

Genetic analysis and identification of SSR markers associated with rice blast disease in a BC₂F₁ backcross population

ABSTRACT

Rice (*Oryza sativa* L.) blast disease is one of the most destructive rice diseases in the world. The fungal pathogen, *Magnaporthe oryzae*, is the causal agent of rice blast disease. Development of resistant cultivars is the most preferred method to achieve sustainable rice production. However, the effectiveness of resistant cultivars is hindered by the genetic plasticity of the pathogen genome. Therefore, information on genetic resistance and virulence stability are vital to increase our understanding of the molecular basis of blast disease resistance. The present study set out to elucidate the resistance pattern and identify potential simple sequence repeat markers linked with rice blast disease. A backcross population (BC₂F₁), derived from crossing MR264 and Pongsu Seribu 2 (PS2), was developed using marker-assisted backcross breeding. Twelve microsatellite markers carrying the blast resistance gene clearly demonstrated a polymorphic pattern between both parental lines. Among these, two markers, RM206 and RM5961, located on chromosome 11 exhibited the expected 1:1 testcross ratio in the BC₂F₁ population. The 195 BC₂F₁ plants inoculated against *M. oryzae* pathotype P7.2 showed a significantly different distribution in the backcrossed generation and followed Mendelian segregation based on a single-gene model. This indicates that blast resistance in PS2 is governed by a single dominant gene, which is linked to RM206 and RM5961 on chromosome 11. The findings presented in this study could be useful for future blast resistance studies in rice breeding programs.

Keyword: Blast inheritance; SSR marker; Pongsu Seribu 2; MR264; Marker-assisted backcrossing