

FROM IN-SILICO PREDICTION TO IN-VIVO VALIDATION: ISOLATING CANDIDATE GENES TO GENETICALLY ENGINEER COTTON FIBERS**Rodrigo Yelin, Sharon Ayal, Rafael Meissner, Dotan Dimet and Hagai Karchi****Evogene
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Fiber yield and quality in cotton is affected by various regulatory and biochemical pathways and thus behaves as a complex, multigenic trait. Shortage in molecular and genomic data in cotton reduces the opportunity for fiber improvement via genetic engineering techniques. Cotton fibers and other trichome cells share many developmental processes. Evogene's plant biologists designed a comparative genomics approach that utilizes data from trichome databases of cotton, Arabidopsis and tomato to identify candidate genes involved in cotton fiber development. Quantitative RT-PCR was performed to obtain an accurate expression profile of these candidates in cotton fiber at different developmental stages and other plant tissues. The expression analysis allowed the isolation of 20 previously unknown genes and the association of these genes to one of the four major stages of cotton fiber development (i.e.: initiation, elongation, cell wall thickening and maturation). In order to correlate between the function of the genes and phenotypic differences in fiber features, the expression pattern of these genes was studied in different commercial cotton lines with a wide variation of fiber characteristics. The phenotypes investigated include very good quality and high lint index (Pima types, originating from Barbadense) and different Hirsutum types: good quality and high lint index (Acala), medium lint index (Coker) and poor quality and short lint index (Tamcot). The correlation between gene expression and fiber phenotype will enable us to pinpoint specific genes that determine the main fiber characteristics between the various cotton lines.

An additional set of evidence to correlate these genes to cotton fiber morphogenesis is being established by transforming Arabidopsis with the above genes under different promoter combinations. The transgenic Arabidopsis plants will then be analyzed for modified trichome development. This type of study, presenting two parallel lines of supporting evidence will accelerate the cotton fiber gene validation process prior to the integration of candidate genes into the crop itself.