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Identification of green leafhopper [*Nephotettix virescens* (Distant.)] resistance genes in rice

G. Padmavathi, N. V. Krishnaiah, G. S. V. Prasad and Y. Kondala Rao

Directorate of Rice Research, Rajendra Nagar, Hyderabad 500 030

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Abstract

The genetics of resistance to green leafhopper, [*Nephotettix virescens* (Distant.)] was studied in four pre-release green leafhopper resistant rice varieties *viz.*, IET 12356 (RP 2432-98-6-3), IET 13268 (HKR 91-102), IET 15359 (BPT 6858), IET 15120 (CRM 47). The parental lines, F_1s and F_2 populations derived from the crosses of resistant varieties with the susceptible variety, TN1 or Phalguna or Sona and inter crosses among resistant varieties were screened against Indian population of green leafhopper in greenhouse at Directorate of Rice Research, Hyderabad. The inheritance of resistance suggested that two dominant complementary genes governed resistance in IET 13268, a single recessive gene in IET 15359, two recessive genes in IET 15120 and a single dominant gene in IET 12356. The single dominant gene of IET 12356 was allelic to *Glh 6* in IR 64.

Key words: Rice, insects, green leafhopper, resistance genes, inheritance, allele tests

Introduction

Green leafhopper [*Nephotettix virescens* (Distant)] is widespread in South and South-East Asia. Though it was considered as a minor pest in the past, of late it has assumed the status of an important pest causing serious losses in rice production in the states of Andhra Pradesh, Tamil Nadu, Karnataka, Uttar Pradesh, Bihar and West Bengal [1]. Both nymphs and adults cause direct damage by sucking plant sap resulting in reduced number of productive tillers, vigour and the number of filled grains. It acts as a vector for transmitting the dreaded rice tungro virus disease causing severe yield loss [2]. Host plant resistance is the most efficient method to control this pest.

Information on the nature of gene(s) controlling resistance is essential for the systematic development of resistant cultivars in the breeding programs. Hence the present study was aimed to identify genetic sources and nature of inheritance of resistance to green leafhopper (GLH) population in India.

Materials and methods

Four pre-release GLH resistant varieties *viz.*, IET 12356, IET 13268, IET 15359 and IET 15120 [16], and one released GLH resistant variety, IR 64 and three susceptible high yielding dwarf varieties *viz.*, Taichung Native 1, Phalguna and Sona were used in the study. The resistant parents were selected on the basis of genetic and geographical diversity (Table 1). These were crossed with susceptible high yielding varieties Taichung Native 1 (TN 1) or Phalguna or Sona; IET 12356 and IET 13268 with Phalguna; IET 13268 with Sona; IET 15359 and IET 15120 with TN 1. IET 12356 crossed with IR 64 to find the allelic relationship between resistance genes present in them. The F_1s thus obtained were selfed to derive F_2 populations for all the crosses.

The parents, F_1s and F_2s were evaluated in greenhouse following standard seed box method at Directorate of Rice Research, Hyderabad during *kharif* season, 1998. Pre-germinated seeds were sown in seed boxes filled with soil to a depth of 3 cm. Each entry was sown in rows following 2.5 cm distance between rows and 1 cm between seeds within rows. TN 1, the susceptible check was sown in the borders and Vikramarya, the standard resistant check was sown in the middle. Seven to eight days old seedlings were uniformly infested with 2nd and 3rd instar nymphs of the insect at the rate of 5-7 insects per seedling.

The observations on the seedling reaction were recorded on single seedling basis using 0-9 scale following Standard Evaluation System [3]. The damage scores were regrouped as resistant (score 0, 1 and 3) and susceptible (score 5, 7 and 9). Data on number of resistant and susceptible seedlings in F_2 generation were tested with chi square test for goodness of fit.

Results and discussion

All the seedlings of susceptible check TN1 were damaged by the nymphs within 7-8 days while IET 12356, IET 13268, IET 15359, IET 15120 and 1R 64 were found to be resistant as revealed by the damage

scores of 1.9 to 2.5. All the susceptible parents *viz.*, TN 1, Phalguna and Sona showed a uniform score of 9 indicating susceptible reaction (Table 1).

The F_1 seedlings from the crosses Phalguna/IET 12356, Phalguna/IET 13268, Sona/IET 13268 and 1R64/IET 12356 exhibited resistant reaction suggesting the dominant nature of resistance whereas those from the crosses TN1/IET 15359 and TN1/IET 15120 exhibited susceptible reaction indicating recessive nature of resistance (Table 2).

