Published online May 18, 2006

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Heritability and Correlations of Agronomic and Fiber Traits in an Okra-Leaf Upland Cotton Population

Mauricio Ulloa*

ABSTRACT

In cotton (*Gossypium hirsutum* L.), the cost and time to develop and evaluate appropriate genetic populations have limited the number of intensive and complete heritability studies. Herein, three agronomic and 17 fiber quality traits were assessed for heritability and correlation analyses on progeny rows in an okra-leaf cotton population of 208 families. Progenies were advanced in succeeding generations by a single-seed descent. Comparison between $F_{2:3}$ and $F_{2:6}$ generations for individual traits and individual progeny by trait revealed significant differences between the two generations. Heritability estimates ($h^2 > 0.60$), and correlations within and between ($r > 0.55$) $F_{2:3}$ and $F_{2:6}$, generations have practical applications for the simultaneous improvement of multiple fiber traits. Fiber strength was positively correlated to 2.5 and 50% fiber span length and negatively correlated to short fiber content. Number of neps was positively correlated to number of seed coats, and short and immature fiber content, and negatively correlated to mean fiber fineness and maturity ratio. The genetic potential for improving agronomic and fiber traits may exist in populations with this alternative leaf morphology, okra-leaf type. Mass selection may be effective for improving most of the above traits ($h^2 > 0.60$). However, pedigree, sibs, and progeny tests need to be used to achieve higher genetic progress. Selection may be applied as early as the F_3 when selection units can be replicated. Thereafter, antagonistic trait correlations may become neutral or favorable in later generations, facilitating improvement of fiber quality.

Cotton is produced as a raw material for the textile industry and is a high value crop. Marketing of this crop is based on measurable quality properties in an industry where manufacturing technology changes are being implemented rapidly (Sawhney et al., 2003). The most widely planted current cotton cultivars are well yielding, day-length neutral and early maturing with easily ginned and abundant fiber. These improved characteristics resulted from human selection from perennial ancestors with shorter and sparser fiber (Fryxell, 1984). The continuing demands for better quality for consumer goods and the recent movement from the preponderance of ring spinning to faster, less labor intensive and versatile spinning methods have been driving research programs to look for alternatives to genetically improve lint and fiber quality (Meredith et al., 1991). All the changes in spinning technology have in common the requirement of unique and often greater cotton fiber quality, especially fiber strength for processing (Deussen, 1992).

Many cotton research programs require measurements of agronomic and fiber quality traits such as lint percentage, boll weight, 2.5 and 50% fiber span length, fiber bundle strength, and fineness (micronaire reading, fiber maturity, fiber perimeter, etc.). The cotton research community has established fiber testing methods (Breeder, Spinning, Areolometer, Sticky, and HVI) for the above traits, which are run in-house, or through public or private institutions such as the International Textile Center (Lubbock, TX) and Starlab Inc. (Knoxville, TN). Fiber span length at 50% (SL 50%) and 2.5% (SL 2.5%) can be measured with a digital Fibrograph instrument. SL 2.5% estimates the length of the longest 2.5% of fibers scanned in a sample, and the distance is presented in millimeter (mm). Fiber strength (T1) is the strength of a bundle of fibers measured by the stelometer. Elongation (E1) is an estimate of the elasticity of the bundle sample. Micronaire reading (Mic) is a measure of fiber fineness and maturity. A relatively new fiber testing method that has been incorporated rather slowly due to the lack of access to some research programs is called the Advanced Fiber Information System (AFIS). This method measures neps, fiber length and diameter, and trash for fibers (Bragg and Shofner, 1993; Hossein et al., 1994). Correlations among traits can be useful in developing selection criteria, but correlations can also present difficult scenarios for interpretation of the association for trait responses. Mic and SL 2.5% length, which both influence lint percentage, are a good example of components of a more complex trait, fiber yield (Ulloa and Meredith, 2000; Ulloa and Meredith, 2002). In addition, multiple traits can be correlated due to linkage or pleiotropy (Miller and Rawlings, 1967; Meredith and Bridge, 1971; Culp et al., 1979). In cotton, several studies have reported negative correlations between fiber quality and agronomic traits, particularly fiber strength and lint percentage (Miller and Lee, 1964; Worley et al., 1976), but other studies did not detect such correlations (Benedict et al., 1999). For negative correlations, several generations of intermating in an isolation block with approximately 50% self-fertilization changed the genetic correlation between lint yield and fiber strength within a population from antagonistic to favorable (Meredith and Bridge, 1971). The negative correlation between lint yield and certain yield components (boll size, number of fiber per seed, and seed index) demonstrates the problem often associated with breeding for specific yield component e.g., increasing one component often results in decreasing another component(s) due to balanced compensation. Breeders face great difficulties in enhancing fiber traits while main-

USDA-ARS-WCIS Res. Unit, 17053 N. Shafter Ave., Shafter, CA 93263. Received 23 Aug. 2005. *Corresponding author (mulloa@pw.ars.usda.gov).

