

A GENOME-WIDE ASSOCIATION STUDY OF FUSARIUM WILT RESISTANCE IN A MAGIC POPULATION OF UPLAND COTTON

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Abstract

Fusarium wilt (FW) is caused by the soil-borne pathogen *Fusarium oxysporum* f. sp. *vasinfectum* (FOV), and FOV race 4 (FOV4) has become a threat to cotton production in the west and southwest U.S. Developing and utilizing resistant cotton cultivars is the most cost-effective disease management strategy. However, current commercial Upland cotton (*Gossypium hirsutum*) is susceptible to FOV4.

In this study, 550 recombinant inbred lines (RILs) were evaluated for FOV4 resistance in two independent replicated tests in the greenhouse using a randomized complete block design with two replicates (10 plants/replicate/line) in each test. The RILs were developed from a multi-parent advanced generation inter-cross (MAGIC) population which was derived from five generations of intermating among 55 half-diallel crosses made from 11 Upland parents (Acala Ultima, Coker 315, Deltapine 90, FM 966, root-nematode resistant M240 with the Deltapine 61 background, Paymaster HS 26, PSC 355, SureGrow 747, Stoneville 474, Stoneville 825, and Tamcot Pyramid). Among the 11 parents, three lines were more resistant to FOV4 with foliar disease severity ratings below 1.0 in the two tests, while three other lines were most susceptible with disease severity ratings above 2.0, based on a rating scale of 0 to 5. Among the 550 MAGIC lines, many lines had consistently low foliar disease severity ratings between the two replicated tests. Many MAGIC lines had consistently high foliar disease severity ratings in the two replicated tests.

Using an Illumina sequencing platform, the 550 MAGIC-RILs were genotyped by re-sequencing (100-150 bp paired-end sequencing) at 3x genome coverage, while the parents were re-sequenced at 20x genome coverage. Based on 473,516 SNPs/Indels identified, a genome-wide association study (GWAS) was performed to identify chromosomal regions that were associated with FW resistance. As a result, a major quantitative trait locus (QTL) for FW resistance on chromosome c14 was identified. The QTL resides on the top of the chromosome. Interestingly, within the QTL region, a major resistance gene (B12) for bacterial blight resistance and one QTL for Verticillium wilt resistance were also identified in this MAGIC population. This QTL region also contains a major resistance gene for root-knot nematode resistance that was previously reported.