (16). Disease reaction was scored by measuring the lesion length (cm) from the point of inoculation of 10 to 15 leaves 14 days after inoculation.

A "virulence index" was used to indicate the virulence of the bacterial strains. This was calculated by averaging the lesion lengths on all 32 rice cultivars produced by particular bacterial strains. Similarly a "susceptibility index" was used to indicate the degree of resistance or susceptibility of rice cultivars. This was done by averaging the lesion lengths produced by all the 51 bacterial isolates inoculated on specific cultivars.

RESULTS

The isolates of X. oryzae differed markedly in their virulence as measured by the lesion length on rice leaves. Figure 1 shows the virulence of 31 isolates on four rice cultivars individually and Table 1 shows the overall virulence of each of the 51 isolates on 32 rice cultivars and the geographical distribution of the isolates. The overall

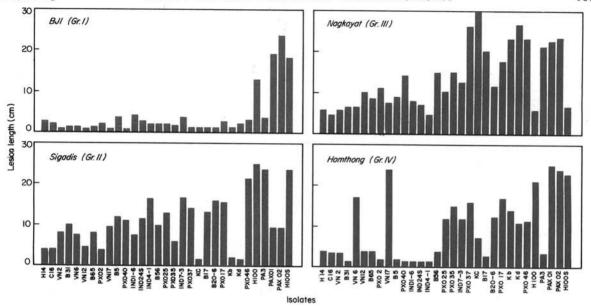


Fig. 1. Susceptibility pattern of four representative rice cultivars to 31 isolates of Xanthomonas oryzae (from left to right increasing average virulence index).

TABLE 1. Virulence of 51 isolates of Xanthomonas oryzae on 32 rice cultivars

Degree of virulence ^a	Virulence index ^b	Isolates and geographic origin ^c B16 ^r , PXO108 ^r , N2 ^l , N4 ^l , KXO2 ^k , B-19 ^t , B46 ^r , B14 ^r , N1 ^l , BU3 ^g , B33 ^r , PXO10 ^r , Sf10 ^r , H257 ^h , N3 ^l . B1 ^r , KXO7 ^k , KXO3 ^k , KXO4 ^k , B-18 ^t , H14 ^h , C1 6 ^s , VN2 ^v , B31 ^r , VN6 ^v , VN12 ^v , B65 ^r , PXO2 ^r .			
LV	0.6 - 4.0				
MV	4.5 - 8.5				
V	9.0 - 12.0	VN17 ^v , B5 ^r , PXO40 ^r , Indl-6 ⁱ , Ind24S ⁱ , Ind4-1 ⁱ , B56 ^r , PXO25 ^r , PXO35 ^r , Ind7-3 ⁱ , PXO37 ^r , KC ⁱ , B-17 ^t , B20-6 ^t , PXO17 ^r , KB ⁱ , KD ⁱ , PXO46-1 ^r .			
HV	16.0 - 19.0	H100 ^h , Pa 3 ^f , PaXO1 ^p , PaXO2 ^p , H100s ^h .			

^aLV = least virulent; MV = moderately virulent; V = virulent; HV = highly virulent.

bVirulence index = overall average lesion length (cm) produced by each isolate on 32 rice cultivars.

TABLE 2. Susceptibility of 32 rice cultivars to 51 isolates of Xanthomonas oryzae

egree of resistance ^a	Susceptibility index ^b	Cultivars RP291-7-1 (A), BJ 1, S. Mangga, Hashikalmi, UCP-28, C. Boro II, Ratna, RP633 (C), IR1545-339, IR20 and IR1514A-E666. TKM6, IR1541-76-3, W. Aikoku, Remadja, IR26, DZ192, Homthong, Sigadis, M. Sungsong, RP633 (E). IR22, Chukei and Nagkayat.				
R	2.2 - 5.0					
MR	6.0 - 9.0					
MS	11.0 - 13.0	W1263, B589A4, Zenith & L(Z)N.				
S	14.0 - 18.0	IR24, Laka, IR8 and IR480.				

