

Title: Germplasm evaluation of cotton accessions from the U.S. Cotton Germplasm Collection, USDA-ARS (Landraces of Mexico)

Part of project P36 (Project 36 is located field 17 (P67)).

Mauricio Ulloa and James Frelichowski

USDA-ARS, WICS Res. Unit, Cotton Enhancement Program.

Project Cooperators:

Universities and USDA-ARS Geneticists/ Breeders.

The *Gossypium hirsutum* gene pool from Mexico encompasses a wide range of habitats and is one of the primary sources for improvement of most of the Acala and Upland cotton growing in the world today. Despite the existence of large collections of landraces of *G. hirsutum*, they are poorly evaluated and difficult to characterize for their value in the collection and potential for cotton improvement. Seed of 439 accessions of landraces, collected from 18 states throughout Mexico from a period of 1946-1997, were planted. These landraces will also be evaluated in a winter nursery in Mexico to ensure accurate evaluations of morphological characteristics (i.e. flowering & fruiting) if funding is available. Molecular markers are being developed at the USDA-ARS, Cotton Enhancement program molecular laboratory from DNA sequences information of cotton that are polymorphic among genotypes of *G. hirsutum*. DNA markers are being developed in cotton for a range of basic and applied scientific objectives in plant improvement. Plant breeders find them useful as a selection tool in monitoring alien genome introgression in cotton breeding programs. Variation in the cotton collections detected by both methods (morphological and molecular data) will be compared to see the value of morphological and genetic markers to characterize the collections, and for possible associations of markers with genes for cotton traits.