The F_2 population derived from the crosses, Phalguna/IET 13268 and Sona/IET 13268 segregated into 9R: 7S ratio suggesting that resistance of IET 13268 is due to two dominant complementary genes (Table 2).

The F_2 population derived from the cross Phalguna × IET 12356 segregated in 3R:1S suggesting the presence of a dominant gene in IET 12356 (Table 2). Dominant gene conferring resistance to GLH have been reported in several varieties in the past. Athwal *et al.* [4] reported resistance in varieties Pankhari 203, ASD 7 and IR 8 to be controlled by single dominant gene *viz.*, *Glh 1*, *Glh 2* and *Glh 3* respectively. Similarly Siwi and Khush [5] identified a dominant gene designated as *Glh 5* in ASD 8. Rezaul Karim and Pathak [6] reported the single dominant gene control in 11 GLH resistant varieties. Avesi and Khush [7] found a single dominant gene in 13 cultivars governing resistance to GLH. Dominant genes were also reported in IR 28 (*Glh 9t*), IR 20965-11-3-3 (*Glh 11t*), Hashikalmi (*Glh 12t*) and Asmaita (*Glh 13t*) [8-10].

The F_2 population of the cross TN 1 × IET 15359 showed a segregation ratio of IR: 3S indicating presence of a recessive gene in IET 15359. Rezaul Karim and Pathak [6] suggested the presence of a single recessive gene conferring resistance against GLH population of Bangladesh in a cultivar Kosatawee. Similar type of recessive gene control of resistance has also been suggested in some rice cultivars [5, 7, 9, 11, 12].

The segregation ratio of 1R:15S in the F_2 generation of the cross TN1 × IET 15120 demonstrated that duplicate recessive genes conditioned resistance in IET 15120.

The F_2 population of the cross of IR 64 with IET 12356 showed resistant reaction indicating that same gene is present in them and hence there is no segregation for susceptibility. The authors in their earlier study also concluded that same single dominant gene governed resistance in IR 64 and IET 12356 (Padmavathi *et al.*, unpublished).

The parentage survey of IET 12356 indicated IR 36 as one of its parent (Table 1). The results of inheritance of resistance observed by Rezaul Karim

Table 1. The parentage and damage scores of varieties used in the study

Name of the variety	Designation	Cross combination	Country of origin	Damage score (0-9 scale)*
IET 12356	RP 2432-98-6-3	IR 36/IET 7916	India	2.3
IET 13268	HKR 91-102	IR 19661-131-1-2/IR 4570-124-3-2-2-2	India	1.9
IET 15359	BPT 6858	MTU 5182/IR 50	India	2.4
IET 15120	CRM 47	-	India	2.3
IR 64	IR 18348-36-3-3	IR 5657-33-23 1-/IR 2061-465-1-5-5	Philippines	2.5
Taichung Native 1			Taiwan	9.0
Phalguna			India	9.0
Sona			India	9.0

*IRRI, 1996

Table 2. Reaction of F_1 hybrids and F_2 segregation ratio

Cross combination	F_1 reaction	F_2 reaction					R:S	χ^2 value	Gene(s)
		Observed			Expected				
		T	R	S	R	S			
Phalguna/IET 12356	R	313	230	75	234.80	78.30	3R:1S	0.228	*Glh 6*
Phalguna/IET 13268	R	313	181	140	180.56	140.44	9R:7S	0.002	2 dominant
Sona/IET 13268	R	332	175	157	186.75	145.85	9R:7S	1.69	2 dominant
TN 1/IET 15359	S	333	80	250	82.50	247.50	1R:3S	0.101	1 recessive
TN 1/IET 15120	S	320	18	312	20.00	300.00	1R:15S	0.213	2 recessive
IR 64/IET 12356	R	330	330	0	-	-	-	-	*Glh 6*

T-total, R-resistant, S-susceptible

and Pathak [6] suggested that the single dominant gene of IR 36 was allelic to that of the differential donor with known gene of resistance i.e., TAPL 796 (*Glh 6*) against GLH population of Bangladesh. Hence IR 36 is assumed to contain *Glh* 6. IET 12356 possessing IR 36 as one of the parents also showed resistant reaction (score of 2.3) against local GLH population of India. It is therefore concluded that IET 12356 derived *Glh 6* gene from IR 36. Likewise, IR 64 possessed the same *Glh 6* gene as the F_2 progenies of cross between IR 64 and IET 12356 were uniform and did not show segregation. Further investigations on the allelic relationship of dominant or recessive genes identified in the present study with known genes of resistance are needed.

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