

**MARKER ASSISTED IDENTIFICATION OF *GOSSYPIMUM TOMENTOSUM*  
CHROMOSOME SUBSTITUTION LINES OF *GOSSYPIMUM HIRSUTUM* L.**

**O.A. Gutiérrez, S. Saha, J.N. Jenkins and J.C. McCarty, Jr.**

**USDA-ARS-CSRL**

**Mississippi State, MS**

**Dwaine A. Raska and D. Stelly**

**Department of Soil & Crop Sciences**

**Texas A & M University**

**College Station, TX**

**Abstract**

The development of interspecific aneuploid chromosome substitution lines in Upland cotton (*Gossypium hirsutum* L.) of *G. tomentosum* Nuttall ex Seemann, one of the most heat resistant species of the genus and the donor of the nectariless trait, have been initiated. Attempts to incorporate genes from other *Gossypium* species into Upland cotton have generally not achieved stable introgression. Associated with these attempts have been poor agronomic qualities of the progeny, distorted segregation, sterility, and limited recombination due to incompatibility between the genomes. An alternative approach to introgress *G. tomentosum* genes into an Upland background would be to rely on chromosome substitution lines. The objectives of this study were to develop and identify chromosome substitution lines of *G. tomentosum* using Simple Sequence Repeat (SSR) markers. Monosomic for *G. tomentosum* chromosomes 1, 2, 3, 4, 9, 16, 18, and 25 as well as monotelodisomic for chromosome arms Te1sh, Te3sh, Te4Lo, Te6sh, Te10sh, Te14Lo, Te15Lo, Te22sh, and Te25sh were developed for assignment of SSR markers. The genetic stocks were fingerprinted using SSR primer pairs that were previously assigned to these specific chromosomes. In addition, the genetic marker TM-1 (*G. hirsutum* L.) and Pima 3-79 (*G. barbadense* L.) and were used as references. Results indicated that SSR markers were able to identify chromosome substitution lines for the chromosomes H2, Te4Lo, H9, H18, and H25 based on deletion analysis.