DEFENSE RESPONSES OF COTTON TO VERTICILLIUM WILT Y. Bolek, C. W. Magill, P. M. Thaxton and K. M. El-Zik Texas A&M University College Station, TX A. A. Bell USDA-ARS, SPARC College Station, TX

Abstract

Verticillium wilt, caused by Verticillium dahliae, is one of the most important diseases of cotton and causes great economic losses. At least five V. dahliae strains were reported to attack Upland cotton cultivars; the most severe is the defoliating strain. Most studies indicate that resistance to the pathogen in Gossypium hirsutum is multigenetic and quantitatively inherited, and can be explained by additive and dominant gene effects. The interaction of Verticillium and several cotton species provides a suitable model system for investigating an important plant disease. An understanding of the genetic events at the molecular level in this disease interaction will increase our ability to utilize the resistance existing in some cotton germplasm to reduce these losses. The objectives of this study were to determine levels of resistance to four isolates of V. dahliae in four cultivars; develop interspecific populations for molecular studies to identify and map genes conferring resistance; and correlate resistance/susceptibility with known defense responses.

In a preliminary experiment, four cultivars (Pima S-7, M-315, Acala 44, and Acala Prema) were tested for disease severity and response to four *V. dahliae* isolates (PH, TS-2, V76, and V44). Plants were inoculated below the cotyledonary node when they had 4-5 true leaves, with the stem puncture technique using a syringe and needle. Data on number of diseased leaves per plant, number of attached leaves, total plant weight, and leaf to stem ratio was collected three weeks after inoculation.

Pima S-7 followed by Acala Prema were the most resistant and Acala 44 the most susceptible to the pathogen. The V76 isolate was the most severe especially on Acala 44. Pima S-7 (*G. barbadense*) was chosen as the resistant parent and Acala 44 (*G. hirsutum*) the susceptible one. Crosses were made in the field, and F1 and F2 generations were grown in the greenhouse along with the parents. All progenies were carried out as single seed descent. The same inoculation technique used in the preliminary experiment was applied to the parents and F2 plants using the V76 isolate. F2 frequency distributions for number of diseased leaves per plant, number of attached leaves, total plant weight, and leaf to stem ratio showed segregation for resistance to *V. dahliae*, and a near normal distribution for the parameters measured, as expected for a quantitative trait. Also, the F2 distribution indicated transgressive segregation for resistance.

DNA was extracted from the parents and 110 F2 plants. Ten resistant and 10 susceptible F2 plants from the extreme phenotypes were bulked (Bulk Segregate Analysis-BSA). Random Amplified Polymorphic DNAs (RAPDs) was used for the BSA and individual F2 plants will be genotyped with the primers that are polymorphic in the BSA. Polymorphic bands were detected between the Pima S-7 and Acala 44 parents and the F2 resistant and susceptible bulks. Twenty-four RAPD primers were screened and three were polymorphic. Work is in progress to screen additional markers for resistance to *V. dahliae*.

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