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GENETICS OF RESISTANCE TO WHITEBACKED PLANTHOPPER IN FIVE RICE STOCKS

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SUMMARY

Five resistant rice stocks, namely, Mudgo, MR1523, ARC11367, NCS2041 and MO1, were crossed with Taichung Native 1 (TN1), a susceptible cultivar, and intercrossed among themselves to study the inheritance of resistance to whitebacked planthopper (WBPH), *Sogatella furcifera* (Horvath) and the allelic relationships among their *Wbph* resistance genes. The reaction of F_1, and segregation pattern for resistance in the F_2 and F_3 generations from the crosses of resistant stocks with TN1 revealed that a recessive gene conferred resistance in MR1523 and ARC11367 each, whereas, resistance in NCS2041 was conditioned by a dominant gene. The resistance in Mudgo and MO1 was governed by two independently inherited dominant genes. The segregation for susceptible plants in the F_2 generation from the intercross of resistant stocks revealed that the resistance genes in all the stocks are non-allelic to each other except that out of the two dominant genes of MO1, one is allelic to a gene in NCS2041. Based on these results, five new genes for resistance to WBPH have been identified and temporarily designated as *WbphM1, WbphM2, wbphAR, WbphN,* and *WbphO.*

Key words: *Sogatella furcifera* (Horvath), *Oryza sativa* L., host plant resistance, inheritance, allelic relationships

The whitebacked planthopper (WBPH), *Sogatella furcifera* (Horvath) (Homoptera: Delphacidae) is a serious pest of rice, *Oryza sativa* L. in Asia. The nymphs and adults suck the phloem sap (Auclair and Baldos, 1982; Khan and Saxena, 1984), which causes reduced plant vigor, stunting, yellowing of leaves, delayed tillering and shriveling of grains. Under heavy infestations, WBPH can cause complete drying and death of the crop, a condition commonly known as "hopperburn" (Kisimoto, 1960; Suenaga, 1963; Pathak, 1968). During 1997-98 (Ambikadevi *et al.*, 1998) the outbreak of WBPH in Southern India caused total crop loss. Several chemicals were effective in the control of this pest. However, the use of insecticides requires additional economic inputs, poses risks such as the development of the pests' resistance to these insecticides, and, causes accumulation of undesirable residues.

The strategies for management of the rice planthoppers in India as well as at the International Rice Research Institute (IRRI) are based on the development of improved germplasm with diverse genes for resistance to the insects (Khush,

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1980). So far, five genes for resistance to WBPH have been identified (Angeles *et al.*, 1981; Hernandez and Khush, 1981; Sidhu *et al.*, 1979; Wu and Khush, 1985) and designated as *Wbph1* through *Wbph5*.

Gupta and Shukla (1986) reported that only two genes, *Wbph3* and *wbph4* are effective against the biotype of northern India. However, the recent studies by Brar (2002) showed that resistance to the biotype in northern India is due to different genes. The present report describes the genetics of these genes for resistance to WBPH from five highly resistant stocks (Mudgo, MR1523, ARC11369, NCS2041, and MO1).

MATERIALS AND METHODS

Five rice stocks showing resistance to WBPH for the last 20 years (Shukla and Saini, 1995, 1996), five lines having known WBPH resistance genes, a susceptible cultivar 'Taichung Native 1' (TN1), and a highly resistant check ARC6248 were used in the study (Table 1).

All the resistant cultivars were intercrossed and crossed with the susceptible cultivar (TN1). A minimum of 30 F_1 seeds were produced for each cross combination. The F_2 seeds were obtained by growing 8-10 F_1 seeds of each cross to maturity. A part of the F_2 seed was saved for simultaneous testing along with the F_3 generation. At least 150 plants were harvested at random from each F_2 population to determine their reaction in the F_3 generation.

The bulk seedling test (Athwal *et al.*, 1971) was utilized for testing the hybrid materials as well as parents for resistance to WBPH. The test consisted of sowing the test material in 60x45x10 cm wooden trays filled with soil to a depth of 6 cm. Each seed box accommodated 13 rows, 45 cm long, subdivided into 26 sub-rows of about 20 cm long. Of these, 22 rows were planted with the test materials and the remaining four border rows was planted with the susceptible check (TN1). Starting from left to right, the 11^{th} row was the resistant check (ARC6248) and the 12^{th} row the susceptible check. Each row accommodated 20-25 seeds. The wooden trays were placed in galvanized iron trays containing water in the screen houses throughout the test. Six days old seedlings were infested for 8-10 second with third instar nymphs of WBPH that had been reared on TN1 (Kalode *et al.*, 1975). The insects belonged to a colony, which was originally started from insects collected from rice fields in Punjab and that had been maintained in the screen house at Punjab Agricultural University. Seven days after release, when more than 90% of the seedlings of the susceptible cultivar TN1 were dead and WBPH damage on the test entries was recorded on a 0-9 damage rating scale used at IRRI given in Table 2 (IRRI, 1980). The reaction of the F_1 and F_2 generations were scored on seedling basis while the F_3 generations were scored on the seedling and row bases. Seedlings and rows with ratings of ≥ 5 were classified as susceptible. Based on the presence of susceptible seedlings within each F_3 family, these were classified as either homozygous resistant (HR), segregating (Segr.), or homozygous susceptible (HS).

