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PATHOGENICITY ASSOCIATION IN *XANTHOMONAS ORYZAE* PV. *ORYZAE*- THE CAUSAL ORGANISM OF RICE BACTERIAL BLIGHT DISEASE

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ABSTRACT

Pathogenicity of the isolates of Xanthomonas oryzae pv. oryzae (Xoo), the incitant of rice bacterial blight disease, collected from different rice growing states of India, were analyzed by calculating (i) virulence frequency (VF) on each host genotype, (ii) pathogenicity association coefficient (PAC) and (iii) virulence association coefficient (VAC) of all possible combinations of two host genotypes, in different sets of rice genotypes involving differential varieties, near isogenic lines (NIL) and gene pyramids each possessing known genes for resistance. Based on the host-pathogen interactions, 4-11 virulence factors could be recognized in the 52 bacterial isolates *viz*. v-1, 2, 3, 4, 5, 6, 7, 10, 11, 12 and 13 which were effective against 11 *Xa* genes conferring resistance to Xoo. A total number of 0-7 avirulence gene factors could also be recognized in the bacterial isolates. The combination of host genes for resistance, which can be effectively deployed in disease control strategy, was characterized by high PAC: low VAC with widest difference between the two and least difference between one and PAC (1-PAC) accompanied by low virulence frequency. The gene combinations responsible for rapid disease spread, which warrant immediate withdrawal from a specific locality, could be characterized by high PAC: high VAC and zero to low difference between PAC and VAC as well as 1-PAC accompanied by high VF for both the genotypes. Such analysis of extensive pathogenicity survey data on large number of isolates representing any particular region would help in taking decision on deployment of desired gene combinations for effective disease control, withdrawal of varieties possessing undesirable gene combinations, breeding varieties possessing resistance genes for specific region and development of NILs.

Keywords: host, genotype, pathogenicity, virulence, association coefficient, frequency.

INTRODUCTION

Bacterial blight disease incited by Xanthomonas oryzae pv. Oryzae (Xoo) is one of the most serious diseases of rice causing huge yield losses in almost all the rice growing countries of Asia. The major epidemics during the sixties and the epidemic in the Punjab state of India are well documented examples of the extensive yield losses even up to the extent of 65-95% due to the disease (Reddy, 1980). Consequent upon the failure of controlling this disease through chemicals, host resistance is given priority in disease control strategy and thus breeding for resistance has become an integral part of the rice improvement programme in all the rice growing countries. The wide variability in virulence among the bacterial strains has become a major constraint in resistance breeding programme. Sincere attempts have been made world wide to group the bacterial strains into virulence groupings through a set of differential varieties and pathotypes have been identified in Japan (Ezuka and Horino, 1974; Endo *et al.*, 1991; Kaku, 1993; Noda *et al.*, 1990; Ogawa, 1993), IRRI, Philippines (Ou *et al.*, 1971; Mew and Vera Cruz, 1979; Horino *et al.* 1980; Mew *et al.*, 1982), Indonesia (Yamamoto *et al.*, 1977) and India (Devadath and Padmanabhan, 1969; Rao *et al.*, 1971; Gupta *et al.*, 1986; Reddy and Reddy, 1990; Nayak and Reddy, 1993).

Based on these grouping and designation of pathotypes, 27 *Xa* genes conferring resistance to Xoo, have been identified in different countries, 21 of which have been compiled by Ogawa (1993), who also suggested the strategy for monitoring the race distribution of *Xoo* by using near-isogenic lines (NIL) and proposed a set of differentials possessing known genes for resistance. Unfortunately, certain Indian isolates possess the virulence factors to overcome the resistance offered by *Xa 1*, *Xa 2*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 7*, *Xa 10* and *Xa 12* (Gupta *et al.* 1986), *Xa 4*, *xa 5*, *Xa 7*, *Xa 11* and *xa 13* (Nayak, 1986), *Xa 1*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 7* and *Xa 11* (Khare and Thrimurty, 2006), *Xa 1*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 7*, *xa 8*, *Xa 10*, *Xa 11*, *xa 13*, *Xa 14* and *Xa 21* (Shanti *et al.* 2001 and Shanti and Shenoy 2005), *Xa 1*, *Xa 2*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 6*, *Xa 7*, *Xa 10*, *Xa 11*, *Xa 12* and *xa 13* (Nayak, 1996), besides the *Xa 14* gene present in Taichung Native-1, which is used as a susceptible check in most of the pathogenicity trials. Shanti and Shenoy (2005) tested 11 near isogenic lines in the genetic background of IR 24 and nine gene pyramids against 10 isolates of *Xoo* and concluded that the effectiveness of genes vary in different regions and to have an effective deployment of gene combinations, regional information on the performance of individual genes is a prerequisite. Under the circumstances, it is essentials to conduct extensive countrywide pathogenicity surveys involving large number of isolates randomly sampled from the entire rice growing tracts, those would adequately describe the pathogen population for studies on pathogenic specialization. The scientific information obtained from such extensive pathogenicity survey data on a set of differential rice genotypes possessing known genes for resistance, through the analysis of virulence frequency, pathogenicity

association coefficients and virulence association coefficients could be best utilized in recognition of desired gene-combinations those can be deployed in effective disease control strategy. An attempt has been made in the present paper to analyze the pathogenicity association of 52 bacterial strains to 16 rice genotypes possessing known genes for resistance to *Xoo* as well as from the published literature (Gupta *et al.*, 1986; Shanti and Shenoy, 2005; Nayak, 1996) and explore the feasibility of deployment of desired gene combinations in bacterial blight disease control strategy.

MATERIALS AND METHODS

Bacterial isolates and rice genotypes

The isolates of Xanthomonas oryzae pv. oryzae (Xoo) were isolated from diseased leaf samples collected from 52 locations situated all over the country, covering 12 rice growing states and one Union Territory of India (Nayak, 1996). The country was divided into four regions *viz*. (i) southern region consisting of Andhra Pradesh (AP), Tamil Nadu (TN), Andaman and Nicobar Islands (AN); (ii) eastern region constituting of Orissa (OR), West Bengal (WB), Assam (AS) and Bihar (BR); (iii) northern region constituting of Uttar Pradesh (UP), Punjab (PB) and Rajasthan (RJ) and (iv) western region consisting of Maharashtra (MH), Gujarat (GT) and Madhya Pradesh (MP). Among the 52 isolates, 13 were collected from southern region, a maximum of 23 isolates from eastern region, nine from northern region and seven from western region. Single cell colonies of each isolate were cultured on potato sucrose agar (PSA) slants and maintained in sterile distilled water at 4^{o}C as stock culture.

The pathogenicity association analysis was made on the virulence pattern of (i) these 52 isolates of *Xoo* on 16 rice genotypes possessing 11 known *Xa* genes for resistance viz. *Xa 1, Xa 2, Xa 3, Xa 4, xa 5, Xa 6, Xa 7, Xa 10, Xa 11, Xa 12* and *xa 13*; present either as single or in combinations of two or three genes (Nayak *et al.*, 2006); (ii) the 52 isolates on five Japanese, five IRRI and five new Indian differentials selected by the authors (Nayak *et al.*,unpublished); (iii) 11 pathotypes identified from 13 isolates of *Xoo* collected from eight districts of Punjab and Haryana states in north-western India on 14 rice genotypes including four IRRI, five Japanese and four new Indian differentials along with the susceptible check Taichung native-1 (TN-1) possessing eight *Xa* genes (Gupta *et al.* 1986) and (iv) 10 isolates of *Xoo* collected from four states of India *viz*. Andhra Pradesh, Orissa, Punjab and Tamil Nadu on 11 near isogenic lines (NILs) each possessing single genes viz. *Xa 1*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 7*, *xa 8*, *Xa 10*, *Xa 11*, *xa 13*, *Xa 14* and *Xa 21*, and nine gene pyramids of two, three or four-gene combinations, in IR 24 genetic background (Shanti and Shenoy, 2005).

