Analysis of simple sequence repeat markers linked with blast disease resistance genes in a segregating population of rice (Oryza sativa).

Abstract

Among 120 simple sequence repeat (SSR) markers, 23 polymorphic markers were used to identify the segregation ratio in 320 individuals of an F(2) rice population derived from Pongsu Seribu 2, a resistant variety, and Mahsuri, a susceptible rice cultivar. For phenotypic study, the most virulent blast (Magnaporthe oryzae) pathotype, P7.2, was used in screening of F(2) population in order to understand the inheritance of blast resistance as well as linkage with SSR markers. Only 11 markers showed a good fit to the expected segregation ratio (1:2:1) for the single gene model (d.f. = 1.0, $P < 0.05$) in chi-square ($\chi(2)$) analyses. In the phenotypic data analysis, the F(2) population segregated in a 3:1 (R:S) ratio for resistant and susceptible plants, respectively. Therefore, resistance to blast pathotype P7.2 in Pongsu Seribu 2 is most likely controlled by a single nuclear gene. The plants from F(2) lines that showed resistance to blast pathotype P7.2 were linked to six alleles of SSR markers, RM168 (116 bp), RM8225 (221 bp), RM1233 (175 bp), RM6836 (240 bp), RM5961 (129 bp), and RM413 (79 bp). These diagnostic markers could be used in marker assisted selection programs to develop a durable blast resistant variety.