

## BREEDING AND GENETICS

### Variation in an Extra-Long Staple Upland X Medium Staple Upland Cotton F2 Population

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#### ABSTRACT

**Development of extra-long staple (ELS) cotton germplasm represented a substantial improvement in upland fiber quality. The objective of this study was to determine the breeding value of an ELS breeding line when crossed to a genotype with average fiber quality. Breeders need to understand how ELS material should be used in a pedigree breeding program to realize the full benefits of the germplasm. Two populations were created from the mating and reciprocal mating of an unreleased ELS breeding line ‘TAM 182-39ELS’ and ‘DP 50’. F2 plants were evaluated at two locations for whole plot and on individual plant basis for yield, plant morphology, and fiber quality performance. Location and genotype effects were significant for lint yield, plant height, and all fiber properties. The ELS parent had superior fiber traits in comparison to DP 50. There were no significant differences between the reciprocal F2 populations for any trait except for length uniformity index and consequently were treated as a single population for individual plant selection analyses. Transgressive segregation and mid-parent heterosis were observed in the F2 population. Broad-sense heritability estimates indicated that Weslaco, TX was a better location for plant selection than College Station, TX. The ELS trait demonstrated a high degree of penetrance in the F2 populations. Capturing the ELS trait in high-yielding germplasm will speed the development of cultivars with improved fiber quality.**

There can be little improvement in crop production attributable to plant breeding without genetic variability. Creation of this variability is a fundamental step towards crop improvement. The cotton industry is facing several challenges on the production and usage ends that plant breeding efforts can address. The solutions include the development of enhanced fiber qualities coupled with better agronomic performances than current germplasm offers.

ELS cotton fiber is longer than 32 mm, which is similar to *Gossypium barbadense* L. cultivars (Cotton Inc., 2011). Recently a set of *Gossypium hirsutum* L. germplasm was developed with ELS properties (Smith et al., 2009b). This *G. hirsutum* germplasm was developed as a result of intraspecific hybridization with no known *G. barbadense* L. parentage (Smith et al., 2008). One of the common parents of this set of ELS lines is ‘TAM 94L-25’ (Smith, 2003). It was speculated that TAM 94L-25 might have received alleles associated with long fiber from a variety of sources, including breeding lines from the USDA Pee Dee breeding program (Smith et al., 2008). This ELS material has spinning properties more comparable to Pima cultivars than current upland cultivars, including Acala and Pee Dee germplasm, and retains an upland-type growth habit (Joy et al., 2010). The breeding value of ELS parents needs to be investigated so plant breeders will understand the best methods of using this unique germplasm.

Diallel breeding schemes are used to determine general and specific combining ability of parents. These studies are particularly useful for hybrid crops and to a lesser extent with self-pollinated crops like cotton. Most cotton breeding programs utilize a pedigree breeding scheme. Individual plants are selected from populations with traits that may or may not be segregating depending upon the diversity of the original parents and the degree of inbreeding. Percy (2003) described efforts to evaluate early generation populations of Pima cotton that had limited success in identifying superior populations at the F2 generation. Cheatham et al. (2003) found that F2 cotton lines produced higher seedcotton yields and longer fiber length than the best parent, but

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other traits were not improved. Meredith and Bridge (1973) suggested that because of large nonadditive genetic effects, selection of individual plants should be delayed at least until the F3 generation, although meaningful additive gene effects for many traits could possibly be determined at the F2 generation.

A study was initiated in 2007 to determine the penetrance of ELS fiber quality into the background of 'Deltapine' (DP 50), which is regarded as having average fiber quality. The pedigree of DP50 is provided by Calhoun et al. (1997). To make the most effective use of ELS germplasm, it is important to know what types of segregating populations can be expected for yield, fiber quality, plant morphology, and breeding objectives. The objective of this study was to determine the agronomic and fiber breeding value of upland cotton lines carrying the ELS trait in a cross with a parent with average fiber quality.

## METHODS AND MATERIALS

Hybridizations between 'TAM 182-39ELS', an unreleased sister line of 'TAM B182-33ELS' (Smith et al., 2009b; PI 654362) and DP 50 (PVP 8400154) occurred in a greenhouse at College Station, TX, in 2007. Twelve plants served as parents for each parental line. A reciprocal population also was made. Approximately 90 F1 plants were self-pollinated to generate the F2 population.

