TOWARD POSITIONAL CLONING OF A MAJOR GLANDLESS GENE IN COTTON

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Abstract

Cotton (*Gossypium* spp.) is not only the leading natural fiber crop, but also an excellent source of oil and protein that are stored in its seed. Cotton breeders have an opportunity to exploit and manipulate many thousands of genes in this important field crop. We report some of our work that is related to the mapping and isolation of a major glandless gene. Regular cottonseed has a high number of dark-colored glands containing toxic gossypol which are primarily responsible for a quality disadvantage. A major co-dominant gene, Gl_2^e, was introduced from an Egyptian cotton "Bahtim 110" to Texas Marker No. 1 (TM-1). Cottons with this gene produce no glands containing gossypol. Linkage between this gene and DNA markers on chromosome 12 has been established via bulked segregants analysis (BSA) of an F_2 population derived from a cross between the TM-1 NILs (with and without Gl_2^e). The nearest marker is 1.9 cM away from the Gl_2^e gene. To isolate genes in cotton via positional cloning, high-quality libraries are needed that are comprised of bacterial artificial chromosome (BAC) clones containing large cotton DNA inserts. Recently, we have constructed such a BAC library from a Gl_2^e-BC_6 nearly isogenic line (NIL) of *G. hirsutum* acc. TM-1. The total number of BAC clones is 115,200, covering 7X haploid genome equivalents. The average size of DNA inserts is 143 Kb, with a range of 90 Kb to 210 Kb. The BAC library currently is being screened with the closest markers for the isolation of the Gl_2^e gene to engineer the glandless cottonseed, and for the development of additional DNA markers around the Gl_2^e locus from a fingerprinted contig of the positive BAC clones. Tightly linked DNA markers would lead to the eventual cloning of the Gl_2^e gene to eliminate gossypol in cottonseed, while retaining glands in other parts of the cotton plant.

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