

Genetic Analysis of Cotton Fiber Traits by Molecular Markers

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1. *Development of EST-SSRs derived from G. barbadense*: One hundred and nineteen EST-SSRs were developed based on 98 unique ESTs from a cDNA library constructed in our laboratory using developing fibers from *G. barbadense* cv. 3-79. Among the SSRs, trinucleotide AAG appeared at a high frequency of 11.76%. Cross-species transferability of the 76 EST-SSRs in diploid *Gossypium* species ranged from 78.95% (in *G. thurberi*) to 94.74% (in *G. arboreum* and *G. herbaceum*), whereas in tetraploid species from 93.42% (in *G. mustelinum*) to 100% (in *G. darwinii*). Twenty-one EST-SSRs exhibited polymorphisms in BC₁ population [(Emian 22 × 3-79) × Emian 22], 24 polymorphic loci were generated, while 22 of the 24 polymorphic loci were integrated with our interspecific BC₁ backbone genetic linkage map, and anchored in 12 chromosomes.

2. *Construction of a high-density interspecific genetic linkage map for QTLs mapping cotton fiber traits*: An interspecific linkage map of allotetraploid cotton was developed based entirely on genome-wide SSR markers in a BC₁ population [(Emian 22 × 3-79) × Emian 22]. A total of 6310 SSR markers (including 13 sets of markers) were employed to screen polymorphisms and yielded 1040 polymorphic loci. The molecular map included 44 linkage groups assigned to 26 chromosomes, and 917 loci spanning 5452.2 cM of the genome. The average distance between loci was 5.9 cM. The method of composite interval mapping was applied to search for QTLs (LOD ≥ 3.0) by the phenotypes of BC₁ plants and corresponding BC₁F₂ families. The analysis yielded 11 QTLs: 2 QTLs controlling fiber length, 1 QTL controlling fiber uniformity, 1 QTL controlling micronaire, 3 QTLs controlling fiber elongation, and 4 QTLs controlling fiber strength. Among them, 6 were mapped on At chromosomes and 5 were mapped on Dt chromosomes, and explained 9.80% and 16.82% of PV, respectively. In three of the QTLs, 3-79 alleles had positive additive genetic effect, with the additive genetic effect values ranging from 0.33 to 1.10.

3. *Construction of a high-density intraspecific genetic linkage map for QTLs mapping cotton fiber traits*: A genetic linkage map was constructed based on F₂ population derived from the intraspecific cross DH962 (an accession from advanced generations of Jimian6 × *G. thurberi*) × Jimian5. A total of 506 loci were obtained and 472 loci were assigned to 50 linkage groups. The map covered 3129.5 cM with a mean density of 6.2 cM per locus. A total of 4 QTLs were detected for fiber-related traits, distributed in 4 groups and explaining to 43.88% of the trait variation.