

GENETIC CORRELATIONS AMONG AGRONOMIC AND FIBER QUALITY TRAITS IN SIX UPLAND COTTON POPULATIONS

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Abstract

Cotton (*Gossypium hirsutum* L.) cultivars are developed using traditional self-pollinated breeding methods, including inbreeding for two or more generations prior to line extraction and testing. Genetic progress for many traits including yield has been limited in recent years. It has been speculated that this is partly due to a narrow genetic base and negative relationships among traits of interest. Six cotton populations were advanced from the F₂ to F₄ generation by two methods of inbreeding: pedigree and single-seed descent (bulk). Our objectives were to compare inbreeding method, and determine genetic correlations among traits of interest. Inbreeding method and previous selection had no influence on line performance for most traits. Lint mass seed⁻¹ and lint yield were increased by pedigree selection in one population. Micronaire was decreased in one population, and fiber length was increased in another. Most trait/population combinations were unaffected by inbreeding method. Genetic correlations varied widely among populations, but strong negative correlations between lint yield and fiber strength continue to be a problem.

Background

Upland cotton is a self-pollinated species, and breeding methods used for its improvement usually involve hybridization followed by generations of inbreeding with or without selection during the inbreeding generations. Most breeders rely on pedigree selection or one of its variations in development of new genetic lines (Bowman, 2000). Early-generation testing has also been suggested as a means of identifying superior populations, but success has been somewhat limited due to inconsistent performance of genotypes across years (Jones and Smith, 2006). Yield-testing of experimental genotypes does not usually begin until the F₄ or later generation (Bowman, 2000). Improvements in yield and fiber quality of upland cotton remain as primary objectives in most cotton breeding programs. Fiber quality traits determine its usefulness by the industry and are largely under genetic control (Meredith, 1984). However, lint yield and fiber quality traits tend to be negatively correlated, which is a major limitation to their simultaneous improvement. Several studies have documented the negative genetic correlation between yield and fiber strength and yield and fiber length (Miller and Rawlings, 1967; Meredith and Bridge, 1971; Fotiadis and Miller, 1973; Scholl and Miller, 1976). Attempts to reduce the association between yield and fiber strength have met with some success (Culp et al., 1979). Progress in the improvement of upland cotton for traits related to yield and fiber properties, particularly fiber strength (Meredith, 2005) has been limited in past years. Yield, along with fiber strength, has actually declined since 1990 (Lewis, 2000). It has been speculated that this is due in part to a narrow genetic base in elite cotton germplasm (Bowman, 1996) and negative genetic relationships between lint yield and important fiber quality traits such as fiber strength and fiber length.

Materials and Methods

Advanced lines from six cotton populations (Table 1) developed by two methods of inbreeding were grown in replicated plots in the field at the Plant Breeding Unit (PBU) in Tallassee, AL during 2005 and 2007.

Table 1. Parents and populations

POP 1	Fibermax 966 × Deltapine 565
POP 2	Arkcot A129 × Stoneville 580
POP 3	PD 94042 × Delta Pearl
POP 4	Miscot 8004 × Fibermax 966
POP 5	PD 94045 × Suregrow 821
POP 6	Miscot 8001 × Suregrow 747

Eleven parents were selected based on adaptation and performance, not necessarily for contrasting phenotypes for the traits of interest or genetic diversity, and represent elite germplasm typical of a modern cotton improvement program in the mid-South and Southeastern production regions. Single-seed descent (modified bulk) populations were advanced by that method to the F_3 generation, when single plants were selected randomly and increased in $F_{3,4}$ plant rows in 2004 to produce seed for testing in replicated, multiple-row plots in 2005 and 2007. Pedigree selection was based on a selection index composed of one yield component and two AFIS fiber quality traits: Lint mass seed⁻¹ (LMS, a component of yield), and short fiber content and upper quartile fiber length (SFC and UQL, AFIS fiber quality traits). These variables were standardized by subtracting the mean and dividing by the standard deviation, and then summed, treating SFC as a negative value since lower values are more desirable. Open-pollinated boll samples (five bolls plant⁻¹) were collected at harvest from three F_3 plants within each F_2 -derived plant row. Within each population, eighteen F_3 -derived genotypes (sixteen for POP 5) were selected for yield testing based on the selection index performance (best combinations of high LMS and UQL, with low SFC).