Published in Crop Sci. 46:1508–1514 (2006).
Crop Breeding & Genetics
doi:10.2135/cropsci2005.08-0271
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677 S. Segoe Rd., Madison, WI 53711 USA

Abbreviations: E1, fiber elongation; millitex, fiber fineness; IFC, immature fiber content; Mic, micronaire reading; no., number; SL 50% and SL 2.5%, fiber span length at 50% and at 2.5%; T1, fiber strength; wt, weight.

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taining yield and fiber quality (Worley et al., 1976; Calhoun and Bowman, 1999).

Although breeding progress has been accomplished for agronomic and fiber traits for the last 70 yr and extensive heritability studies have been done, the number of intensive and complete studies is limited. The cost of obtaining reliable heritability estimates is very high for most traits due to the time required to develop appropriate genetic populations and evaluate them over years and across locations. Broad and narrow-sense heritability studies have been preferred using individual plants and progeny rows, but many traits have been incompletely studied (Miller and Rawlings, 1967; Meredith and Bridge, 1971). In addition, there are only a few studies that have reported heritability for the AFIS fiber testing method (USTER, AFIS, Knoxville, TN). Knowledge of heritability and type of genetic variation involved in the expression of fiber traits would facilitate further improvement of cotton fiber properties (May and Green, 1994).

Okra-leaf type cottons are not commercially grown extensively in the USA. The FiberMax 832 cultivar, however, is grown extensively in the Texas Coastal Bend area, but little elsewhere. The okra-leaf type usually confers earlier maturity and produces similar yield to its normal-leaf isoline cotton (Heitholt and Meredith, 1998), less boll rot (Andries et al., 1969), reduced leaf area index (Kerby et al., 1980), higher single-leaf photosynthesis per unit leaf area (Pettigrew et al., 1993), moderate resistance to pink bollworm (*Pectinophora gossypiella* Saunders) (Wilson, 1990), and growth characteristics such as fewer branches, fewer nodes, greater production of flower buds and flowers when compared with normal-leaf types (Karami and Weaver, 1979). The genetic potential for improving cotton yield and fiber traits may exist in okra-leaf cottons and their use could be considered for producing future cultivars (Heitholt and Meredith, 1998). Herein is presented the first report of correlations and heritability estimates in a cotton population with alternative leaf morphology, okra-leaf type, over two generations $F_{2:3}$ and $F_{2:6}$, and its assessment and genetic potential for improving agronomic and fiber quality traits, using the single-seed descent (SSD) method for rapidly advancing progeny generations.

MATERIALS AND METHODS

The genetic population was developed from crossing 'Fiber Max 832' (FiberMax–Bayer Corp.) and an okra-leaf isoline of 'MD51ne'. The MD51ne parent had high yield, high fiber strength, and fine fiber. MD51ne was a BC_2F_2 plant selection that originated from a cross of MD65–11 and 'Deltapine 90' (Meredith, 1993). Four backcrosses to MD51ne with normal leaf followed by two generations of selection for okra leaf type beginning in the BC_4F_3 generation were performed to obtain the okra leaf isoline of MD51ne. The ne abbreviation means that this cultivar is nectariless. Fiber Max 832 is a commercial okra-leaf cultivar bred by CSIRO in Australia (CSIRO, Cotton Research Unit, Narrabri, NSW, AU). The population used in this study consisted of 208 F_2 derived-families. Generations were advanced from the F_2 to the F_6 generation by single seed descent (SSD), without selection for agronomic or fiber quality traits.