Inoculation and observation

The rice plants were clip inoculated (Kauffman *et al.*,1973) at boot leaf stage with a pair of scissors every time dipped into the bacterial suspension containing ca. 10^9 cfu.ml^{-1}, prepared from a 48 h old actively growing culture of each isolate grown on modified Wakimoto-agar-medium. The lesion length developed below the point of inoculation was measured on the 21st day of inoculation. The development of necrotic lesions progressing up to a maximum of 3-5 cm was considered as resistant (R) and water-soaked lesions initiated within 4-5 days of inoculation, followed by rapid progress thereafter with typical yellowish-grey colour, was characterized as susceptible (S) reaction. The lesion length < 4.00 cm were considered as resistant and > 4.00 cm as susceptible by Shanti and Shenoy (2005), while those with < 25% of the lesion length recorded on the susceptible check TN-1 were considered as resistant and > 25% as susceptible by Gupta *et al*. (1986).

STATISTICAL ANALYSIS

The response of the host genotypes to the pathogen isolates was expressed as resistant (R) or susceptible (S). The pathogenicity of the corresponding isolate was expressed as avirulent (A) or virulent (V), respectively. The terminology pathogenicity, as used in the present context, means the capacity to produce disease in the host plant. Virulence is used to mean the capacity to produce severe disease and avirulence means the inability to produce severe disease. The tabulated data on the disease reaction of the host genotypes to each of the isolates expressed as susceptible (S) or resistant (R) were transformed into pathogenicity terminology of virulent (V) or avirulent (A), respectively with the basic assumption, within the gene-for-gene relationship, that if a host genotype possesses a gene for resistance, then the pathogen isolate possesses a corresponding gene for avirulence and vice versa. The pathogenicity data were sorted out into four geographic regions of the country according to their place of origin of the states in each region.

The virulence frequency of the isolates on each of the rice genotypes was calculated by dividing the number of virulent isolates by the total number of isolates in each sample. When the pathogenicity of a specific isolate to a specific host genotype is recognized as avirulent or virulent, the pathogenicity of that isolate to any pair of host genotypes, A and B, can be recognized as either Avirulent A : Avirulent B (A_A : A_B), or Avirulent$_A$: Virulent$_B$ (A_A : V_B) or Virulent$_A$: Avirulent$_B$ (V_A : A_B) or Virulent$_A$: Virulent$_B$ (V_A : V_B). The pathogenicity data were classified in this manner with regard to all possible combinations of any two genotypes in each set of rice genotypes. The Pathogenicity Association Coefficient (PAC) and Virulence Association Coefficient (VAC) were calculated in a similar way as coefficients of resemblance in numerical taxonomy (Sokal and Sneath 1963) as:

$$PAC_{AB} = \frac{\text{(No. of isolates } A_A{:}A_B\text{)+(No.of isolates } V_A : V_B\text{)}}{\text{Total number of isolates in the sample}}$$

$$VAC_{AB} = \frac{\text{Number of isolates } V_A{:}\ V_B}{\text{Total number of isolates in the sample}}$$

The PAC and VAC values were calculated for each possible pairs of host-genotype combinations in each of the four geographic regions as well as the country as a whole, by this method; and also for each set of pathogenicity data included in the present investigation.

RESULTS

The virulence frequency (VF) of the isolates of Xoo on 16 rice genotypes in each of the four regions as well as the country as a whole, revealed wide differences ranging from 8-100% in southern region, 26-100% in eastern region, 11 to 100% in northern region, zero to 100% in western region and 15 to 100% in the country (Table 1). The VF of all the isolates to the Japanese differential Rantai Emas (*Xa 1+Xa 2*) , the IRRI differentials IR 8 (*Xa 11*) and IR 20 (*Xa 4*) were 100%, suggesting that these genes are ineffective to overcome the virulence factors present in the isolates in all the regions of the country. The next higher VF of 56% was expressed by the isolates collected from the northern region, on the genotypes Java-14 (*Xa 1+3+12*) and Cas-209 (*Xa 10*) ; compared with the VF of 14, 15 and 35% expressed by the isolates from western, southern and eastern regions, respectively. There was a wide variation (0.00-35%) in VF expressed by the isolates from four regions, in respect of rest of the genotypes. The highest overall VF of 44% was expressed by the isolates from eastern region, followed by 35% from southern region, 34% from northern region, 31% from western region compared with 38% for the country as a whole.

Table-1. Virulence frequency (%) of 52 Indian isolates of Xanthomonas oryzae pv. oryzae on 16 rice genotypes with known genes for resistance.

	Genotypes	**Virulence frequency** (%)				
		Southern region* (N = 13)	**Eastern region** (N = 23)	**Northern region** (N = 9)	**Western region** (N = 7)	**India** (N = 52)
1.	Kogyoku (*Xa 1+Xa 3+Xa 12*)	30.77	30.43	11.11	28.57	26.92
2.	Rantai Emas (*Xa 1+Xa 2*)	100.00	100.00	100.00	100.00	100.00
3.	Wase Aikoku 3 (*Xa 3*)	30.77	30.43	22.22	28.57	28.85
4.	Java 14 (*Xa 1+Xa 3+Xa 12*)	15.38	34.78	55.56	14.29	30.77
5.	IR 8 (*Xa 11*)	100.00	100.00	100.00	100.00	100.00
6.	IR 20 (*Xa 4*)	100.00	100.00	100.00	100.00	100.00
7.	IR 1545-339 (*xa 5*)	7.69	26.09	11.11	0.00	15.38
8.	Cas 209 (*Xa 10*)	15.38	34.78	55.56	14.29	30.77
9.	DV 85 (*xa 5+Xa 7*)	7.69	34.78	11.11	0.00	19.23
10.	TKM 6 (*Xa 4*)	30.77	30.43	11.11	28.57	26.92
11.	Tetep (*Xa 1+Xa 2*)	30.77	30.43	11.11	28.57	26.92
12.	Semora Mangga (*Xa 4*)	7.69	30.43	11.11	0.00	17.31
13.	CB II (*Xa 3+xa 5+xa 13*)	30.77	30.43	11.11	28.57	26.92
14.	BJ 1 (*xa 5+xa 13*)	30.77	30.43	11.11	28.57	26.92
15.	Zenith (*Xa 6*)	7.69	30.43	11.11	0.00	17.31
16.	M.Sung Song (*Xa 6*)	7.69	30.43	11.11	0.00	17.31
	Overall frequency (%)	34.61	44.02	34.02	31.25	38.22

*Southern region = Andhra Pradesh, Tamil Nadu, Andaman and Nicobar Islands
Eastern region = Assam, Bihar, Orissa, West Bengal
Northern region = Punjab and Haryana, Uttar Pradesh, Rajasthan
Western region = Gujarat, Madhya Pradesh, Maharashtra

The VF of the isolates to Indian differential varieties showed wide variations ranging from 8-100% in southern, 22-100% in eastern, 0-100% in northern as well as western regions and 17-100% for the country as a whole (Table-2). A comparatively narrower range of variation in VF was expressed to all the three sets of differential varieties in eastern region. A critical insight into the data revealed that the VF were the pathogenicity expressed by the pathotypes 1+7+15+16 in the southern region, while 1+4+14+15+16 in the eastern region, 4+14+16 in the northern region, 7+15+16 in the western region and 1+4+7+14+15+16 in the country as a whole. This suggests the existence of the respective pathotype groups in the corresponding regions of the country.

The VF of the isolates from Punjab and Haryana states (Gupta *et al.*, 1986) ranged between 18 and 100%. Highest VF of 100% was expressed on the rice genotypes IR 20 (*Xa 4*), IR 1545 (*xa 5*), Tetep (*Xa 1+Xa 2*), Java 14 (*Xa 1+Xa 3+Xa 12*) and Taichung Native-1 (*Xa 14*); while that on DV 85 (*xa 5, Xa 7*) and Wase Aikoku 3 (*Xa 3*) was 91%. These findings suggest that these genes/gene combinations are ineffective against the virulent isolates of the locality.

