

STACKING PIMA S-6 FIBER LENGTH ALLELES IN A TAMCOT 2111 BACKGROUND

Christopher L. Souder, C. Wayne Smith, and Peggy Thaxton

Texas A&M University

Andrew H. Paterson

University of Georgia

Abstract

Molecular markers can be used to stack fiber quality alleles among recombinant inbred lines and thus, aid in the development of unique genotypes. The objective of this study was to determine the potential for stacking *Gossypium barbadense* (Pima S-6) quantitative trait loci (QTLs) for upper half mean (UHM) fiber length in a *G. hirsutum* (Tamcot 2111) background through marker-assisted selection. Near isogenic lines that contained unique combinations of 0, 1, and 2 homozygous QTLs for upper half mean fiber length were grown under greenhouse culture at College Station, TX during 2001 and 2002. Genotypes containing *G. barbadense* alleles for RFLP markers pGH679, A1296, and A1580 improved UHM above the recurrent parent, Tamcot 2111 used to develop the families (Table 1). Genotypes containing a combination of QTLs pAR077a and A1580 increased UHM fiber length above Tamcot 2111. Two other stacked combinations failed to increase UHM fiber length above the recurrent parent, Tamcot 2111. Differences in micronaire, fiber bundle strength, uniformity index, and elongation also existed among genotypes, some of which could be explained by the QTLs selected for in each family. The techniques and results in this study suggest that marker-assisted selection is possible and practical in upland cotton.

Table 1. Summary of marker genotype performance, relative to Tamcot 2111, grown under greenhouse conditions in College Station, TX.

Marker	Fiber property				
	UHM	MIC	STR	UI	ELO
pAR206a (family A / family D)	- / 0 [†]	+ / +	0 / +	0 / 0	0 / -
pGH399b (family A / family C)	- / -	+ / 0	0 / +	0 / 0	0 / -
pAR077	0	+	+	0	-
pGH679	+	-	0	+	-
A1296	+	0	+	+	0
A1580	+	0	0	0	0
pAR206a / pGH399b	0	+	0	0	0
pAR077 / pGH679	0	0	0	-	0
pAR206a / A1580	+	0	+	0	-

[†]Each +, -, or 0 indicates the effect of the marker on the phenotype of a particular genotype relative to the performance of Tamcot 2111.