

## Abstract

Rice (*Oryza sativa* L.), the most important crop of the world population, is severely devastated by the brown planthopper (BPH, *Nilaparvata lugens* Stål.). Host plant resistance is generally regarded as the most effective and economical mean for controlling this insect. More than 46 genes for BPH resistance have been identified from rice cultivars and wild relatives. Understanding of genetic locations and resistance performances of genes are necessary to exploit resistance plants efficiently and sustainably in field condition.

In the first study, we developed seven near-isogenic lines (NILs) (*BPH2*-NIL, *BPH3*-NIL, *BPH17*-NIL, *BPH20*-NIL, *BPH21*-NIL, *BPH32*-NIL and *BPH17-ptb*-NIL) carrying a single BPH resistance gene and fifteen pyramided lines (PYLs) carrying two or three genes on the genetic background of the *japonica* rice variety, 'Taichung 65' (T65). The NILs and PYLs were assessed for resistance levels against two BPH populations collected in Japan in 1966 (Hadano-66) and 2013 (Koshi-2013). Many of the NILs and PYLs were resistant against the Hadano-66 population but were less effective against the Koshi-2013 population. Among PYLs, *BPH20+BPH32*-PYL and *BPH2+BPH3+BPH17*-PYL had relatively high BPH resistance against Koshi-2013.

In the second study, the locations of *BPH2*, *BPH17-ptb*, and *BPH32* were delimited using chromosome segment substitution lines derived from crosses between T65 and NILs for *BPH2* (*BPH2*-NIL), *BPH17-ptb* (*BPH17-ptb*-NIL), and *BPH32* (*BPH32*-NIL). The resistance mechanism of *BPH2*, *BPH17-ptb* and *BPH32* were determined by applying the tests for antibiosis, antixenosis and tolerance. *BPH2* was delimited as approximately 247.5 kbp between RM28449 and ID-161-2 on chromosome 12. *BPH17-ptb* and *BPH32* were located between RM1305 and RM6156 on chromosome 4 and RM508 and RM19341 on chromosome 6, respectively. The

antibiosis, antixenosis, and tolerance were estimated by several tests using *BPH2*-NIL, *BPH17-ptb*-NIL, and *BPH32*-NIL. *BPH2* and *BPH17-ptb* showed resistance to antibiosis and antixenosis, while *BPH17-ptb* and *BPH32* showed tolerance.

The third research topic was conducted for identifying quantitative trait loci for BPH resistance from two *O. nivara* accessions (IRGC 89073 and IRGC 93005) and Sri Lanka rice variety, 'Rathu Heenati'. The segregation populations for these three-rice variety/accessions were developed. The frequency distributions of segregation populations showed continuous distribution, suggesting that IRGC 89073, IRGC 93005, and 'Rathu Heenati' contain multiple genes for BPH resistance.

These results will be useful in the monitoring of BPH virulence prior to deploying resistant rice varieties, and in the improvement of BPH resistance of rice varieties in the context of regionally increasing levels of virulence.