

**ESTs CONTAINING SSRs: USEFUL MARKERS TO
STUDY GENETIC DIVERSITY IN COTTON**

Samina N. Qureshi

Dept. of Plant & Soil Sciences

Mississippi State University

Mississippi State, MS

S. Saha and J.N. Jenkins

USDA, ARS

Crop Science Research Laboratory

Mississippi State, MS

R.V. Kantety

Dept. of Plant Breeding

Cornell University

Ithaca, NY

D.M. Stelly

Dept. of Soil & Crop Sci.

Texas A&M University

College Station, TX

Abstract

ESTs (expressed sequence tags) containing SSRs (simple sequence repeats) represent a new class of genetic markers for cotton (*Gossypium sp.*). One hundred and thirty-three ESTs containing SSR (SSR-ESTs) were identified by analyzing 36,000 sequences from publicly available cotton database using bioinformatic tools. A diversity of di-, tri- and tetra nucleotide SSR motifs (34%, 54% and 12% respectively) were present among these SSR-ESTs. Primers were designed for 80 of these SSR-ESTs and were tested on ten different diverse cotton lines, DP-90 (*Gossypium hirsutum*), ACALA MEXA (*G. hirsutum*), ST-472 (*G. hirsutum*), PIMA S6 (*G. barbadense*), TM1 (*G. hirsutum*-AD₁), PIMA 3-79 (*G. barbadense*) and wild accession of *G. arboreum* (A₂) and *G. raimondii* (D₅), to study genetic diversity. An average of 3-4 amplicons were obtained per primer pair. The intraspecific (*G. hirsutum*) and interspecific polymorphism rate among the cotton cultivars was very high. Polymorphism was widely distributed among the various repeat types and structures (e.g., pure, imperfect and compound repeats) without any specific patterns.

To explore the potential utility of the SSR-EST loci for comparative mapping, these sequences were compared using BLAST search against different plant species with minimum E-value<-10. Blast results showed that about 74% of SSR-ESTs were from fiber related genes in *G.hirsutum* and 26% were matching with sequences from other tissues, e.g. Cotton boll abscission, cotton seed catalase, etc. Fifty five percent of these SSR-EST sequences matched with *G. arboreum*. About 33% of the sequences were syntenic to the *Arabidopsis thaliana*. We also identified chromosomal locations of some of these SSR-EST markers by using chromosomal substitution lines.

Our results showed that EST-derived SSRs in cotton are useful, as they are polymorphic and highly transferable across species. This will be the first report on such kind of functional gene markers in cotton that can be utilized for comparative mapping.