

Genetic dissection of rice blast resistance by QTL mapping approach using an F3 population

ABSTRACT

Rice blast is one of the major fungal diseases that badly reduce rice production in Asia including Malaysia. There is not much information on identification of QTLs as well as linked markers and their association with blast resistance within local rice cultivars. In order to understanding of the genetic control of blast in the F3 families from indica rice cross Pongsu seribu2/Mahsuri, an analysis of quantitative trait loci against one of the highly virulent Malaysian rice blast isolate *Magnaporthe oryzae*, P5.0 was carried out. Result indicated that partial resistance to this pathotype observed in the present study was controlled by multiple loci or different QTLs. In QTL analysis in F3 progeny fifteen QTLs on chromosomes 1, 2, 3, 5, 6, 11 and 12 for resistance to blast nursery tests was identified. Three of detected QTLs (qRBr-6.1, qRBr-11.4, and qRBr-12.1) had significant threshold (LOD >3) and approved by both IM and CIM methods. Twelve suggestive QTLs, qRBr-1.2, qRBr-2.1, qRBr-4.1, qRBr-5.1, qRBr-6.2, qRBr-6.3, qRBr-8.1, qRBr-10.1, qRBr-10.2, qRBr-11.1, qRBr-11.2 and qRBr-11.3) with Logarithmic of Odds (LOD) <3.0 or LRS <15) were distributed on chromosomes 1, 2, 4, 5, 6, 8, 10, and 11. Most of the QTLs detected using single isolate had the resistant alleles from Pongsu seribu 2 which involved in the resistance in the greenhouse. We found that QTLs detected for deferent traits for the using isolate were frequently located in similar genomic regions. Inheritance study showed among F3 lines resistance segregated in the expected ratio of 15: 1 for resistant to susceptible. The average score for blast resistance measured in the green house was 3.15, 1.98 and 29.95 % for three traits, BLD, BLT and % DLA, respectively.

Keyword: F3 families; Linkage map and QTL; Rice blast disease; SSRs markers