SSRs for marker assisted selection for blast resistance in rice (Oryza sativa L.).

ABSTRACT

Rice blast caused by the fungus Magnaporthe oryzae is one of the most devastating diseases of rice in nearly all rice growing areas of the world including Malaysia. To develop cultivars with resistance against different races of M. oryzae, availability of molecular markers along with marker-assisted selection strategies are essential. In this study, 11 polymorphic simple sequence repeat (SSR) markers with good fit of 1:2:1 ratio for single gene model in F2 population derived from the cross of Pongsu seribu 2 (Resistant) and Mahsuri (Susceptible) rice cultivars were analysed in 296 F3 families derived from individual F2 plants to investigate association with Pi gene conferring resistance to M. oryzae pathotype. Parents and progeny were grouped into two phenotypic classes based on their blast reactions. Chi-square test for the segregation of resistance and susceptibility in F3 generation fitted a ratio of approximately 3:1. Association of SSR markers with phenotypic trait in F3 families was identified by statistical analysis. Four SSR markers (RM413, RM5961, RM1233 and RM8225) were significantly associated with blast resistance to pathotype 7.2 of M. oryzae in rice ($p \leq 0.01$). These four markers accounted for about 20% of total phenotypic variation. So, these markers were confirmed as suitable markers for use in marker-assisted selection and confirmation of blast resistance genes to develop rice cultivars with durable blast resistance in Malaysian rice breeding programmes.

Keyword: Rice (Oryza sativa L.); Rice blast (Magnaporthe oryzae); Simple sequence repeats (SSRs) markers; F2 and F3 population; Marker assisted selection; Resistance gene.