Introgression of Day-Neutral Genes in Primitive Cotton Accessions: I. Genetic Variances and Correlations

J. C. McCarty, Jr.,* J. N. Jenkins, and J. Zhu

ABSTRACT

Many of the primitive accessions of cotton, *Gossypium hirsutum* L., are photoperiodic and not readily useable by plant breeders. Five generations of day-neutral progenies (F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5) derived from 16 accessions crossed to 'Deltapine 16' were evaluated for agronomic and fiber traits for 3 yr. Genetic variance components for each trait and correlation among these traits were studied. Variation of accession generation was highly significant for all traits studied. Main effects for accessions and generations were significant; however, the magnitude was relatively small compared with the interaction variation. The breeding merit of day-neutral progenies should be evaluated according to specific accessions. Lint yield had significant but small positive phenotypic correlation with lint percentage, boll size, and 2.5% span length, but not with the other traits studied. Highly significant positive correlations were found for effects of accession, generation, and accession × generation between lint yield and lint percentage. With the use of multiple backcrosses to introgress day-neutral genes in primitive cotton accessions large interaction can be expected between accession and backcross generation; therefore, specific generations should be evaluated for the trait of interest.

C ROP IMPROVEMENT requires diverse plant genetic resources. These resources may extend from commercial cultivars to wild or exotic species. A narrow genetic base could result in a crop being highly vulnerable to stresses. Therefore, it is important that attempts be made to expand the genetic diversity by utilizing new and unrelated sources of germplasm.

Research has shown that primitive accessions of cotton have useful genetic variability (Percival, 1987; Meredith, 1991; McCarty and Jenkins, 1992; McCarty et al., 1995). Percival and Kohel (1990) reviewed the collection, distribution, and evaluation of *Gossypium* germplasm. The number of primitive accessions in the *Gossypium* collection currently numbers more than 2000 (Percival, 1987).

The utilization of the genetic variability of the primitive accessions has been limited because most require short days to initiate flowers and produce fruit. A back-cross-breeding program has been in place for a number of years to incorporate day-neutral genes in the primi-

tive accessions (McCarty et al., 1979; McCarty and Jenkins, 1992, 1993).

McCarty et al. (1995) evaluated F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5 progenies for 16 day-neutral germplasm accessions for several agronomic and fiber traits. Results indicated there was useful genetic variability yield and fiber traits in the day-neutral lines. The objective of the present study was to determine genetic variances and correlations for the agronomic and fiber traits to aid cotton breeders in utilizing these accessions in their breeding programs.

MATERIALS AND METHODS

Sixteen photoperiodic primitive germplasm accessions (Table 1) were selected as male parents and crossed with Deltapine 16. The crosses were made at a winter breeding nursery in Mexico where the plants would flower. The F_1 generation was self-pollinated at the winter nursery. Then the F_2 generation was grown in field plots at Mississippi State, MS, and F_2 progeny with day-neutral flowering habit were selected. Seeds from one F_2 day-neutral plant in each accession cross were grown as F_3 in the tropical winter nursery and backcrossed to their respective germplasm accession parent. One open-pollinated boll was harvested from each F_2 that set fruit, seeds were bulked and advanced to the F_5 generation. This procedure was described by McCarty et al. (1979). Except for selection for day-neutrality after each backcross cycle, no other selection pressure was applied.

Experiments were conducted at the Plant Science Research Center, Mississippi State, MS, in 1989, 1990, and 1991 on a Marietta sandy loam (fine loamy, siliceous thermic fluvaquentic Eutrochrepts) soil. Eighty F_5 populations consisting of the F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5 generations derived from 16 single-cross combinations were planted in a randomized complete block design with four replicates in a split-plot arrangement of treatments. Generations were whole plots and accessions were sub-plots. Plots consisted of a single row, 13 m in length, with 1 m between rows. Standard cultural and insect control practices were followed throughout the growing seasons.

Plots were harvested with a mechanical picker for yield determination. Boll samples containing 25 bolls were hand harvested in each plot prior to mechanical picking. Boll samples were weighed, and ginned on a 10-saw laboratory gin to determine boll weight, lint percentage, and seed index (weight of 100 seed). Lint samples were sent to Starlab Inc. (Knoxville, TN) for determination of elongation (E_1), fiber strength, 2.5% span length (2.5% S. L.), 50% span length (50% S. L.), and micronaire.

