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COMPARATIVE MICROARRAY ANALYSIS OF GENES DIFFERENTIALLY EXPRESSED DURING FIBER DEVELOPMENT OF UPLAND AND PIMA COTTON

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Abstract

A comprehensive study was initiated to determine the genes responsible for the superior fiber quality traits found in the extra-long stable (ELS) Pima variety of cultivated cotton. The cultivars selected for fiber gene expression analysis were the *Gossypium hirsutum* cultivar Acala 1517-99 and the *Gossypium barbadense* cultivar Phytogen 76. The time points at which total RNA's were extracted from ovule and fiber cells were DPA -1, 3, 5, 8, 13, 20, and 26, which represent all stages of fiber cell development including initiation, elongation, and expansion. Identification of candidate fiber quality genes was accomplished using cotton oligo (70-mer) fiber gene chips containing 12,227 genes generated from a non-redundant 7-10 DPA fiber EST library of the diploid cotton species *Gossypium arboreum* cv. AKA8401. A total of 6 cotton gene chips were utilized for each time point with 3 dye-swaps. Each of the 12,227 genes and control features are represented twice on each chips allowing for 12 replications with 6 cotton gene chips. On chip spike controls were used to normalize data among all chips for each time point. Statistical analysis of microarray data consisted of an initial feature intensity cutoff to eliminate low hybridization signals that still produce a statistically significant log-ratio. A t-test was performed on gene and control feature IDs with 12 replications to produce the initial gene lists. Intensity log ratios from 1 to -1 were considered genes that are constitutively expressed and removed from the gene list. The final gene list for each time point was generated based on an individual feature p-value of 4×10^{-6} which was calculated based a chip global p-value of 0.05 and the feature population of 12,227. Due to the enormity of data collected from this study, data processing is still in progress at the time of this writing. Currently, candidate genes are being selected from the final data sets to corroborate the microarray data. Primer design will allow for sequence comparison between Acala 1517-99 and Phytogen 76, and identification of polymorphic markers.