S3-2

# New Classification of *Plasmodiophora brassicae* Races Using Differential Genotypes of Chinese Cabbage

**Hun Kim and Gyung Ja Choi**

*Center for Eco-friendly New Materials, Korea Research Institute of Chemical Technology, Daejeon 305-600, Korea*

**Email:hunkim@krict.re.kr*

Clubroot disease caused by *Plasmodiophora brassicae* induces severe losses of cruciferous vegetables worldwide. To control clubroot of Chinese cabbage, many CR (clubroot resistance) $F_1$ hybrid cultivars have been bred and released in Korea, China and Japan. In this study, we determined the race of *P. brassicae* 12 field isolates, which collected from 10 regions in Korea, using Williams' differential varieties including two cabbage ('Jersey Queen', 'Badger Shipper') and two rutabaga ('Laurentian', 'Whilhelmsburger'). By Williams' differential varieties, 12 clubroot pathogens were assigned into one (GN2), two (HS and YC), two (HN1 and HN2), three (DJ, KS and SS) and four (GS, GN1, JS and PC) isolates for races 1, 2, 4, 5 and 9, respectively. In addition, the degree of resistance of 45 CR cultivars that were from Korea, China and Japan was tested with the 12 isolates. The 45 CR cultivars of Chinese cabbage were differentiated into three genotypes according to their resistance responses. Even though the 12 *P. brassicae* isolates were same race by Williams' differential varieties, three CR genotypes showed different resistance response to the isolates. These results indicate that races of *P. brassicae* by Williams' differentials were not related with resistance of CR cultivars, and three CR genotypes represented qualitative resistance to the *P. brassicae* isolates. CR genotype I including 'CR-Cheongrok' showed resistance to GN1, GN2, JS, GS, HS, DJ and KS isolates and susceptibility to YC, PC, HN1, HN2 and SS isolates. And CR genotype II such as 'Hangkunjongbyungdaebaekchae' was resistant to GN1, GN2, JS, GS, HS, YC, PC and HN1 and susceptible to DJ, KS, SS and HN2. CR genotype III including 'Chunhajangkun' and 'Akimeki' represented resistance to 10 isolates except for SS and HN2 isolates. Based on these results, we selected 'CR-Cheongrok', 'Hangkunjongbyungdaebaekchae', and 'Chunhajangkun' as a representative cultivar of three CR genotypes and 'Norangkimjang' as a susceptible cultivar. Furthermore, we investigated the resistance of 15 lines of Chinese cabbage, which were provided by seed companies, to 11 isolates except for HN1 of *P. brassicae*. The results showed that three lines were susceptible to all the tested isolates, whereas five, four, and three lines represented the similar responses corresponding to the CR genotypes I, II, and III, respectively; there is no line of Chinese cabbage showing different resistance patterns compared to three CR genotypes. In particular, line 'SS001' showing resistance responses of CR genotype II was a parent of 'Saerona' that have been commercialized as a CR $F_1$ cultivar of Chinese cabbage. Together, we divided 12 isolates of *P. brassicae* into 4 races, designated by wild type, mutant type 1, mutant type 2, and mutant type 3. Wild type including GN1, GN2, JS, GS, and HS isolates of *P. brassicae* was not able to infect all the cultivars of three CR genotypes, whereas, mutant type 3 such as SS and HN2 isolates developed severe clubroot disease on all the CR genotype cultivars. To mutant type 1 including DJ and KS isolates, CR genotypes I, II and III were resistant, susceptible and resistant, respectively. In contrast, to mutant type 2 including YC, PS, and HN1 isolates, CR genotypes I, II and III showed susceptibility, resistance and resistance, respectively. Taken together, our results provide the extended knowledge of classification of *P. brassicae* races, which is useful information for the breeding of resistant crops, with a suggestion that 'Norangkimjang', 'CR-Cheongrok', 'Saerona' and 'Chunhajangkun' cultivars of Chinese cabbage could be used as new race differentials of *P. brassicae* for clubroot disease assay.