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GENETIC DIVERSITY OF U.S. COTTON CULTIVARS USING MICROSATELLITE MARKERS Priyanka Tyagi Vasu Kuraparthy Daryl Bowman NC State University Raleigh, NC Michael Gore USDA-ARS Maricopa, AZ

<u>Abstract</u>

Establishing genetic diversity is essential for the germplasm enhancement and genomic analysis in crop improvement programs. We characterized genetic relationships of 384 upland cotton (*Gossypium hirsutum* L.) cultivars, representing breeding programs across the U.S. cotton belt. Genotyping was done with 65 SSR markers uniformly distributed across the genome using high-resolution capillary-based SSR genotyping. The 65 SSR markers amplified a total of 280 alleles with an average of 4.3 alleles per locus. The average Polymorphic Information Content (PIC) value of microsatellite markers was 0.19 with a range of 0.00 to 0.72. Phylogenetic analysis revealed significant diversity among the cultivars. This information is useful for selection of cultivars which can represent the most of the cotton diversity.