The VF of the 10 isolates from Andhra Pradesh, Orissa, Tamil Nadu and Punjab states tested on the NILs

as well as the gene pyramids (Shanti and Shenoy 2005), ranged between zero to 60%. The isolates expressed zero VF on IRBB-14 (*Xa 14*), M. Sung Song (Xa *6*) and the pyramid with *Xa 4 + xa 5* genes; while it was 10% on IRBB 8 (*xa 8*) and the pyramids with *xa 5+xa 13*, *xa 5+Xa 21*, *xa 13+Xa 21*, *Xa 4+xa 5+xa 13*, *Xa 4+xa 5+Xa 21*, *xa 5+xa 13+Xa 21* and *Xa 4+xa 5+xa 13+Xa 21*. The highest degree of resistance expressed by the presence of *Xa 14* gene in IRBB 14, in contrast with the highest degree of susceptibility expressed by TN-1 possessing the same gene, however, need further investigation on the genetic constitution of the latter.

Table-2. Virulence frequency (%) of 52 Indian isolates of Xanthomonas oryzae pv. oryzae on the sets of Indian, IRRI, and Japanese differential varieties.

Differentials varieties	**Virulence frequency** (%)				
	Southern region* (N = 13)	**Eastern region** (N = 23)	**Northern region** (N = 9)	**Western region** (N = 7)	**India** (N = 52)
Indian differentials:					
IR 8 (*Xa 11*)	100.00	100.00	100.00	100.00	100.00
TKM 6 (*Xa 4*)	30.77	30.43	11.11	28.57	26.92
DV 85 (*xa 5+Xa 7*)	7.69	30.43	11.11	0.00	17.31
PN 13 (?)	7.69	21.74	55.56	0.00	21.15
IET 8585 (?)	38.46	30.43	0.00	42.86	28.85
IRRI differentials:					
IR 8 (*Xa 11*)	100.00	100.00	100.00	100.00	100.00
IR 20 (*Xa 4*)	100.00	100.00	100.00	100.00	100.00
IR 1545 (*xa 5*)	7.69	30.43	11.11	0.00	17.31
Cas 209 (*Xa 10*)	15.38	34.78	55.56	14.29	30.77
DV 85 (*xa 5+Xa 7*)	7.69	30.43	11.11	0.00	17.31
Japanese differentials:					
Kinmaze (?)	100.00	100.00	100.00	100.00	100.00
Kogyoku (*Xa 1+Xa 3+Xa 12*)	30.77	30.43	11.11	28.57	26.92
Rantai Emas (*Xa 1+Xa 2*)	100.00	100.00	100.00	100.00	100.00
Wase Aikoku 3 (*Xa 3*)	30.77	30.43	11.11	28.57	26.92
Java 14 (*Xa 1+Xa 3+Xa 12*)	15.38	34.78	55.56	14.29	30.77

*Southern region = Andhra Pradesh, Tamil Nadu, Andaman and Nicobar Islands
Eastern region = Assam, Bihar, Orissa, West Bengal
Northern region = Punjab and Haryana, Uttar Pradesh, Rajasthan
Western region = Gujarat, Madhya Pradesh, Maharashtra

Table-3. Distribution of the virulence factors present in 52 isolates of Xanthomonas oryzae pv. Oryzae in different regions of India.

	Virulence factors											
	1	**2**	**3**	**4**	**5**	**6**	**7**	**10**	**11**	**12**	**13**	**Total**
Southern region (N = 13)												
6 AP (16)*	+	+	-	+	-	-	-	-	+	-	-	4
7 AP (16)	+	+	-	+	-	-	-	-	+	-	-	4
8 AP (16)	+	+	-	+	-	-	-	-	+	-	-	4
25 AP (15)	+	+	+	+	-	-	-	+	+	+	-	7
26 AP (1)	+	+	+	+	+	+	+	+	+	+	+	11
27 AP (16)	+	+	-	+	-	-	-	-	+	-	-	4
39 AP (7)	+	+	+	+	+	-	-	-	+	+	+	8
41 AP (16)	+	+	-	+	-	-	-	-	+	-	-	4
42 AP (16)	+	+	-	+	-	-	-	-	+	-	-	4
45 AP (7)	+	+	+	+	+	-	-	-	+	+	+	8
48 AP (7)	+	+	+	+	+	-	-	-	+	+	+	8
9 TN (16)	+	+	-	+	-	-	-	-	+	-	-	4
10 AN (16)	+	+	-	+	-	-	-	-	+	-	-	4
Frequency (%)	**100.00**	**100.00**	**38.46**	**100.00**	**30.77**	**7.69**	**7.69**	**15.38**	**100.00**	**38.46**	**30.77**	

Eastern region (N = 23)												
1 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
2 OR (14)	+	+	+	+	-	-	-	+	+	+	-	7
3 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
4 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
5 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
18 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
19 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
20 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
21 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
22 OR (15)	+	+	+	+	-	-	-	+	+	+	-	7
23 OR (4)	+	+	+	+	+	+	+	-	+	+	+	10
24 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
38 OR (1)	+	+	+	+	+	+	+	+	+	+	+	11
46 OR (4)	+	+	+	+	+	+	+	-	+	+	+	10
47 OR (1)	+	+	+	+	+	+	+	+	+	+	+	11
49 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
50 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
51 OR (16)	+	+	-	+	-	-	-	-	+	-	-	4
52 OR (4)	+	+	+	+	+	+	+	-	+	+	+	10
31 BR (1)	+	+	+	+	+	+	+	+	+	+	+	11
40 AS (15)	+	+	+	+	-	-	-	+	+	+	-	7
28 WB (1)	+	+	+	+	+	+	+	+	+	+	+	11
44 WB (15)	+	+	+	+	-	-	-	+	+	+	-	7
Frequency (%)	**100.00**	**100.00**	**47.83**	**100.00**	**30.43**	**30.43**	**30.43**	**34.78**	**100.00**	**47.83**	**30.43**	
Northern region (N = 9)												
32 UP (16)	+	+	-	+	-	-	-	-	+	-	-	4
11 PB (14)	+	+	+	+	-	-	-	+	+	+	-	7
12 PB (14)	+	+	+	+	-	-	-	+	+	+	-	7
13 PB (14)	+	+	+	+	-	-	-	+	+	+	-	7
14 PB (14)	+	+	+	+	-	-	-	+	+	+	-	7
15 PB (14)	+	+	+	+	-	-	-	+	+	+	-	7
16 PB (4)	+	+	+	+	-	-	-	-	+	+	+	10
17 PB (16)	+	+	-	+	+	+	+	-	+	-	-	4
43 RJ (16)	+	+	-	+	-	-	-	-	+	-	-	4
Frequency (%)	**100.00**	**100.00**	**66.67**	**100.00**	**11.11**	**11.11**	**11.11**	**55.56**	**100.00**	**66.67**	**11.11**	
Western region (N = 7)												
29 MP (7)	+	+	+	+	+	-	-	-	+	+	+	8
30 MP (16)	+	+	-	+	-	-	-	-	+	-	-	4
37 MH (15)	+	+	+	+	-	-	-	+	+	+	-	7
33 GT (16)	+	+	-	+	-	-	-	-	+	-	-	4
34 GT (16)	+	+	-	+	-	-	-	-	+	-	-	4
35 GT (16)	+	+	-	+	-	-	-	-	+	-	-	4
36 GT (7)	+	+	+	+	+	-	-	-	+	+	+	8
Frequency (%)	**100.00**	**100.00**	**42.86**	**100.00**	**28.57**	**0.00**	**0.00**	**14.29**	**100.00**	**42.86**	**28.57**	

* Numerals in parentheses are pathotypes designate (cf. Nayak, 1996)
+ = Virulence factor present - = Virulence factor absent

Virulence frequency has two dimensions i.e. the relative occurrence of virulence factors between isolates (inter-isolate) and the occurrence within an individual isolate (intra-isolate). The inter-isolate frequency of virulence factors V-1, 2, 4 and 11 was 100% among the isolates of all the four regions, next in order being 67% for V-3 and 12, followed by 56% for V-10 among the isolates from northern region of the country (Table-3). The V-6 and 7 were absent in the western region but occurred in low frequencies in southern (8%) region. The V-5, 6 and 7 occurred in low frequencies in northern (11%) and moderately low in eastern (30%) region, as well as for V-10 in southern (15%) region. The frequency of occurrence

of rest of the v-factors ranged between 28-48% among the isolates from all the four regions of the country.

