Molecular mapping of quantitative trait loci (QTLs) associated with whitebacked planthopper in rice

P. Kadirvel, M. Maheswaran, Marker-Aided Selection Laboratory,
Center for Plant Breeding and Genetics; and
K. Gunathilagaraj, Department of Entomology, Tamil Nadu Agricultural University,
Coimbatore 641003, India

The whitebacked planthopper (WBPH), *Sogatella furcifera* (Horvath) (Homoptera: Delphacidae), has emerged as a major pest of rice in India and other Asian countries. Classical genetic analysis of selected rice accessions resulted in the identification of five major genes: *Wbph 1* (Sidhu et al 1979), *Wbph 2* (Angeles et al 1981), *Wbph 3* and *Wbph 4* (Hernandez and Khush 1985), and *Wbph 5* (Wu and Khush 1985). These genes have been incorporated into improved germplasm to broaden the genetic base for resistance to WBPH. The need to identify gene loci conferring durable resistance to insect pests, however, led to the molecular marker-based QTL (MBQTL) analysis involving 96 doubled-haploid lines derived from IR64/Azucena.

Parents and 96 doubled-haploid lines were evaluated by screening at the seedling and maturity stage. For seedling screening, the mass screening method was adopted. Pre-germinated seeds of test lines were sown 3 cm apart in 20-cm rows in 50 × 50 × 10-cm wooden boxes. Each line was planted in a replication across the width of the seedbox with 15 plants per row. One row each of the susceptible check, TN1, and the resistant check, PTB33, was sown at random in all seed boxes. Ten days after seeding, each seedling was exposed to 5-8 first- to third-instar WBPH nymphs. After infestation, the wooden seed boxes with seedlings were covered with wire-mesh wooden cages. Test plants were observed daily for WBPH damage. A damage rating of test plants was made by row when 90% of the plants in the susceptible check row were killed.

For mature plants, the pot screening method was adopted. Pre-germinated seeds of each test line and TN1 were sown in 16-cm-diameter pots. Thirty days after sowing, seedlings were thinned to 2/ pot and covered with cylindrical mylar film cages (13 × 90 cm). Two treatments using first-instar nymphs were used for the 35-day-old plants: 0 and 50/ pot. Treatments were replicated twice.

At 32 days after infestation, visual plant damage ratings were taken on all test lines and the WBPH progenies were collected in glass vials with a suction device. Insects were dried in an oven at 50 °C for 60 hours and weighed. Infested and uninfested test plants (both shoots and roots) were removed from the pots and air-dried for 3 hours, dried in an oven at 50 °C for 70 hours, and weighed. From the data, tolerance parameters such as functional plant loss index (FPLI), tolerance index (TI), antibiosis index (AI), and plant dry weight loss per milligram of WBPH dry weight produced (PDLOSS) were computed.

Phenotypic data gathered for various parameters were subjected to QTL analysis using marker data for IR64/Azucena doubled-haploid populations. The results of interval mapping indicated the presence of a major QTL on chromosome 11 for the phenotypic values of PDLOSS. Data on PDLOSS were obtained using the formula above (Panda and Heinrichs 1983).

PDLOSS = Dry weight of uninfested plant (mg) – dry weight of infested plant (mg)/ Dry weight of WBPH progeny produced on the test line (mg)

The phenotypic value of this parameter varied greatly between the parents (221.6 for IR64 and 377.0 for Azucena). The doubled-haploid lines ranged from 23.3 to 201.3 and had a mean value of 248.0. TN1 had a value of 98.1. The frequency distribution of the phenotypic values is given in Figure 1. The skewed nature of the distribution indicated the qualitative nature of the trait. The heritability estimate was high for this parameter (72%). The QTL mapped on chromosome 11 was flanked by markers RG103 and RG167 and explained the phenotypic variance of 79% with a LOD score of 7.31 (Fig. 2). No QTL could be detected

when phenotypic data of other parameters were used. The single-marker analysis for the markers identified for PDLOSS also indicated the association of markers with QTLs. The single-marker analysis for the markers in between and outside the interval of RG103-RG167 indicated no marker-QTL association, suggesting the possibility of two QTLs for the trait (see table). The analysis of the phenotypic effect of QTLs identified for WBPH resistance indicated that IR64 contributed more toward resistance. We anticipate identifying newer QTLs when additional phenotypic screening methods are used for screening rice varieties for WBPH resistance.

References

Angeles ER, Khush GS, Heinrichs EA. 1981. New genes for resistance to whitebacked planthopper in rice. Crop Science 21:47-50.

Hernandez JE, Khush GS. 1985. Genetics of resistance to whitebacked planthopper in some rice (*Oryza sativa* L.) varieties. Oryza 18:44-50.

Panda N, Heinrichs EA. 1983. Levels of tolerance and antibiosis in rice varieties having moderate resistance to brown planthopper *Nilaparvata lugens* (Stål.) Hemiptera:Delphacidae. Environmental Entomology 12:1204-1214.

Sidhu GS, Khush GS, Medrano FG. 1979. A dominant gene in rice for resistance to whitebacked planthopper and its relationship to other plant characteristics. Euphytica 28:227-232.

Wu CF, Khush GS. 1985. A new dominant gene for resistance to whitebacked planthopper in rice. Crop Science 25:505-509.

Putative QTLs identified for PDLOSS based on single-marker analysis. [a]/

	No. of individuals with		Mean of PDLOSS for DHLs with [b]/		
Marker	IR 64 allele	Azucena allele	IR 64 allele	Azucena allele	F value
RG1094	76	16	242.21	287.65	0.54
RG167	78	12	203.06	339.99	5.600 [c]/
Npb44	78	12	247.06	269.27	0.101
RG247	78	12	237.59	269.27	0.213
RG103	52	38	209.17	312.37	4.780 [c]/
RG1109	76	16	242.21	287.65	0.54

[a]/ The markers present in between RG167 and RG103 do not show linkage.

[b]/ DHL = doubled-haploid line. [c]/ Significant at 1% level.

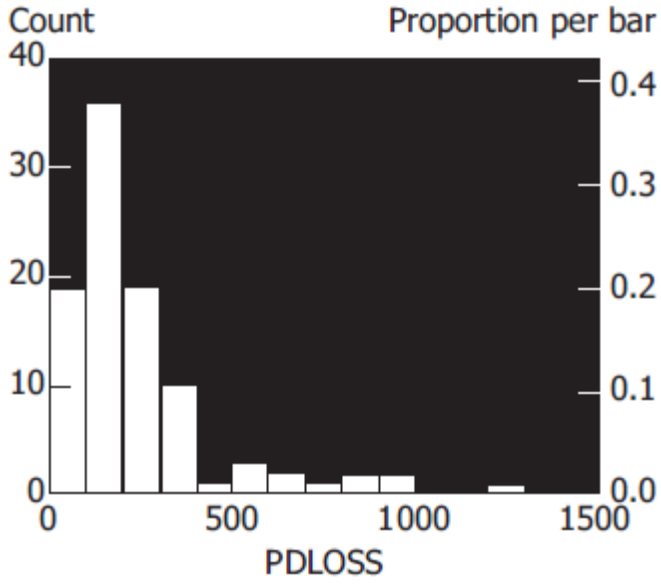

Fig. 1. Frequency distribution among doubled-haploid lines of IR64/Azucena.

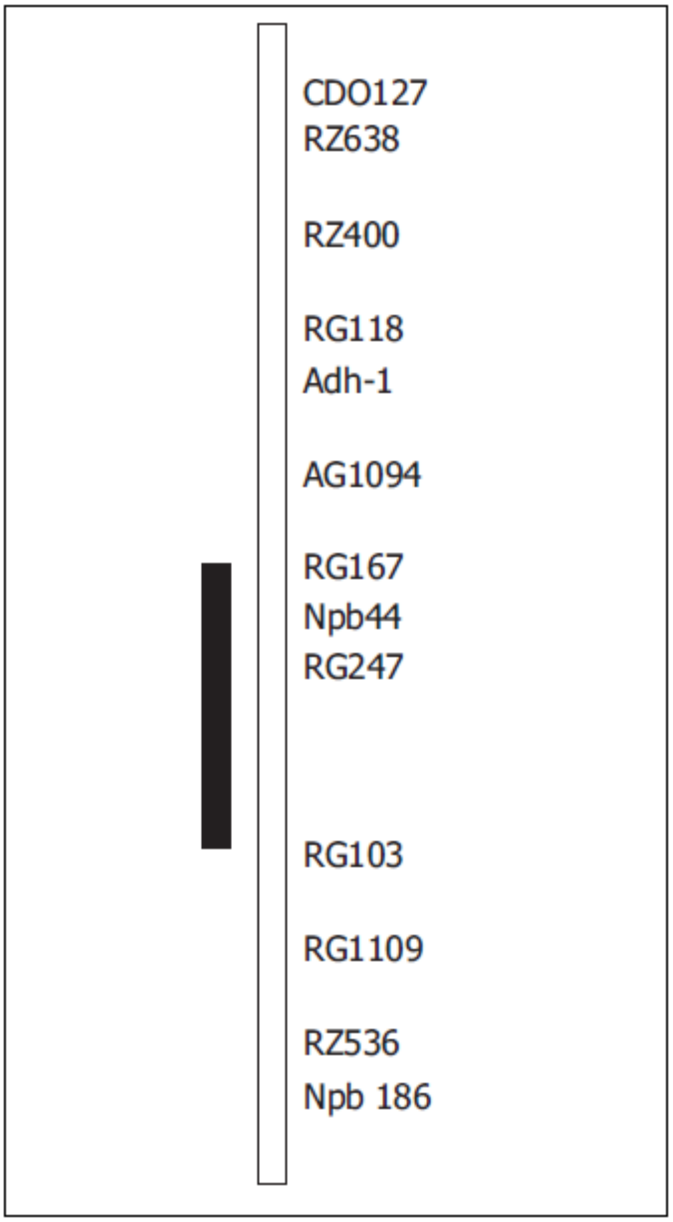

Fig. 2. Marker interval indicating the presence of a QTL for PDLOSS.

Kadirvel P, M Maheswaran, K Gunathilagaraj. 1999. Molecular mapping of quantitative trait loci (QTLs) associated with whitebacked planthopper in rice. International Rice Research Notes 24 (3) 12-14.