IDENTIFICATION AND MAPPING OF FIBER LENGTH AND STRENGTH QTLS IN AN INTERSPECIFIC COTTON POPULATION

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Abstract

There is a need to improve fiber characteristics of Upland (*Gossypium hirsutum*) cotton cultivars to meet market and textile demands. The objective of this study was to identify and map genes associated with fiber length and strength. In order to develop a mapping population that was sufficiently polymorphic for fiber characteristics, an interspecific cross between Pima S-7 (*G. barbadense*) and Tamcot SP37 (*G. hirsutum*) was made, and single seed descent segregating F_2 and F_3 plants obtained. Each field grown F_2 and F_3 plant was harvested separately and measurements for fiber length and strength were made using individual instruments. A large amount of high quality DNA was extracted from leaf tissue samples of individual plants for molecular analysis.

The F_2 frequency distributions showed segregation for both fiber length and strength, and a near normal distribution, as expected for a quantitative trait. The population appeared to include transgressive segregants on both the short and long fiber extremes, and on the stronger fiber extreme. Mean fiber length was 0.95 inches for Tamcot SP37 and 1.17 inches for Pima S-7, and fiber strength of Tamcot SP37 was 19 g/tex and 28.1 g/tex for Pima S-7.

In performing bulk segregant analysis (BSA), three bulks; i.e. high, low and intermediate were analyzed for each trait. Ten samples representing each of the longest fibers, the shortest fibers, and the mean were bulked together, and similar three samples for fiber strength were also bulked. Molecular markers including Amplified Fragment Length Polymorphism (AFLP), Cleaved Amplified Polymorphic Sequences (CAPS), and microsatellites were used to create a structural map for quantitative trait loci (QTLs). AFLP polymorphism between Pima S-7 and Tamcot SP37 was obtained for both fiber length and strength. BSA was used as a preliminary step to screen individual F_2s to determine how informative currently available microsatellite markers are. Thirty microsatellites that exhibited polymorphism between the parents were screened over the bulks. One of these markers displayed a segregation pattern linked with the bulk containing high strength individuals. The marker is codominant and is associated with the Tamcot SP37 parent. Analysis of the F_2 and F_3 individuals will be performed to confirm stability and character of markers. Work is in progress to screen additional markers for fiber length and strength.

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