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PROMOTER ANCHORED AMPLIFIED POLYMORPHISM IN COTTON

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ABSTRACT

Genome sequence information and high-throughput gene expression profiling methods such as cDNA micoarray to measure gene expression abundances open the door for investigating genome-wide gene expression and regulations in plants. However, non-coding sequences especially regulatory regions also play an important role in gene regulation and plant development. In our efforts to design molecular marker systems to search polymorphism associated with higher fiber yield and better fiber qualities, we are trying to examine a methodology that could specifically target different regulatory regions of the genome in cotton. In this study we designed 10-nucleotide degenerate promoter primers based on the conserved core promoter sequences and tested their applicability in PCR amplifications in combination with 10-mer random primers. To increase the specificity of PCR amplifications, we also designed longer primers consisting of filler sequences and the conserved core promoter sequences based on TATA box, GC box, G box and CA box. The primers were combined with AFLP primers in a PCR reaction. The markers amplified using RAPD-based and AFLP-based techniques were collectively called promoter anchored amplified polymorphism (PAAP).

Forty cotton germplasm with diverse genetic and geographical backgrounds were used to test the RAPD-based primers, while eight germplasm were used to test the AFLP-based primers. Based on RAPD-PAAP markers amplified from 12 primer combinations, the 40 genotypes were grouped into 5 distinctive groups (2 Upland cotton groups from China, 2 Upland cotton groups from the US and 1 from Pima cotton), consistent with their genetic and geographical origins. Based on AFLP-PAAP, the 8 genotypes were divided into three groups, congruent with their genetic backgrounds.

The new PAAP marker system is being used to map PAAP markers in a backcross inbred line (BIL) population and to identify QTLs controlling fiber quality and yield.