

## **1497 QTL Analysis of resistance to verticillium wilt using *Gossypium hirsutum* × *G. barbadense* backcross populations**

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In order to introgress elite alleles of *Gossypium barbadense* L. for resistance to verticillium wilt into *G. hirsutum* L, the elite *G. hirsutum* cultivar 'CCRI36' and *G. barbadense* 'Hai1' were used as recurrent and donor parent, respectively, to produce BC<sub>1</sub>, BC<sub>1</sub>S<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub> populations. After screening the two parents and F<sub>1</sub>, 226 SSR primer pairs were used to screen the BC<sub>1</sub>F<sub>1</sub> population. Linkage test indicated that 220 loci could be mapped to 32 linkage groups and covered a total genetic distance of 2408 cM. Twenty three QTLs for verticillium wilt were identified in the BC<sub>2</sub>F<sub>1</sub> and BC<sub>1</sub>S<sub>1</sub> generations, 17 for disease index, and 6 for the ratio of susceptibility. Each QTL could explain 6.4% to 24.5% of the phenotypic variance. One QTL for disease index on linkage LG17 was detected in the BC<sub>2</sub>F<sub>1</sub> verticillium wilt nursery and in the BC<sub>2</sub>F<sub>1</sub> and BC<sub>1</sub>S<sub>1</sub> field populations, which could explain 24.5% of the phenotypic variance, suggesting stable genetic effects for resistance to verticillium wilt. This QTL should be useful in marker assisted breeding.