In 1998 the $F_{2:3}$ and in 2000 the $F_{2:6}$ families were grown in one-row plots 5m long with 1m row spacing. The 208 F_2 derived-families and parental checks were grown on two sites at Stoneville, MS. A randomized complete block design with two replications at each location was used to determine yield components and fiber properties. Yield components and fiber trait evaluations were determined from 50 boll samples taken randomly from each plot. Plant density was about 113 000 plants ha^{-1} for $F_{2:3}$ and $F_{2:6}$ generations. One site, planted 7 May 1998 and 9 May 2000, was a Beulah fine sandy loam soil type (coarse-loamy, mixed, active, thermic typic dystrudepts), and the other site, planted 15 May 1998 and 17 May 2000, was a Dubbs silt loam (fine-silty, mixed, active, thermic typic hapludalfs) with three plots of Fiber Max 832 and MD51ne okra each used as controls. Nitrogen rates were 112 kg ha^{-1} applied about 30 d before planting while remaining cultural practices were consistent with those recommended by the Mississippi Cooperative Extension Service.

The agronomic and fiber traits were determined from 50 randomly hand-harvested bolls from each plot for the $F_{2:3}$ and $F_{2:6}$ generations. The following agronomic traits were evaluated on harvested bolls from progeny rows: lint percentage, boll and seed weight. Lint percentage was determined from the harvested boll sample by ginning on a small 10-saw experimental gin and calculated by weighing the seed cotton, ginning samples (lint), and weighing seed, expressing this yield component as a percentage of the total sample. Boll weight was calculated by dividing the fiber weight of the 50 boll sample by the number of bolls. Seed weight was determined by the weight of 100 fuzzy seeds from each sample. The following single-instrument fiber quality traits were evaluated: E1, Mic, SL 2.5%, SL 50% presented in mm, and T1 presented in kN m kg^{-1}. A commercial testing company, Starlab Laboratories of Knoxville, TN, determined the above fiber properties.

In addition, the AFIS at the USDA-ARS, Crop Genetics & Production Research Unit at Stoneville, MS, was also used to determine fiber properties. The following fiber quality traits were evaluated: Number of neps (no. g^{-1}), number of seed coats (g^{-1}), average length of all fibers by weight (wt) [mm], average length of all fibers by number (no.) [mm], upper quartile of fiber length by wt (mm), short fiber content by wt (g kg^{-1}), short fiber content by no. (g kg^{-1}), SL 5.0% no. (mm), SL 2.5% no. (mm), fiber fineness (millitex), immature fiber (g kg^{-1}), and maturity ratio (Unit).

Data from $F_{2:3}$ and $F_{2:6}$ generation progeny were analyzed with two replications at two locations using SAS PROC GLM (SAS Institute Inc., Cary, NC) for variance components and mean separation. In addition, comparison of $F_{2:3}$ with $F_{2:6}$ generations was done for each trait using locations (average over replications) as replications. Comparison of $F_{2:3}$ with $F_{2:6}$ generation for each progeny by trait was performed separately. Correlations among agronomic and fiber properties within and across generations were calculated by PROC CORR. Means were tested for normal distribution, skewness, and kurtosis by PROC UNIVARIATE.

Heritability estimates for the agronomic and fiber traits were calculated by two methods using the variance components from the analyses of variance, hierarchal ($a - h^2 = V_G/V_G + V_{GXE} + V_E$) and one-way layout-interclass correlation ($b - h^2 = V_G/V_P$) in the following generations $F_{2:3}$ and $F_{2:6}$. The variance (V) calculated from the observed variations in the quantitative character constituted the phenotypic variance (V_P). V_P equals genetic variance (V_G) plus nongenetic or environmental variance (V_E) (Ponzoni and James, 1978; Williams et al., 1965). To investigate additive type gene actions with generation means, deviation between mid-parent (mean of parents) and family mean values from each generation were tested using a paired t test (Ramey, 1962).

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RESULTS AND DISCUSSION

Significant variation was observed among 208 F_2 derived-families for agronomic and fiber quality traits in $F_{2:3}$ and $F_{2:6}$ generations, except for seed coat fragments ($F_{2:6}$) (Table 1). Genotype by site (g × s) interaction ($P < 0.05$) was significant for lint percentage, micronaire reading, and E1 in the $F_{2:3}$ generation. In the $F_{2:6}$ generation, g × s was significant for lint percentage, micronaire reading, T1, SL2.5%, fiber fineness, and immature fiber (data not shown). The genetic variance of the families was high in magnitude and therefore provided sufficient variability for assessment of almost all traits presented herein. With the exception of the number of seed coats, the heritability estimates for traits measured in these families were moderate to high, depending on the heritability method used (Table 2). The environmental variation might not be great enough for most traits described herein to mask the genetic variation in this population e.g., lint percentage (h^2 = 0.64–0.95), Mic (h^2 = 0.60–0.81), and T1 (h^2 = 0.56–0.85). Similar observations were presented in other studies (May and Jividen, 1999; May and Taylor, 1998), where genotype × environment interactions for fiber samples were smaller relative to genetic variation.

