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Genetic Mapping of Clubroot Resistance Gene in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*)

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Objectives

1. Genetic analysis of clubroot disease.
2. genetic mapping of clubroot resistance gene named *CRb*

Materials and Methods

1. Materials: An F_2 population of 143 individuals derived from a cross between CR Shinki DH line and susceptible line 94SK was used to map the *CRb* gene.
2. Methods
   - Inoculation of F_3 family against single spore isolate.
   - Identification of DNA markers linked to *CRb* using AFLP technique.
   - Mapping of the *CRb* gene with converted SCAR markers from AFLP marker.

Results and discussion

Result of inoculation indicated that clubroot resistance was controlled by a single dominant gene. Using AFLP technique combined with BSA, 6 co-dominant AFLP markers, 4 and 7 dominant AFLP markers linked in coupling and repulsion could be identified, respectively. Out of 17 AFLP markers, 6 markers showing a few recombination events in 138 F_2 lines were cloned. Among them, five markers were converted into CAPS and SCAR markers. Survey of 143 F_2 plants with these marker a genetic map around *CRb* was constructed. One dominant marker, TCR08, was located on the end of map at 0.74 cM from *CRb*. The remaining markers (TCR04, TCR01, TCR09, TCR07, and TCR02) were located on the other side of *CRb*, where the nearest marker to *CRb* was TCR04 at genetic distance of 1.97 cM.

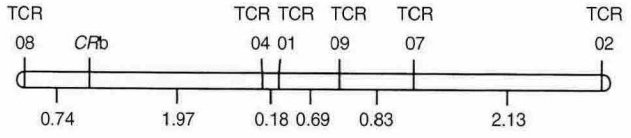

Figure 1. Linkage map of the *CRb* gene. Genetic distance was calculated with Kosambi mapping function

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