Field trials were conducted at College Station and Weslaco, TX, in 2008. Soil type at Weslaco was Hidalgo sandy clay loam, a fine-loamy, mixed, active, hyperthermic Typic Calciustolls; and a Westwood silt loam, a fine-silty, mixed thermic Fluventic Ustochrept, intergraded with Ships clay, a very fine, mixed, thermic Udic Chromustert at College Station. The trial at Weslaco was planted 5 March 2008 and the trial at College Station was planted 21 April 2008. Crops were grown under irrigation at both locations and all other crop management decisions were standard for the growing region.

Trials were planted in a randomized complete block design with four replications at both locations. Entries included the two parents, DP 50 and TAM B182-39ELS, and the two reciprocal F2 progeny populations. Plots consisted of two rows, 12.2 m by 1 m. Seeds were sown at a rate of 7.4 seed per meter. Plants in one row (the left row of each plot) of each plot were thinned at the V5 stage of growth (Elsner et al., 1979) to a stand of six plants per meter. This row was used to sample individual plants and the

unthinned row (the right row of each plot) was used for whole-plot performance evaluation.

Rows used to evaluate performance were harvested with a one-row mechanical picker. To determine lint percent and fiber properties, a 25-boll sample was hand harvested from each plot and ginned on a laboratory gin at the Cotton Improvement Lab in College Station, TX. Fibers were measured with high-volume instrumentation (HVI) by the Fiber and Biopolymer Research Institute (FBRI) at Texas Tech University in Lubbock, TX. Plant mapping data [e.g., nodes above white flower (NAWF), first sympodium (FS), total sympodia (TS), and plant height] were ascertained from the unthinned performance rows. NAWF data was ascertained 76 d after emergence (DAE) at Weslaco, and 81 DAE at College Station. Other plant mapping data were collected just prior to harvest. FS was determined by counting the nodes after the cotyledons on the monopodium. A total of 10 plants per plot were mapped and the mean of those 10 plants were pooled for analysis.

At Weslaco, 15 IPSs were hand harvested from each plot. At College Station, 10 plants from each plot were individually hand harvested. Plants were selected at random to harvest at both locations to avoid a possible yield bias through preferential selection (Bowman et al., 2004). Seedcotton from each plant was ginned on a laboratory gin and fiber samples sent to FBRI for HVI fiber measurements. Data were analyzed using PROC GLM (SAS Institute, 2009). Means were separated at the  $k = 100$  probability level as calculated by the Waller-Duncan  $K$ -ratio  $t$ -test. Broad-sense heritability was estimated by pooling all F2 IPS plant data by location and determining the variance. The mean of the parental variance was used to estimate the environmental variance ( $V_E$ ). By subtracting the variance of the F2 ( $V_{F2}$ ) from  $V_E$ , the genetic variance ( $V_G$ ) was calculated. In turn, the broad-sense heritability was estimated with the formula  $V_G/V_{F2}$ .

## RESULTS AND DISCUSSION

The ANOVA for the whole plot samples indicated significant differences between locations for lint yield, NAWF, plant height, and all fiber traits (Table 1). Genotype effects were significant for all traits except lint percent. Apart from plant height, no traits had significant genotype x location interactions. Therefore data for all traits, excluding plant height, from both locations were pooled.

**Table 1. Significance levels as determined by the F-test for cotton lint yield, lint percent, plant morphology, and fiber traits across two locations (College Station and Weslaco, TX) in 2008.**

Source	df	Significance of F-ratio									
		Lint yield	Lint percent	NAWF	1 <sup>st</sup> sympodium	Total sympodia	Plant height	Micronaire	Length	UI	Strength
Location (L)	1	**	ns <sup>z</sup>	**	ns	ns	**	**	*	**	**
Rep (loc)	6	ns	ns	**	**	ns	**	ns	ns	ns	ns
Genotype (G)	3	*	ns	*	**	*	**	**	**	**	**
L x G	3	ns	ns	ns	ns	ns	**	ns	ns	ns	ns
Error	18										

<sup>z</sup> ns, not significant.

\*Significant at the 0.05 level.

\*\* Significant at the 0.01 level.

