

Analysis of SSR markers linked with brown planthopper resistance genes ('Bph') using high-resolution melting (HRM) in rice

ABSTRACT

Developing rice cultivars with host-plant resistance is widely considered the best strategy for the long-term control of the brown planthopper (BPH). The use of molecular markers in many aspects of rice ('*Oryza sativa*' L.) studies, such as the genetic analysis of insect and disease resistance, is increasing. In the present study, 110 simple sequence repeat (SSR) markers that are associated with Bph resistance genes were selected from the Gramene database and used to develop SSR marker-based strategies for the reliable selection of BPH-resistant genotypes. Fifty-seven of the best polymorphic markers were used to identify the segregation ratio in 176 individual F2 rice progeny from a MR276 (susceptible) x Rathu Heenati (resistant) interspecific cross. Thirty-five SSR markers, including RM544, RM547, and RM8213, showed a good fit to the expected segregation ratio (1:2:1) for the single gene model (d.f. = 1.0, $p \leq 0.05$) in chi-square (χ^2) analyses. The remaining markers did not fit the expected Mendelian segregation ratios. The genetic information generated in this research will be useful in rice breeding programmes to provide varieties with durable resistance to BPH. Additionally, this research showed that high-resolution melting analysis (HRM) is powerful and applicable for accurately and quickly genotyping many samples.

Keyword: Rice (*Oryza sativa* L.); Brown planthopper (BPH); Resistance genes; Simple sequence repeat markers; F2 population.