DISCOVERY OF SINGLE NUCLEOTIDE POLYMORPHISMS IN SELECTED FIBER GENES IN CULTIVATED TETRAPLOID COTTON

Yingzhi Lu, J. Curtiss and Jinfa Zhang
Las Cruces, NM
Richard Percy
USDA-ARS
Maricopa, AZ
R. G. Cantrell
Cotton Incorporated
Cary, NC

Abstract

Single nucleotide polymorphisms (SNPs) are useful for characterizing allelic variation, QTL mapping, and markerassisted selection. Information on the frequency and nature of SNPs in cotton, especially in coding DNA regions is lacking. This study was conducted to estimate the nucleotide diversity in cotton fiber genes among cultivated tetraploid cotton for the development of SNP-based cotton linkage map and quantitative trait loci detection. DNA sequence polymorphism of selected fiber genes was analyzed using polymerase chain reaction (PCR) and PCRbased direct sequencing technique. Single DNA fragments were amplified from genomic DNA of TM-1 and 3-79 by 56 of 93 primer pairs that were designed based on ca. 50 fiber genes. Sequence-tagged site (STS) was uncovered by 7 primer pairs between three Upland cotton genotypes (TM-1, NM24016, and Acala 1517-99) and five Gossypium barbadense genotypes (3-79, PHY 76, PS-32, K239, K240). Twenty-one primer pairs giving single products were used for DNA sequence analysis among the two cultivated tetraploid species. A total of 94 SNPs including 36 single-base changes (38.3%) and 58 indels (61.7%) were identified in 112 DNA fragments for 16 fiber gene fragments. The average frequency of SNPs, approximately one SNP per 500bp DNA sequences detected in the selected fiber genes of cotton was lower than the coding sequences of most other plant species. The three Upland cotton genotypes displayed a lower level of SNPs than the five G. barbadense. An uneven distribution of SNPs between and within the genes was observed with more indels than base substitutions and A-T, A-G changes, and Aindels are the most frequent SNPs. Heterogeneity of nucleotide diversity was revealed by DNA sequencing in tetraploid cotton.