TAM 182-39ELS had significantly improved fiber over that of DP 50 in terms of micronaire, length, length uniformity index, and strength (Table 2). In addition, TAM 182-39ELS first fruiting branch occurred at a higher mainstem node. The reciprocal F2 populations were not different between each other for all traits except for fiber length uniformity index. The lack of reciprocal effects was not unexpected due to the similarities of parental cytoplasm sources. DP50/TAM 189-39ELS (F2) produced more lint yield than DP 50. Both F2 populations had a higher NAWF value than DP 50 and both F2 populations exceeded the parents in terms of total number of sympodium branches. Moreover, the F2 populations had intermediate values between the parents for fiber micronaire, length, and strength. There was no difference between the reciprocal F2 populations for plant height at either location, but both tended to be taller in College Station than in Weslaco (Table 3). There was a change in rank for the parents. DP 50 was taller than TAM 182-39ELS at Weslaco, but was the shortest genotype at College Station.

Reciprocal F2 population IPS data were pooled because the whole plot evaluation indicated little differences among these progeny populations. Cotton germplasm generally is developed through a pedigreed breeding program in which individual plants are selected from a segregating population. A higher coefficient of variation (CV) would imply a greater likelihood of finding a transgressive segregant. Identification of transgressive segregating plants is important to improving fiber quality in cotton breeding programs (Bowman and Gutierrez, 2003). DP 50 generally had lower CV values than TAM 182-39ELS and the F2 progeny at College Station, which could be a result of a higher degree of inbreeding for DP 50 and/or the result of the high-end genetic potential of fiber traits associated with ELS genotypes (Table 4). Based on the maximum and minimum values of IPSs, there is evidence of transgressive segregation expression for fiber micronaire, length, and strength at both College Station and Weslaco when fiber qualities of an individual plant exceeded the mean fiber values of TAM 182-39ELS (Table 5).

**Table 2. Lint yield, lint percent, plant morphology, and fiber traits of parents and reciprocal F2 progeny across locations.**

Genotype	Lint <sup>z</sup> kg/ha	Lint Percent <sup>†</sup> %	NAWF <sup>z</sup> -no.-	1 <sup>st</sup> sympodium <sup>z</sup> no.	Total sympodia <sup>z</sup> no.	Micronaire <sup>†</sup> units	Length <sup>z</sup> mm	UI <sup>z</sup> %	Strength <sup>z</sup> k N m kg <sup>-1</sup>
DP 50	921b	35.4a	4.1b	5.4c	15.3b	5.2a	27.6c	82.6b	256c
TAM 182-39ELS	1088ab	35.5a	4.5ab	7.0a	15.3b	4.3c	33.6a	84.5a	324a
DP 50/TAM 182-39ELS(F2)	1102a	36.1a	4.7a	6.5b	16.6a	5.0b	30.9b	84.0a	302b
TAM 182-39ELS/ DP 50(F2)	1052ab	36.9a	4.7a	6.6ab	16.4a	4.9b	30.4b	82.8b	292b
Mean	1041	36.0	4.5	6.4	15.9	4.9	30.6	83.5	293
C.V.	11.7	4.1	9.3	6.6	5.8	3.1	2.5	0.9	3.6

<sup>z</sup> Means with the same letter are not significantly different at the 0.05 probability level as calculated by the Waller-Duncan *K*-ratio *t*-test.

**Table 3. Plant height of parents and reciprocal F2 progeny at College Station and Weslaco, TX.**

Genotype	Plant height <sup>z</sup> , mm	
	Weslaco	College Station
DP 50	89b	95c
TAM 182-39ELS	74c	102b
DP 50/ TAM 182-39ELS (F2)	97a	112a
TAM 182-39ELS/ DP 50 (F2)	98a	112a
Mean	89	105
C.V.	3.2	2.3

<sup>z</sup> Means with the same letter are not significantly different at the 0.05 probability level as calculated by the Waller-Duncan *K*-ratio *t*-test.

**Table 4. Comparison of individual plant traits from DP 50, TAM 182-39ELS, and F2 progeny at College Station, TX.**

Genotypes	C.V., %	Max	Min	Mean <sup>z</sup>
<b>Lint Percent (%)</b>				
DP 50	5.7	41.7	30.8	36.3b
TAM 182-39ELS	8.1	42.7	27.2	35.8b
F2 Progeny	7.3	43.2	25.1	37.9a
<b>Micronaire (units)</b>				
DP 50	6.9	6.2	4.6	5.3a
TAM 182-39ELS	9.7	5.4	3.5	4.4b
F2 Progeny	8.9	6.3	4.0	5.0a
<b>Fiber length (mm)</b>				
DP 50	2.8	28.4	24.9	27.2b
TAM 182-39ELS	6.1	35.6	27.7	32.4a
F2 Progeny	5.3	32.5	26.4	29.4b
<b>Fiber strength (k N m kg<sup>-1</sup>)</b>				
DP 50	5.6	287	232	255c
TAM 182-39ELS	8.3	358	234	309a
F2 Progeny	7.8	329	234	274b

<sup>z</sup> Means with the same letter are not significantly different at the 0.05 probability level as calculated by the Waller-Duncan *K*-ratio *t*-test.

