

**DISSECTING QUANTITATIVE VARIATION INTROGRESSED INTO FOUR DIFFERENT  
BACKGROUNDS OF UPLAND COTTON USING VARIANCE COMPONENTS ANALYSIS AND  
COMPARATIVE TRANSCRIPTOMICS**

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**Abstract**

Limited genetic diversity within the elite cotton germplasm base could be hindering the potential for significant improvement in the fiber quality of upland cotton (*Gossypium hirsutum* L.). *G. barbadense*, a closely related species with superior fiber length, strength and fineness, has been used with some success for introgressing traits into upland cotton. In prior studies, Sealand 883 (SL883) was discovered to be carrying introgressed segments from *G. barbadense* harboring several quantitative trait locus (QTL) for fiber quality traits. One QTL region in particular, located on distal region of Chromosome 25, showed a large effect on fiber length (qFL-Chr.25) in the original mapping populations. This chromosomal region was introgressed using marker-assisted selection into GA089, Acala SJ4, Paymaster HS26, and DP50 cultivar genetic backgrounds representing the four major cotton growing regions within the United States. A modest but significant effect was consistently shown with the presence of qFL-Chr.25. The near-isogenic introgression lines (NILs) harboring the QTL would serve as an important resource to further understand the inheritance of fiber length.

In 2020, we planted the parents, QTL positive, QTL negative, and QTL heterozygous lines in a randomized complete block design with three replications for each of the four backgrounds. In late 2019 and early 2020 we sequenced 60 RNA-seq libraries corresponding to Paymaster HS26 genetic background and the donor parent SL883. RNA was extracted from three biological replications of fiber samples at 7, 10, 15, and 21 days post anthesis (DPA) and sequenced using Novogene services (en.novogene.com). Two genes of interest were discovered in the QTL positive Paymaster HS26 line that could be traced to the SL883 parent line responsible for fiber length.