GENETIC ANALYSIS AND QUANTITATIVE TRAIT LOCUS MAPPING FOR FUSARIUM WILT RACE 4 RESISTANCE IN A RECOMBINANT INBRED LINE POPULATION OF PIMA COTTON

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Abstract

Fusarium wilt (FW) is caused by Fusarium *oxysporum* f. sp. *vasinfectum* Atk. Sny & Hans, FOV) and is becoming a serious problem in the US cotton production. FW causes leaf chlorosis and necrosis, vascular discoloration, plant wilting, defoliation and plant death. Although Upland cotton is more resistance to FW than Pima cotton, Pima S-6 is resistant to FOV race 4 (FOV4). Therefore, intraspecific genetic and breeding populations with FOV4-resistant Pima S-6 can be used as a parent to develop promising lines with resistance to FOV4 and to identify molecular markers associated with FOV4 resistance. In this study, 163 recombinant inbred lines (RILs) with their two parents Pima S-6 and FOV4-susceptible 89590 were used to assay FOV4 resistance based on two replicated tests in the greenhouse or controlled conditions using a randomized complete block design with two replications in each test. Foliar disease severity ratings (DSR) at 30 days after inoculation (DAI) were determined based on a rating scale from 0 to 5, with 0 for no symptoms and 5 for plant death. Significant genotypic variations were detected for FOV4 resistance in both tests and in a combined analysis of variance. Although a significant genotype × test interaction was detected for DSR, 10 RILs had significantly lower DSR than the susceptible parent and were consistently resistant to FOV4 in both tests. The estimated heritability values for DSR were moderate (0.683), indicating that 68% of the phenotypic variation for FOV4 resistance in the Pima RIL population was due to genetic factors. A total of five and four quantitative trait loci (QTL) were detected in test 1 and test 2, respectively, on six chromosomes (c14, c17, c19, c21, c24, and c25), and each explained 15 to 29 % of the phenotypic variation. Three QTL were in common for both tests, accounting for 60% and 75% of the QTL detected in test 1 and 2, respectively. The QTL were validated by comparing them with previous reported QTL, indicating that chromosomes (c6, c17, c18, c19, c24, and c25) carry most FW resistance QTL. Thus, the common QTL detected in this study will be useful for marker-assisted selection for FOV4 resistance in cotton.