

**ADDITION OF NEW MARKERS
TO THE TRISPECIFIC COTTON MAP**

M. Altaf Khan and G. O. Myers

Louisiana State University

Baton Rouge, LA

J. McD. Stewart and J. Zhang

University of Arkansas

Fayetteville, AR

R. G. Cantrell

New Mexico State University

Las Cruces, NM

Abstract

SSRs are new marker types recently added to the existing trispecific linkage map of *Gossypium*. At present this map comprises 332 AFLP, 91 RAPD, 12 SSR and 3 morphological markers. Of the 12 SSRs, 7 markers are specific to 5 chromosomes of the cotton genome (chromosomes 2-S, 5-L, 6-L, 9-L and 10-L), and 4 SSRs were found linked with existing molecular markers on 3 different linkage groups. Initially the collection of polymorphic markers comprised 43 linkage groups and a set of markers that were unlinked with any of the anchored linkage groups. When grouped among themselves, these markers formed 8 more groups and the number of linkage groups increased from 43 to 51 and covered a total distance of 6663 cM. We used only the anchored 43 linkage groups for QTL analyses of seven agronomic traits scored from the same trispecific F₂ population. A total of 67 QTLs were detected for these agronomic traits. They consisted of 10 QTLs for leaf main lobe length, 9 for leaf main lobe width, 12 for length of leaf second lobe, 14 for sinus depth, 11 for bract teeth number, 6 for internode length, and 5 for petal length. All QTL analyses were performed by the MapMaker program using a LOD threshold of 2.0 or above. Number of QTLs may increase with the addition of more markers.