6. Molecular breeding of clubroot disease resistant cultivars in Chinese cabbage (Brassica rapa ssp. pekinensis)

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Clubroot disease, caused by Plasmodiophora brassicae Wor., is a most damaging problem in Chinese cabbage. Most CR cultivars were released by introducing CR gene from turnip into Chinese cabbage in Japan. However, many CR cultivars were breakdown because of newly generated races and/or a few races mixed together in the field. The presence of several races in one gall was confirmed by inoculation to other CR cultivars with isolate separated from one infected CR cultivar. The presence of several resistance genes in B. rapa would support a possibility to pyramid these genes into one plant with the aids of molecular markers. Ten CR lines were developed by anther culture of CR F₁ hybrids. All of the DH lines showed resistance to clubroot disease. Genetic analysis of CR gene with their offsprings showed that clubroot resistance was controlled by a single dominant gene in eight out of ten lines. However, the others showed skewed segregation. The CR Shinki DH line of Chinese cabbage that confers a resistance to race 2, 4 and 8 was crossed to a susceptible line 94SK to construct a mapping population. Bulked segregant analysis combined with AFLP technique was carried out to identify molecular markers linked to the resistant gene. With 256 AFLP primer combinations, 6 co-dominant markers, 4 cis-linked and 7 trans-linked markers could be identified. Analysis in an F₂ population (138 plants), the resistance gene was mapped in 12cM intervals consisting of 17 AFLP and SCAR markers. The two nearest flanking markers named P10 and TCR01 were 0.2 and 1.9cM, respectively. The infection of different CR cultivars with different isolates showed race specific resistance. The marker TCR01 was examined in Chinese cabbage hybrid cultivars and ECD 01 to 05. Out of seventeen CR cultivars, only six were identical to the resistant pattern of the marker, while others showed susceptible pattern. ECD 01 showed resistant pattern. The CR cultivars of Chinese cabbage could be divided into three groups based on survey of some F₁ hybrids with TCR01 and inoculation with race 4.

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