

Genetic Linkage Analysis of the Natural Colored Fiber and Fuzzless Traits in Cotton

LI Fu-zhen¹, QIU Xin-mian¹, WANG Ju-qin¹, LU Yan-ting¹, BAO Li-sheng²

(1. Center of Crop Molecular Breeding, Institute of Crop and Nucleonic Technology Utilization, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China; 2. Technical Popularization Station of Economic Specialty, Jinhua 321017, China)

Genetic linkage relationship of the natural colored fiber and six fuzzless seed germplasms in obsolete backgrounds of *Gossypium hirsutum* (AD genome) and *G. barbadense* were analyzed in the past two years. Three lines of natural brown fiber that were controlled by single dominant genes and two lines of green fiber controlled by another single dominant gene. One line of natural brown fiber was controlled by a major dominant gene or Quantitative Trait Locus (QTLs). Genetic analysis showed the six fuzzless lines were controlled by a recessive gene, temporally named n3. Genetic linkage analysis showed that there was 45% genetic recombination between the green fiber gene and fuzzless gene, which indicated that the two genes were independent. Because of the epistasis, modification, genetic complementation relationships, and environmental effects among the different brown fiber genes, the brown lint and the fuzz, it is probably necessary to map and localize the important genes with the Recombinant Inbred Lines (RILs) population, which included the fuzzless gene and the excellent colored fiber identification techniques. The relative RIL populations are being constructed and will be mapped for these important genes of cotton fiber, and agricultural traits are being processed in our laboratory.

Key words: natural colored fiber genes; fuzzless gene; genetic linkage analysis; recombinant inbred lines