Data of yield and fiber traits were analyzed by mixed linear model approaches. A linear model was used that included years as environments (E), accessions (A), generations (G), and their interactions (AG, AE, GE, and AGE) along with

J.C. McCarty, Jr., and J.N. Jenkins, USDA-ARS, Crop Sci. Res. Lab., P.O. Box 5367, Mississippi State, MS 39762; J. Zhu, Agronomy Dep., Zhejiang Agriculture Univ., Hangzhou 310029, China. Work was completed while J. Zhu was a visiting scientist at Mississippi State Univ. Contribution of the USDA-ARS in cooperation with the Mississippi Agric. and Forestry Exp. Stn. Received 16 Sept. 1996. *Corresponding author (jcm@ra.msstate.edu).

Table 1. Texas number, PI number, and collection location of primitive accessions that were crossed to Deltapine 16.†

Texas no.	PI no.	Collection location		
		Country	State	Site
53	154080	Mexico	Chiapas	Comitan de Dominguez
78	153969	Guatemala	–	–
87	153975	Guatemala	–	Coronado
88	153976	Guatemala	–	San Jose El Idolo
91	153980	Guatemala	–	–
106	163712	Guatemala	Chiquimula	Chiquimula
119	163645	Guatemala	Jutiapa	Valle Nuevo
158	163714	Guatemala	Chiquimula	Chiquimula
168	163634	Guatemala	Jutiapa	Jacarro Grande
174	163647	Guatemala	Jutiapa	Progreso
175	163661	Guatemala	Jutiapa	Santa Catarina Mita
228	163672	Guatemala	Jalapa	Chaparron
257	165253	Mexico	Oaxaca	Mitla
326	165326	Mexico	Guerrero	Asoyu
612	154023	–	–	–
1149	529966	–	–	–

† Plant descriptors for these accessions were published by Percival (1987) and are accessible through the Germplasm Resource Information Network (GRIN).

block factor (B) and residual error (e). All of these factors were defined as random effects.

Variance components for each trait and covariance components among all traits studied were estimated by MINQUE (1) method (Rao, 1971; Zhu, 1992; Zhu and Weir, 1996). Total phenotypic variance was estimated as

$$V_P = V_E + V_A + V_G + V_{AG} + V_{AE} + V_{GE} + V_{AGE} + V_e$$

This partitioning was also applicable for phenotypic covariance,

$$C_P = C_E + C_A + C_G + C_{AG} + C_{AE} + C_{GE} + C_{AGE} + C_e$$

Correlation coefficients among components were calculated. Jackknifing over blocks within year was used for estimates and standard errors of variances and correlations (Miller, 1974; Zhu, 1989). Since there were a total of 12 blocks for 3 yr, the degrees of freedom were 11 for the jackknifing. Testing significance of genetic parameters was conducted by a one-tail t-test for proportion of variances but by a two-tail t-test for correlation coefficients. All the data were analyzed on a PC computer with programs written in C language.

RESULTS AND DISCUSSION

Estimated proportions of variance components to total phenotypic variance are listed in Table 2 for yield and fiber traits. Variation of year effects (V_E/V_P) and residual errors (V_e/V_P) was large as compared with other factors for both yield and fiber traits. Variation of accession × generation (V_{AG}/V_P) was highly significant and

important for all the traits studied. Although variation of main effects of accession (V_A/V_P) or generation (V_G/V_P) was significant, the magnitude was relatively small as compared with the interaction variation. The accession by generation interaction indicates that the breeding values of accessions may vary by generation. The environment interaction variation was small for AE, GE, and AGE, respectively. Therefore, effects of accession, generation and accession × generation are stable in different environments.