**Table 5. Comparison of individual plant traits from DP 50, TAM 182-39ELS, and F2 progeny at Weslaco, TX.**

Genotypes	C.V., %	Max	Min	Mean <sup>z</sup>
<b>Lint Percent (%)</b>				
DP 50	5.1	40.5	29.1	35.6b
TAM 182-39ELS	8.2	47.1	30.4	36.8a
F2 Progeny	6.6	43.0	30.2	36.4a
<b>Micronaire (units)</b>				
DP 50	6.5	5.5	3.8	4.9a
TAM 182-39ELS	9.2	5.5	3.1	4.2b
F2 Progeny	9.8	5.7	3.2	4.6ab
<b>Fiber length (mm)</b>				
DP 50	3.9	31.5	25.9	29.0c
TAM 182-39ELS	4.9	36.6	28.4	33.9a
F2 Progeny	5.8	34.5	27.2	30.6b
<b>Fiber strength (k N m kg<sup>-1</sup>)</b>				
DP 50	7.1	325	247	279c
TAM 182-39ELS	5.0	352	283	322a
F2 Progeny	6.9	340	260	297b

<sup>z</sup> Means with the same letter are not significantly different at the 0.05 probability level as calculated by the Waller-Duncan *K*-ratio *t*-test.

Broad-sense heritability estimates generally were higher for fiber traits at Weslaco than in College Station (Table 6). This suggests that Weslaco was a better location in which to select ELS fiber-related traits than College Station. It was interesting to note broad-sense heritability for fiber length was 0.48 at Weslaco, but only 0.07 at College Station. Given the large difference in fiber length between DP 50 and TAM 182-39ELS, one would have expected this heritability to be much larger at College Station.

Mid-parent heterosis in the F2 populations was low for most agronomic and fiber-related traits (Table 7). The largest expression of heterosis was for plant height with a calculated value of 14.3% at College Station and 19.8% at Weslaco. Heterosis in F2 populations can contribute to enhanced lint yield (Meredith 1990; Meredith and Brown, 1998; Tang et al. 1996). The estimated broad-sense heritability for lint yield was 11.4% in College Station and 1.9% in Weslaco. Consequently, DP50/TAM 189-39ELS (F2) outperformed DP 50 in terms in lint yield (Table 2).

**Table 6. Broad-sense heritability of lint percent and fiber traits of DP 50/TAM 182-39ELS (F2) progeny at College Station and Weslaco, TX, in 2008.**

Trait	College Station	Weslaco
	H <sup>2</sup>	
Lint percent	0.16	-
Fiber micronaire	0.18	0.39
Fiber length	0.07	0.48
Fiber length uniformity index	0.22	0.22
Fiber strength	0.07	0.43

**Table 7. Mid-parent heterosis estimations of DP 50/TAM 182-39ELS (F2) progeny based on whole-plot performance at College Station and Weslaco, TX, in 2008.**

Trait	College Station	Weslaco
	%	
Lint percent	4.3	1.8
Lint kg ha <sup>-1</sup>	11.4	1.9
NAWF	7.0	9.4
Plant height	14.3	19.8
1 <sup>st</sup> sympodium	11.4	0.4
Total sympodia	9.0	7.4
Fiber micronaire	3.5	4.1
Fiber length	0.5	0.4
Fiber length uniformity index	-	-
Fiber strength	2.2	2.8

## CONCLUSIONS

Neither of the F2 populations exceeded the high parental value for any economically beneficial trait (i.e., lint yield and fiber quality). The value of these populations likely will be derived from IPSs in a pedigreed breeding program. Ideally breeders would create segregating populations with considerable variation which would increase the odds of finding beneficial transgressive segregating plants. Smith et al. (2009a) suggested that transgressive segregates for UHML in upland cotton can be expected at low frequencies when crossing contrasting parents or similar parents. Yield performance and fiber quality of F2 progeny demonstrated the high degree of penetrance of the ELS germplasm. Capturing the ELS trait in high-yielding germplasm will speed the development of cultivars with improved fiber quality.

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