MAPPING COTTON GENOME WITH MOLECULAR MARKERS

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Abstract

Cultivated cotton (*G. hirsutum* L. and *G. barbadense* L.) is the leading natural fiber crop. Fiber strength is the main property of the fiber that is limiting in textile processing. Inheritance of cotton fiber strength, as measured by fiber bundles, displays additive quantitative nature. Classical cotton breeding has been successful in improving fiber strength only through the tedious process of selection based on measuring fiber strength in advance generation of the selected lines. Molecular markers in cotton create unprecedented opportunities for improving competitiveness of U.S. cotton production, by targeting genetic changes and accelerating breeding progress. We are currently identifying DNA markers that are linked to fiber strength and other important traits (*Glandless*, *Photoperiod sensitivity*, *immature fiber*, and *Ligon lintless-2*) in cotton.

F_2 progeny from an interspecific cross between two commercially important cottons, *G. hirsutum* L. acc. TM-1, and *G. barbadense* L. acc. 3-79 were used to construct the molecular map and to determine the location of QTLs for the fiber strength and other fiber quality properties. Based on replicated field tests at College Station, the fiber properties are: for strength 20.2 vs. 30.2 cN/tex, for length 1.10 vs. 1.34 inches, and for fineness 4.47 vs. 3.20 micronaire units for TM-1 vs. 3-79, respectively. F_2 fiber strength values ranged from 17 to 34.6 cN/tex, with a normal distribution. The unique high quality fiber characteristics of 3-79 and the high productivity and wide adaptability of TM-1 led to our choice of this mapping population. Furthermore, we have analyzed this population by use of naturally polymorphic morphological mutants: *Petal spot*, *Pollen color*, *Leaf shape*, and *Lint color* in four different linkage groups. Segregation of these mutants in the F_2 did not deviate significantly from normal mendelian expectations.

Hundreds of DNA markers (RAPDs, RFLPs, AFLPs, and SSRs) have been generated and their segregations have been determined among 152 F_2 individuals of TM-1 X 3-79. A framework map has been constructed that consists of 141 RAPDs and 62 RFLPs in 28 linkage groups. About an half of these groups have been assigned to the cotton chromosomes by use of substitutional aneuploid cottons (monosomics and monotelodisomics) developed by David Stelly at TAMU. Three putative QTLs for fiber strength were detected among the 28 linkage groups. The relationship and relative contribution of these QTLs are being determined. Once the putative QTLs are verified, they will be transfered into intraspecific crosses of *G. hirsutum* L. for cotton fiber improvement.

Mapping of monogenic traits are underway by use of respective crosses segregating for these genes: *Glandless* (TM-1 X ESP; ESP X 3-79); *Photoperiod sensitivity* (TM-1 X Lengupa; T-586 X Lengupa); *immature fiber* (TM-1 X *imim*); and *Ligon lintless-2* (TM-1 X Li_2Li_2). The *Glandless* gene was transfered to TM-1 from an Egyptian cotton Bahtim 110 (*G. barbadense* L.), resulting in a new alternative genetic system to glandless cottonseed breeding programs. A cotton plant with or without the *Photoperiod sensitivity* gene will result in flowering or non-flowering. Currently, these two dominant genes have been mapped to different linkage groups via DNA markers at about 25-30 cM. Tighter linkages of these genes to additional DNA markers will provide cotton geneticists and breeders with a valuable tool for revealing the genetic basis and improving cotton production. Information on the mapped DNA markers and their map locations will be available to the cotton community through cotton genome database, Cotton DB, maintained in our research unit.

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