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Identification of Novel Clubroot Resistance Loci in *Brassic rapa*

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Plasmodiophora brassicae, the causal agent of clubroot disease, does the most serious damage to the *Brassica* crops. The limited control approaches make that the identification of clubroot resistance (CR) is more important for developing CR cultivars of the *Brassica* crops. So far, 8 CR loci were mapped. However, the variation of *P. brassicae* leads to the rapid erosion of its resistance. To identify novel CR genes, we employed three mapping population, derived from crosses between Chinese cabbage and turnip inbred lines (59-1×ECD04 and BJN3-1×Siloga) or between Chinese cabbage inbred lines (BJN3-1 x 85-I-II), to perform QTL analysis. Totally, 8 CR loci were indentified and showed race-specific resistance. Physical mapping of these 8 loci suggested that 4 were located previously mapped position, indicating they might be the same allele or different alleles of the same genes. Other 4 loci were found to be novel. Further, CR near isogenic line carrying each CR locus was developed based on the marker assisted selection. Verification of these CR loci was underway. Identification of these novel CR genes would facilitate to breed broad-spectrum and durable CR cultivars of *B. rapa* by pyramiding strategies.