

### Mapping of *Wbph6(t)* — a new gene resistant to white-backed planthopper

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Whitebacked planthopper (WBPH, *Sogatella furcifera* Horváth) is one of the most destructive insects for rice. The utilization of WBPH resistance genes is always an efficient solution to this problem. Besides five WBPH resistance genes registered, *Wbph1*, *Wbph2*, *Wbph3*, *wbph4*, and *Wbph5*, classical segregation analysis and allelism test showed that several rice landraces from Yunan Province, China, carried a new dominant resistance gene *Wbph6(t)*. We herein reported the mapping of *Wbph6(t)* by using DNA markers.

An F<sub>3</sub> population was derived from the cross of TN1/Guiyigu. TN1 is an indica rice variety commonly used as a susceptible control, and Guiyigu (GYG) is a landrace carrying *Wbph6(t)*. The F<sub>3</sub> population, as well as the two parents, was evaluated for WBPH resistance in CNRRI in 2000, by employing the standard bulk-screening test modified by IRRI. One row of 25 plants was for each F<sub>3</sub> line with three replications. At 2-leaf stage, each plant was infested with 7-8 insects of 1-2 instar nymphs. The resistance reaction of each line was scored when the mortality of the susceptible check TN1 seedlings reached

95%. The percentage of dead seedlings (DS) was used to evaluate the resistance to WBPH. The average values of DS for TN1 and GYG were 97.2% and 18.3%, respectively. Of the F<sub>3</sub> lines tested, 90 lines showed consistent reaction among the three replications and they were used for further analysis. The average DS of the F<sub>3</sub> lines ranged from 12% to 100% (Fig. 1).

Leaves were collected from a single plant for each parent, and from a mixture of 20 plants for each F<sub>3</sub> line. DNAs were extracted for RFLP and SSCP analyses. Of a total of 131 RFLP probes and 150 primer pairs used for parental survey, 54 probes and 45 primer pairs detected polymorphism between TN1 and GYG. DNA pools were constructed from 10 susceptible (S pool) and 10 resistant extremes (R pool), respectively, and they were assayed by using polymorphic RFLP probes and SSR primers. Positive markers were only detected with SSR primer RM167. The PCR product of the S pool consisted of a single DNA fragment from the susceptible parent TN1, while that of the R pool consisted of fragments both from TN1 and GYG.

The RM167 genotypes of each F<sub>3</sub> line were determined. Of the 10 susceptible extremes, 6 had the TN1 homozygote, 4 had the heterozygote, and none had the GYG homozygote. The genetic distance between *Wbph6(t)* and RM167 was 21.2 cM. When the F<sub>3</sub> population was divided into three sub-populations based on the genotypes at RM167 locus, it was found that the majority of F<sub>3</sub> lines having GYG and TN1 homozygotes could be classified as resistant and susceptible lines, respectively, and the majority of the F<sub>3</sub> lines having the heterozygote had moderate DS values (Fig. 1). This result was in support of the linkage between *Wbph6(t)* and RM167.

