

**Genetic analysis of the resistance to rice blast in the BC2F1 population
derived from MR263 × Pongsu Seribu 1**

ABSTRACT

Rice blast disease, caused by *Magnaporthe oryzae*, is the most important and most devastating rice disease globally. For genetic analysis of resistance to rice blast, the present study used a BC2F1 population developed through marker-assisted backcrossing from a cross between blast susceptible MR263 and blast resistant Pongsu Seribu 1 (PS1). We selected out of 450 markers, 65 polymorphic simple sequence repeat markers, including the Pi gene-based markers, and identified 16 markers associated with blast resistance that showed heterozygous bands in the BC2F1 population. Of the 16 polymorphic markers, only eight (RM5961, RM263, RM163, RM224, RM262, RM168, RM229 and RM169) showed a good fit to the expected segregation genotypic ratio (1:1) for the single dominance gene model ($df=1.0$, $P<0.05$), according to chi-square (χ^2) analysis. An analysis of phenotypic data of the BC2F1 population also showed a good fit to the expected phenotypic ratio (1:1; R:S) for resistant and susceptible plants. The resistance to blast pathotype P7.2 in PS1 is most likely controlled by a single dominant gene that is linked to the eight markers we identified. These markers could be used in marker-assisted selection programmes to develop a durable blast resistant rice variety.