MAPPING QUANTITATIVE TRAIT LOCI FOR RESISTANCE TO VERTICILLIUM WILT (*VERTICILLIUM DAHLIAE*) USING A RECOMBINANT INBRED LINE POPULATION

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Abstract

Cotton is one of the most important cash crops in the world and is the leading natural fiber crop worldwide. Verticillium wilt (VW) is one of the most devastating diseases in cotton, causing severe yield and quality loss. Utilization of resistant cultivars is often considered the most cost-effective method to control the disease. However, the lack of effective resistant germplasm and inadequate knowledge of relevant genetic mechanisms on VW resistance have been the major challenges in breeding for resistant cultivars. Most of the linkage maps and QTLs for VW resistance from previous studies were based on F_2 or $F_{2:3}$ progenies which could not be repeatedly screened. In this study, a recombinant inbred line (RIL) population with 94 lines, developed from a cross between a VW resistant genotype, NM 24016 and a susceptible genotype TM-1, was used to map quantitative trait loci (QTLs) for VW resistance. The RILs together with the two parents were evaluated twice using artificial inoculation in the greenhouse. In each test, seed was planted in a 4-inch plastic pot-containing potting soil with 10 seed/pot and seedlings were thinned to 5 - 6 plant/pot after emergence. The experiment was arranged based on randomized complete block design with 4 replicates (a total of 40 plants were screened for each RIL). Seedlings at the $2^{nd}/3^{rd}$ true leaf stage were inoculated with the pathogen, *V. dahliae* by pouring conidia suspension to each pot. Disease incidence and VW symptom severity were assessed using a 0 - 5 scoring system. Significant phenotypic variation in VW resistance was detected in this RIL population from both of the tests. Based on a total of 491 simple sequence repeat (SSR) markers with 236 loci placed on 54 linkage groups, 3 QTLs for VW resistance were detected. Two QTLs were located on Chromosome 3 and 11, and the third one was on a linkage group with chromosome unknown. These QTLs explained 11.1-16.6% of the phenotypic variation.