^aR = resistant; MR = moderately resistant; MS = moderately susceptible; S = susceptible.

Geographic origin: Bangladesh, Burma, India, Indonesia, Japan, Korea, S., Pakistan, Philippines, Sri Lanka, Thailand, Vietnam, S.

^bSusceptibility index = overall average lesion length (cm) of each cultivar to 51 bacterial isolates.

virulence indices varied from 0.6 for isolate B16 to 18.9 of isolate H100s. Japanese and Korean isolates were only weakly virulent; all the virulent isolates were from the

tropics.

Marked differences in resistance or susceptibility to the parents DZ192. The spectrum of resistance to the bacterial isolates Cl 6, KD, and B20-6 of progenies of isolates were observed among the rice cultivars. The overall susceptibility indices (against 51 X. oryzae isolates) of rice cultivars ranged between 2.2 for RP291-7-1 (A) and 18.0 for IR480. The rice cultivars BJ1, Semora Mangga, Hashikalmi, UCP-28, Chinsurah Boro II, Ratna, IR20, and hybrid lines, RP291-7-1 (A), RP633 (C), IR1514-E666, and IR1545-339, had a broad spectrum of resistance (Table 2). The spectrum of resistance of BJ1 to the 31 isolates is shown in Fig. 1.

Semidwarf hybrid lines showed greater resistance to specific virulent isolates than did the parental cultivars (Table 3). The level of resistance of RP291-7-1 (A) and RP633 (C) to isolate PaXO2 was higher than that of its resistant parent BJ1. The resistance of IR1545-339 to isolates Cl 6 and H14 was greater than that of the resistant

TKM6 (IR20, IR1514A-E666, IR26, and Ratna) was better than that of TKM6.

Rice cultivar groups and bacterial isolates also showed differential reaction patterns (Table 4, Fig. 1). BJ1, S. Mangga, UCP-28, Hashikalmi, C. Boro II, and DZ192 of group I had a broad spectrum of resistance to most of the isolates, but they were susceptible to isolates PaXO2 and H100 (also to PaXO1 and H100s, not shown in Table 4). The group II, namely Remadja, Sigadis, and TKM6, had a moderate level of resistance to PaXO2 (and PaXO1) to which group I was susceptible. However, group II was susceptible to PXO46-1 and several other isolates to which the group I rices were resistant. Cultivar TKM6 was different from Sigadis and Remadja of this group II in that it had resistance to Ind7-3 and was susceptible to bacterial isolates KD and Cl 6. Group III (M. Sungsong, Nagkayat, W. Aikoku, and Chukei) was resistant to isolates H100 (and H100s) and was susceptible to isolates KD (also KB and KC). Cultivars W. Aikoku and Chukei were resistant to bacterial isolate PXO46-1, but M. Sungsong and Nagkayat were not resistant to PXO46-1. Cultivar Homthong of group IV was resistant to bacterial

TABLE 3. Reactions of resistant parents and their progenies of some rice cultivars to specific isolates of Xanthomonas oryzae

Parental cultivar or		Isolates						
progeny line	Cross	PaXO2	H100	Pa 3	Cl 6	KD	B20-6	
BJ 1		23.6ª	12.7	3.3	2.3	1.8	1.1	
RP291-7-1 (A)	IR8/BJ1	9.2	11.7	3.0	2.3	0.6	1.0	
RP633 (C)	IR8/BJ1//IR22	7.5	12.7	13.6	4.8	1.8	5.2	
DZ 192	//4	30.6	27.0	27.3	16.6	4.3	4.0	
IR1545-339	IR24/DZ192	24.5	22.9	20.6	8.9	2.0	2.6	
гкм6		9.9	15.1	17.9	14.1	12.9	11.5	
IR20	IR262/TKM6	7.9	9.2	11.6	3.2	8.5	7.5	
IR1514A-E666	IR20/TKM6	7.7	12.9	9.0	3.5	5.9	7.1	
IR26	IR24/TKM6	7.8	16.2	13.7	3.6	12.0	8.0	
Ratna	TKM6/IR8	14.7	13.6	9.9	8.4	3.9	4.6	

[&]quot;Average lesion length (in centimeters) of inoculated leaves 14 days after inoculation.

