NEW GENOMIC TOOLS FOR COTTON IMPROVEMENT

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Abstract

Cotton germplasm development has lagged behind that of other major crops including maize, soybean, and wheat. At present, less than one percent of the U.S. cotton germplasm has been exploited in the development of cotton varieties. Until now, without portable molecular markers and an integrated physical/genetic map, there has not been an efficient way to find useful genes from this genebank. To leverage cotton genomic resources and tools, we have constructed six complementary libraries of approximately 280,000 bacterial artificial chromosome (BAC) clones from the cotton genome (*G. hirsutum* acc. TM-1, the genetic standard of Upland cottons and its glandless isoline ESP). These libraries cover 18 cotton genome equivalents, and the average size of DNA inserts in the cotton is about 150 kb, the largest ever reported in cotton. These clones contains most full-length gene sequences and DNA marker loci for application to cotton improvement. New SSR markers are isolated from the positive TM-1 BAC clones to facilitate integrative genetic and physical mapping of the cotton genome. One of the six libraries is the only transformation-ready cotton library currently available in the world, and it facilitates direct transfer of cotton genes via *Agrobacterium*. A preliminary survey indicates that about 5-10% of *Arabidopsis* ESTs would be conservative and readily applicable in cotton. Detailed analysis of this portion of *Arabidopsis* genes in relation to cotton genes will greatly facilitate cotton improvement programs. An integrative physical/genetic map, consisting of the large number of genes and markers on the BAC contigs, will provide new tools to open up cotton genetic resources for higher yield, stronger and longer fiber, seed quality, and stress tolerance.

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