Identification of Key Genes in Cotton Fiber

LI Fu-ruang

(Cotton Research Institute, Chinese Academy of Agricultural Sciences; Key Laboratory of Cotton Genetic Improvement, Ministry of Agriculture, Anyang, Henan 455000, China)

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 ΔCO3 and POX improved fiber strength of the variety, CCI 21, by about 23 cN × tex$^2$. 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 cN × tex$^1$ were identified. These plants were selected for further advancement in the breeding program. A molecular marker map of a G. hirsutum × G. hirsutum population, consisted of 565 markers, is the largest G. hirsutum × 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 GZm3 mutant by molecular marker location method, was transformed. Its transgenic cotton plants will be obtained this year.