The intra-isolate frequency of occurrence of v-factors revealed the presence of a maximum of 11 v-factors in 5 isolates from eastern and southern regions, 10 v-factors in 4 isolates from eastern and northern regions, 8 v-factors in 5 isolates from southern and western regions, 7 v-factors in 11 isolates and a minimum of 4 v-factors in 27 isolates, both distributed over all the four regions of the country. Re-interpretation of the earlier reports revealed the presence of V-1, 2, 3, 4, 5, 7, 10, 12 and 14 in Punjab and Haryana states (Gupta *et al.,* 1986); V-1, 3, 4, 5, 7, 11 and 14 in Chhattishgarh state (Khare and Thrimurty 2006) and V-1, 3, 4, 5, 7, 8, 10, 11, 13, 14 and 21 in Andhra Pradesh, Orissa, Tamil Nadu and Punjab states (Shanti and Shenoy 2005). Compilation of these results indicated that, out of the total number of 14 v-factors, a maximum number of 14 v-factors were present in isolates from Andhra Pradesh and Orissa, followed by 12 from Punjab and Haryana, 11 from West Bengal and Bihar, 8 from Gujarat and Madhya Pradesh, 7 from Assam and Chhatishgarh and 4 from Rajasthan, Uttar Pradesh and Andaman and Nicobar Islands. Besides, there are isolates possessing no virulence factors like MRF-06 from Andhra Pradesh (Shanti and Shenoy 2005) and 10 isolates from five states of Andhra Pradesh, Bihar, Manipur, Orissa and Rajasthan (Nayak 1986). This indicated the existence of a wide range of variability in pathogenicity among the Indian isolates.

The pathogenicity association coefficient (PAC) and virulence association coefficient (VAC) data obtained from the pathogenicity association analysis between each possible combination of the set of 16 host genotypes consisted of 120 PACs and 120 VACs with regard to each of the regions as well as the country as a whole. A critical insight into the entire data (Table-4) revealed that all the possible combinations could be broadly classified into four groups viz. (i) High PAC : high VACs, (ii) High PAC : low VAC, (iii) Low PAC : low VAC, and (iv) variable PAC : VAC. Among these categories, the combination with high PAC: high VAC is associated with the high level of virulence of all or most of the isolates to both the host genotypes in the combination. Only a small portion or none of the isolates would be avirulent to one or both the genotypes in the combination and hence is of little value in direct disease control. Three such combinations of host genotypes viz. Rantai Emas (Xa 1+Xa2): IR 8 (*Xa 11*) and IR-20 (*Xa 4*), IR-8 (*Xa 11*): IR-20 (*Xa 4*) (Sl. Nos. 18, 19 and 55 in (Table-4) showed 1: 1 PAC: VAC in respect of all the four regions of the country due to highest levels of virulence of all the isolates to both the genotypes in each of the combinations. The pathogenicity data further revealed that these isolates belonged to the pathotypes-1, 4, 7, 14, 15 and 16; which indicated that all the prevailing pathotype groups are capable of overcoming the resistance genes (*Xa 1*, *Xa 2*, *Xa 4* and *Xa 11*) present alone or in combinations, in these host genotypes. Similarly, the genotype combinations of IR 8: IR 20 as well as Kinmaze: Rantai Emas among the differential sets resulted in such high PAC: high VAC of 1: 1 in all four regions of the country (Table-5). The 10 genotype combinations IR-20: IR-1545, Tetep, Java-14, TN-1; IR-1545: Tetep, Java-14, TN-1; Tetep: Java-14, TN-1 and Java-14: TN-1 (Table-6) are also few such examples of high PAC: high VAC with the VF of 100% on the corresponding host genotypes against all the pathotypes tested (Gupta *et al.* 1986). Besides, there are 26 combinations with high PAC: high VAC and 29 combinations with both PAC and VACs of medium range, VF ranging from 45-100% and 1-PAC ranging from 0.09 to 0.55. These gene combinations warrant immediate withdrawal from the locality.

Low PAC: low VAC indicates that most of the protection offered by the host genotype combination would be by only one or the other of the two genes in the combination, thus resulting in lower disease control efficiency. Several such genotype combinations involving different gene combinations were detected in different regions of the country. Among the 39 such combinations showing low PAC : low VAC (Sl. Nos. 1, 4, 5, 16, 17, 20-29, 31, 32, 43, 44 and 56-75 in Table 4), seven combinations (Sl. Nos. 17, 21, 43, 44, 46, 57 and 67) showed both PAC and VAC of mid-range in northern region, while 15 combinations (Sl. Nos. 20, 22, 25, 28, 29, 56, 58, 61, 64, 65, 66, 68, 71, 74 and 75) in western region showed both PAC : VAC as zero.

High PAC: low VAC indicates that majority of the pathogen population are avirulent and a few or none are virulent on the combination of genotypes, which is a most desirable attribute in any successful disease control strategy. Such attributes were present in 78 combinations of host genotypes in all the four regions, except for 22 combinations (Sl. Nos. 3, 7, 30, 34, 45, 47-54, 76, 85 to 92), which showed high PAC : low VAC in all the regions but low PAC : low VAC in the northern region. Although high PAC and zero to low VAC accompanied by low VF could be observed in 56 combinations of genotypes listed under serial numbers 2, 6, 8-15, 33, 35-42, 46, 77-84, 93-120 in Table-4 the 10 combinations *viz*. 78, 80, 83, 84, 95, 98, 99, 113, 114 and 120 with PAC : VAC of 1 : 0 and six combinations *viz*. 95, 98, 99, 113, 114 and 120 with PAC : VAC of 1 : 0.08, zero difference between one and PAC (1-PAC) and low VF for the respective genotypes, could be deployed directly for disease control in western and southern regions, respectively. Similar genotype combinations for northern and eastern region as well as all India level for direct deployment for disease control need to be determined through fresh pathogenicity surveys and tests on genotypes possessing resistance to the virulent isolates.

Table-4. Pathogenicity Association Coefficient (PAC) and Virulence Association Coefficient (VAC) data on the isolates of Xanthomonas oryzae pv. oryzae to 16 rice genotypes possessing known genes for resistance, estimated in samples from southern, eastern, northern, western regions and India as a whole.

S. #	Genotype combinations	Southern region		Eastern region		Northern region		Western region		India	
		PAC	VAC	PAC	VAC	PAC	VAC	PAC	VAC	PAC	VAC
1.	1 : 2*	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
2.	1 : 3	1.00	0.31	1.00	0.30	0.89	0.11	1.00	0.29	0.98	0.25
3.	1 : 4	0.69	0.08	0.70	0.17	0.22	0.00	0.57	0.00	0.63	0.10
4.	1 : 5	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
5.	1 : 6	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
6.	1 : 7	0.62	0.00	0.96	0.26	1.00	0.11	0.71	0.00	0.87	0.13
7.	1 : 8	0.69	0.08	0.70	0.17	0.22	0.00	0.57	0.00	0.63	0.10
8.	1 : 9	0.77	0.08	0.96	0.30	1.00	0.11	0.71	0.00	0.90	0.17
9.	1 : 10	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
10.	1 : 11	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
11.	1 : 12	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
12.	1 : 13	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
13.	1 : 14	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
14.	1 : 15	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
15.	1 : 16	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
16.	2 : 3	0.31	0.31	0.30	0.30	0.22	0.22	0.29	0.29	0.27	0.27
17.	2 : 4	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
18.	2 : 5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
19.	2 : 6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
20.	2 : 7	0.08	0.08	0.26	0.26	0.11	0.11	0.00	0.00	0.15	0.15
21.	2 : 8	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
22.	2 : 9	0.08	0.08	0.35	0.35	0.11	0.11	0.00	0.00	0.19	0.19
23.	2 : 10	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
24.	2 : 11	031	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
25.	2 : 12	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.19	0.19
26.	2 : 13	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
27.	2 : 14	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
28.	2 : 15	0.08	0.08	0.30	0.36	0.11	0.11	0.00	0.00	0.17	0.17
29.	2 : 16	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
30.	3 : 4	0.69	0.08	0.61	0.17	0.11	0.00	0.57	0.00	0.62	0.10
31.	3 : 5	0.31	0.31	0.30	0.30	0.22	0.22	0.29	0.29	0.27	0.27
32.	3 : 6	0.31	0.31	0.30	0.30	0.22	0.22	0.29	0.29	0.27	0.27
33.	3 : 7	0.62	0.08	0.96	0.26	0.89	0.11	0.71	0.00	0.85	0.13
34.	3 : 8	0.69	0.08	0.70	0.17	0.22	0.00	0.57	0.00	0.62	0.10
35.	3 : 9	0.77	0.08	0.96	0.30	0.89	0.11	0.71	0.00	0.88	0.15
36.	3 : 10	1.00	0.31	1.00	0.30	0.89	0.11	1.00	0.29	0.98	0.25
37.	3 : 11	1.00	0.31	1.00	0.30	0.89	0.11	1.00	0.29	0.98	0.25
38.	3 : 12	0.77	0.08	1.00	0.30	0.89	0.11	0.71	0.00	0.90	0.17
39.	3 : 13	1.00	0.31	1.00	0.30	0.89	0.11	1.00	0.29	0.98	0.25
40.	3 : 14	1.00	0.31	1.00	0.30	0.89	0.11	1.00	0.29	0.98	0.25
41.	3 : 15	0.77	0.08	1.00	0.30	0.89	0.11	0.71	0.00	0.90	0.17
42.	3 : 16	0.77	0.08	1.00	0.30	0.89	0.11	0.71	0.00	0.90	0.17
43.	4 : 5	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
44.	4 : 6	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
45.	4 : 7	0.92	0.08	0.65	0.13	0.33	0.00	0.86	0.00	0.69	0.08
46.	4 : 8	1.00	0.15	1.00	0.35	0.56	0.56	1.00	0.14	1.00	0.31
47.	4 : 9	0.85	0.08	0.65	0.17	0.33	0.00	0.86	0.00	0.69	0.10