Correlations

Correlations between traits within generations for $F_{2:3}$ and $F_{2:6}$ on family-mean basis are given in Tables 3 to 5. Number of neps was positively correlated to number seed coats, short fiber content by weight and number, and immature fiber and negatively correlated to average length of fiber by number, fiber fineness, and maturity ratio. Mic was positively correlated to fiber fineness and maturity ratio and negatively correlated to number of neps and immature fiber. T1 was positively correlated to SL 50 and 2.5% and negatively correlated to short fiber by weight and number and average length of all fiber by number. (Tables 3–5).

There is no way in which cotton yield can be changed without changing one or more of the yield and fiber components. Correlations among traits in this cotton population with alternative leaf morphology okra-leaf type suggest that individual families can be identified within this population for the simultaneous improvement of multiple traits. Components of fiber strength, such as SL 50 and SL 2.5%, and maturity ratio (Meredith, 1992; Ulloa and Meredith, 2000) were correlated with mean family generations. The positive correlation of SL 2.5 and 50% with T1 suggests that families with superior length and strength can be identified in this population (Table 3).

Negative correlations between lint yield and T1 have long been recognized by cotton breeders (Meredith and Bridge, 1971; Culp et al., 1979). A major contribution for yarn tenacity is provided by T1 (Meredith et al., 1991; May and Taylor, 1998) as well as for the durability of knit and woven fabric (Faeber, 1995). This type of negative effect suggests that breeding for high fiber strength would sacrifice/deteriorate the primary trait, lint yield. In this okra-leaf population the negative association between lint percentages (which is a major indicator of yield) and T1 can be reduced or changed to be even less detrimental in advanced generations, making selection more favorable for the combination of increased yield potential and high fiber strength (Table 3).

In contrast to the negative effect between lint percentage and T1, the negative correlations for Mic with some fiber traits are indicators of positive effects. The longer the fiber (SL 2.5%, SL 5%, and upper quartile of fiber length) the more fine (lower Mic) the fibers should be, but at the same time it could be an indicator that some F_2 derived-families posses a higher number of immature fiber content and/or lower maturity ratio value in these fibers, which affects the dyeing process of fibers (Tables 3 and 4). Improvement of the cotton crop re-

Table 1. *F* values, means and standard deviations (SD) of three agronomic and 17 fiber traits from 208 $F_{2:3}$ and $F_{2:6}$ progeny developed from a cross between FiberMax 832 and MD51ne.

	$F_{2:3}$		$F_{2:6}$	
Trait name	*F* value	Mean ± SD	*F* value	Mean ± SD
Lint percentage (%)	6.16**	37.1 ± 1.4	16.10**	35.5 ± 1.7
Boll weight (g)	2.84**	4.7 ± 0.3	1.75**	4.7 ± 0.4
Seed weight (g)	2.84**	10.0 ± 0.8	4,69**	9.4 ± 0.9
Fiber strength (kN m kg^{-1})	6.24**	242.0 ± 13.0	6.23**	235.0 ± 14.0
Micronaire reading (Unit)	5.79**	4.6 ± 0.2	6.87**	3.8 ± 0.3
Elongation (%)	6.83**	6.3 ± 0.5	3.99**	6.6 ± 0.6
50% fiber span length (mm)	2.03**	14.8 ± 0.3	2.58**	14.3 ± 0.3
2.5% fiber span length (mm)	3.91**	29.8 ± 0.8	12.07**	29.8 ± 0.3
Number of neps (no. g^{-1})†	2.06**	102.6 ± 14.4	1.90**	147.9 ± 28.0
Number of seed coats (g)†	1.23*	11.0 ± 2.0	0.92	7.1 ± 1.5
Average length of all fibers by wt (mm)†	4.35**	25.8 ± 0.5	4.61**	25.8 ± 0.8
Average length of all fibers by no. (mm)†	3.27**	21.0 ± 0.5	3.38**	20.8 ± 0.8
Upper quartile of fiber length by wt (mm)†	6.82**	30.8 ± 0.8	8.20**	31.0 ± 1.25
Short fiber content by wt (g kg^{-1})†	3.22**	67 ± 8	3.46**	72 ± 11
Short fiber content by no. (g kg^{-1})†	3.85**	225 ± 21	4.39**	231 ± 27
5.0% fiber span length no. (mm)†	7.19**	34.8 ± 0.8	8.85**	35.0 ± 1.3
2.5% fiber span length by no. (mm)†	6.88**	37.0 ± 1.0	8.22**	37.5 ± 1.5
Fiber fineness (millitex)†	5.02**	175.7 ± 5.8	7.67**	164.3 ± 5.9
Immature fiber (g kg^{-1})†	2.96**	47 ± 6	3.29**	59 ± 6
Maturity ratio (Unit)†	4.47**	0.95 ± 0.02	4.26**	0.93 ± 0.02

* Significant at $P < 0.05$.
** Significant at $P < 0.01$.
† AFIS = Advanced Fiber Information System measurements (number of neps − maturity ratio).