Data analysis

Standard errors for the damage rating of all the stocks used in the present study were estimated. For testing the goodness of fit of the genetic ratios, a simple χ^2 (Chi-square) test was applied to F_2 and F_3 data.

Table 1. Rice stocks used for genetic studies, their origin, seed source, and reaction to whitebacked planthopper.

S. No.	Name of stocks and *Wbph* genes	Origin	Source *	Damage Rating (±S.E.)
(A) Resistant				
1.	Mudgo	India	CRRI	2.83 ± 0.200
2.	MR1523	India	DRR	4.01 ± 0.235
3.	ARC11367	India	DRR	3.01 ± 0.260
4.	NCS2041	Not known	CRRI	2.06 ± 0.197
5.	MO1	Not known	DRR	1.81± 0.129
(B) Susceptible				
1.	Taichung Native 1	Taiwan	IRRI	8.54 ± 0.195
(C) Lines/Cultivars having known genes				
1.	N22 (*Wbph1*)	India	IRRI	6.98 ± 0.199
2.	ARC10239 (*Wbph2*)	India	IRRI	6.43 ± 0.188
3.	ADR52 (*Wbph3*)	India	IRRI	5.27 ± 0.253
4.	Podiwi A8 (*wbph4*)	Sri Lanka	IRRI	4.09 ± 0.218
5.	N'Diang Marie (*Wbph5*)	Senegal	IRRI	5.72 ± 0.245
(D) Resistant Check				
1.	ARC6248	India	CRRI	1.23 ± 0.115

*CRRI = Central Rice Research Institute, Cuttack, India.
*DRR = Directorate Rice Research, Hyderabad, India.
*IRRI = International Rice Research Institute, Philippines.

Table 2. Standard rating for damage by *Sogatella furcifera* (IRRI, 1980).

Grade of damage	Seedling damage	Rating
0	No damage	Highly resistant
1	First leaf yellow-orange	Resistant
3	50% of leaves or their tips are yellow-orange, slight stunting	Moderately resistant
5	Most leaves or their tips are yellow-orange, stunting	Moderately susceptible
7	50% plants dead, severe wilting and stunting	Susceptible
9	Plants dead	Highly susceptible

RESULTS

Mode of inheritance of resistance

The F_1 seedlings from the crosses of TN1 with Mudgo, NCS2041 and M01 showed resistant reactions, whereas the crosses from MR1523 and ARC11367 were susceptible (Table 3). The F_2 population from the cross of TN1 with Mudgo segregated in 15 resistant (R): 1 susceptible (S) ratio, indicating that resistance in Mudgo is conditioned by two dominant genes. The F_3 families segregated in a digenic ratio of 7 homozygous resistant (HR): 8 segregating (Segr.): 1 homozygous susceptible (HS), thus confirming two dominant genes in Mudgo. The F_2 seedlings from the cross of TN1 with MR1523 and ARC11367 segregated

Table 3. Reaction to whitebacked planthopper of F_1, F_2, and F_3 populations from the crosses of resistant rice stocks with Taichung Native 1 (TN1).

Cross	Generation/Reaction*											
	F_1	F_2			Ratio	χ^2	F_3				Ratio	χ^2
		Res.	Susc.	Total			Res.	Segr.	Susc.	Total		
TN1 X Mudgo	Resistant	334	28	362	15:1	1.362	55	67	8	130	7:8:1	0.125
TN1 X MR1523	Susceptible	203	677	880	1:3	1.751	Not Tested					
TN1 X ARC11367	Susceptible	80	274	354	1:3	1.088	16	46	17	79	1:2:1	2.164
TN1 X NCS2041	Resistant	227	90	317	3:1	1.944	29	61	33	120	1:2:1	0.268
TN1 X MO1	Resistant	282	64	346	13:3	0.015	35	43	5	83	7:8:1	0.109

* Res.= Resistant, Susc.= Susceptible, Segr.= Segregating.

as 1 resistant: 3 susceptible, which indicates that resistance in each of these cultivars to WBPH is controlled by a single recessive gene. The F_3 generation from the cross of TN1 with ARC11367 showed a close fit to a 1 HR: 2 Segr. : 1 HS ratio and thus confirmed that resistance in ARC11367 is governed by a recessive gene. The F_3 families from the cross TN1 with MR1523 were not available during the experimentation. In the cross of TN1 with NCS2041, the F_2 generation gave a perfect fit to a 3 resistant: 1 susceptible ratio, indicating a dominant gene conferring resistance to WBPH in this line. The F_3 families segregated 1 HR: 2 Segr. : 1 HS. This confirmed that a dominant gene governs resistance in NCS2041. The F_2 population of the cross of TN1 with M01 gave a good fit of 13 resistant: 3 susceptible ratio expected for the segregation of one dominant and one recessive gene. The F_3 generation contained 35 HR, 43 Segr., and 5 HS families that segregated 7 HR : 8 Segr. : 1 HS ($\chi^2 = 0.11$). Thus, these confirmed the conclusion that two dominant genes controlled the resistance in M01.

