Phylogenetic Analysis of *Gossypium hirsutum* Spp. Collected from the Caribbean Basin and Florida

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**RESEARCH PROBLEM**

The evolution of cotton is a complex story that is continuing in many places of the world even today. Its study helps identify primitive accessions that may harbor unique traits for improvement of yield and reduction of vulnerability to pests. The idea behind this project came from a 1985 report written by Dr. A. Edward Percival entitled “Collection of *Gossypium* spp. obtained by exploration on several Caribbean Islands” (Percival, 1985). A common characteristic among some of those species was reported to be their brown lint. The finding of natural populations of brown-lint cotton varieties along the west coast of Florida in 2003 by James McD. Stewart generated the hypothesis that there may be a connection between the Florida and Caribbean wild accessions. An additional criterion for the selection of these accessions was their proximity to the sea, which may have facilitated their dispersal to the area.

**BACKGROUND INFORMATION**

*Gossypium hirsutum* L. (upland cotton) has a polyploid genome as a result of the union of ancestral diploid genomes that currently are restricted to different hemispheres of the world. The New World tetraploid cottons are allopolyploids and contain one genome of the Old World diploids (the A genome) and one of those found in New World diploids (the D genome) (Wendel, 1989). This fusion of genomes from very distant regions of the world demonstrates the complexity of cotton evolution. Also, most of the wild allopolyploid species occur in coastal habitats (Brubaker and Wendel, 1994) which suggests a means for rapid dispersal coupled with salt-tolerant seeds. Because of this, a close genetic relationship between the Florida accessions and some of the Island accessions was expected, but with some genetic diversity among them. The objectives of this study were to identify the degree of genetic similarity among the accessions, to

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establish the evolutionary relationship of these naturally occurring plants, and to address
the theory that long-distance dispersal can lead to the evolution of endemics.

**RESEARCH DESCRIPTION**

The study employed forty-six *G. hirsutum* L. (Malvaceae) accessions, including five designated as race yucatanense, eleven accessions from Florida, and one *G. tomentosum* (AD3) of Hawaiian origin as a reference for wild genotypes, and three plants from each accession were examined. Their DNA was extracted by a cetyltrimethylammonium bromide (cTAB) method (Zhang and Stewart, 2000), and the extracted DNA quality was estimated by the Å260/Å280 ratio. Six Amplified Fragment Length Polymorphism (AFLP) selective primer sets were used to assess the genetic diversity among the accessions. DNA fragments were amplified by polymerase chain reaction and separated by polyacrylamide gel electrophoresis. Each genotype was scored for presence (1) and absence (0) of each fragment. A heuristic search was performed with PAUP* (4b2) software using Parsimony, an unrooted dendrogram was generated and one thousand Bootstrap operations were performed on the dataset to aid in identification of the best phylogenetic tree.

**RESULTS AND DISCUSSION**

The six primer combinations yielded 243 usable DNA fragments across all accessions. Of these, 77 (32%) were polymorphic (absent in at least one genotype). The least genetically similar accession was from Cuba with only 57 bands in common with the Florida accessions, and the most genetically similar island accession was from Puerto Rico with 81 bands in common. The Florida accessions shared 142 bands while all accessions shared 52 bands. The outgroup species *G. tomentosum* from Maui, Hawaii, differed from the Florida cottons by at least 13 markers, but was more closely related to the Florida accessions than to most of the other cotton accessions examined. The *G. hirsutum* race yucatanense differed from the Florida accessions by at least 48 polymorphic markers but from the Caribbean accessions by at least 58 markers. Since Mexico is the center of diversity for the D-genome diploids and the wild accession of race yucatanense, all of which have brown fiber, it can be suggested that brown lint represents a primitive character, and that the wild cotton of Florida was established from a wild progenitor and did not result from escaped or feral cultivated cotton. The clustering of most of the Florida accessions in the dendogram indicates the establishment of an endemic population of wild cotton on the Florida peninsula.

**PRACTICAL APPLICATION**

The center of origin of the wild crop progenitors contains the greatest genetic diversity (Frankel, 1998). Thus, establishing the origin and the genetic diversity of the wild accessions from the Florida peninsula and the Caribbean basin will increase the probability of finding unique genotypes. The usefulness of an accession is proportional
to the number of unique genes in that accession. Further study of these exotic and diverse germplasm resources increases the possibility of detecting useful alleles, if transferred into commercial cotton cultivars. At the very least the diversity will improve genetic buffering against environmental stress and, thereby, aid in yield increase.

**LITERATURE CITED**