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Table 2. Correlation between $F_{2:3}$ and $F_{2:6}$ generations and heritability estimates for three agronomic and 17 fiber traits obtained from 208 $F_{2:3}$ and $F_{2:6}$ progeny developed from a cross between FiberMax 832 and MD51ne.

Trait name	Correlation between $F_{2.3}$, $F_{2.6}$	$F_{2:3}$ a-h^2†	$F_{2:3}$ b-h^2‡	$F_{2:6}$ a-h^2†	$F_{2:6}$ b-h^2‡
Lint percentage (%)	0.54**	0.79	0.64	0.95	0.89
Boll weight (g)	0.30**	0.64	0.34	0.46	0.26
Seed weight (g)	0.52**	0.85	0.55	0.86	0.57
Fiber strength (kN m kg^{-1})	0.42**	0.85	0.56	0.80	0.74
Micronaire reading (Unit)	0.32**	0.80	0.60	0.78	0.81
Elongation (%)	0.47**	0.83	0.61	0.74	0.62
50% fiber span length (mm)	0.13	0.52	0.27	0.64	0.46
2.5% fiber span length (mm)	0.42**	0.74	0.43	0.89	0.86
Number of neps (g^{-1})§	0.21**	0.46	0.35	0.43	0.37
Number of seed coats (g)§	0.20**	0.16	0.28	−0.08	−0.03
Average length of all fibers by wt (mm)§	0.41**	0.76	0.57	0.81	0.65
Average length of all fibers by no. (mm)§	0.39**	0.67	0.57	0.73	0.56
Upper quartile of fiber length by wt (mm)§	0.48**	0.84	0.63	0.89	0.79
Short fiber content by wt (g kg^{-1})§	0.35**	0.67	0.57	0.71	0.56
Short fiber content by no. (g kg^{-1})§	0.38**	0.72	0.59	0.77	0.64
5.0% fiber span length (mm)§	0.48**	0.85	0.64	0.89	0.80
2.5% fiber span length (mm)§	0.45**	0.84	0.63	0.89	0.78
Fiber fineness (millitex)§	0.34**	0.78	0.58	0.82	0.80
Immature fiber (g kg^{-1})§	0.39**	0.63	0.47	0.62	0.61
Maturity ratio (unit)§	0.43**	0.77	0.56	0.73	0.68

*Significant at $P < 0.05$.
** Significant at $P < 0.01$.
† $a - h^2 = V_G/V_G + V_{G\times E} + V_E$.
‡ $b - h^2 = V_G/V_P$
§ AFIS = Advanced Fiber Information System measurements (number of neps − maturity ratio).

quires reliable selection criteria based on trait performances. It may be possible to increase lint percentage without increasing Mic up to levels that do not penalize growers (above 5.0). For example, selection for Mic in this population may be possible by simultaneously monitoring traits such as fiber fineness, immature fibers and maturity ratio, because their associations are indicators of high or low micronaire reading (Tables 3–5). In addition, multiple-selection against correlated traits such as number of neps, number of seed coats, and immature fiber could reduce the problems of foreign matter in the lint/fibers, yarn evenness, and visual appearance of fabrics (Tables 3–5).

Fiber fineness, immature fiber content, and maturity ratio were highly correlated to micronaire reading. For fiber quality traits, single instrument, conventional measurements were correlated with measurements taken by AFIS such as SL 2.5% span length from Starlab and AFIS with $r = 0.85$ and $r = 0.90$ for $F_{2:3}$ and $F_{2:6}$, respectively (Table 4). Much of the fiber properties exhibited by *G. hirsutum* at the textile mill have been reported to be under genetic control (Meredith et al., 1991). Across generations ($F_{2:3}$ and $F_{2:6}$), most analyzed measurements were moderately correlated, and after six generations by SSD, the okra-leaf population still possessed sufficient genetic variability to show a significant selection response (Table 2).

