

**GENETIC SIMILARITY AMONG IMPROVED COTTON  
CULTIVARS BASED ON SSR MARKERS AND THEIR  
RELATIONSHIP WITH F<sub>2</sub> HYBRID PERFORMANCE  
IN AGRONOMIC AND FIBER TRAITS**

**S. Basu and C. Cheatham**

**Mississippi State University**

**Mississippi State, MS**

**D. B. Shoemaker**

**Delta and Pine Land Company**

**Scott, MS**

**S. Saha, J. N. Jenkins, J. C. McCarty, Jr. and O. A. Gutiérrez**

**USDA-ARS-CSRL**

**Mississippi State, MS**

**Abstract**

Knowledge of genetic diversity and relationships among breeding materials has a significant impact on crop improvement. Molecular markers are increasingly being used to determine the genetic distance between individuals. Association between parental divergence and progeny performance has been detected in other crops. However, in cotton (*Gossypium hirsutum* L.) such information is limited. The objectives of this study were to estimate genetic diversity based on SSR markers among selected improved upland cotton cultivars and to investigate any association between the genetic distance based on SSR markers and agronomic performance of the F<sub>2</sub> progenies of their crosses. Nine cultivars from five private cotton-breeding programs and two exotic germplasms were genotyped using 90 SSR primer pairs providing 139 polymorphic markers. Genetic similarity (*GS*) between lines was calculated using the Nei and Li's formula with the PAUP\* software. *GS* among all lines including two exotic germplasms ranged from 0.66 to 0.94 but among the commercial cultivars varied from 0.78 to 0.94 indicating a narrow genetic base in improved cultivars. Correlations between four groups of F<sub>2</sub> hybrids and *GS* values were calculated under four different categories based on genetic and geographic origin of the materials as follows: 1) Cultivars of U.S. commercial companies, 2) Cultivars of Australian commercial companies, 3) U.S. commercial varieties and two exotic germplasms and 4) Australian commercial varieties and two exotic germplasms. Significant correlations were observed between many agronomic traits and F<sub>2</sub> hybrids groups. Lint percentage and boll size were significantly correlated with the genetic similarity. Results indicated that the correlation directions between genetic distance and agronomic traits in the F<sub>2</sub> hybrids would depend on the genetic background. Even though SSR markers explained only a small amount of the variation among F<sub>2</sub> populations, these results revealed that SSR markers can be a useful tool in the genetic analysis of breeding populations. Additional SSR markers would improve the merit of this approach.