EVALUATION AND QTL MAPPING OF FUSARIUM WILT AND VERTICILLIUM WILT RESISTANCE IN AN INTREGRESSED MAGIC POPULATION DERIVED FROM INTERMATING BETWEEN CHROMOSOME SUBSTITUTION LINES AND UPLAND COTTON

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Abstract

Fusarium wilt (FW) and Verticillium wilt (VW) are major disease problems in cotton production. Both diseases cause leaf chlorosis, necrosis, stem discoloration, plant wilting, defoliation and plant death, which results in yield loss and reduction of fiber quality. Pima cotton (*Gossypium barbadense*) is resistant to VW, and Upland cotton (*G. hirsutum*) is more resistant to FW than Pima cotton. Therefore, genetic and breeding populations between Upland and Pima can be created to identify introgressed lines with resistance to both VW and FW and to identify molecular markers associated with VW and FW resistance. In this study, 180 introgressed lines were used to assay FW and VW resistance based on four replicated tests in the greenhouse using a randomized complete block design with two replicates. The lines were developed from a multi-parent advanced generation inter-cross (MAGIC) population which was derived from three generations of intermating among crosses between 3 Upland cultivars including SG 747, FM 966, and PSC 355 and 18 chromosomal substitution lines (CSLs) each carrying a pair of Pima 3-79 chromosomes or arms in the TM-1 background. The 18 CSLs together with TM-1, Pima 3-79, SG 747, FM 966 and PSC 355 were also included in the greenhouse evaluations. Foliar disease severity ratings at 30 days after inoculation (DAI) were determined for each plant based on a rating scale from 0 to 5, with 0 for no symptoms and 5 for full plant defoliation or plant death. Significant genotypic differences were detected for FW and VW resistance. Pima 3-79 showed the highest level of VW resistance with the lowest disease severity rating, and SG 747 had the lowest severity rating to FW, while PSC 355 was most susceptible to both VW and FW. Among the 18 CSLs, CS-B04 was most resistant to VW, while CS-B17 was most resistant FW. Among the 180 MAGIC lines, resistant lines to VW or FW were identified. Although there was no overall correlation between VW and FW resistance, a few MAGIC lines were resistant to both diseases. All the MAGIC lines were re-sequenced and single nucleotide polymorphic markers (SNPs) are being identified. Once SNPs are called, a genome-wide association study for FW and VW will be performed.