QTL Analysis of Watermelon Mosaic Virus 2 Resistance with a Novel Watermelon Germplasm

Nanjoo Yeo, Yoon Jeong Jang, Bal Kum Han, Hui Joo Cho, Jin Hyuck Huh, Yoo Jin Park, and Gung Pyo Lee*
Department of Integrative Plant Science, Chung-Ang University, Ansan-gu, 1568, Korea

Watermelon mosaic virus 2 (WMV2) is a member of the genus Potyvirus, which consists of ca. 10kbp monopartite RNA genome. The virus is distinguished from watermelon mosaic virus 1 by its ability to infect papaya. WMV2, transmitted by aphids with non-persistent stylet-borne mode, causes very severe damages to the production of watermelon as well as those of other cucurbit crops. The virus is often found to be co-infected with other viruses in the field. We have isolated and purified WMV2 from watermelon leaves co-infected with zucchini yellow mosaic virus. A novel WMV2-resistant breeding resource (CR019) has been found and genetically fixed. To analyze genetic heredity, F1, BC1P1, BC1P2, and F2 population from resistant line CR019 and susceptible line SBB were generated. Virus detection was accomplished by RT-PCR and the resistance was revealed to be dominated by multiple loci. For QTL analysis, we applied bulked-segregant analysis and next generation sequencing method and the detailed result will be presented.

T. 031-670-3037, gplee@cau.ac.kr