MOLECULAR MAPPING OF THE COTTON GENOME AND ITS APPLICATIONS TO COTTON IMPROVEMENT

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Abstract

The recent application of DNA marker technology offers a valuable tool for revealing the genetic basis of both simple and complex traits in crop plants. In agriculture, it brings extraordinary promise for streamlining many plant breeding efforts, particularly for introgression of valuable genes from exotic germplasm and breeding for traits affected by many quantitative trait loci (QTLs). DNA markers in cotton create unprecedented opportunities for improving competitiveness of U.S. cotton (*Gossypium hirsutum* L. and *G. barbadense* L.) production, by accelerating breeding progress and targeting genetic changes. 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.

To determine the location of QTLs for the fiber strength and other fiber quality properties, we use F_2 progeny from an interspecific cross between two commercially important cottons, *Gossypium hirsutum* acc. TM-1 and *G. barbadense* acc. 3-79. We have produced 152 F_2 plants for which we have detailed morphological data, individual plant fiber samples, and screening for RAPD and RFLP markers. Recombinant inbred (RI) lines of the above cross are being developed for the verification of putative QTLs. To map other monogenic traits, F_2 segregants from other crosses are made available for *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).

We analyzed the fiber strength mapping population by use of naturally polymorphic morphological mutants: *Petal spot, Pollen color, Leaf shape*, and *Lint color* in four different linkage groups. We found that their segregation in the F_2 did not deviate significantly from normal Mendelian expectations. Fiber samples large enough for analysis of bundle fiber strength and single fiber strength were obtained for 152 F_2 segregants. The variation of bundle fiber strength in the parents (TM-1 X 3-79) and F_2 had a normal distribution. From three years of 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. Therefore, they are directly applicable for mapping of agronomic traits such as the unique high quality fiber characteristics of 3-79 and the high productivity and wide adaptability of TM-1.

We have surveyed RFLPs for 7 mapping parents (TM-1, 3-79, T-586, ESP, HS-427-10, PD-6992, and Lengupa) with a core set of mapped probes from A. H. Paterson. 3-79 and Lengupa are *G. barbadense* cottons, the other five are *G. hirsutum* cottons. Over 90% of probes show polymorphism between *G. hirsutum* and *G. barbadense* with at least one of four restriction enzymes: *Eco*RI, *Eco*RV, *Hin*dIII, and *Xba*I. Polymorphism within *G. hirsutum* ranges from 38% to 44%. A majority of the mapped probes detect a single copy of polymorphism, but a few produce multiple copies. Polymorphism within *G. hirsutum* offers an opportunity to transfer and monitor the gene from an interspecific cross to an intraspecific cross. As ESP is a BC_6 product of Bahtim 110 (a donor of *Glandless* gene) to TM-1, few probes we found polymorphic from surveys for the cross of TM-1 X ESP could be putatively positive markers linked to the *Glandless* gene.

We have completed the optimization of the RAPD-PCR reaction for each of 200 RAPD primers, 10-mer. An anchor set of RAPD fragments has been developed from screening cotton aneuploids. A subset of 40 F_2 plants, based on a range of fiber strength, were selected, and screened with 234 DNA fragments from 85 primers. Larger RAPD experiments on 152 F_2 plants for fiber strength are underway by use of the primers giving polymorphic fragments.

Polymorphic RFLP markers based on the parental survey were used to probe respective F_2 blots. Segregation of DNA fragments in F_2 populations were monitored. Data from 40 RFLP probings and 50 RAPD amplifications on the 152 F_2 plants of TM-1 X 3-79 have been analyzed with data from 3 replicates of fiber strength using MapMaker 3.0b and MapMaker/QTL 1.1b. Preferential amplification of RAPD markers in particular regions of the cotton genome has been noticed. Preliminary results indicate the potential for QTL associations of bundle fiber strength. Once the candidate QTLs are confirmed, they will be transferred into intraspecific crosses of *G. hirsutum* for cotton fiber improvement. Mapping of monogenic traits is underway by use of specific F_2 populations. As the chromosome assignment of cotton molecular linkage groups is currently not complete, we are going to use additional aneuploid cottons to complete the assignment of the linkage groups to the remaining cotton chromosomes during this mapping project. Information on the mapped DNA markers and their map locations will be available to the cotton community through cotton genome database, CottonDB 1.0, maintained in our research unit.

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