Heritability

For agronomic traits, lint percentage was the most consistently heritable trait across the two generations,

Table 3. Correlation coefficients for three agronomic and 17 fiber traits obtained from 208 $F_{2:3}$ and $F_{2:6}$ progeny developed from a cross between FiberMax 832 and MD51ne.

Cotton traits	Lint percentage	Boll weight	Seed weight	T1	Micronaire	E1	50% span	2.5% span
Boll weight	0.09†							
	−0.07‡							
Seed weight	0.31**	0.55**						
	0.30**	0.62**						
Fiber strength (T1)	−0.14*	−0.17*	0.17*					
	−0.08	−0.06	0.10					
Micronaire reading	0.39**	0.23**	0.07	0.00				
	0.37**	0.12	0.04	−0.21**				
Fiber elongation (E1)	0.13	−0.04	−0.10	0.05	−0.15*			
	0.16	−0.03	−0.14*	−0.08	−0.11			
50% fiber span length	−0.00	0.17*	0.34**	0.56**	0.23**			
	−0.11	0.29**	0.40**	0.30**	0.05			
2.5% fiber span length	−0.04	0.27**	0.32**	0.56**	0.03	−0.15*	0.66**	
	−0.22**	0.32	0.47**	0.30**	−0.29**	−0.17*	0.60**	
Number of neps§	−0.20**	−0.08	−0.02	−0.29**	−0.37**	−0.044	−0.11	0.20**
	0.21**	−0.11	−0.10	−0.18*	−0.53**	0.13	−0.17*	0.11

* Significant at $P < 0.05$.
** Significant at $P < 0.01$.
† Correlation coefficients for generation $F_{2:3}$.
‡ Correlation coefficients for generation $F_{2:6}$.
§ AFIS = Advanced Fiber Information System measurements (number of neps – maturity ratio).

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Table 4. Continuation of correlation coefficients for two agronomic and 17 fiber traits obtained from 208 F2:3 and F2:6 progeny developed from a cross between FiberMax 832 and MD51ne.

Cotton traits	Lint percentage	Boll weight	Seed weight	T1	Micronaire	E1	50% span	2.5% span	No. of neps§
Number of seed coats§	−0.06†	−0.10	0.06	−0.16*	0.09	0.00	−0.08	−0.10	0.53**
	0.04‡	−0.13	−0.05	−0.10	−0.05	−0.01	−0.20**	−0.17*	0.37**
Average length of all fibers by wt§	−0.24**	0.20**	0.36**	0.35**	0.06	−0.20**	0.64**	0.74**	−0.11
	−0.21**	0.30**	0.41**	0.33**	−0.16*	−0.17*	0.57**	0.79**	−0.23**
Average of all fibers by no.§	−0.25**	0.08	0.27**	0.52**	0.20**	−0.12	0.59**	0.34**	−0.37**
	−0.15*	0.21**	0.25**	0.41**	0.10	−0.11	0.54**	0.41**	−0.51**
Upper quartile of fiber length by wt§	−0.18*	0.25**	0.33**	0.13	−0.06	−0.24**	0.50**	0.87**	0.10
	−0.21**	0.32**	0.44**	0.22**	−0.28**	−0.19**	0.475**	0.41	−0.03
Short fiber content by wt§	0.15*	0.05	−0.13	−0.56**	−0.31**	0.00	−0.45**	0.08	0.52**
	0.03	−0.05	−0.03	−0.36**	−0.34**	0.00	−0.38**	0.10	0.65**
Short fiber content by no.§	0.15*	0.12	−0.04	−0.51**	−0.27**	−0.02	−0.31**	0.25**	0.51**
	−0.01	0.00	0.07	−0.32**	−0.36**	−0.03	−0.26**	0.27**	0.63**
5.0% fiber span length§	−0.19*	0.21	0.29**	0.12	−0.12	−0.24**	0.47**	0.87**	0.13
	−0.22**	0.30**	0.41**	0.21	−0.33**	−0.19*	0.46**	0.91**	0.03
2.5% fiber span length§	−0.20**	0.18*	0.26**	0.15*	−0.19**	−0.22**	0.45**	0.85**	0.14*
	−0.24**	−0.26**	0.38**	0.24**	−0.39**	−0.18*	0.45**	0.90**	0.06
Fiber fineness§	0.17*	0.17*	0.06	0.07	0.80**	−0.08	0.14	−0.16*	−0.50**
	0.29**	0.18*	0.08	0.13	0.83**	0.05	0.06	−0.30**	−0.61**
Immature fiber§	−0.11	−0.09	−0.03	0.26**	−0.67**	0.173	−0.27**	0.05	0.55**
	−0.31**	−0.14*	0.07	−0.06	−0.79**	0.17*	−0.19	0.115	0.64**
Maturity ratio§	0.12	0.12	0.11	0.33**	0.74**	−0.25**	0.36**	0.01	−0.56**
	0.26**	0.16*	0.07	0.16*	0.77**	−0.25**	0.23**	−0.13	−0.72**

