

## **GENETIC RELATIONSHIPS AMONG U.S. UPLAND COTTON**

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### **Abstract**

Genetic diversity can be defined by the allelic variation of genes. It is the basis upon which breeders can select traits to improve cotton. It is also useful in a macro-environmental sense to buffer the crop against the physical environment and pests. Lack of genetic diversity as a reason for a perceived cotton yield plateau seen since about 1987-88 has also been a topic of conversation in the hallways of the Beltwide Cotton Conferences and at other informal gatherings of cotton researchers. The genetic diversity in this study of 330 historically important U.S. Upland cotton cultivars and germplasm lines using 261 codominant RFLP markers was 0.075. This is very low compared to other major crop species like wheat, soybeans, corn, and sorghum. This measure of cotton genetic diversity is consistent with a Principle Coordinate Analysis (PCoA) with four interspecific outgroup species of *G. barbadense* and *G. darwinii* and one interspecific outgroup of *G. hirsutum* race palmeri. The Upland cotton was separated into groups based on breeding program and production location. The three breeding programs, MAR, Pee Dee, and Acala, were clustered by PCoA with very little overlap. This may be an indication of a natural biological substructure or of differential selection pressure by the environment or the breeder. Adding a group of commercial stripper type cultivars to the PCoA chart placed this cluster on top of the Acala cluster with some spread beyond that to the MAR group. A small group of cultivars from the Mississippi Delta region clustered away and past the Pee Dee cluster. A group of cultivars considered extra-long staple (ELS) type clustered on top of the Pee Dee and the MidSouth cluster. Both of the overlapping cluster groups can be explained based on the shared pedigrees between them. This also gives a close genetic source for traits between the Acala and the stripper type as well as between the ELS and the Pee Dee with the MidSouth cultivars as illustrated by the differences of fiber quality in each of these clusters.