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# INTEGRATED GENETIC, PHYSICAL, AND COMPARATIVE MAPPING OF THE COTTON GENOME

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## Abstract

Integrated genetic, physical, and comparative maps of the cotton genome are important to cotton functional genomics and other advanced biological studies. We are using the BAC libraries, developed from an Upland cotton genetic standard TM-1, to construct physical contigs and isolate SSR markers that are genetically mapped with an RIL population of TM-1 x 3-79 cross. Many fiber genes or EST sequences are physically located in the integrated map through the 2-D Overgo hybridization. Understanding where these genes are located in chromosomes and how they interact is crucial for improving fiber yield and quality. In addition to cotton EST sequences, TM-1 BAC ends are sequenced for comparative studies between cotton and Arabidopsis, of which comparative mapping with some conserved ortholog genes uncovers syntenic relationships and facilitates cross-utilization of genetic resources and tools of both species. Development of such an integrated cotton genome map would lead to many applications including eventual sequencing of the cotton genome and ultimately to improvement of the world's most important fiber crop.