MOLECULAR AND GENETIC DIVERSITY OF CULTIVARS IN THE U.S. COTTON GERMPLASM COLLECTION Lori Hinze Richard Percy USDA-ARS College Station, TX Jane Dever Texas Agrilife Research Lubbock, TX

<u>Abstract</u>

Although a large range of untapped genetic diversity exists within the U.S. Cotton Germplasm Collection, much of this diversity has not been characterized and its sources identified. Our objective in this study was to characterize a subset of cultivated Gossypium hirsutum germplasm within the collection using phenotypic and molecular tools, with the goals of determining the level of genetic variation present in the cultivar subset and identifying useful variation. Sixty G. hirsutum cultivars from five geographic regions (12 each from northern Africa, southern Africa, China, U.S. obsolete, and U.S. recent) along with two controls (G. hirsutum TM-1 and G. barbadense 3-79) were grown in two environments with four replications to evaluate agronomic and fiber traits. All cultivars were also genotyped with SSR markers to assess molecular diversity. There were significant differences (P=0.001) among cultivar groups for the agronomic traits of yield, lint percent, lint index, and seed index. Significant cultivar-bylocation interaction occurred for lint yield. Cultivars within each group varied widely for the agronomic traits, as observed in the range of minimum and maximum values obtained. Differences (P=0.001) among groups and cultivars occurred for micronaire, upper half mean length, strength, and short fiber content as measured by HVI. Several multivariate measures were used to analyze molecular diversity. Genetic distances indicate that these five groups are closely related, with the largest genetic distances occurring between North African and South African cultivars. The range of values for agronomic and fiber traits along with molecular diversity measures indicate a large pool of genetic diversity with the potential to provide alleles useful in developing new cultivars.