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Genetic analysis of resistance to green leafhopper, *Nephotettix virescens* (Distant) in rice (*Oryza sativa* L.)

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Abstract

The genetics of resistance to green leafhopper *Nephotettix virescens* (Distant) in five rice (*Oryza sativa* L.) donors including two pre-release varieties with unknown genes for resistance *viz.*, IET 13341 and IET 12175; three differentials with known genes *viz.*, TAPL 796, Maddai Karuppan and Ptb 8 was studied. The donors, F_1 hybrids and F_2 populations from the crosses of donors with the susceptible variety, TN1 and inter crosses among resistant donors were screened against Indian population of green leafhopper in green house. Inheritance of resistance suggested that a single dominant gene governed resistance in IET 13341, IET 12175, TAPL 796 and Maddai Karuppan and a single recessive gene in Ptb 8. Allelic tests with known gene donors i.e., TAPL 796 and Maddai Karuppan showed that the dominant genes present in IET 13341 and IET 12175 were different and independent of *Glh 6* and *Glh 7* of TAPL 796 and Maddai Karuppan, respectively.

Key words: Rice, green leafhopper, resistance, inheritance, allelic tests

Introduction

Rice (*Oryza sativa* L.), a major staple food crop of India is affected by several pests and diseases causing considerable yield losses. Leafhoppers which were earlier considered as minor pests have of late emerged as major pests. Green leafhopper *Nephotettix virescens* (Distant) is widespread in south and south east Asia. Both nymphs and adults cause direct damage by sucking plant sap resulting in reduced vigour, number of productive tillers and filled grains. It causes great harm by transmitting the dreaded Rice Tungro Virus disease and sometimes even 100% loss has been recorded [1]. Host plant resistance is the most efficient and logical method to control this pest.

A large number of germplasm lines have been screened against green leafhopper (GLH) at the International Rice Research Institute (IRRI), Philippines, India, China and Bangladesh and many resistant donors have been identified [2]. Genetic analyses of resistance identified thirteen genes so far, they are designated as *Glh 1* in Pankhari 203, *Glh 2* in ASD 7, *Glh 3* in IR 8 [3], *glh 4* in Ptb 8 and *Glh 5* in ASD 8 [4], *Glh 6* in TAPL 796 and *Glh 7* in Maddai Karuppan [5], *glh 8* in DV 85 [6], *Glh 9*(t) in IR 28 [7], *glh 10* (t) in IR 36 and *Glh 11* (t) in IR 20965-11-3-3 [8], *Glh 12* (t) in Hashikalmi and *Glh 13* (t) in Asmaita [9]. The genes *glh 4*, *glh 8* and *glh 10* (t) are recessive while the rest are dominant. Many of these genes have already been incorporated into improved cultivars which are now widely cultivated in many rice growing areas. In addition to major genes, polygenic control of GLH resistance has been reported in RILs derived from *japonica/indica* crosses [10].

Knowledge about the number, nature and diversity of genes controlling resistance is very much needed for the exploitation of resistant cultivars in the breeding programs. Hence the present study on genetics of GLH resistance aims to identify genetic sources of resistance to GLH in India and to investigate the inheritance of resistance for their use in future breeding.

Materials and methods

The test material included three resistant donors with known genes *viz.*, Ptb 8 (*glh 4*) and Maddai Karuppan (*Glh 7*) and TAPL 796 (*Glh 6*); two pre-release GLH resistant lines [11] with unknown genes (IET 13341 and IET 12175); Vikramarya (resistant check) and Taichung Native 1 (susceptible check). The resistant donors, Ptb 8, Maddai Karuppan and TAPL 796 are traditional tall *indicas* from India, Sri Lanka and Bangladesh respectively whereas IET 13341 and IET 12175 are new dwarf breeding lines developed at Directorate of Rice Research (DRR), Hyderabad. TN1 is a known susceptible check from Taiwan with no resistance gene(s) for GLH while Vikramarya is a high yielding GLH resistant variety from India used as a standard check in GLH screening programs. The five resistant donors were crossed with susceptible check to study the mode of inheritance to GLH and among them to know the allelic relationship between resistant genes. The F_1s thus obtained were advanced to derive F_2 populations for screening.

