

**DETERMINATION OF CHROMOSOME EFFECTS FOR COTTON CULTIVARS  
CROSSED WITH CHROMOSOME SUBSTITUTION LINES AND TM-1**

**Jixiang Wu**

**Mississippi State University**

**Mississippi State, MS**

**Johnie N. Jenkins**

**USDA-ARS-GAPARU**

**Mississippi State, MS**

**Jack C. McCarty**

**USDA-ARS**

**Mississippi State, MS**

**Sukumar Saha**

**USDA-ARS, Crop Science Research Laboratory**

**Mississippi State, MS**

**Ted P. Wallace**

**Mississippi State Univ.**

**Mississippi State, MS**

**Abstract**

Determination of desirable chromosome effects associated with traits of interest in inbred lines or crosses will provide useful genetic information for crop improvement. In this study, using recently developed genetic model, we analyzed the data set including 13 cotton chromosome substitution (CS-B) lines and their recurrent parent TM-1, five commercial cultivars, and their 70 F<sub>2</sub> hybrids. The chromosome additive and dominance variance components for eight agronomic and fiber traits regarding 13 chromosomes or chromosome arms among these parents and their crosses were estimated. Chromosome additive effects among these parents regarding a specific chromosome or chromosome arm for a quantitative trait with a large contribution to the phenotypic variance (>20%) were predicted as well. Results showed that chromosome 16 in CS-B16 had additive effects associated with decreased seed cotton yield and lint yield while chromosome 16 in FM966 had additive effects associated with increased seed cotton yield and lint yield. Chromosome 25 in CS-B25 was associated with negative additive effect for micronaire, positive additive effects for 2.5% fiber span length and fiber strength. Chromosome 25 of FM966 had desirable additive effects for fiber length and strength. The results from this study should provide valuable genetic information for pure lines development with several improved traits such as yield and fiber strength.