Pedigree-selected $F_{3,5}$ and $F_{3,7}$ lines were yield-tested during 2005 and 2007 and compared with a group of non-selected lines advanced to the same level of inbreeding without selection using single-seed descent, a modified bulk method. For POP 6, only 6 single-seed descent lines were available for testing. Plots were 2 rows, 6.1 m long with 1 m spacing between rows. Fifty-boll samples were hand harvested for fiber analysis followed by machine picking for yield determination. Fiber traits were determined by HVI analysis at Cotton Incorporated, Cary, NC. Experimental design was a randomized complete block with 3 replications and genotypes nested within inbreeding methods. Data were analyzed using SAS[®] PROC MIXED with genotypes as a random factor and inbreeding methods and blocks as fixed factors. Genetic correlations among traits and their standard errors were calculated (ignoring inbreeding method) using the multivariate restricted maximum likelihood approach (Holland, 2006). Due to convergence issues in PROC MIXED, some variables were transformed. Lint yield was transformed from lbs acre⁻¹ to tons acre⁻¹, boll mass was multiplied by 100, and 50% span length in inches was multiplied by 10.

Results and Discussion

For most traits, inbreeding method had little impact on mean line performance (Table 2). Lint yields were essentially equal regardless of inbreeding method with the exception of POP 2, where yield was higher for pedigree-selected lines. Lint percentage was unaffected by inbreeding method across all populations. Lint mass seed⁻¹, one of the traits included in the selection index, was increased in only one population by selection, and that was POP 2, the population with the lowest mean LMS. Micronaire values were affected by inbreeding method for two populations, but the effect was in opposite directions: POP 2 had an increase in micronaire as a result of pedigree selection, POP 6 had a reduction. Fiber length (upper-half mean, UHM) was increased by selection in POP 6, but this population tended to have lower fiber length overall. Fiber elongation was slightly reduced in POP 4 by selection. All other traits were unaffected by inbreeding method. Efforts to reduce SFC by including this trait as part of the selection index were entirely unsuccessful.

Table 2. Yield and fiber quality traits for six cotton populations advanced by two methods of inbreeding.

Method	Lint yield lbs/A	Lint %	Lint mass seed ⁻¹ g ($\times 10^{-2}$)	Boll mass g	Mic	UHM in	T ₁ g/tex	UI %	E ₁ %	SFC %
Population 1 (Fibermax 966 $\times$ Deltapine 565)										
PED [†] (18)	1223.5	41	7.0	5.1	4.7	1.12	29.6	82.1	5.2	7.1
SSD (18)	1228.1	41	7.0	4.9	4.6	1.11	29.9	82.1	5.4	7.4
P-contrast	0.87	0.81	0.88	0.24	0.37	0.39	0.48	0.99	0.23	0.32
Population 2 (Arkcot A 129 $\times$ Stoneville 580)										
PED [†] (18)	1121.8	38	6.0	5.0	4.7	1.12	31.5	83.3	5.7	5.9
SSD (18)	1040.4	37	6.0	5.0	4.5	1.13	31.6	83.2	5.8	5.6
P-contrast	0.06	0.16	0.08	0.59	0.09	0.67	0.83	0.86	0.53	0.19
Population 3 (PD 94042 $\times$ Delta Pearl)										
PED [†] (18)	1157.3	45	7.0	4.5	4.8	1.12	28.6	82.5	5.7	7.4
SSD (18)	1153.8	45	7.0	4.5	4.8	1.12	28.3	82.3	5.8	7.2
P-contrast	0.95	0.50	0.70	0.82	0.99	0.45	0.50	0.67	0.46	0.63
Population 4 (Miscot 8004 $\times$ Fibermax 966)										
PED [†] (18)	925.2	42	7.0	4.8	4.8	1.04	28.2	81.6	6.1	7.4
SSD (18)	938.0	42	7.0	4.7	4.8	1.03	27.5	81.5	6.3	7.5
P-contrast	0.76	0.79	0.75	0.28	0.95	0.36	0.14	0.86	0.07	0.79
Population 5 (PD 94045 $\times$ Suregrow 821)										
PED [†] (18)	1017.4	40	7.0	4.8	4.4	1.12	31.5	83.6	5.3	5.9
SSD (18)	1009.4	40	7.0	4.7	4.4	1.11	31.6	83.5	5.4	5.8
P-contrast	0.82	0.66	0.58	0.09	0.62	0.20	0.86	0.76	0.60	0.51
Population 6 (Miscot 8001 $\times$ Suregrow 747)										
PED [†] (18)	884.4	41	7.0	4.7	4.5	1.08	27.9	82.0	6.4	7.7
SSD (18)	929.9	42	7.0	4.7	4.7	1.05	27.6	82.2	6.6	7.1
P-contrast	0.44	0.71	0.51	0.91	0.10	0.01	0.71	0.52	0.36	0.33

