IDENTIFICATION OF *LIGON LINTLESS-1* SPECIFIC TRANSCRIPTS IN COTTON

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Abstract

Gene identification and isolation is frequently the bottleneck in the genetic manipulation of fiber properties. We report: 1) an improved method for differential gene expression studies using fluorescently labeled SSR-specific primers and 2) isolation of transcripts specific to a Mendelian dominant mutant *Ligon Lintless -1* (*Li-1*). Near-isogenic lines, developed by six backcrosses with the TM-1 line as the recurrent parent as well as F_1 and F_2 plants, developed from the cross of the TM-1 and *Li-1* lines, were used for this study. cDNA libraries were constructed using a commercial kit. We confirmed the earlier reports of a simple Mendelian dominance for the *Li-1* locus based on progeny analysis of 147 F_2 plants. Histological studies revealed no distinct differences between the mutant and normal leaf cells, unlike the fiber cells which are very short in the mutant. As per our knowledge there is no report of using SSR-specific primers to screen cDNAs because the conventional idea is that SSRs are located predominantly in non-functional regions of the genome. We identified two putative transcripts specific to *Li-1* plants using SSR-specific primers. The DNA sequence information revealed the presence of dinucleotide repeats in ESTs, further confirming the merit of utilizing SSR-specific primers for differential gene expression. A preliminary BLAST search indicated the homology of the repeats with the untranslated regions of mRNAs of several plants. The SSR-based differential gene screening method has the specific advantages of being a simple, PCR-based technique, the markers are normally polymorphic and few enough in number for easy isolation and analysis.

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