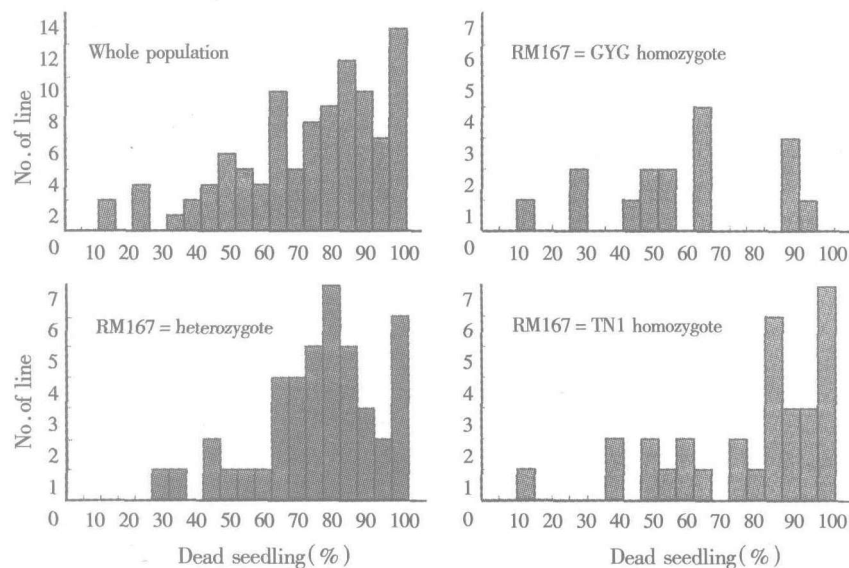


Fig. 1. Resistance segregation in the TN1/Guiyigu F<sub>3</sub> population.

The  $F_3$  lines were also assayed with two more SSLP markers on chromosome 11, RM287 and RM21. *Wbph6(t)* was located on the off-end of the RM167-RM287-RM21 segment (Fig.2). Work is underway to construct recombinant inbred line population from the cross of TN1/ GYG, with which the precise location of *Wbph6(t)* could be determined. □

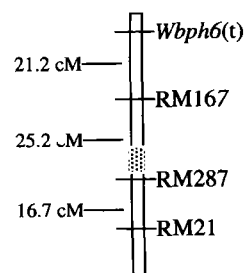


Fig.2. Location of *Wbph6(t)* on chromosome 11 of rice.

The chromosome is drawn as a blank bar with dotted portion referring to centromere.

### QTL × Environment interaction for rice panicle characteristics

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Genotype by environment (GE) interaction is a very important factor that determines yielding stability of crop varieties, and it has received considerable attention in plant breeding. In a two-year experiment, an  $F_9$  recombinant inbred line population derived from the cross between Zhenshan 97 and Minghui 63, the parents of Shanyou 63, were used to analyze QTL and GE interaction. In the 1997 test, the seeds were sown on May 15 in large plastic boxes, and in the 1998 test, the seeds were sown on Jun 5 in seedling bed. Two kinds of DNA markers, representing 220 polymorphic loci, 174 RFLPs and 46 SSRs, were used to construct the genetic linkage map by using Mapmaker

3.0 (Lincoln et al., 1992).

QTLs for 5 characters were determined by the computer software Mapmaker/ QTL 1.0 based on a mixed linear model approach. A total of 34 QTLs were detected (see table), of which alleles for increasing traits values were identified in high value parent at 17 QTLs and in low value parent at the other 17 QTLs.

QTL clustering was observed in six intervals. QTL located in the genomic region C1087-RZ403 on chromosome 3, influenced spikelets per panicle, grains per panicle, seed setting rate, and spikelet density simultaneously. In the four cases, Minghui 63 alleles had a negative effect. QTLs located in the intervals G359-RG532 on chromosome 1, R2510-RM211 on chromosome 2, and R2549-C962 on chromosome 6, had effects simultaneously on spikelets per panicle and spikelet density. For the three intervals, the same genotype of each locus had the same direction effect on their associated traits. The loci in the interval C2340-C86 on chromosome 1 and C405A-C223 on chromosome 10 had effects simultaneously on three and two different traits, respectively, but with the opposite direction of effects on the traits.

The difference in planting times between 1997 and 1998 provided different environmental conditions of the field trials. In this study, 6 of 34 QTLs were identified to be interacted significantly with environment (see table), including one QTL for panicle length, two QTLs for spikelets per panicle, and three QTLs for seed setting rate. The contribution was slightly larger for each interaction than that for the QTL involved in the interaction. However, the total amounts of the effects ascribed to GEs were small for all the five traits. QTL with major effect did not show environmental interaction. No environmental interaction was detected for traits with high heritabilities such as grains per panicle and spikelet density. Results indicated that major QTLs could be used to improve rice variety under the help of the closely linked markers. □