The parental lines, F_1s and F_2s were evaluated in the greenhouse for GLH reaction following standard seed box method (Fig. 1). Pre-germinated seeds were

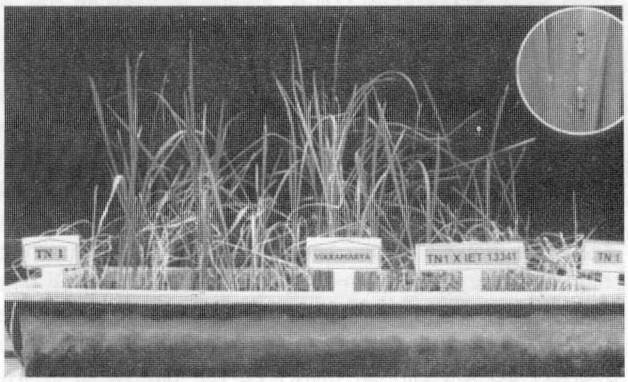

Fig. 1. Greenhouse screening for GLH reaction

sown in seed boxes filled with soil upto a depth of 3 cm. Each entry was sown in rows following 2.5 cm distance between rows and 1 cm between seeds within a row. TN1 was sown on the borders and Vikramarya in the middle. Seven to eight days old seedlings were infested with 2nd and 3rd instar nymphs when seedlings were in 3-4 leaf stage. The seedlings were infested uniformly by distribution of nymphs approximately 6-7 nymphs per seedling throughout the seed box.

Observations on the plant reaction were recorded on single plant basis when all the seedlings of susceptible check TN1 were dead, usually about one week after infestation following 0-9 scale of Standard Evaluation System for rice [12]. The parents, F_1s and F_2 seedlings were scored individually as resistant (Score 0, 1, 3) and susceptible (Score 5, 7, 9). Chi square (χ^2) method was applied to test the goodness of fit.

Results and discussion

Mode of inheritance: Damage scores of parental lines indicated that the donors were resistant to local GLH population. The donors namely Ptb 8, Maddai Karuppan, TAPL 796, IET 13341 and IET 12175 recorded mean damage scores of 2.0, 2.4, 3.0, 1.3 and 1.9, respectively (Table 1).

The F_1 crosses of donors with TN1 were found to be resistant except with Ptb 8 indicating the presence of dominant gene in IET 13341, IET 12175, TAPL 796 and Maddai Karuppan and recessive gene in Ptb 8 (Table 2). The four F_2 populations of TN1 with resistant donors *i.e.*, TN1 × IET 13341, TN1 × IET 12175, TN1 × TAPL 796 and TN1 × Maddai Karuppan showed a good fit to a segregation ratio of 3 R : IS (χ^2 = 2.81, 0.74, 0.14 and 0.24 respectively) indicating that each resistant cultivar carried a single dominant gene. Single gene governing GLH resistance recorded in this study

Table 1. Parental lines and their damage score in rice

Variety	Resistance gene	Country of origin	Damage score (0-9 scale)*
Ptb 8	*glh 4*	India	2.0
Maddai Karuppan	*Glh* 7	Sri Lanka	2.4
TAPL 796	*Glh* 6	Bangladesh	3.0
ET 13341	?	India	1.3
IET 12175	?	India	1.9
Vikramarya (Resistant check)	?	India	1.0
TN 1 (Susceptible check)	None	Taiwan	9.0

*IRRI (1996)

confirmed the earlier findings involving *Glh 7* in Maddai Karuppan [5] and *Glh 6* in TAPL 796 [4] against IRRI biotype of GLH.

In the F_2 population of TN 1 × Ptb 8, a ratio of 1 R: 3 S (χ^2 = 0.05) was observed showing that Ptb 8 carried a single recessive gene. Similar finding of single recessive gene inheritance in Ptb 8, DV 85 and IR 36 has also been reported earlier [4, 13, 8].

Allelic tests: All the resistant donors were intercrossed to determine the allelic relationship of their respective resistance genes. Data on the reaction of ten F_1 crosses and F_2 populations derived from intercrossing donors is furnished in Table 3. The F_1 hybrids from all the crosses were resistant. The F_2 populations of IET 13341 and IET 12175 with TAPL 796 and Maddai Karuppan showed a segregation pattern of 15 R : 1S. These results showed that the single resistant gene present in IET 12175 and IET 13341 are dominant and distinct and also independent of genes *Glh 6* and *Glh 7* present in TAPL 796 and Maddai Karuppan respectively.

A segregation ratio of 15 R : 1 S observed in the F_2 populations of TAPL 796 × Maddai Karuppan with a non significant χ^2 value (0.27) demonstrated a good fit and confirmed that the dominant genes, *Glh 6* and *Glh 7* were non allelic to each other.

