

## **Virus-induced gene silencing to test the function of genes that may affect cotton fiber quality**

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### Abstract

We aim to generate an agronomically preferred upland cotton plant (*Gossypium hirsutum*) that produces high-quality fiber resembling the Pima cotton (*G. barbadense*) used in the highest quality textiles. Currently, Pima cotton composes less than 5% of the worldwide supply due to its restricted growth environments and lower yield. Our group is focused on reducing upland cotton fiber diameter, which, in turn, supports better fiber fineness (mass per unit length, which is ideally lower). While Pima cotton has all narrow fibers, our lab and collaborators previously linked lower fineness in mature upland fibers to a higher proportion of narrow fibers shortly after they start elongating. We identified five differentially expressed candidate genes held in common between RNA sequencing data (comparing upland and Pima fiber at two early days of development) with a high-confidence Quantitative Trait Locus (QTL) on a D genome chromosome that was identified in a Genome-Wide Association Study (GWAS). We targeted these candidates using a *Cotton leaf crumple virus* (CLCrV)-based virus-induced gene silencing (VIGS) approach. Notably, silencing of one candidate gene, involved in epigenetic control, increased the proportion of narrow fibers compared to empty vector controls. These combined approaches present promising opportunities to improve fiber quality through cotton breeding or biotechnology, ultimately benefiting the agricultural and textile industries. We thank Cotton Inc. (Cary NC) for research support and the groups of C. Haigler (B.P. Graham; NC State) and A. Hulse-Kemp (G. Billings; USDA-ARS and NC State) for the generation of unpublished data necessary for this study.