48.	4 : 10	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
49.	4 : 11	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
50.	4 : 12	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
51.	4 : 13	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
52.	4 : 14	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
53.	4 : 15	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
54.	4 : 16	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
55.	5 : 6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
56.	5 : 7	0.08	0.08	0.26	0.26	0.11	0.11	0.00	0.00	0.15	0.15
57.	5 : 8	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
58.	5 : 9	0.08	0.08	0.35	0.35	0.11	0.11	0.00	0.00	0.19	0.19
59.	5 : 10	0.30	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
60.	5 : 11	0.30	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
61.	5 : 12	0.31	0.31	0.30	0.30	0.11	0.11	0.00	0.00	0.19	0.19
62.	5 : 13	0.08	0.08	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
63.	5 : 14	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
64.	5 : 15	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
65.	5 : 16	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
66.	6 : 7	0.08	0.,08	0.26	0.26	0.11	0.11	0.00	0.00	0.15	0.15
67.	6 : 8	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
68.	6 : 9	0.08	0.08	0.35	0.35	0.11	0.11	0.00	0.00	0.19	0.19
69.	6 : 10	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
70.	6 : 11	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
71.	6 : 12	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.19	0.19
72.	6 : 13	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
73.	6 : 14	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.25	0.25
74.	6 : 15	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
75.	6 : 16	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
76.	7 : 8	0.92	0.08	0.65	0.13	0.22	0.00	0.86	0.00	0.69	0.08
77.	7 : 9	0.85	0.00	0.91	0.26	1.00	0.11	1.00	0.00	0.92	0.13
78.	7 : 10	0.62	0.00	0.96	0.30	1.00	0.11	0.71	0.00	0.87	0.13
79.	7 : 11	0.62	0.00	0.96	0.30	1.00	0.11	0.71	0.00	0.87	0.13
80.	7 : 12	0.85	0.00	0.96	0.30	1.00	0.11	1.00	0.00	0.94	0.13
81.	7 : 13	0.62	0.00	0.96	0.30	1.00	0.11	0.71	0.00	0.87	0.13
82.	7 : 14	0.62	0.00	0.96	0.30	1.00	0.11	0.71	0.00	0.87	0.13
83.	7 : 15	0.85	0.00	0.96	0.30	1.00	0.11	1.00	0.00	0.94	0.13
84.	7 : 16	0.85	0.00	0.96	0.30	1.00	0.11	1.00	0.00	0.94	0.13
85.	8 : 9	0.92	0.08	0.65	0.17	0.33	0.00	0.86	0.00	0.69	0.10
86.	8 : 10	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
87.	8 : 11	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
88.	8 : 12	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
89.	8 : 13	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
90.	8 : 14	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.63	0.10
91.	8 : 15	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
92.	8 : 16	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.71	0.10
93.	9 : 10	0.77	0.08	0.96	0.30	1.00	0.11	0.71	0.00	0.90	0.17
94.	9 : 11	0.77	0.08	0.96	0.30	1.00	0.11	0.71	0.00	0.90	0.17
95.	9 : 12	1.00	0.08	0.96	0.30	1.00	0.11	1.00	0.00	0.98	0.17
96.	9 : 13	0.77	0.08	0.96	0.30	1.00	0.11	0.71	0.00	0.90	0.17
97.	9 : 14	0.77	0.08	0.96	0.30	1.00	0.11	0.71	0.00	0.90	0.17
98.	9 : 15	1.00	0.08	0.96	0.30	1.00	0.11	1.00	0.00	0.98	0.17
99.	9 : 16	1.00	0.08	0.96	0.30	1.00	0.11	1.00	0.00	0.98	0.17

100.	10 : 11	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
101.	10 : 12	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
102.	10 : 13	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
103.	10 : 14	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
104.	10 : 15	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
105.	10 : 16	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
106.	11 : 12	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
107.	11 : 13	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
108.	11 : 14	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
109.	11 : 15	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
110.	11 : 16	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
111.	12 : 13	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
112.	12 : 14	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
113.	12 : 15	1.00	0.08	1.00	0.30	1.00	0.11	1.00	0.00	1.00	0.17
114.	12 : 16	1.00	0.08	1.00	0.30	1.00	0.11	1.00	0.00	1.00	0.17
115.	13 : 14	1.00	0.31	1.00	0.30	1.00	0.11	1.00	0.29	1.00	0.25
116	13 : 15	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
117.	13 : 16	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
118.	14 : 15	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
119.	14 : 16	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.92	0.17
120.	15 : 16	1.00	0.08	1.00	0.30	1.00	0.11	1.00	0.00	1.00	0.17

*1 = Kogyoku (*Xa 1*, *Xa 3*, *Xa 12*)	5 = IR 8 (*Xa 11*)	9 = DV 85 (*xa 5*, *Xa 7*)	13 = CB II (*Xa 3*, *xa 5*, *xa 13*)
2 = Rantai Emas (*Xa 1*, *Xa 2*)	6 = IR 20 (*Xa 4*)	10 = TKM 6 (*Xa 4*)	14 = BJ 1 (*xa 5*, *xa 13*)
3 = Wase Aikoku 3 (*Xa 3*)	7 = IR 1545-339 (*xa 5*)	11 = Tetep (*Xa 1*, *Xa 2*)	15 = Zenith (*Xa 6*)
4 = Java 14 (*Xa 1*, *Xa 3*, *Xa 12*)	8 = Cas 209 (*Xa 10*)	12 = Semora Mangga (*Xa 4*),	16 = M.Sung Song (*Xa 6*)