* Significant at $P < 0.05$.
** Significant at $P < 0.01$.
† Correlation coefficients for generation $F_{2:3}$.
‡ Correlation coefficients for generation $F_{2:6}$.
§ AFIS = Advanced Fiber Information System measurements (number of neps – maturity ratio).

while for fiber traits, E1, fiber fineness, Mic, SL 2.5%, SL 5.0%, and T1 showed the same results (Table 2). The heritability estimates for number of neps were observed to be moderate in $F_{2:3}$ progeny rows (a-b-h^2 = 0.46–0.35) and $F_{2:6}$ progeny rows (a-b-h^2 = 0.43–0.37). A nep is a knot of fibers that results from ginning or pre-spinning fiber preparation that can cause flaws in the finished textile product. The genetic control of neps has not been extensively studied. In a previous study, Pearson (1949) reported that cultivar variation was more important in explaining the variation in neps than the main effect of location and the cultivar × location interaction. However, May and Jividen (1999) did not find genetic variation for neps, which was found to be non-heritable in the two cotton populations used in their study. Further research is needed to understand the expression of neps and other traits that may contribute to them, such as micronaire reading, fiber length, immature fiber, maturity ratio, and seed coat fragments (Tables 4 and 5).

Number of seed coat fragments heritability estimates were found to be nonexistent and/or conflicting, precluding efficient selection against this trait (Table 2). Genetic variation for this trait was only found in $F_{2:3}$ (significant at $P < 0.05$) and not $F_{2:6}$ generation. Several

Table 5. Continuation of correlation coefficients for three agronomic and 17 fiber traits obtained from 208 F2:3 and F2:6 progeny developed from a cross between FiberMax 832 and MD51ne.

Cotton traits	Average length of all fibers by wt§	Average length of all fibers by no.§	Upper quartile of fiber length by wt§	Short fiber content by wt§	Short fiber content by no.§	5.0% Fiber span length§	2.5% Fiber span length§	Fiber fineness§	Immature fiber§
Average length of all fibers by no.§	0.82**								
	0.83**								
Upper quartile of fiber length by wt§	0.91**	0.54**							
	0.93**	0.59**							
Short fiber content by wt§	−0.45**	−0.86**	−0.07						
	−0.38**	−0.81**	0.04						
Short fiber content by no§.	−0.27**	−0.76**	0.97**	0.97**					
	−0.20**	−0.70**	0.97**	0.97**					
5.0% Fiber span length§	0.88**	0.50**	−0.02	−0.02	0.16*				
	0.91**	0.55**	0.01	0.01	0.18*				
2.5% Fiber span length§	0.86**	0.47**	0.00	0.00	0.17*	0.99**			
	0.90**	0.53**	0.02	0.02	0.19*	0.99**			
Fiber fineness§	0.08	0.41**	−0.57**	−0.57**	−0.58**	−0.21**	−0.28**		
	−0.11	0.21**	−0.45**	−0.45**	−0.48**	0.32**	−0.40**		
Immature fiber§	−0.25**	−0.56**	0.70**	0.70**	0.68**	0.06	0.11	−0.84**	
	−0.04	−0.26**	0.44**	0.44**	0.42**	0.15	0.21**	−0.80**	
Maturity ratio§	0.31**	0.61**	−0.72**	−0.72**	−0.68**	−0.01	−0.07	0.86**	−0.94** $F_{2.3}$
	0.15*	0.46**	−0.64**	−0.64**	−0.63**	−0.12	−0.17*	0.80**	−0.93** $F_{2.6}$

* Significant at $P < 0.05$.
** Significant at $P < 0.01$.
† Correlation coefficients for generation $F_{2:3}$.
‡ Correlation coefficients for generation $F_{2:6}$.
§ AFIS = Advanced Fiber Information System measurements (number of neps − maturity ratio).