Correlation coefficients among yield and fiber traits for different components are presented in Table 3. Phenotypic correlation was usually different in magnitude or even in direction as compared with the correlation of component effects. Lint yield had highly significant but small positive phenotypic correlation with lint percentage, boll size, and 2.5% span length, but not with other traits. Strong positive correlations were found for effects of A, G, and AG between lint yield and lint percentage. It was suggested that selection of high lint percentage in accessions, generations, or generations within accessions could significantly increase the lint yield. There were positive correlations between lint yield and boll size for AG and GE effects. Since variation of GE for boll size is small relative to main effects, selecting generations with large bolls might be efficient in increasing yield in specific accessions. Selection for high yield in accessions or generations could result in small seeds because of the strong negative correlation between lint yield and seed size (Table 3).

Although lint yield had highly negative correlations of R_{GE} with elongation, and of R_G with micronaire, 50% span length, and strength, yield would not be affected by selection of generations for these fiber traits because of the very small variation for these effects. Improvement of yield could be expected along with elongation while selecting generations, or with 50 and 2.5% span length while selecting accessions. Positive R_{GE} between lint yield and fiber strength indicated the possibility of simultaneous improvement for these two traits while selecting generations in certain environments. In this study, BC_3F_5 and BC_4F_5 in 1991 tended to have high lint yield and strong fiber strength (data not shown).

Accessions with large bolls, long but weak fiber tended to have high lint percentage. Since the correlation between lint percentage and seed index for A and AG effects, was not significant selection of accessions with high lint percentage might not result in reduced

Table 2. Estimates of proportion of variance components for yield and fiber traits of cotton.

Parameter†	Lint yield	Lint percentage	Boll size	Seed index	Elongation	Micronaire	50% Span length	2.5% Span length	Strength
V_E/V_P	0.219**	0.196**	0.042**	0.260**	0.268**	0.381**	0.131**	0.361**	0.260**
V_A/V_P	0.049**	0.097**	0.026**	0.032*	0.071**	0.051**	0.073**	0.118**	0.053**
V_G/V_P	0.094**	0.091**	0.012**	0.015*	0.041**	0.025**	0.010**	0.000	0.019*
V_{AG}/V_P	0.094**	0.202**	0.031**	0.120**	0.106**	0.086**	0.143**	0.172**	0.137**
V_{AE}/V_P	0.000	0.020**	0.007**	0.012**	0.016**	0.000	0.034**	0.000	0.027**
V_{GE}/V_P	0.069*	0.000	0.001**	0.010*	0.013	0.000	0.022*	0.013**	0.056**
V_{AGE}/V_P	0.070*	0.074**	0.019**	0.090**	0.000	0.060*	0.057**	0.026**	0.000
V_e/V_P	0.405**	0.321**	0.145**	0.462**	0.483**	0.397**	0.531**	0.309**	0.447**

*, ** Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.
† Phenotypic variance (V_P) was partitioned into environment (V_E), accessions (V_A), generations (V_G), accession by generation (V_{AG}), accession by environment (V_{AE}), generation by environment (V_{GE}), accession by generation by environment (V_{AGE}), and residual (V_E).

Table 3. Estimates of correlation coefficients among yield and fiber traits of cotton.

