

QTL Mapping for Fiber Quality Traits Based on a Dense Genetic Linkage Map with SSR, TRAP, SRAP and AFLP Markers in Cultivated Tetraploid Cotton

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Cotton is one of the most important economic crops in the world, and it provides natural fiber for the textile industry. With the advancement of the textile technology and increased consumption demands on cotton fiber, both cotton yield and quality should be enhanced. However, cotton yield and fiber quality are complex quantitative traits and are usually negatively associated that hampers the simultaneous improvement of lint yield and fiber quality by traditional breeding. In an attempt to overcome the limitations of the conventional breeding, molecular breeding based on marker-assisted selection is a reality as marker technology has become cheaper and higher throughput. We have undertaken an effort in establishing a marker-assisted selection program aimed at introgressing fiber quality genes or quantitative trait loci (QTLs) from *Gossypium barbadense* L. ($2n = 4x = 52$, AADD) into Upland cotton (*G. hirsutum* L., $2n = 4x = 52$, AADD). A high-density linkage map was constructed for an F_2 population of 186 individuals derived from an interspecific cross of cultivated allotetraploid species between Upland cotton 'CRI 36' and *G. barbadense* L. 'Hai 7124'. The F_2 and $F_{2:3}$ populations also were tested in the field for fiber quality traits. Of a total of 1,252 polymorphic loci, included in the map construction there were 1,097 markers consisting of 697 simple sequence repeats (SSRs), 171 target region amplification polymorphisms (TRAPs), 129 sequence-related amplified polymorphisms (SRAPs), 98 amplified fragment length polymorphisms (AFLPs), and two morphological markers. The map spanned 4,536.7 cM with an average genetic distance of 4.1 cM per marker, and covered > 90% of the tetraploid cotton genome. By using 45 duplicated SSR loci between the two subgenome (A and D) chromosomes, 11 of the 13 pairs of homoeologous chromosomes were identified. QTL analysis for fiber-related traits based on F_2 individuals and $F_{2:3}$ families were performed by means of composite interval mapping using WinQtlCart ver 2.0. A total of 28 significant QTLs were detected including, 6 QTLs for fiber length (4 from F_2 and 2 from $F_{2:3}$), 5 QTLs for fiber strength (2 from F_2 and 1 from $F_{2:3}$), 5 for Micronaire value (2 from F_2 and 3 from $F_{2:3}$), 9 for fiber uniformity (8 from F_2 and 1 from $F_{2:3}$), and 3 for fiber elongation (1 from F_2 and 2 from $F_{2:3}$). Common QTLs for the fiber quality traits were detected between F_2 and $F_{2:3}$ populations. Further field tests have been conducted for identifying consistent and stable QTLs across generations and environments. The present map and QTL analysis provide additional useful information for cotton genomics and for breeders to identify and transfer desirable QTLs from *G. barbadense* to the predominantly cultivated Upland cotton.