## A MAJOR LOCUS FOR FUSARIUM WILT RACE 4 RESISTANCE IDENTIFIED IN GOSSYPIUM HIRSUTUM ACALA NEMX USING AN INTERSPECIFIC PROGENY WITH G. BARBADENSE

Congli Wang
NIGA-CAS
Harbin, China
Mauricio Ulloa
USDA-ARS-SPA-CSRL
Lubbock, TX
Philip A. Roberts
University of California Department of Nematology
Riverside, CA

## Abstract

Fusarium wilt, caused by the soil-borne pathogen Fusarium oxysporum f. sp. vasinfectum race 4 (FOV4), is a vascular disease of cotton (Gossypium spp.) which causes plant injury and yield loss in most Pima (G. barbadense L.) and Acala/Upland (G. hirsutum L.) cultivars without co-infection with root-knot nematode (Meloidogyne incognita). QTL analysis on an interspecific progeny from a cross of Pima-S7 × Acala NemX revealed a major locus conferring resistance to FOV4 in Acala NemX. Two SSR markers (BNL2650-0/196 and CIR112-0/226) were closely linked to the resistance locus, which accounted for 18% (LOD > 3.5) to 40% (LOD > 9.70) of resistance response of FOV4 foliar disease index at 10 and 20 days after inoculation (DAI), and up to 35% for the ratio of vascular discoloration/plant height (VDL/PH) using interval mapping analysis. Additional minor QTLs contributing to the resistance were identified at early DAI (10 and 13) on chromosomes 8, 11, and 21. Positive alleles of these minor OTLs were contributed by either Pima-S7 or Acala NemX. Genetic linkage analysis based on this progeny suggests that the major resistance locus may be located on chromosome 17. BNL2650/CIR112 alleles were linked to previously reported SSRs CIR180 and BNL0834 (BNL0834 also was linked to resistance locus Fov4 in Pima S-6). The BNL2650 and CIR112 SSR markers provide additional valuable resources for incorporating FOV4 resistance into elite germplasm using marker-assisted selection. In addition, some recombinant inbred lines from the Pima S7 x Acala NemX population with resistance to both root-knot nematode and Fusarium wilt races 1 and 4 provide multiple resistance sources for breeding.