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NOVEL GENES FOR IMPROVING FIBER QUALITY VALIDATED THROUGH TOMATO SEED HAIR AS A UNIQUE MODEL SYSTEM

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Abstract

One of the major bottlenecks in the development of improved cotton via transgenic means is the long period it takes to characterize the new genes in cotton. Currently, the state of the art cotton transformation is slow; it takes around two years from day of transformation till the transformed gene is ready for first function validation in field trials. For this reason it is crucial to have access to good biological models that enable a first round of validation in a shorter time period.

We identified a novel set of 70 candidate genes for cotton fiber improvement using a unique comparative genomics-based bioinformatics approach leveraging a propriety computational platform. Cotton fibers and other trichome cells share many developmental processes. We designed a comparative genomics approach that utilizes data from trichome databases of cotton, Arabidopsis and tomato. Moreover, additional elongated tissues were compared, such as etiolating seedling and poplar xylem.

A unique tomato Micro-Tom tomato model for cotton fiber was developed in order to validate and prioritize the candidate genes overcoming the slow validation process of cotton transformation. Tomato seed hairs and cotton fibers originate from similar seed epidermal cells. This observation supported by molecular analysis suggests that the readily transformable tomato plant can provide a good model for cotton fiber gene validation. To check whether the expression of a known cotton fiber gene has an effect on tomato seed hair development, we over-expressed cotton Expansin under the regulation of the 35S promoter. Previous studies have shown that transgenic cotton lines over-expressing Expansin produce fiber of increased length (patent application US20040006794). In line with the results obtained with transgenic cotton, the average length of the tomato seed hairs of Expansin expressing transgenic plants (0.361mm) was significantly longer than that of WT (0.319mm).

Expression levels of our novel candidate genes were measured and correlated with seed hair length. As found for the Expansin gene, a clear positive correlation was found between transgene Evo104, Evo103 and Evo116 expression and seed hair length (0.493, 0.415 and 0.400 respectively). Evo104 produced tomato seed hairs significantly longer then those of Expansin.