

1207 Intraspecific linkage map construction of tetraploid cotton using PCR markers and QTLs mapping for yield and fiber-related traits

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An intraspecific F₂ segregation population of DH962 (an introgression line of *G. thurberi* with good fiber quality) and Jimian5 was constructed, and used for linkage map construction and QTL mapping for yield and fiber related traits. A total of 600 RAPD primers, 929 SSR primer pairs and 238 SRAP primer combinations were used to screen the parental polymorphisms. One hundred and fifty six loci generated from these primers and 139 loci mapped into 32 linkage groups including 79 SSR loci, 15 RAPD loci and 45 SRAP loci with 2-14 markers in each group. The mean interlocus distance was , and this map covered 1018.5cM, about 21.86% of the total cotton genome. A total of 14 QTLs associated to yield-related traits were detected by composite interval mapping and explained 7.35%-43.78% of the trait variation. Eight QTLs were detected for fiber-related traits and explained 8.14%-30.05% of the trait variation.