

**MAPPING OF VERTICILLIUM WILT
RESISTANCE GENES IN COTTON**

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Abstract

Verticillium wilt, caused by the soil inhabiting fungus *Verticillium dahliae* is one of the most important cotton diseases and causes significant economic losses. A molecular mapping population derived from the interspecific cross of the resistant cv Pima S-7 (*Gossypium barbadense*) and the susceptible cv Acala 44 (*G. hirsutum*) was phenotyped for disease incidence. Phenotyping of plant reaction to the disease was quantified using a set of growth parameters measured three weeks after inoculation. The F₂ phenotypic distribution of these parameters- total plant weight (TPW), stem weight, leaf weight, number of attached leaves, leaf to stem ratio, and number of diseased leaves- suggest that resistance is polygenic. Total plant weight had the strongest correlation with the other traits measured. A set of 500 microsatellites was recently made available for identification of linked marker loci. Ten plants each of extreme resistant and susceptible progeny were selected for bulked segregant analysis (BSA). Out of 240 primers screened so far, 24 were positive in BSA, either in coupling or repulsion phase. The individuals of the bulks and the entire F₂ population were tested for linkage of SSR markers to resistance traits. Single point regression analysis using QGENE software was employed as the primary method of detecting associations between markers. Of all loci linked, JESPR-F25 located on chromosome 3, and JESPR-U65 located on chromosome 10 were linked to Verticillium wilt resistance loci (P=0.007 and 0.004, respectively), with LOD scores of 2.28 and 1.24. CM50B located on chromosome 1 was also linked to TPW (P=0.004 and LOD=2.45). Further experiments to identify additional markers linked to resistance, and anchoring of these markers to currently available genetic maps are in progress.