

INTEGRATED GENOME MAPPING FOR COTTON IMPROVEMENT

Russell J. Kohel, John Z. Yu, Jianmin Dong, and Nicole L. Steele

USDA-ARS

College Station, TX

Hongbin Zhang and Zhanyou Xu

Texas A&M Univ

College Station, TX

Abstract

Integrated genome maps have been developed or initiated in other major crops such as maize, soybean, and wheat, providing an essential infrastructure to rapidly advance current genomic research in these species. A whole-genome, integrated physical and genetic map for cultivated allotetraploid cottons is much needed to streamline the identification and transfer of beneficial genes and QTLs for cotton improvement. We are now working toward such a map by use of three complementary BAC and BIBAC libraries that were constructed from TM-1, the genetic standard of Upland cottons (*Gossypium hirsutum*). A permanent mapping population of 191 recombinant inbred lines (RIL-F₇) was developed from a cross between TM-1 and 3-79, the genetic standard line for *G. barbadense*. The feasibility, strategies, and approaches to developing the map of the AD cotton genome have been tested. Integrative DNA markers (mainly SSRs) have been developed from TM-1 BAC clones for mapping of the cotton chromosomes. Approximately 1,000 markers from the existing cotton genetic map are being physically located to TM-1 BAC contigs and about 1,000 new markers, isolated from the contigs, are being genetically mapped by use of the RILs. Fingerprints from more than 42,000 clones of TM-1 BAC/BIBAC libraries have been produced with an improved automated procedure that uses a robotic workstation, capillary sequencers, and advanced computer programs, and the fingerprints were assembled into contigs. The initial results showed that the cotton physical contigs representing respective subgenomic origins (A vs. D) can be readily assembled, sorted, and anchored to the cotton genetic map, thus making it feasible to develop a robust genome-wide map that integrates physical and genetic mapping information for the cultivated AD cotton. In addition, we are also developing databases and bioinformatics facilities to effectively manipulate, disseminate, access, and use abundant information that is being generated from the cotton integrated genome mapping. The integrated cotton genomic information and resources will significantly benefit the cotton research community.