Pathogenicity association analysis of the 52 isolates of *Xoo* to three sets of differential varieties (Table-5) revealed high PAC : low VAC for the genotype combinations of TKM-6 : DV-85, PN-13, IET 8585; DV-85 : PN-13, IET-8585 and PN-13 : IET 8585 in southern, eastern as well as western regions of the country, while similar results were recorded in northern region only for TKM-6 : DV-85, IET-8585 and DV-85 : IET 8585, among the Indian differentials. Both PAC and VAC were either zero or low or of mid-range values in rest of the genotype combinations in all the four regions of the country. The combinations possessing most desirable attributes of high PAC: low VAC, least difference in 1-PAC, widest differences between PAC and VAC accompanied by low VF, were DV-85: PN-13 in southern as well as western regions and TKM-6: DV-85 for northern regions. The isolates expressed high PAC: low VAC only among three genotype combinations of IRRI differentials viz. IR 1545-339: Cas 209 and DV-85 and Cas 209: DV-85 in southern, eastern and western regions, while only between IR 1545-339: DV-85 combination in northern region of the country. Among them the combination of IR 1545: DV 85 possessed the most desirable attributes for all the four regions of the country. Rest of the genotype combinations exhibited equal PAC: VAC of either high or medium or low values or zero in all the four regions of the country. A similar expression of the isolates was recorded for the genotype combinations among the Japanese differentials, with high PAC: low VAC for Kogyoku : Wase Aikoku-3 in all the four regions and Kogyoku : Java-14 as well as Wase Aikoku-3 : Java-14 in southern and eastern regions. Among them, only gene combination *viz*. Kogyoku: Wase Aikoku-3 is worth deployment in disease control strategy. Rest of the combinations exhibited equal PAC and VACs of either high or of mid-range or low values. Such prevalence of more number of undesirable genotype combinations among the IRRI as well as Japanese differential sets, might be due to the high VF of 100% for IR 8 and IR 20 in the former and Kinmaze and Rantai Emas in the later sets, leading to the highest PAC: VAC of 1.00: 1.00 for the respective genotype combinations all over the country which deserve immediate withdrawal.

Table-5. Pathogenicity Association Coefficient (PAC) and Virulence Association Coefficient (VAC) data on the isolates of Xanthomonas Oryzae pv. oryza to the Indian, IRRI and Japanese differential varieties, estimated in samples from four regions of India.

Genotype combinations	Southern region (N = 13)		Eastern region (N = 23)		Northern region (N = 9)		Western region* (N = 7)		India (N = 52)	
	PAC	VAC	PAC	VAC	PAC	VAC	PAC	VAC	PAC	VAC
Indian differentials:										
IR 8 : TKM 6	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.27	0.27
IR 8 : DV 85	0.08	0.08	0.30	0..30	0.11	0.11	0.00	0.00	0.17	0.17
IR 8 : PN 13	0.08	0.08	0.22	0.22	0.56	0.56	0.00	0.00	0.21	0.21
IR 8 : IET 8585	0.38	0.38	0.30	0..30	0.00	0.00	0.43	0.43	0.29	0.29
TKM 6 : DV 85	0.77	0.08	1.00	0.30	1.00	0.11	0.71	0.00	0.90	0.17
TKM 6 : PN 13	0.77	0.08	0.83	0.17	0.33	0.00	0.71	0.00	0.71	0.10
TKM 6 : IET 8585	0.92	0.38	0.74	0.17	0.89	0.00	0.86	0.29	0.83	0.19
DV 85 : PN 13	1.00	0.08	0.83	0.17	0.33	0.00	1.00	0.00	0.79	0.10
DV 85 : IET 8585	0.69	0.08	0.76	0.17	0.89	0.00	0.57	0.00	0.69	0.10
PN 13 : IET 8585	0.69	0.08	0.83	0.17	0.44	0.00	0.57	0.00	0.69	0.10
IRRI differentials:										
IR 8 : IR 20	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
IR 8 : IR 1545	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
IR 8 : Cas 209	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
IR 8 : DV 85	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
IR 20 : IR 1545	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
IR 20 : Cas 209	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
IR 20 : DV 85	0.08	0.08	0.30	0.30	0.11	0.11	0.00	0.00	0.17	0.17
IR 1545 : Cas 209	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.69	0.10
IR 1545 : DV 85	1.00	0.08	1.00	0.30	1.00	0.11	1.00	0.00	1.00	0.17
Cas 209 : DV 85	0.92	0.08	0.70	0.17	0.33	0.00	0.86	0.00	0.69	0.10
Japanese differentials:										
Kinmaze : Kogyoku	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.27	0.27
Kinmaze : Rantai Emas	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Kinmaze:Wase Aikoku 3	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.27	0.27
Kinmaze : Java 14	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
Kogyoku : Rantai	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.27	0.27
Kogyoku : WK 3	0.92	0.31	1.00	0.30	1.00	0.11	1.00	0.11	1.00	0.27
Kogyoku : Java 14	0.69	0.08	0.70	0.17	0.33	0.00	0.57	0.00	0.62	0.10
Rantai Emas:Wase Aikoku 3	0.31	0.31	0.30	0.30	0.11	0.11	0.29	0.29	0.27	0.27
Rantai Emas : Java 14	0.15	0.15	0.35	0.35	0.56	0.56	0.14	0.14	0.31	0.31
Wase Aikoku 3 : Java 14	0.69	0.08	0.70	0.17	0.30	0.00	0.57	0.00	0.62	0.10

* Southern region = Andhra Pradesh, Tamil Naldu, Andaman and Nicobar Islands
Eastern region = Assam, Bihar, Orissa, West Bengal
Northern region = Punjab and Haryana, Uttar Pradesh, Rajasthan
Western region = Gujarat, Madhya Pradesh, Maharashtra

Pathogenicity association analysis involving VF, PAC and VAC on the virulence pattern of 11 pathotypes reported among 13 isolates of Xoo, collected from the states of Punjab and Haryana (Gupta *et al.*, 1986) on 14 rice genotypes including four IRRI, five Japanese and four new breeding lines used as Indian differentials, along with Taichung Native-1 as the susceptible check, revealed some interesting results (Table-6). The VF was very high with a wide range from 18-100%. The pathogenicity to 36 of 91 genotype combinations was highly associated with similar high virulence associations. Both PAC and VAC were low in 21 of 91 combinations and of mid-range in 29 of 91 combinations of genotypes. The desired pathogenicity association of high PAC: low VAC was recorded only in 5 of 91 combinations namely; Kogyoku: B-76 and CNGS-20083; ARC-10l464: B-76, CNGS-20083 and B-76: CNGS-20083. Thus the pathogenicity association suggests that 95% of the genotype combinations involving *Xa 1*, 2, 3, 4, *xa 5*, *Xa 7*, 12 and 14 genes are ineffective against the virulent isolates prevailing in Punjab and Haryana states.

Similar pathogenicity association among 18 isolates of *Xoo* collected from six states namely Andhra Pradesh, Orissa, West Bengal, Bihar, Manipur and Rajasthan on eight rice genotypes possessing known genes for resistance (Nayak 1986), revealed PACs were ranging from 0.72 to 1.00. VACs from 0.11-0.44, but VF from 22-44% (Table-7). Among the 18 isolates, eight isolates possessed 4-5 v-factors against the Xa genes 4, 5, 7, 11 and 13. Inspite of the fact that 10 of the 18 isolates did not possess any v-factors, none of the 28 genotype combinations was worth deployment for bacterial blight disease control.

Table-6. Pathogenicity Association Coefficient (PAC), Virulence Association Coefficient (VAC) and Virulence Frequency (VF) data on the isolates of Xanthomonas oryzae pv. oryzae on 14 differential varieties estimated from published data of Gupta *et al*. (1986).

