

**CHROMOSOMAL ASSIGNMENT OF BAC-DERIVED SSR MARKERS IN COTTON (GOSSYPIMUM
HIRSUTUM L.)****Yufang Guo****Plant and Soil Sciences department****Mississippi State, MS****Sukumar Saha and Johnie N. Jenkins****USDA-ARS, Crop Science Research Laboratory****Mississippi State, MS****John Z. Yu and R. J. Kohel****USDA-ARS, Southern Plain Research Center, Crop Germplasm Research Unit****College Station, TX****David M. Stelly****Texas A&M University****College Station, TX****Abstract**

Integrated physical and genetic maps of the cotton genome will expedite genetic improvement, and facilitates positional candidate gene cloning, comparative genomics, and the organization of genome sequencing at the chromosome level. The overall objective of this research was to identify chromosomal locations of BAC-derived SSR markers in cotton. One hundred and ninety-two BAC-derived SSR primer pairs were screened against three tetraploid cotton species, *Gossypium hirsutum* (TM-1, DP61, T-701), *G. barbadense* (3-79), *G. tomentosum* (CMD-11) and two diploid species of A₂ (*G. arboreum*) line (CMD-9) and D₅ (*G. raimondii*) (CMD-10). Interspecific aneuploid chromosome substitution lines were used to identify chromosomal locations of these SSR markers. Overall, 48% of these BAC-derived SSR primers were polymorphic at the interspecific level. 40% are polymorphic between TM-1 and 3-79, 31% are polymorphic between TM-1 and *G. tomentosum*. 21% common primer pairs were polymorphic between TM-1, 3-79 and *G. tomentosum*.