

**GENETIC DIVERSITY IN DIPLOID AND
TETRAPLOID COTTON SPECIES EXAMINED BY
AMPLIFIED FRAGMENT LENGTH
POLYMORPHISM (AFLP)**

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Abstract

To determine inter- and intraspecific genetic relationships among and within a diverse collection of 29 genotypes representing five *Gossypium* species, 16 AFLP primer combinations were tested for selective amplification of DNA fragments. *Gossypium* accessions studied were three diploid species; *G. herbaceum* (A1), *G. arboreum* (A2) and *G. raimondii* (D5), and 26 (AD) allotetraploid cultivars (*G. barbadense* and *G. hirsutum*). A total of 1180 major AFLP bands were observed; 368 of these (31%) exhibited polymorphism within the collection. The number of polymorphic bands generated by individual primer pairs ranged from 9 (E-AAC/M-CAC) to 33 (E-AAG/M-CTG and E-AGG/M-CTG). Genetic similarities among all genotypes ranged from 0.21 (between *G. arboreum* and *G. raimondii*) to 0.72 (between *G. barbadense* and *G. hirsutum*), with a 0.54 mean similarity. The mean genetic similarity within our geographically and historically diverse set of *G. barbadense* accessions (0.89) was similar to our *G. hirsutum* collection, which consisted of Upland cultivars (0.86). The level of similarity between the (A) and (D) diploid species were extremely low (0.21 to 0.22) indicating that AFLP is a reliable source of markers for phenetic studies of cultivated diploid and allotetraploid *Gossypium* species.

By UPGMA clustering, the taxa fell into four well-supported clusters that are consistent with the cytogenetic genome groups and traditional taxonomic species: 17 cultivars fell into a *G. barbadense* cluster, eight cultivars into a *G. hirsutum* cluster, three taxa into an 'A genome' cluster, and one taxa, *G. raimondii* comprised the (D) genome cluster. Among the limited taxa included in our study, *G. barbadense* has a greater diversity, or broader 'genetic base' than *G. hirsutum*. In some cases, well-supported phylogenetic relationships, as well as evidence of genetic reticulation, could also be inferred. UPGMA trees and principle coordinate analysis based on genetic similarity matrices were used to identify genetically distinct cultivars that are potentially important sources of germplasm for cotton improvement, particularly of fiber quality traits.