Genotypes (genes)		**IR 1545** (*xa 5*)	**DV 85** (*xa 5+Xa 7*)	**Cas 209** (*Xa 10*)	**Tetep** (*Xa 1+Xa 2*)	**Java 14** (*Xa 1+Xa 3+ Xa 12*)	**Kogyoku** (*Xa 1+Xa 3 +Xa 12*)	**Wase Aikoku 3** (*Xa 3*)	**Kinmaze** (?)	**IR 1160-8-6-1** (?)	**ARC-10464** (?)	**B-76** (?)	**CNGS-20083** (?)	**TN-1** (*Xa 14*)	**VF** (%)
IR 20 (*Xa 4*)	PAC	1.00	0.91	0.45	1.00	1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	100.00
	VAC	1.00	0.91	0.45	1.00	1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	
IR 1545 (*xa 5*)	PAC		0.91	0.45	1.00	1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	100.00
	VAC		0.91	0.45	1.00	1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	
DV 85 (*xa 5+Xa 7*)	PAC			0.36	0.91	0.91	0.36	0.82	0.73	0.64	0.55	0.45	0.27	0.91	90.91
	VAC			0.36	0.91	0.91	0.27	0.82	0.73	0.64	0.45	0.36	0.18	0.91	
Cas 209 (*Xa 10*)	PAC				0.45	0.45	0.45	0.55	0.64	0.55	0.45	0.55	0.55	0.45	45.45
	VAC				0.45	0.45	0.09	0.45	0.45	0.36	0.12	0.18	0.18	0.45	
Tetep (*Xa 1*+2)	PAC					1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	100.00
	VAC					1.00	0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	
Java 14 (*Xa 1*+3+12)	PAC						0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	100.00
	VAC						0.27	0.91	0.82	0.73	0.45	0.36	0.18	1.00	
Kogyoku (*Xa 1*+3+12)	PAC							0.27	0.27	0.55	0.64	0.73	0.73	0.27	27.27
	VAC							0.27	0.18	0.18	0.18	0.18	0.09	0.27	
Wase Aikoku (*Xa 3*)	PAC								0.91	0.82	0.55	0.45	0.27	0.91	90.91
	VAC								0.82	0.73	0.45	0.36	0.18	0.91	
Kinmaze (?)	PAC									0.73	0.64	0.55	0.36	0.82	81.82
	VAC									0.64	0.45	0.36	0.18	0.82	
IR1160-8-6-1 (?)	PAC										0.73	0.64	0.45	0.73	72.73
	VAC										0.45	0.36	0.18	0.73	
ARC-10464 (?)	PAC											0.91	0.73	0.45	45.45
	VAC											0.36	0.18	0.45	
B-76 (?)	PAC												0.82	0.36	36.36
	VAC												0.18	0.36	
CNGS-20083 (?)	PAC													0.18	18.18
	VAC													0.18	
TN-1 (*Xa 14*)	PAC													-	100.00
	VAC													-	

Table 7. Pathogenicitry Association Coefficient (PAC), Virulence Association Coefficient (VAC) and Virulence Frequency (VF) data on the isolates of Xanthomonas oryzae pv. oryzae, estimated from the published data of Nayak (1986).

Genotypes (genes)		**IR 20** (*Xa 4*)	**TKM 6** (*Xa 4*)	**Ramakrishna** (*Xa 4*)	**CB-II** (*Xa 3+xa 5+xa13*)	**IR 1545** (*xa 5*)	**BJ-1** (*xa 5+xa 13*)	**DV 85** (*xa 5+Xa 7*))	**VF** (%)
IR 8 (*Xa 11*)	PAC	0.83	0.89	0.94	0.94	0.94	0.94	0.72	38.89
	VAC	0.22	0.28	0.33	0.28	0.39	0.39	0.22	
IR 20 (*Xa 4*)	PAC		0.83	0.89	0.78	0.78	0.78	0.78	22.22
	VAC		0.17	0.22	0.17	0.22	0.22	0.11	
TKM 6 (*Xa 4*)	PAC			0.94	0.83	0.83	0.83	0.78	27.78
	VAC			0.28	0.22	0.28	0.28	0.17	
Ramakrishna (*Xa 4*)	PAC				0.78	0.89	0.89	0.78	33.33
	VAC				0.22	0.33	0.33	0.17	
CB-II (*Xa 3+xa 5+ xa13*)	PAC					0.89	0.89	0.89	33.33
	VAC					0.33	0.33	0.22	
IR 1545 (*xa 5*)	PAC						1.00	0.78	44.44
	VAC						0.44	0.22	
BJ-1 (*xa 5+xa 13*)	PAC							0.78	44.44
	VAC							0.22	
DV 85 (*xa 5+Xa 7*)	PAC							-	22.22
	VAC							-	

The pathogenicity association analysis of 10 isolates of Xoo, collected from the four states of Andhra Pradesh, Orissa, Punjab and Tamil Nadu, to 11 isogenic lines and nine gene pyramids revealed that the PACs were highly associated but the VACs were zero to low for all the combinations of host genotypes (Table-8). The high PACs ranging from 0.40 to 1.00 accompanied by low VACs of 0.00-0.10 with the lowest VF of 0 and 10% were observed for all combinations involving IRBB-8, IRBB-14 and most of the gene pyramids. Among them, the combination IRBB 14 : MSS as well as pyramid *Xa 4 + xa 5* showed the most desirable attributes of high PAC : low VAC of 1.00 : 0.00 with zero VF expressed on the respective host genotypes. This was followed by PAC: VAC of 0.90: 0.00 by the combinations IRBB 8: IRBB 14, pyramid *Xa 4 + xa 5* and MSS; IRBB 14: all the pyramids, except *Xa 4 + xa 13* and each of the pyramids: MSS; pyramid *Xa 4 + xa 5*: all other pyramids except *Xa 4 + xa 13*, with the VF of 0-10% for the respective genotypes. The PAC: VAC among different combinations of the pyramids 5+13, 5+21, 13+21, 4+5+13, 4+5+21, 5+13+21 and 4+5+13+21 were 1.00: 0.10 with VF of 10% for each of the pyramids. The highest PAC, least VAC, zero to 0.10 differences between 1-PAC as well as highest difference between PAC - VAC for the combinations suggest that these gene combination would offer highest protection against the disease if deployed in disease control strategy in the corresponding localities. The pathogenicity of 10 diagnostic strains of *Xoo* from eastern India (Shanti *et al.* 2001) to 11 NILs and three gene pyramids (data not presented) revealed the presence of most desirable attributes of high PAC : low VAC of 1.00 : 0.00 only in three combinations of pyramids *viz.* (*Xa 4 + xa 5*) : (*xa 5 + Xa 21*) and (*Xa 4 + xa 5 + Xa 21*) and (*xa 5 + Xa 21*) : (*Xa 4 + xa 5 + Xa 21*) accompanied by zero VF.

Table-8. Pathogenicitry Association Coefficient (PAC), Virulence Association Coefficient (VAC) and Virulence Frequency (VF) data on the isolates of Xanthomonas oryzae pv. oryzae to 11 near isogenic lines (NIL) and nine gene pyramids, estimated from the published data of Shanti and Shenoy (2005).

Xa/xa genes		**3**	**4**	**5**	**7**	**8**	**10**	**11**	**13**	**14**	**21**	**4 + 5**	**4 + 13**	**5 + 13**	**5 + 21**	**13 + 21**	**4 + 5 +13**	**4 + 5 +21**	**5+13 +21**	**4+5+3+21**	**MSS** (Xa6)	**VF** (%)
Xa 1	PAC	0.60	0.90	0.70	0.50	0.60	0.50	0.40	0.60	0.70	0.70	0.70	0.70	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.70	30.00
	VAC	0.10	0.20	0.10	0.10	0.00	0.20	0.10	0.10	0.00	0.10	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 3	*PAC*		0.70	0.90	0.70	0.60	0.70	0.60	0.70	0.70	0.90	0.70	0.90	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.70	30.00
	VAC		0.20	0.20	0.20	0.00	0.30	0.20	0.20	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 4	PAC			0.80	0.60	0.50	0.60	0.50	0.80	0.60	0.80	0.60	0.80	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.60	40.00
	VAC			0.20	0.20	0.00	0.30	0.20	0.30	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
xa 5	PAC				0.80	0.70	0.60	0.70	0.80	0.80	1.00	0.80	1.00	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	20.00
	VAC				0.20	0.00	0.20	0.20	0.20	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 7	PAC					0.50	0.60	0.90	0.60	0.60	0.80	0.60	0.80	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.60	40.00
	VAC					0.00	0.30	0.40	0.20	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
xa 8	PAC						0.50	0.60	0.50	0.90	0.70	0.90	0.70	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.90	10.00
	VAC						0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Xa 10	PAC							0.70	0.40	0.40	0.60	0.40	0.60	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.40	60.00
	VAC							0.40	0.20	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 11	PAC								0.50	0.50	0.70	0.50	0.70	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.50	50.00
	VAC								0.20	0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
xa 13	PAC									0.60	0.80	0.60	0.80	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.60	40.00
	VAC									0.00	0.20	0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 14	PAC										0.80	1.00	0.80	0.90	0.90	0.90	0.90	0.90	0.90	0.90	1.00	00.00
	VAC										0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Xa 21	PAC											0.80	1.00	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	20.00
	VAC											0.00	0.20	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
Xa 4 + 5	PAC												0.80	0.90	0.90	0.90	0.90	0.90	0.90	0.90	1.00	00.00
	VAC												0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Xa 4 + 13	PAC													0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	20.00
	VAC													0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.00	
xa 5 + 13	PAC														1.00	1.00	1.00	1.00	1.00	1.00	0.90	10.00
	VAC														0.10	0.10	0.10	0.10	0.10	0.10	0.00	
xa 5 +21	PAC															1.00	1.00	1.00	1.00	1.00	0.90	10.00
	VAC															0.10	0.10	0.10	0.10	0.10	0.00	
xa 13+21	PAC																1.00	1.00	1.00	1.00	0.90	10.00
	VAC																0.10	0.10	0.10	0.10	0.00	
Xa 4 +5+13	PAC																	1.00	1.00	1.00	0.90	10.00
	VAC																	0.10	0.10	0.10	0.00	
Xa 4 + 5 + 21	PAC																		1.00	1.00	0.90	10.00
	VAC																		0.10	0.10	0.00	
xa 5 + 13 + 21	PAC																			1.00	0.90	10.00
	VAC																			0.10	0.00	
Xa 4+5+3+ 21	PAC																				0.90	10.00
	VAC																				0.00	
MSS (*Xa 6*)	PAC																				-	00.00
	VAC																				-	