Allelic relationships

The F_1 plants from all the crosses, as expected, were resistant. The F_2 population from the crosses of Mudgo with MR1523, NCS2041, and MO1 segregated for susceptible seedlings (Table 4), indicating that the dominant genes for resistance to WBPH in Mudgo are non-allelic to and independent of the resistance genes in MR1523, NCS2041, and MO1. Similarly, the F_2 population from the crosses of MR1523 with ARC11367 and NCS2041 showed segregation (Table 4), which indicates that the recessive gene for resistance to WBPH in MR1523 is non-allelic to and independent of the resistance genes in ARC11367 and NCS2041. In the F_2 population from the cross of ARC11367 with NCS2041 and MO1, only four out of 312 and five out of 316 seedlings, respectively, were susceptible; thus, the dominant gene for resistance to WBPH in ARC11367 is non-allelic to and independent of the resistance genes in NCS2041 and MO1. A similar proportion of seedlings in the resistant checks were also killed in our tests. The mortality of these otherwise resistant seedlings may be ascribed to their late germination and slow growth because of the differences in micro climate and many other variables beyond control including soil-borne fungi. The F_2 population in the cross NCS2041 x MO1 showed no segregation for susceptibility, indicating that one of the two dominant genes in MO1 is allelic to the dominant gene in NCS2041.

Table 4. Segregation* for susceptible seedlings in F_2 generation from intercrosses of resistant stocks.

Cultivars	MR1523	ARC11367	NCS2041	MO1
Mudgo	Seg. (300)	NT	Seg. (632)	Seg. (326)
MR1523	-	Seg. (351)	Seg. (333)	NT
ARC11367		-	Seg. (316)	Seg. (321)
NCS2041			-	No Seg. (323)

*Seg. : Segregation; No Seg. : No Segregation; NT : Not Tested
Figures in parenthesis indicate the population size.

DISCUSSION

At present, only five genes for resistance to WBPH have been identified and designated as *Wbph1* (Sidhu *et al.*, 1979), *Wbph2* (Angeles *et al.*, 1981), *Wbph3, wbph4* (Hernandez and Khush, 1981), and *Wbph5* (Wu and Khush, 1985). Earlier studies by Gupta and Shukla (1986) reported that only *Wbph3* and *wbph4* genes are effective against the biotype of WBPH in northern India. The present studies indicate that the lines having known genes (*Wbph1* to *Wbph5*) were susceptible to the biotype of WBPH in northern India except *wbph4*, which is recessive in nature and shows moderate resistance with a damage rating of 4.09 to this insect (Table1). Therefore, the dominant genes conferring resistance to WBPH in Mudgo, NCS2041, and MO1 identified here are different to all the known genes. The lines with all the known genes for WBPH were resistant in IRRI (Nair *et al.*, 1982 and Saini *et al.*, 1982), which indicates that the biotype in IRRI is different from that in India. In the present studies, the cultivar MR1523 showed the presence of a single recessive gene with the reaction score of 4.01, which is comparable with the reaction of Podwi A8 with the gene *wbph4* (4.09). Thus, the recessive gene in MR1523 may be *wbph4*. Because the F_2 generation from the cross MR1523/ARC11367 segregated for susceptible plants, both lines cannot be presumed to have *wbph4* as the reaction score of ARC11367 (3.01) was lower than that of *wbph4*. Based on these results it is therefore, proposed that the stocks tested carry at least five new genes for wbph resistance. The dominant genes have been temporarily designated as *WbphM1, WbphM2, WbphN*, and *WbphO*. There is at least one recessive gene that is different from *wbph4* and that has been designated as *wbphAR* (Table 5). These new genes are thus useful sources of resistance against WBPH in northern India. The five new genes identified in the present study will not only add to the genetic diversity for resistance against WBPH in northern India but these will also facilitate systematic development of WBPH resistant cultivars.

Table 5. Genotypes (temporary gene symbols) of five whitebacked planthopper resistant stocks.

Stock	Nature and number of genes	Genotype based on temporary symbols
Mudgo	Digenic, dominant	*WbphM1WbphM1, WbphM2 WbphM2*
MR1523	Monogenic, recessive	*wbph4 wbph4* ?
ARC11367	Monogenic, recessive	*wbphAR wbphAR*
NCS2041	Monogenic, dominant	*WbphN WbphN*
MO1	Digenic, dominant	*WbphN WbphN, WbphO WbphO*

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