

A CYTOGENETIC SNAPSHOT OF THE COTTON GENOME – 2.5 BILLION BASE PAIRS OF DNA

B. Liu

A. M. Hulse-Kemp

D. M. Stelly

Texas A&M AgriLife Research

College Station, TX

Abstract

The ongoing whole-genome sequencing project on upland cotton *Gossypium hirsutum* is using BAC libraries constructed with DNA from this tetraploid AD-genome species. BACs selected from the sequencing libraries were physically localized to pachytene bivalents by using fluorescence *in situ* hybridization techniques, thus cytogenetic maps have been constructed. The integration of cyto-genomic, physical maps and linkage maps offers a unique perspective, because it combines multiple genetic interests, such as gene and marker locations, recombination rates, genomic organization and structure, large-scale comparisons between subgenomes, et cetera.