

QTL Analysis of Fiber Yield and Quality and Resistance to *Verticillium* Wilt Using *Gossypium hirsutum* and *G. barbadense* Advanced Backcross Populations

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To introgress elite QTL alleles of *Gossypium barbadense* L. for fiber yield and quality and resistance to *Verticillium* wilt into *G. hirsutum* L., enlarge the genetic base of *G. hirsutum*, and provide new germplasm resources for the variety development, the cultivars Zhongmiansuo 36, *G. hirsutum*, and Hai 1, *G. barbadense*, were used as recurrent and donor parent, respectively, to produce BC₁F₁, BC₁S₁, and BC₂F₁ populations. QTL analyses of fiber quality, yield-related, and *Verticillium* wilt traits were conducted by the Composite Interval Mapping (CIM) method. Most traits fit the normal distribution in the Kolmogorov-Smirnov test. Fiber length had a significantly positive correlation with fiber strength and a negative correlation with micronaire value; seed index had a significantly positive correlation with boll weight and a negative correlation with lint percentage; lint percentage had negative correlations with fiber length and strength. These correlations could be genetically explained by QTLs co-location in this experiment. A total of 6200 SSR primer pairs were used to screen polymorphism among two parents and the F₁ progeny, which resulted in 857 polymorphic primer pairs with the unique band for Hai 1, and 776 of them were used to screen the BC₁F₁ population. Linkage test indicated 769 of 800 polymorphic loci could be mapped into 28 linkage groups, covering 2968.66 cM, approximately 66.7% of the 4450 cM cotton genome. Each linkage group averaged 27.46 markers, spanned 106.02 cM, with 3.86 cM between markers. Eighty-three QTLs for fiber quality traits were mapped among the three generations. There were 20, 12, 12, 21, and 18 QTLs for fiber length, strength, micronaire, uniformity, and elongation ratio, respectively, which explained 5.39% ~ 23.29% of phenotypic variance. One QTL for fiber elongation, and one for fiber length were detected in the three generations. Additionally, four for fiber elongation, two for fiber length, one for micronaire, and three for fiber strength could be detected in two of the three generations or in the normal field and the disease-nursery field. Twenty-seven QTLs for yield-related traits were mapped among the three generations. QTL numbers for lint percentage, boll weight, and seed index were 7, 7, and 13, respectively, which accounted for 6.61% ~ 19.03% of phenotypic variance. Two QTLs for lint percentage could be detected in the three generations. Additionally, two for lint percentage and two for seed index could be detected in the two of the three generations, which indicated that these QTLs had stable genetic effects, and could be used for marker assisted selection. Thirty QTLs for *Verticillium* wilt resistance were mapped in BC₂F₁ and BC₁S₁ generations, and each could explain 6.54% ~ 16.96% of phenotypic variance. Three QTLs for resistance to *Verticillium* wilt were detected in the wilt nursery and the normal field or in the BC₂F₁ and BC₁S₁ generations, which showed the stable genetic effects. These resistance alleles were derived from the *G. barbadense* parent and could be used for marker assisted breeding.

Key words: interspecific backcross; AB-QTL; fiber quality; yield; *Verticillium* wilt resistance