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# AN INTRASPECIFIC SSR LINKAGE MAP OF COTTON

**Osman A. Gutierrez**
**USDA-ARS**
**Mississippi State, MS**
**Jixiang Wu**
**Mississippi State University, Dept. of Plant & Soil Sciences**
**Mississippi State, MS**
**Johnie N. Jenkins and Jack C. McCarty**
**USDA-ARS**
**Mississippi State, MS**
**Dwaine A. Raska and David M. Stelly**
**Texas A&M University**
**College Station, TX**

Most of the linkage maps that have been assembled in cotton are of interspecific nature, i.e. Upland cotton X Pima cotton (*Gossypium hirsutum* L. x *Gossypium barbadense* L.). Low polymorphism within the Upland cotton genotypes and insufficient numbers of Simple Sequence Repeat (SSR) markers has been responsible for this situation. We have constructed an intraspecific *Gossypium hirsutum* L. linkage map using 188 recombinant inbred lines (RIL) that were developed by single hill (bulked progeny row) procedure from the cross of HS-46 X MARCABUCAG8US-1-88. The 188 RIL were genotyped with 943 SSR markers (BNL, CIR, JESPR and CM). A total of 211 markers (22%) were found to be polymorphic between the parents. In addition, chromosomal locations of the polymorphic SSR markers were assigned using aneuploid lines. The number of established linkage groups was higher than the chromosome number but most of them matched the previously assigned chromosomal locations. The resulting intraspecific map will provide a valuable resource for the cotton research community.