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## Characterization and Utilization of the Clubroot Resistant Genes in Chinese Cabbage (*Brassica rapa* L.)

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Clubroot disease is the major threat to the production of Chinese cabbage (*Brassica rapa* L.) in Japan. Although the breeding of the clubroot resistant (CR) cultivars is one of the most efficient ways to control this disease, the CR cultivars do not always have effects due to the breakdown of resistance. Therefore, it is necessary to develop the breeding strategy to accumulate multiple CR genes in a single cultivar effectively. We have identified two incomplete dominant CR loci, *Crr1* and *Crr2*, which are originated from the European CR turnip Siloga. To investigate the effectiveness of marker-assisted selection (MAS) for CR breeding, the inbred line with *Crr1* and *Crr2* was crossed with parental lines of the existing CR F<sub>1</sub> cultivar of Chinese cabbage, followed by 5 times of MAS and backcrossing. The F<sub>1</sub> derived from a cross between the resulting parental lines improved the clubroot resistance as expected and had the same morphological characters as the original F<sub>1</sub> cultivar.

We have shown that the *Crr1* locus comprised two loci: *Crr1a*, which by itself conferred resistance to the mild isolate; and *Crr1b*, which had a minor effect, but was not required for *Crr1a*-mediated resistance. Further genetic analysis suggested that *Crr1b* was necessary to acquire resistance to the more virulent isolate in combination with *Crr2*. Molecular characterization of *Crr1a* encoding TIR-NB-LRR class of R protein revealed that there were at least 4 alleles in Japanese CR cultivars of Chinese cabbage. PCR analysis with *Crr1a*-specific markers demonstrated that the functional alleles were predicted to be present in European CR turnips, Debra and 77b besides Siloga, whereas rarely in Japanese CR cultivars, indicating that *Crr1a* is an useful source to improve the resistance of Chinese cabbage cultivars.