TABLE 4. Susceptibility pattern of specific rice cultivars to specific virulent isolates of Xanthomonas oryzae

Susceptibility group	Rice cultivar	Isolates						
		PaXO2	H100	Pa 3	Cl 6	PaXO46-1	KD	Ind7-3
I	BJ 1	23.6ª	12.7	3.3	2.3	3.1	1.8	3.5
	S. Mangga	19.2	11.8	3.5	2.4	3.3	1.3	2.0
	UCP-28	23.7	18.6	22.0	3.7	2.5	1.9	3.1
	Hashikalmi	18.7	16.6	11.4	2.7	1.1	1.4	2.7
	DZ 192	30.6	27.0	27.3	16.6	7.7	4.3	4.9
П	Remadja	8.9	18.0	17.1	3.8	21.3	0.7	12.9
	Sigadis	9.5	19.3	23.6	3.8	21.4	1.6	16.3
	TKM6	9.9	15.1	17.9	14.1	12.0	12.9	4.9
ш	M. Sungsong	16.6	7.7	18.7	2.6	23.6	21.7	10.8
	Nagkayat	23.0	5.3	20.8	4.5	22.9	26.5	6.3
	W. Aikoku	15.1	3.9	12.3	3.9	5.8	15.8	8.0
	Chukei	21.9	6.6	21.0	3.1	5.5	18.7	10.7
IV	Homthong	23.7	21.1	2.0	3.6	13.7	1.0	13.4

^aAverage lesion length (in centimeters) of inoculated leaves 14 days after inoculation.

isolate Pa 3, but the rices of groups II and III and some in group I were not.

The differential reaction between the rice cultivars and bacterial isolates also was observed among the 20 selected bacterial strains on 11 rice cultivars inoculated separately (Reddy and Ou, *unpublished*).

DISCUSSION

The results indicate wide variability in virulence among the bacterial isolates and great difference in the susceptibility of rice cultivars to the bacterial isolates. These results confirm the earlier studies on bacterial strains.

distinct groups according to differences in susceptibility and/or resistance to isolates of the blight organism (Table 4) suggests a vertical host-pathogen relationship. The cultivars of each of these groups may have identical genes governing blight resistance; this concurs with earlier studies (8) and tends to confirm the differential interactions reported with strains of the blight pathogen of India (3, 6, 10), Australia (1, 2), and The Philippines (14). The vertical relationship between the weakly virulent pathotypes and rice cultivars are not easily recognized because of the smaller lesions developed. It is recognized only occasionally with such isolates as VN6, PXO2, VN17 etc. on Sigadis, Nagkayat, and Homthong in Fig. 1. The general aspect of disease caused by the weakly virulent isolates is that of a horizontal host-pathogen relationship. These host-pathogen relationships may have been the result of the evolution of the blight pathogen in Asia on a large number and continuously changing cultivars of rice.

The spectrum of resistance of rice cultivars, such as BJ1 (Table 4, group I), may be further broadened by combining the resistance of cultivars such as Sigadis, M. Sungsong, and others (Table 4, group II and III). An improved spectrum of resistance to the blight pathogen in semidwarf hybrid lines suggests the presence of minor genes, which may have additive effects on resistance.

These findings may be useful to rice breeding programs designed to develop a stable broad spectrum of resistance to bacterial blight in rice cultivars. Work on the genetics of resistance is needed to clarify the vertical host-pathogen relationship of resistant rice cultivars against virulent strains of the bacterial blight pathogen.

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