Earlier studies also reported independent segregation of the dominant genes in test cultivars with respect to known resistance genes *i.e.*, the dominant genes found in cultivars, DS 1, Khama 49/8, ARC 6602 and ARC 7007 were non allelic to *Glh 5* present in ASD 8 [14]; the dominant genes present in cultivars Ghaiya, ARC 10313, and Garia were independent and non alleic to *Glh 1* of IR 5491, *Glh 2* of IR 5492, *Glh 3* of IR 8 and *Glh 5* of ASD 8 [15]; the dominant genes of Dumai, Gadur and ARC 7012 were independent of *Glh 1* in IR 5491 and *Glh 2* of IR 5492, *Glh 3* of IR 8 [6]; dominant genes of IR 28, Aus Murali, and IR 34 were independent of *Glh 1* gene of IR 5491, *Glh 2* of IR 5492 and *Glh 3* of IR 8 [5]; the dominant

Table 2. Reaction of F_1 and F_2 populations against green leafhopper in rice

Cross combination	F_1 reaction	F_2 reaction					χ^2 value	
		Observed			Expected		3R:1S	1R:3S
		T	R	S	R	S		
TN1 × IET 13341	R	250	199	51	187.5	62.5	2.81	-
TN1 × IET 12175	R	180	140	40	135.0	45.0	0.74	-
TN1 × Ptb 8	S	250	61	189	62.5	187.5	-	0.05
TN1 × TAPL 796	R	195	145	50	146.3	48.7	0.14	-
TN1 × Maddai Karuppan	R	196	150	46	147.0	49.0	0.24	-

T - Total, R - Resistant, S - Susceptible

Table 3. Allelic relationship based on the reaction of F_1 and F_2 populations in rice

Cross combination	F_1 reaction	F_2 reaction					χ^2 value		Genes
		(Observed)			(Expected)				
		T	R	S	R	S	13R:3S	15R:1S	
IET 13341 × IET 12175	R	270	250	20	253.1	16.90	-	0.63	Duplicate dominant
IET13341 × Ptb 8	R	197	155	42	160.1	36.90	0.85	-	One dominant one recessive
IET 13341 × TAPL 796	R	300	280	20	281.3	18.70	-	0.09	Duplicate dominant
IET 13341 × Maddai Karuppan	R	248	230	18	232.5	15.50	-	0.43	Duplicate dominant
IET 12175 × Ptb 8	R	224	185	39	182	42.00	0.26	-	One dominant one recessive
IET 12175 × TAPL 796	R	285	265	20	267.2	17.80	-	0.29	Duplicate dominant
IET 12175 × Maddai Karuppan	R	187	172	15	175.3	11.70	-	1.00	Duplicate dominant
Ptb 8 × TAPL 796	R	130	103	27	105.6	24.40	0.35	-	One dominant one recessive
Ptb 8 × Maddai Karuppan	R	164	142	22	133.3	30.70	3.04	-	One dominant one recessive
TAPL 796 × Maddai Karuppan	R	290	274	16	271.8	18.12	-	0.27	Duplicate dominant

T - Total, R - Resistant, S - Susceptible

gene *Glh 13* (t) present in Asmaita segregated independently of *Glh 12* (t) of cultivars Hashikalmi, Ghaiya, ARC 10313 and Garia [16].

The cultivars were crossed with Ptb 8 in order to know the identity of genes with respect to *glh 4* gene. In the F_2 populations of IET 13341 and IET 12175 with Ptb 8, a segregation ratio of 13 R : 3 S was found. This suggested that resistance in each of the test cultivars, IET 13341 and IET 12175 was controlled by a single dominant gene and segregated independently of *glh 4* gene of Ptb 8.

In the crosses between TAPL 796 and Maddai Karuppan with Ptb 8, the F_2 population segregated in the ratio of 13 R : 3 S as expected. This suggested that the dominant gene of TAPL 796 (*Glh 6*) and Maddai Karuppan (*Glh 7*) were non allelic and segregated independently of *glh 4* of Ptb 8.

However the conclusions drawn based on F_2 population in the present investigation need to be confirmed from the reaction of F_3 progenies of those crosses for application in future breeding. The present study indicated that breeding lines IET 13341 and IET 12175 possessed a single dominant gene conferring resistance to Indian population of green leafhopper. The genes are non allelic and segregated independently of each other. These genes are also non allelic to *Glh 6* of TAPL 796 and *Glh 7* of Maddai Karuppan. Further investigations on the allelic relationship of these dominant genes with other known genes governing resistance are needed.

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