[†]PED = Pedigree and SSD = Single-seed Descent. Numbers in parentheses indicate number of lines tested for each method/population combination.

In order to calculate estimates of genetic correlation, certain conditions must be satisfied. Positive genetic variance estimates must exist for any two traits for which genetic correlations are being estimated. Zero or negative estimates of genetic variance for lint yield in 2 of the 6 populations (POP 1 and POP 4), made it impossible to estimate genetic correlations between lint yield and any other variable for those populations. POP 2 had a negative or zero genetic variance for lint percentage. A lack of genetic variation for some traits is not surprising in these populations, given the lack of genetic diversity among the parents. Otherwise, genetic correlations, mostly positive, were found to exist between lint yield and yield component traits across populations (Table 3). Genetic correlations between lint yield and lint percentage, and lint yield and LMS component traits were fairly strong, although standard errors tended to be large. Estimable genetic correlations between lint yield and boll weight were variable.

Table 3. Genetic correlations between lint yield and yield components (and their associated standard errors) for six cotton populations.

Population	Lint %	Lint mass seed ⁻¹	Boll wt.
POP 1	†	†	†
POP 2	‡	0.57 (0.27)	-0.40 (0.77)
POP 3	0.59 (0.21)	1.18 (0.28)	0.66 (0.29)
POP 4	†	†	†
POP 5	*	**	**
POP 6	0.22 (0.33)	0.04 (0.39)	-0.06 (0.46)

† Negative variance component estimate for lint yield.

‡ Negative variance component for lint percentage.

* No maximum likelihood estimate could be calculated.

** Nonsensical maximum likelihood estimate obtained.

Estimable genetic correlations, both positive and negative, were found to exist between lint yield and fiber quality traits (Table 4). Again, negative or zero estimates of genetic variance for certain trait combinations prevented estimation of genetic correlations for all possible trait pairs. In particular, there was a consistent negative genetic correlation between lint yield and fiber strength, as has been shown previously in experiments going back over 40 years. This continues to be a formidable barrier to the simultaneous improvement of both yield and fiber strength. There was a general lack of genetic correlation between lint yield and fiber length. Genetic correlations between lint yield and fiber elongation were mostly positive.

Table 4. Genetic correlations between lint yield and fiber quality traits (and their associated standard errors) for six cotton populations.

Population	Micronaire	UHM	Strength	Uniformity Index	Elongation
POP 1	†	†	†	†	†
POP 2	0.16 (0.25)	0.02 (0.39)	-0.26 (0.24)	-0.34 (0.43)	0.33 (0.22)
POP 3	0.56 (0.25)	-0.16 (0.43)	-0.44 (0.26)	‡	0.79 (0.23)
POP 4	†	†	†	†	†
POP 5	‡	‡	‡	‡	1.24 (8.70)
POP 6	0.09 (0.37)	‡	-0.91 (0.45)	-1.33 (3.67)	-0.04 (0.36)

† Negative variance component estimate for lint yield.

‡ Negative variance component for trait listed in column header.

The lack of effects on lint yield, yield components and fiber traits due to inbreeding method were probably the result of the particular selection index used. The traits used in the selection index were a yield component (LMS), a measure of fiber length (UQL), and SFC. The yield component trait and the fiber quality trait are known historically to be negatively related, and SFC is known to be poorly heritable and highly variable among single plants (Weaver and Badger, 2006). Selection for SFC therefore probably had little effect, and selection for the other two traits were largely negating.

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