## MOLECULAR DIVERSITY AMONG G. HIRSUTUM ACCESSIONS IN THE GOSSYPIUM DIVERSITY **REFERENCE SET** Lori Hinze USDA-ARS, Southern Plains Agricultural Research Center **College Station**. TX David Fang **USDA-ARS, Southern Regional Research Center** New Orleans, LA **Michael Gore** USDA-ARS, Arid Lands Agricultural Research Center Maricopa, AZ **Brian Scheffler** USDA-ARS, Jamie Whitten Delta States Research Center Stoneville, MS John Yu James Frelichowski **Richard Percy USDA-ARS, Southern Plains Agricultural Research Center College Station**, TX

## <u>Abstract</u>

A core set of 105 SSR markers were employed to develop accession profiles and analyze genetic relationships among 2,254 plant introductions of cotton (Gossypium spp.) including wild species, landraces, and adapted cultivars from around the world as represented in the US National Cotton Germplasm Collection. This group of plant introductions (accessions) is collectively known as the Gossypium Diversity Reference Set (GDRS). 1,540 G. hirsutum accessions are included in the GDRS. NTSYS software was used to generate a Jaccard similarity matrix of the GDRS accessions which was double-centered and used to calculate eigenvectors based on Principal Coordinate Analyses (PCoA). PCoA plots were used to show the molecular relationships among and within genomes, species, types of G. hirsutum, races of wild type G. hirsutum, and geographic distribution of races. The first two principal coordinate axes explain ~27% of molecular variation among accessions. When comparing Gossypium genomes, two distinct clusters can be discerned among AD genome accessions, a third distinct cluster composed of A genome accessions can be detected, and accessions of the remaining diploid genomes form a fourth intermixed but distinct cluster. When making comparisons among the AD tetraploid genome species, G. hirsutum and G. barbadense accessions form distinct clusters, while G. tomentosum and G. mustelinum accessions cluster together and remain distinct from G. hirsutum and G. barbadense accessions. Within the G. hirsutum and G. barbadense clusters are putative misclassified or introgressed accessions requiring confirmation. Wild type G. hirsutum accessions form a long loose cluster, assumed to be attributable to significant diversity, while cultivated accessions form a smaller, tighter group at the lower extreme of the G. hirsutum cluster. The majority of G. hirsutum wild types are "not classified" into races, and those that are classified do not form distinct clusters based on race. Following assignment of geographic origins to wild type accessions, there appear to be some correspondences between race and geographic origin. The structure of genetic diversity revealed in the PCoA tends to support the geographic distribution of races, but it does not show races to be distinct discrete entities.