IDENTIFICATION OF MICRONAIRE-RELATED GENES BASED ON COMPARATIVE OLOGONUCLEOTIDE MICROARRAY ANALYSIS BETWEEN INTROGRESSION LINES

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Abstract

Upland cotton, Gossypium hirsutum with wide adaptation and high yield, accounts for more than 90% of the world cotton fiber production, while Pima or Egyptian cotton, G. barbadense with high fiber quality produces 5-8% of the world's cotton fibers. Micronaire is one of the most important fiber characteristics for international cotton classers and spinners. It is regarded as an indication of both fineness (linear density) and maturity (degree of cell-wall development). High micronaire fibers are normally coarse, which is undesirable from the point of view of spinning and yarn evenness. A relatively low micronaire has been used as a predictor of problems in processing, but a low micronaire may also indicate fine fibers with adequate maturity. Cotton breeding indicates that with the improvement of yield, micronaire is becoming higher. Cotton micronaire is complex quantitative traits. With the advancement of molecular biology, quantitative trait loci (QTLs) of micronaire and fiber-related genes have been reported. However, little is known about the molecular genetic basis of fiber micronaire trait and candidate genes associated with micronaire or its QTLs.

It is difficult to directly transfer the high fiber quality traits from G. barbadense to G. hirsutum because of hybrid breakdown in offspring of interspecific crosses. In order to solve this problem, backcross inbred lines (BIL) have been developed and used for genetic and molecular analysis. The main objective of this study was to identify differentially expressed genes in developing fibers at 10 days post-anthesis between two groups of BIL lines with contrasting micronaire readings using Affymetrix cotton microarray. Each group contained three BIL lines. Of the 24029 transcripts, 259 (1.1%) showed significantly differential expression, including 161 up-regulated and 98 down-regulated transcripts. These genes were further analyzed using COG database and Gene Ontology. A selected set of genes was validated using RT-PCR and quantitative RT-PCR analysis.