GENETIC MAPPING FOR RESISTANCE TO FUSARIUM WILT IN TWO INTROGRESSED POPULATIONS OF UPLAND COTTON

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Abstract

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) race 4 (FOV4), is an early season fungal disease, causing poor seedling establishment and death. Resistance sources in Upland and Pima cotton are limited. Interspecific genetic and breeding populations between the two cultivated tetraploid species can be developed to identify introgressed lines with resistance to FOV4 and to further identify molecular markers associated with FOV4 resistance. In this study, two interspecific populations including 120 introgressed lines (ILs-122) and 180 backcross inbred lines (BILs-182) were derived from backcrossing the same recurrent Upland parent (CCRI 36) to two different *G. barbadense* parents. The two populations and their parents were evaluated in three replicated tests under temperature-controlled conditions at 20-23ºC to assess FOV4 resistance at 7, 14, 21, and 28 days after inoculation (DAI). Disease severity ratings (DSR), disease incidence (DI) and mortality rate (MR) were calculated at each DAI. Because it takes into consideration both DI and MR, DSR at 28 DAI was used to assess FOV4 resistance and perform QTL analysis in this study. DSR had a mean of 3.10 and 3.55 in the ILs-122 and BILs-182 populations, respectively. A combined analysis of variance across the three tests in each population showed significant genotypic differences for FOV4 resistance. A total of 34 ILs and 36 BILs had a significant lower DSR than the susceptible parents and were consistently resistant to FOV4 across the three tests. For the ILs-122 population, 2,292 simple sequence repeat (SSR) markers that covered the 26 Upland cotton chromosomes were used to construct a genetic map. Quantitative trait locus (QTL) analysis for this population is still ongoing. For the BIL-182 population, 7,709 single nucleotide polymorphic (SNP) markers were used to perform QTL analysis for FOV4 resistance across the three tests. A total of 18 QTL were detected on 10 chromosomes (A04, A06, A07, A08, A10, A11, A12, D08, D10 and D12), and each explained 5 to 13 % of the phenotypic variation. Eight QTL had negative additive effects from the Pima parent, while 10 QTL had positive additive effects from the recurrent Upland parent. Except for one QTL, 17 QTL detected were identified within narrow chromosomal regions between 0.5 and 5.0 Mb, indicating a high resolution power in detecting QTL in this study. The results will be useful for marker-assisted selection for FOV4 resistance in cotton.