

**INTEGRATED MOLECULAR MAP BASED ON A
TRISPECIFIC F₂ POPULATION OF COTTON**

M. Altaf Khan, Jinfa Zhang and James McD. Stewart

Department of Agronomy

University of Arkansas

Fayetteville, AR

Roy G. Cantrell

Department of Agronomy and Horticulture

New Mexico State University

Las Cruces, NM

Abstract

A trispecific F₂ mapping population was developed by crossing *G. arboreum* (A₂) cv. Nanking with *G. trilobum* (D₈). The diploid hybrid was treated with colchicine to produce a synthetic allotetraploid 2(A₂D₈). This hybrid was crossed with *G. hirsutum* (AD₁) cv. T-586, and the resulting hybrid was self-pollinated to obtain the segregating F₂ population. A total of 426 markers (332 AFLPs, 91 RAPDs and 3 morphological markers) were scored among 90 F₂ plants. Fifty-seven percent of the markers showed distorted segregation perhaps due to chromosomal rearrangements, divergence of the three genome species and areas of low recombination among the genomes. A linkage map was constructed comprising 51 linkage groups that spanned over 6663 cM of the cotton genome with an average distance of 18 cM between markers. Out of 51, eighteen linkage groups possessed 2 markers each and 13% of the markers remained unlinked. Fourteen linkage groups were assigned to the A subgenome that covered a map distance of 2270 cM and thirty groups assigned to the D subgenome covered 4066 cM map units. Seven linkage groups could not be assigned to either subgenome. We observed higher levels of recombination and polymorphism in the D genome compared to the A genome. It was suggested that the diploid D genome is more divergent from its allopolyploid D_h subgenome than A is from the A_h subgenome. Three morphological markers, pilose (T₁), red plant color (R₁) and naked seed (N₁), that are located on chromosomes 6, 16 and 12 of the cotton classical genetic map, were found to be linked with molecular markers on three different linkage groups. The results are discussed in relation to published information on genomic maps of *Gossypium* and other species with specific reference to the genomic organization of cotton.