## GENETIC DIVERSITY IN THE U.S. COTTON GERMPLASM COLLECTION AS REVEALED BY SSR MARKERS **Richard Percv** USDA-ARS, Southern Plains Agricultural Research Center **College Station**, TX David Fang **USDA-ARS, Southern Regional Research Center** New Orleans, LA Lori Hinze John Z. Yu J. Frelichowski **USDA-ARS, Southern Plains Agricultural Research Center College Station, TX Brian Scheffler USDA-ARS** Stoneville, MS **Michael Gore** USDA-ARS, Arid Lands Agricultural Research Center Maricopa, AZ

## <u>Abstract</u>

A comprehensive knowledge of the genetic diversity within the U.S. *Gossypium* Germplasm Collection is necessary to achieve its most effective utilization and the greatest efficiency in its maintenance. To improve our knowledge of the collection's diversity, 2,256 accessions representing 31 species of *Gossypium*, or approximately a quarter of the collection, were genotyped using a core SSR marker set of 105 markers. Labeled primers for the SSRs were created using FAM, HEX, or NED labels, creating 35 primer sets for multiplex PCR amplification. Good amplification occurred for 104 of the 105 markers. A total of 1702 alleles were observed across all markers, for an average of 16.4 alleles per SSR primer. A PIC value of 0.71 was obtained for the set of 2,256 accessions. Within *G. hirsutum*, an average of 7.5 alleles per marker. This was reflected in PIC values of 0.65 in race stocks and 0.46 in cultivars of *G. hirsutum*. Lower PIC values were observed in *G. barbadense*, with cultivars producing a value of 0.47 and commensal cottons producing a value of 0.52. PIC values for wild diploid species ranged from 0.62 in the D genome to 0.06 in the F genome. There appeared to be large differences in detectable genetic variation within species of genomes. Sixty one percent of the SSRs were polymorphic within *G. aridum* of the D genome, whereas only six percent of the SSR markers were polymorphic in *G. raimondii*. Data analyses are still in the initial stages and continue.