Mapping of QTLs conferring resistance in rice to brown planthopper, Nilaparvata lugens

ABSTRACT

Brown planthopper (BPH), Nilaparvata lugens Stål (Hemiptera: Delphacide), is a destructive insect pest of rice, Oryza sativa L. (Poaceae), in rice-producing areas worldwide. Host plant resistance is a major aspect of managing this pest. In this study, a mapping population consisting of 150 F3 lines, derived from a cross of MR276 and Rathu Heenati, was used to detect and analyse quantitative trait loci (QTLs) for the resistance to BPH. Composite Interval Mapping (CIM) was used for QTL detection. In total 10 QTLs controlling BPH resistance were mapped on chromosomes 1, 3, 6, 7, 9, 10, and 12. Four QTLs ï qBph-1-1, qBph-3-1, qBph-6-1, and qBph-7-1 ï were mapped on chromosomes 1, 3, 6, and 7 in the standard seedbox screening test, explaining 41% of the phenotypic variance. Two QTLs, qBph-6-1 and qBph-9-1, were detected on chromosomes 6 and 9 in the honeydew test, accounting for 32% of the total phenotypic variance. Moreover, four QTLs ï qBph-3-1, qBph-6-1, qBph-10-1, and qBph-12-1 ï were identified on chromosomes 3, 6, 10, and 12 expressing antixenosis to BPH and explaining 41% of the phenotypic variance. QTL qBph-3-1 was located in the chromosomal region between markers RM231 and RM3872 on chromosome 3, and QTL qBph-6-1 was located in the region between RM588 and RM204 on chromosome 6, indicating that these regions have a major effect in controlling the resistance to BPH in the population studied. The molecular markers linked to QTLs that are identified will be useful in the development of varieties resistant to BPH. Our study contributes to the development of genetic material for breeding programmes and marker-assisted selection (MAS) in rice to improve BPH resistance.

Keyword: Antibiosis; Antixenosis; Composite interval mapping; Delphacidae; F3 population; Hemiptera; Oryza sativa L.; Poaceae; Quantitative trait locus; Seedbox screening test