The NILs *Xa 1* – 21 = IRBB 1 – IRBB 21

DISCUSSION

Any disease control strategy using host resistance depends on the deployment of cultivars possessing combination of genes for high degree of resistance. The determination of the useful combination of genes for resistance can be attained from the pathogenicity surveys through the analysis of pathogenicity associations. We have used virulence frequencies (VF), pathogenicity association coefficient (PAC) and virulence association coefficient (VAC) of the isolates of Xanthomonas oryzae pv. oryzae to different sets of rice genotypes possessing known *Xa* genes, for such an analysis to determine the desired combination of genes useful for deployment in disease control strategy as well as breeding program. The VF of a set of isolates to specific host genotypes shows the potential value of the resistance/virulence genes in minimizing the disease severity. In other words, low VF of the isolates to specific host lines indicates high level of resistance and *vice versa*. The deployment of cultivars with combination of genes for low reactions to the

isolates, prevailing in a specific locality, is essential in disease control program. The virulence of an isolate to a specific host genotype is the resultant effect of the interaction between the resistance factor in the host and corresponding virulence factor present in the pathogen isolate. The presence of higher number of matching v-factors in the pathogen isolate corresponding to the resistance factor in the host genotype is closely associated with high degree of susceptibility (Nayak, 1996). Knowledge on the geographic distribution of the v-factors among the pathogen population enables the breeders to direct their breeding program towards proper utilization of host resistance factors for which the frequency of matching v-factors in the pathogen population is low.

The genetic system between the host and the pathogen is dynamic in nature and genes in one part of the system interact with the corresponding genes in other part, in a manner similar to the gene-for-gene hypothesis. Rice bacterial blight pathosystem is no exception. In addition to the v-gene factors mentioned above, it is possible to recognize the avirulent gene factors present in each isolate based on the data presented in Table-3. The rice genotypes showing resistant reaction to specific isolates of the pathogen indicate that such isolates possess avirulent gene factors against the corresponding resistant genes. Thus 27 isolates possessing 4 v-gene factors and belonging to pathotype-16 possess 7 Avr. Gene factors viz. Avr. gene factors-3, 5, 6, 7, 10, 12 and 13. Similarly, the 11 isolates belonging to pathotype-14 and 15, each with 7 v-factors, possess 4 Avr. gene factors-5, 6, 7 and 13. The 5 isolates belonging to pathotype-7 with 8 v-factors possess 3 Avr. gene factors-6, 7 and 10 and the 4 isolates belonging to pathotype-4 with 10 v-factors possess a single Avr. gene factor-10. The five most virulent isolates belonging to pathotype-1 each with all the 11 v-factors possessed no avirulent gene factors.

The genes in any plant-pathosystem function as:

(i) virulence when there is no corresponding R-gene,

(ii) avirulence when there is a matching R-gene and

(iii) inhibitor or innate immunity of the host plant.

The first category of gene effect is commonly found in all the Indian isolates tested on the rice genotype Taichung (Native)-1 which is used as a susceptible check. The present set of Avr. gene factors are of second category acting against matching R-genes of *Xa* 1, 2, 3, 4, 5, 6, 7, 10, 11, 12 and 13. The third category of the avr. genes are rarely found against the most virulent Indian isolates of Xoo., although such type of immunity has been reported in the wild rice species Oryza barthii (Devadath, 1981).

It is important for the breeders to have detailed information on the useful gene combinations effective in a particular locality for transfer into high yielding background. This could be determined through the analysis of PAC and VAC from the data on pathogenicity of a set of maximum number of isolates representing the locality/region to a set of host genotypes possessing known genes for resistance. The difference between PAC and VAC for a given pair of genotypes indicate the frequency of the population that has avirulence to both the lines. In other words, the wider the difference better is the gene combination for control of the disease, either by direct deployment or by genetic manipulations. The difference between one and PAC (1-PAC) indicate the proportion of the pathogen population those attack one or the other of the two genotypes in the combination *i.e.* the total A_A: V_B plus V_A: A_B. The frequencies for A_A: V_B and V_A: A_B could be calculated by subtraction if VF of A and B are known. Thus the proportion of the pathogen population those will attack either none or one or both the genotypes of a pair of the combinations could be expressed from PAC and VAC along with VF. In other words, the least the difference between one and PAC, accompanied by lowest VF, the better is the combination.

Till date, 27 *Xa* genes have been identified by different researchers. Following the detailed procedures on development of isogenic lines (Ogawa, 1993), NILs have been developed in IR 24 genetic background, which have been tested against bacterial isolates from different areas (Adhikari *et al.*, 1999; Shanti *et al.*, 2001; Shanti and Shenoy, 2005; Khare and Thrimurty, 2006). The VF of the isolates tested on the NILs ranged between 20-70% (Shanti *et al.* 2001) and 0-60% (Shanti and Shenoy, 2005), which suggests the necessity to identify new resistant genes operative against the most virulent Indian isolates and develop NILs possessing such genes. However, the expression of the desired attributes of high PAC: low VAC accompanied by zero to low VF for a few combinations of gene pyramids, is a hopeful feature which can be exploited successfully for disease control in future. The present analysis emphasizes the genes expressed as resistance factor or virulence factor as the entity, within basic assumption of the theory of 'gene-for-gene relationship', rather than a group of isolates designated as race/pathotype; since genes are the biologically functional units. The focal point of the parasite becomes the pathogen isolate with known differential pathogenicity that can be utilized in manipulating host genes for low reaction in breeding program. Two cultures, one with A_AV_B and the other with V_AA_B are needed to easily combine the two genes A and B. Individual isolates/cultures are controllable experimental entities, rather than a taxonomic group of isolates represented by race/pathotype names.

The pathogenicity association analysis is simple, systematic, provides detailed information to the breeder for guidance in the breeding programme, deals with individual isolates as an experimental entity rather than a taxonomic group of isolates designated as race/pathotype; but lacks a central nomenclature system which can be developed in future. One more important aspect that needs attention is that the samples must be collected in a random manner covering random plants/cultivars/plots in a locality. Although the present analysis has been done manually as a simple model with limited number of isolates, necessary computer programme can be developed in future, in order to deal with a large number of representative samples collected through extensive pathogenicity surveys. Such analysis involving pathogenicity of large samples to the complete set of NILs as well as gene pyramids will provide useful scientific

information that will help in (i) monitoring the distribution of virulence factors as well as races of the pathogen, (ii) identification of new resistant genes and their incorporation into high yielding background, (iii) development of new NILs possessing such single genes, (iv) recognition of desirable gene combinations for deployment in effective disease control strategy and also undesirable gene combinations responsible for high disease pressure those deserve immediate withdrawal from cultivation and (v) development of synthetic multiline cultivars for specific regions of the country.

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