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reasons could explain the low variability observed in this population: the choice of cultivars without enough variability for this specific trait, the trait is not genetically inherited, environmental variance plays a major role in its expression, measurement error, or all of the above. The reduction of seed coat fragments needs further research on heritability and correlation with fiber strength, length, neps, seed size and weight, and fiber per seed density. Except for number of seed coats, highest heritability estimates were observed among $F_{2:3}$ (a-b-h^2 = 0.46–0.85) and $F_{2:6}$ progeny rows (a-b-h^2 = 0.43–0.95), indicating that high selection efficiency could be accomplished in early and advanced generations (Table 2).

Comparisons of individual traits between $F_{2:3}$ and $F_{2:6}$ revealed significant differences for all traits between the two generations. Individual progeny by trait comparison between $F_{2:3}$ and $F_{2:6}$ were significant for all traits. For lint percentage and fiber traits (fiber fineness, micronaire reading, and number of neps), approximately 64% of the F_2–derived families by trait comparisons (one by one) between $F_{2:3}$ and $F_{2:6}$ generations were observed to be significantly different ($P > 0.05$). Even though the SSD method was used without breeding selection pressure to rapidly advance the population to the next generation in this okra-leaf type, at least 5% of the progeny were not significantly different ($P > 0.90$) between the two generations for at least four fiber traits (data not shown), which may indicate that the rule of thumb often practiced by breeders may be practiced by keeping the highest (5–10%) of superior plants. In practice, the lower the heritability, the greater the number of plants that should be selected to ensure that some of the selected plants are superior (Poehlman, 1987). The heritability estimates of some of these traits (Table 2) in this population showed that genetic variation was greater for most traits than environmental variation. After six generations by SSD, the okra-leaf population still possessed sufficient genetic variability to show a significant selection response in early and advanced generations and selection could be made to select for plants with superior fiber properties (Table 2). Similar variation was observed for T1 in another study (McCall et al., 1986). Selection for T1 was effective after four cycles of selection under an enforced self-pollination regime.

In this okra-leaf population, the fact that heritability estimates for most of the agronomic and fiber traits were greater than 0.6 on $F_{2:3}$ and $F_{2:6}$ progeny rows (Table 6) may indicate that a large proportion of the variance in these traits is additive and/or additive × additive in nature (Verhalen and Murray, 1967). However, differences were detected between means of the F_2-derived family generations ($F_{2:3}$ and $F_{2:6}$) and mid-parent (mean of the parent) for fiber span length traits (average length of all fiber by weight, SL 2.5%, SL 2.5% no., SL 5% no., and upper quartile length of fibers). These differences may indicate that not only additive, but also dominance or epistatic gene action may cause the means to deviate from halfway position (Ramey, 1962). No significant differences between the means of the F_2-derived family generations ($F_{2:3}$ and $F_{2:6}$) and the mid-parent (mean of the parent) were detected for the rest of the traits in both generations (data not shown).

The correlations among traits and trait variation observed within each generation in this population have practical applications for the simultaneous improvement of multiple fiber traits. Based on yield potential and/or fiber properties most cotton breeders begin making plant selections in the F_2 from a particular cross displaying a large amount of variability. May and Jividen (1999) reported that early generation selection for T1 measurement has resulted in desirable fiber profiles, and F_2 bulk with low selection intensity may be adequate to identify populations with superior fiber traits (May and Green, 1994). Even though mass selection may be effective for improving most of the traits ($h^2 > 0.60$), especially lint percentage, Mic, T1, E1, and SL 2.5%, emphasis may have to be placed on pedigrees, sibs, and progeny tests to achieve a high degree of genetic progress (Meredith and Bridge, 1971; Verhalen and Murray, 1967). Breeders may begin making selections as early as the F_3 when selection units can be replicated. Thereafter, antagonistic trait correlations may become neutral or favorable in later generations, facilitating the concurrent improvement of fiber yield and quality.

ACKNOWLEDGMENTS

The author would like to thank the USDA-ARS, C.G. & P. Res. Unit at Stoneville, Mississippi for the support of this project. In addition, the author would like to thank Dr. William R. Meredith, Jr. for providing the original ($F_{2:3}$) seed and support to this project. Special thanks to Debbie Boykin for her great assistance in the statistical and data analysis and Robin Jordan for field assistance. The author would like to thank Dr. James Frelichowski, Dr. Bob Hutmacher and the anonymous reviewers for their suggestions and comments to improve this manuscript. Names are necessary to report factually in available data, however, the USDA neither guarantees nor warrants the standard of products or service, and the use of the name by the USDA implies no approval of the product or service to the exclusion of others that may also be suitable.

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