Parameter†	Lint percentage	Boll size	Seed index	Elongation	Micronaire	50% Span length	2.5% Span length	Strength
Lint yield								
R_A	0.55**	0.26	-0.58**	0.15	0.01	0.45**	0.51**	0.04
R_G	0.95**	0.04	-0.76**	1.00**	-0.51**	-1.00**	0.00	-1.00**
R_{AG}	0.76**	0.44**	0.00	0.25	0.34**	0.19	0.19	-0.30**
R_{AE}	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
R_{GE}	0.00	0.58**	0.36*	-1.00**	0.00	-0.22	0.25	0.28*
R_{AGE}	0.33	0.01	-0.23	0.00	-0.01	0.08	0.00	0.00
R_e	0.15*	0.12*	0.06	0.01	-0.04	0.07	0.10	0.06
R_P	0.37**	0.15**	-0.05	0.08	-0.02	0.04	0.12*	-0.07
Lint percentage								
R_A		0.55**	-0.22	0.04	0.14	0.60**	0.76**	-0.34*
R_G		0.20	-0.75**	0.64**	-0.40	-0.79**	0.00	-1.00**
R_{AG}		0.48**	-0.03	0.17	0.33**	0.07	0.17*	-0.49**
R_{AE}		-0.11	0.08	0.14	0.00	0.12	0.00	-0.31
R_{GE}		0.00	0.00	0.00	0.00	0.00	0.00	0.00
R_{AGE}		0.33**	-0.09	0.00	0.10	-0.06	-0.14	0.00
R_e		0.04	-0.12	0.04	-0.02	-0.02	0.02	-0.06
R_P		0.21**	-0.13*	0.11*	0.04	0.04	0.15**	-0.24**
Boll size								
R_A			-0.16	-0.46**	0.61**	-0.34**	-0.03	-0.59**
R_G			0.18	0.21	0.52**	0.75**	0.00	0.12
R_{AG}			0.50**	-0.10	-0.08	0.03	0.18	-0.21**
R_{AE}			0.39*	0.67**	0.00	0.15*	0.00	-0.62**
R_{GE}			0.10	-0.87**	0.00	-0.46*	0.49**	-0.30
R_{AGE}			0.41**	0.00	0.45*	0.52**	0.48**	0.00
R_e			0.57**	-0.04	0.25*	0.15*	0.11	-0.08
R_P			0.47**	-0.08	0.27**	0.11**	0.14**	-0.12**
Seed index								
R_A				0.07	0.42*	-0.30**	-0.34*	-0.08
R_G				-0.19	0.78**	0.86**	0.00	0.92**
R_{AG}				-0.30*	-0.27	-0.02	0.11	0.06
R_{AE}				0.74**	0.00	0.72**	0.00	-0.31
R_{GE}				-1.00**	0.00	0.17	0.97**	0.02
R_{AGE}				0.00	0.76**	0.29*	0.35**	0.02
R_e				-0.05	0.23	0.12	0.05	-0.06
R_P				-0.07	0.22**	0.11*	0.07	0.01
Elongation								
R_A					-0.53**	0.16	0.14	0.11
R_G					-0.48**	-0.89**	0.00	-0.85**
R_{AG}					0.15	0.16	0.03	-0.25*
R_{AE}					0.00	0.27	0.00	-0.01
R_{GE}					0.00	-0.36	-1.00**	-0.39*
R_{AGE}					0.00	0.00	0.00	0.00
R_e					-0.13*	0.06	0.10*	-0.09
R_P					0.11**	0.04	0.04	-0.15**
Micronaire								
R_A						-0.22	-0.24*	0.09
R_G						1.00**	0.00	0.75**
R_{AG}						-0.20	-0.52**	0.03
R_{AE}						0.00	0.00	0.00
R_{GE}						0.00	0.00	0.00
R_{AGE}						0.36**	0.25	0.00
R_e						-0.02	-0.22**	-0.11*
R_P						-0.00	-0.20**	0.01
50% span length								
R_A							0.94**	0.47**
R_G							0.00	0.87**
R_{AG}							0.86**	0.43**
R_{AE}							0.00	0.13
R_{GE}							-0.04	0.28
R_{AGE}							0.34*	0.00
R_e							-0.67**	0.13*
R_P							0.69**	0.24**
2.5% span length								
R_A								0.10
R_G								0.00
R_{AG}								0.24**
R_{AE}								0.00
R_{GE}								0.11
R_{AGE}								0.00
R_e								0.12*
R_P								0.14*

*, ** Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.
† Correlation coefficient for accession (R_A), generation (R_G), accession by generation (R_{AG}), accession by environment (R_{AE}), generation by environment (R_{GE}), accession by generation by environment (R_{AGE}), residual (R_E), and phenotype (R_P).

seed size. Selection of accessions with large bolls might result in lower elongation, 50% span length and fiber strength. Seed size was positively correlated with micronaire for accessions or with elongation for accessions in some environments ($\hat{R}_{AE} = 0.74**$). Simultaneous improvement was possible for fiber strength with 50% span length while selecting accessions or generations in accessions, and with 2.5% span length while selecting generations in accessions. Highly positive correlations were observed for R_A and R_{AG} between 50 and 2.5% span length.

Since there were large interaction between accession generation for the yield and fiber traits studied, evaluation of accessions should be considered for specific generations. We will predict breeding merits for accessions, generations, and their combinations in a companion paper (McCarty et al., 1998).

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