

Identification of Key Genes in Cotton Fiber

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Twenty-eight candidate genes provided by other sub-projects were used to produce transgenic cotton plants. There were over 1000 individuals, and some of them were generation T_2 or T_3 . All plants were identified by molecular methods, and some were evaluated for fiber qualities, and included in genetics analyses. The results showed, that if the recipient line had poor fiber quality, the transgenic plant's fiber quality was improved; such as the genes ACO3 and POX improved fiber strength of the variety, CCRI 24, by about $2-3 \text{ cN} \cdot \text{tex}^{-1}$. But, if the recipient line had good fiber quality, the transgenic plants had little change in fiber quality. In other words, the genes effects were overwhelmed. At the same time, most of the negative-genes had evident effects, especially in decreasing fiber length and fiber strength. After field experiments and selections, a few plants of T_2 or T_3 with fiber strengths of more than $34 \text{ cN} \cdot \text{tex}^{-1}$ were identified. These plants were selected for further advancement in the breeding program. A molecular marker map of a *G. hirsutum* \times *G. hirsutum* population, consisted of 565 markers, is the largest *G. hirsutum* \times *G. hirsutum* map. The map is capable of chromosome associations with the new EST or genes cloned by other researchers. A new gene, which was cloned from the GZnn mutant by molecular marker location method, was transformed. Its transgenic cotton plants will be obtained this year.