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QTL analysis identifies genomic regions associated with clubroot disease in Brassica rape seed

ADDRESS

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Clubroot disease is one of the most serious soil contagious diseases caused by *Plasmodiophora brassicae* in Brassicaceae crops. Several studies for QTL identification and Genome-Wide Association Study (GWAS) were conducted to investigate the genetic factors of *Brassica rapa* related to clubroot disease resistance in South Korea. Traditional QTL mapping with bi-parental mapping population is an efficient method to find significant locus. Alternatively, GWAS is another approach used for predicting genetic loci/candidate genes associated with disease related traits in natural population. In this study, we have carried QTL analysis in 82 DH lines generated from F1 population of O9CR-500 (resistant) and O9CR-501 (susceptible) parental lines screened for two years. As a result, a QTL mapped in chromosome A08 that consists of 11 R genes. Further, association-mapping analysis in 232 inbred lines with three years replication allowed to predict 15 associated SNP markers related to clubroot disease. Among these, few markers located in chromosome A02 and A03 are known and in addition to that new candidate SNPs also identified in A06 and A09 chromosomes. These results will be useful as additional resource in the future studies for identification of clubroot resistance or defense-associated genes, through marker-assisted selection in breeding.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS