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Genotype X Environment Interactions Over Seven Years for Yield, Yield Components, Fiber Quality, and Gossypol Traits in the Regional High Quality Tests

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ABSTRACT

Since the 1960s, many changes in cotton (*Gossypium hirsutum* L.) cultivar tests have been made. This study partitioned the total variation for 26 traits into environment (E), genotype (G) and genotype X environment (GE) variance components for the 2001 through 2007 Regional High Quality (RHQ) tests with 98 genotypes. It evaluated 26 traits and 56 year-location environments. There were four yield traits, five yield components, six traditional breeder-geneticists (BG) fiber traits, seven High Volume Instrumentation (HVI) fiber traits, and four gossypol traits. Yield variance components for lint, seed, oil, and N were similar with an average of 87, 5, and 8% of the total variance due to E, G, and GE, respectively. Lint% E, G, and GE were 57, 33, and 10%, respectively and were similar to oil% E, G, and GE which were 53, 37, and 10%, respectively. Length, strength, and micronaire's G components for BG fiber was 28, 52, and 16%, respectively. For the HVI samples, G was similar with 36, 48, and 18%, respectively. Average G for total gossypol and its two isomers, plus (+) and minus (-) was 36, 47, and 29%, respectively. The

plus (+) percent of total gossypol was 17, 72, and 11% for E, G, and GE, respectively. This was the lowest E% and highest G% of all the 26 traits. The results of this study suggested that during the last 50 yrs, little changed in E, G, and GE variance components occurred.

Genotype X environment interactions (GE) have long been of major interest to cotton breeders. Long-term cultivar and/or germplasm trials provide an excellent source of extensive data to study GE interactions. The National Cotton Variety Testing program (NCVT), which began in 1960, has provided a wealth of valuable information for cotton breeders, agronomists, and producers. Miravalle (1987) reviewed the history of the NCVT and reported its first objective was to study “the interaction of principal cultivars or types of cotton and the location effects for the Cotton Belt as a whole and the principal regions within the Belt.” Research by Miller et al. (1958, 1959, 1962), Abou-El-Fittouh et al. (1969), and Pope and Ware (1945) gave direction on organizing NCVT programs and subsequently five regions were identified for the NCVT. Because of the long-term, continuous nature of the program and its design, the NCVT provides an excellent dataset to study GE interactions for cotton fiber and seed traits.

The first GE investigations for agronomic and fiber quality traits involved early generation progeny selection within states (Miller et al., 1958) and larger geographic areas were evaluated by Pope and Ware (1945) and Miller et al. (1962). Additional research using NCVT data by Abou-El-Fittouh et al. (1969) investigated within and across regions. These investigations indicated the environmental (E) source of variability for lint yield was great, frequently accounting for more than 80% of the total variability. Generally, the Location (L) source of variability was greater for yield, yield components, and fiber quality traits than that for years (Y). For yield, the GE component of variance was equal to or greater than that for genotype (G). This relationship held true for

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variations among states and within states (Abou-El-Fittouh et al. 1969; Miller et al. 1959). The GE for yield components and fiber quality traits was smaller than G in most studies.

More recently, six studies reported similar yield and fiber quality GE results. These studies involve widely different E, G, and GE analyses methods. DeLacy et al. (1990) reported on two studies, one in Thailand and one in Australia. Kerby et al. (2000) conducted two GE analyses on private sector in-house cultivar trials, which involved cotton of different maturity and involved 16 USA states. Meredith (2003) reported on 36 yr (1964–1999) of results of the Regional High Quality (RHQ) Test. In that analysis, Meredith (2003) evaluated 19.2 genotypes per year and the average number of locations was 9.2 per year in eight states from North and South Carolina to Texas. Campbell and Jones (2005) characterized GE for commercial cultivars evaluated in South Carolina Official Variety Trials from 2000 to 2003. Blanche et al. (2006) conducted bi-plot analysis and characterized GE for conventional and transgenic cultivars. Campbell et al. (2011) estimated E, G, and GE contribution on 82 germplasm lines and cultivars produced from 70 yr of improvement by the USDA-ARS Pee Dee germplasm enhancement program located in Florence, SC. These unique germplasm lines were produced by introgression of genes from wild *Gossypium* species and the researchers' major objective was to develop germplasm with improved combinations of yield and fiber traits. This study involved 14 year-location environments involving four states. These six previous GE studies are summarized for yield and yield components in Table 1 and for fiber quality traits in Table 2. Most noticeable is that for yield, 86% of total variation was due to E, 5% due to G, and 9% to GE. These results are similar to the earlier GE studies.

Other economically important cotton production traits in need of GE analyses are cottonseed oil and protein. An early GE evaluation for cottonseed oil and protein was conducted by Pope and Ware (1945). It involved 16 cultivars grown in 11, 13, and 14 environments from North Carolina to Texas in 1935, 1936, and 1937, respectively. Results showed large effects on both oil and protein were due to E. Pope and Ware (1945) concluded that despite large E effects, the rank for G was not greatly influenced by ecology and weather. Using data from the 1973 to 1975 NCVT, Turner et al. (1976) calculated mean squares for oil content of 15.6, 0.9, and 1.0 for E, G,

and GE, respectively. Cherry et al. (1978) used the same cultivars as that of Turner et al. (1976) and both studies showed large E effects. However, the ratio of G to GE was 0.9 for Turner et al. (1976) and 3.7 for Cherry et al. (1978).

Table 1. Average results of previous studies partitioning percent of total contributions of environments (E), genotype (G), and GE for yield and yield components

Study Author	% of Total components		
	E	G	GE
Lint Yield			
DeLacy et al., 1990 (T) ^z	90	3	8
DeLacy et al., 1990 (A)	80	11	9
Kerby et al., 2000 (E) ^y	94	1	6
Kerby et al., 2000 (M)	90	1	9
Meredith, 2003	80	7	13
Campbell and Jones, 2005	90	2	8
Blanche et al., 2006	92	3	5
Campbell et al., 2011	72	9	19
AVERAGE	86	5	9
Lint Percent			
Kerby et al., 2000	55	24	21
Kerby et al., 2000	82	6	12
Meredith, 2003	57	26	17
Campbell and Jones, 2005	23	57	20
Blanche et al., 2006	28	38	34
Campbell et al., 2011	66	21	13
AVERAGE	52	29	19
Boll Weight			
Meredith, 2003	55	27	19
Blanche et al., 2006	36	38	26
Campbell et al., 2011	44	10	46
AVERAGE	45	25	30
Seed Weight			
Meredith, 2003	47	36	18
Blanche et al., 2006	26	48	27
Campbell et al., 2011	43	29	28
AVERAGE	39	38	24

^z T and A data reported by DeLacy et al., 1990 are summarizations from research conducted in Thailand and Australia, respectively.

^y E and M data reported by Kerby et al., 2000 from early- and mid-maturing tests, respectively.

Table 2. Results of previous studies partitioning percent of total variability contributed by environments (E), genotypes (G), and genotype X environments (GE) interactions for fiber quality traits.

Study Author	% of Total components		
	E	G	GE
Length, %			
DeLacy et al., 1990 (A) ^z	38	49	13
Kerby et al., 2000 (E) ^y	85	6	9
Kerby et al., 2000 (M)	85	6	9
Meredith, 2003	50	31	19
Campbell and Jones, 2005	47	45	8
Blanche et al., 2006	57	19	23
Campbell et al., 2011	32	33	35
AVERAGE	56	27	17
Strength, %			
DeLacy et al., 1990 (A)	22	65	13
Kerby et al., 2000 (E)	29	54	17
Kerby et al., 2000 (M)	66	15	19
Meredith, 2003	34	44	22
Campbell and Jones, 2005	14	63	8
Blanche et al., 2006	56	27	17
Campbell et al., 2011	58	38	20
AVERAGE	40	44	16
Micronaire, %			
DeLacy et al., 1990 (A)	56	25	19
Kerby et al., 2000 (E)	59	21	20
Kerby et al., 2000 (M)	78	6	16
Meredith, 2003	61	21	18
Campbell and Jones, 2005	81	10	9
Blanche et al., 2006	49	33	18
Campbell et al., 2011	82	7	11
AVERAGE	66	18	16

^z A data reported by DeLacy et al., 1990 are summarizations from research conducted in Thailand and Australia, respectively.

^y E and M data reported by Kerby et al., 2000 from early- and mid-maturing tests, respectively.

In addition to yield, fiber quality, seed oil, and protein, GE studies involving other cotton production traits would be beneficial to cotton breeders. One such trait involves gossypol, which is located in pigment glands and is a constituent in the leaves, flower buds, squares, bolls, and seeds of the cotton plant. Gossypol provides resistance to

many cotton insect pests (Lukefahr and Houghtaling, 1969). Gossypol is not desired in the seed as it limits the proportion of seed that can be safely used as cattle and chicken rations (Bailey et al., 2000). Because of gossypol's toxicity to cattle and chicken, there is a great deal of interest in eliminating seed gossypol. The genetic basis of gossypol has been extensively studied and Calhoun (1997) proposed that the genetic variability of two genes (*Gl*₂ and *Gl*₃) had potential of reducing seed gossypol, while maintaining high levels of gossypol in other plant parts. However, the impact of GE interactions on seed and/or plant gossypol levels has not been addressed.

The need for continued GE research is the ever-changing effect of technology on changing GE. Three constantly changing factors in cotton production systems are G, the management component of E, and the need to estimate the GE for new instruments and equipment used to further improve experimentation or measure new traits. Genetics and breeding have undergone great changes involving breeding organizations, numbers of cultivars evaluated, introduction of transgenes, introduction of foreign cultivars and germplasm lines, and a reduction in time of evaluation before cultivar release.

Twenty-eight breeding organizations were reported in 1981 by the USDA-Agricultural Marketing Service (AMS) (USDA-AMS, 1981). The number reported by USDA-AMS (2010) for 2010 was nine. In 1981, it required 10 breeding organizations to account for 87.0% of the USA's land area planted to cotton. In 2010, three breeding organizations accounted for 87.9% of the USA planted land area. The number of cultivars planted in the USA in 1981 and 2010 (USDA-AMS 1981, 2010) was 74 and 113, respectively. A major change in G was the introduction of transgenic cultivars in 1995 (USDA-AMS, 1995). In 1996, there were four transgenic cultivars that accounted for 12.1% of the USA planted area. In 2010, there were 100 transgenic cultivars that accounted for 95.9% of the USA planted area (USDA-AMS, 1996, 2010). Jones et al. (1996) reported large GE interactions between transgenic cultivars carrying the *Bacillus thuringiensis* (Bt) gene and the related recurrent non-transgenic cultivar parents. Bauer et al. (2006), Blanche et al. (2006), Bourland (2005), Ethridge and Hequet (2000), Moser et al. (2001), and Verhalen et al. (2003) demonstrated

no major differences between transgenic cultivars and the non-transgenic recurrent parent for yield, fiber quality traits, or GE unless target insects or herbicide drift was not controlled. Another change in G occurred when germplasm under the trade name 'FiberMax' was broadly introduced from Australia into the USA in 1996. In 1998, FiberMax cultivars accounted for 0.38% of the USA planted area (USDA-AMS, 1998); in 2010, the FiberMax brand accounted for 39.0% of the total USA plantings, (USDA-AMS, 2010).

In addition to changes in G, USA cotton production areas have shifted significantly in recent years. Today, more than 50% of the total USA cotton production area is concentrated in Texas. Other traditional cotton production areas in the Western, Midsouth, and Southeastern USA have decreased cotton production significantly. The recent development of new instruments to measure fiber quality properties also highlights the importance of continuing GE analyses on new traits. In 1991, the High-Volume Instrument (HVI) system entered into the automatic classing of the USA cotton crop (Frydrich and Thibodeaux, 2010). This system is rapid and more objective than the previous system of human classing but little is known about the extent to which GE interactions affect these traits.

The present study had three objectives. The first objective was to compare a new GE analysis with results from earlier studies. The second was to compare GE studies for fiber traits as measured by HVI with fiber traits measured by older fiber quality instruments. The third was to measure GE for seed characteristics of oil%, N, and gossypol and compare the results with yield, yield components, and fiber quality traits.

MATERIALS AND METHODS

RHQ Test Procedures. The RHQ Tests were initiated in 1964 and have continued every year since inception. The RHQ is part of the NCVT and conducted annually in approximately 12 states. The number of locations varies due to changes in personnel and programs. The NCVT is conducted by volunteers involving USDA-ARS, Land Grant University Systems, and commercial companies. However, all field evaluations are conducted by public researchers. Entries are nominated each year and those selected have proven to generally have

better combinations of yield and fiber quality than those cultivars being grown by the cotton growers. The genetic population of the RHQ is different from that of the NCVT because a greater priority on improving fiber traits is placed on the RHQ than that for the NCVT. Field data are collected by the cooperators and forwarded to the USDA-ARS Crop Genetics Research Unit at Stoneville, MS. Yield is determined on site using various harvesting equipment and laboratory type gins. In the NCVT studies from 2001 to 2007 (Meredith and Keene, 2001-2007), the number of tests per year averaged eight.

Fiber quality testing was conducted by Starlab, Inc. (Knoxville, TN) with 150-g fiber samples provided by each field test cooperator. Two methods were used to determine fiber properties. The first method, the breeder-geneticist (BG) method, has been used since 1963 and measures 50 and 2.5% span lengths (SL), stelometer strength (T_1), elongation (E_1), micronaire, and yarn tenacity. The second method is the HVI, which is the AMS – Cotton Division standard for all USA cotton bales and many foreign countries. There were some slight changes in fiber data reporting as new versions of HVI evolved. The HVI classing for all USA bales was initiated in 1991 and first used by the RHQ in 1980. HVI estimates seven fiber quality traits. Two of these, upper-half mean (UHM) length and micronaire were expected to produce the same values as that for 2.5% SL and micronaire, respectively, in the BG samples. Other traits were uniformity index, HVI strength and elongation. BG and HVI provide strength and elongation percent values. However, the BG and HVI do not generally produce the same strength and elongation means but might produce similar variance components. Yarn tenacity measures the combined effects of length, strength, and micronaire and their interactions and is only measured in the BG. Also included in the HVI analysis is colorimeter, which measures Rd and Hunter's +b value. Rd is the percentage of the reflectance, the higher the value, the brighter the fiber. Hunter's b value is a measure of increasing cotton yellowness. Both the BG and HVI fiber analyses were from the same 150-g sample forwarded to StarLab, Inc.

Gossypol is determined from de-hulled, oven-dried meal. It uses the American Oil Chemists' Society (AOCS) recommended practice Ba 8a-99 (AOCS, 1998). Formulation of this complex al-

lows the (+) and (-) gossypol enantiomers to be determined by HPLC. Total gossypol is calculated as the sum of (+) and (-) gossypol. Percentage + gossypol is the amount of + divided by the total amount of gossypol. The percentage of the + contribution is determined by the total weight of + gossypol divided by the total weight of + and - gossypol as expressed as a percent. Oil and N percent are determined by AOCS official methods. All seed analyses for oil, N, and gossypol were made from the seed sample sent to Eurofins Scientific (Memphis, TN).

Field Tests. The locations for each year’s study, the region where the tests were conducted, and the number of entries are given in Table 3. The average number of locations per year was eight and the average number of genotypes was 20.9 per year. The total number of genotypes evaluated was 98. The total number of location-year environments was 56. Each location uses the crop management system typical of that particular area. The experimental design was a randomized complete block with four to six replications. Seed and lint samples were obtained from 50 to 150 hand-picked bolls per plot. Usually the number of replications for seed and lint is a sample from two replications. Plot size varies but usually is two rows, 12 m X 1 m. Lint percents were determined on common laboratory gins. Boll weights were determined by dividing the weight of the boll sample by the number of bolls in a sample. Seed weights were determined as the

weight (g) of 100 fuzzy seeds. Results from each individual location and an over-all location average was statistically analyzed and reported through internet websites.

Statistical Analysis. Variance components for years (Y), locations (L), Y-L, Genotypes (G), G-Y, G-L, and G-Y-L were determined for all 26 traits and expressed as a percent of the sum of seven sources of variation. Statistical analyses from all 26 traits were determined for variance. For these analyses Y, L, and G and their interactions were considered random effects. All statistical evaluations were conducted in SAS ver. 9.2 (SAS Institute, 2008) as described by Holland (2006). The approximate t-test was computed by dividing the variance or covariance for each case by its standard error.

RESULTS AND DISCUSSION

The variance components and their “t” estimate for 26 traits are given in Tables 4, 5, and 6. Table 4 consists of nine traits that are involved in lint and seed traits and their yield components. Table 5 consists of 13 fiber traits that estimate E, Y, L, and G variance components, and their interactions. Table 6 involves gossypol and its two isomers. The three tables are partitioned into the estimates of E, G, and GE. The data are reported as a percent of the total of the three sources of variability, E + G + GE = 100%.

Table 3. Locations and number of genotypes evaluated in Regional High Quality Tests, 2001-2007.

Location	NCVT Region	Year							Number of Years in Test
		01	02	03	04	05	06	07	
Florence, SC	Eastern	X	X		X	X	X	X	6
Tifton, GA	Eastern	X	X						2
Bell Mina, AL	Eastern	X	X	X	X	X	X	X	7
Stoneville, MS	Delta	X	X	X	X	X	X	X	7
Portageville, MO	Delta	X			X	X	X	X	5
Bossier City, LA	Central	X	X	X	X	X		X	6
Keiser, AR	Delta	X	X	X	X	X	X	X	7
College Station, TX	Central	X	X	X	X	X	X	X	7
Lubbock, TX	Plains			X	X	X	X	X	5
Las Cruces, NM	Western					X	X	X	3
Rocky Mount, NC	Eastern	X							1
Number of Genotypes		20	24	20	19	20	21	22	146

Table 4. Means for nine yield, yield component, and seed traits and their variance components expressed as a percent of the total variance from RHQ Test data from 2001-2007.

Trait	Mean	Environmental				Genotype Total	Genotypic X Environment			
		Year (Y)	Loc (L)	YL	Total %	(G)	GY	GL	GYL	Total %
Lint, kgha ⁻¹	1227	0	39.6	44.7	84.3	7.4	0.0	1.7	6.6	8.4
		(.) ^z	1.7	4.4		5.9	(.)	2.0	7.2	
Seed, kgha ⁻¹	1818	0.4	37.5	50.4	88.6	3.6	0.0	2.1	5.7	7.8
		0.1	1.5	3.6		3.8	(.)	2.0	5.2	
Oil, kgha ⁻¹	358	1.9	38.6	43.9	84.4	6.9	0.03	1.9	6.4	8.6
		0.3	1.6	3.6		5.1	0.6	2.4	5.5	
N, kgha ⁻¹	62	2.6	34.9	52.6	90.1	1.0	1.5	2.2	5.2	8.9
		0.4	1.5	3.6		0.8	1.4	2.1	4.9	
Oil, %	19.5	1.6	32.4	18.9	52.8	36.7	0.7	1.7	8.1	10.5
		0.6	1.8	4.0		6.7	1.1	1.1	6.0	
N, %	3.43	14.3	30.6	36.7	81.6	10.8	1.3	1.0	5.4	7.7
		1.2	1.6	4.1		5.0	1.7	1.3	6.2	
Lint %	40.1	0.0	20.2	36.8	57.0	33.1	1.1	4.7	4.0	9.8
		(.)	1.3	3.6		4.5	3.3	1.5	2.9	
Boll weight	5.11	4.2	35.2	31.6	71.0	16.2	0.0	0.0	12.8	12.8
		0.7	1.7	3.9		6.0	(.)	(.)	11.0	
Seed weight	9.72	1.3	70.1	11.0	82.4	10.8	0.3	4.1	2.4	6.8
		0.6	0.6	3.6		5.9	1.9	6.6	4.1	

^z estimated “t” value is given directly under its respective variance

^t estimated by variance component divided by standard error. t values for 40, and 100 + df are 2.02 and 1.98, respectively for 0.05 probability levels and 2.70 and 2.62, respectively for 40 and 100 + df at the 0.01 probability level.

Yield and Yield Components. The results given in Table 4 are similar to data in earlier studies summarized in Table 2. Most of the variability with yield is associated with E. The percent of total variability associated with E 56 Y-L is 84.3, 88.6, 84.4, and 90 for lint, seed, oil, and N, respectively. Environments used in these studies involve locations within the Eastern, Delta, Central, and Plains regions of the NCVT.

The traditional lint yield components are similar to previous studies with E being a major source of variability for lint percent, boll weight, and seed weight (Tables 1 and 4). In the current investigation, E was 57, 71, and 82% of the total variance for these three components, respectively. Nevertheless, G was highly significant for all three components resulting in 33, 16, and 11% of the total variability for lint%, boll weight, and seed weight, respectively. GE was significant and lower than that for G in all three components. Environmental variance for oil % was 52.8, which was lower than that for any of

the three traditional yield components; whereas N% at 81.6% was higher than any of the three yield components. Variances for oil%, a component of oil yield, was similar with that for lint%. Lint% and oil% were 57 and 52.8%, respectively. The two G components were 33.1 and 36.7%, respectively. The GE components were 9.8 and 10.5%, respectively. The variance profile for N% was different than that for lint% and oil%. Its variance for E, G, and GE was 81.6, 10.8, and 7.7%, respectively. Because of its higher energy content and relative contribution of the genetic component to overall variation, Chapman et al. (2008) suggested that oil% could be genetically manipulated such that its energy could be redirected to producing higher lint yield.

The Y-L interaction was the largest E source of variability in the analysis of variance for lint yield, seed yield, oil, N, N%, but not for oil% or boll weight (Table 4). For lint yield the Y influence was estimated to vary greatly over the range of environments (data not shown).

Table 5. Fiber trait means and their Breeder-Geneticist and High Volume Instrument variance components expressed as a percent of the total variance.

Trait	Mean	Environmental				Genotype Total	Genotypic X Environment			
		Year (Y)	Loc (L)	YL	Total %	(G)	GY	GL	GYL	Total %
Breeder-Geneticist Samples										
50 %, mm	14.4	11.1	25.1	31.5	67.7	22.0	1.1	0	9.3	10.4
		1.1 ^z	1.6	4.0		5.6	1.3	(.)	16.4	
2.5%, mm	29.5	13.7	14.3	34.9	62.9	28.1	1.2	0.3	7.6	9.1
		1.1	1.4	3.9		5.6	2.1	0.6	5.6	
Strength, T ₁	216	0.9	6.5	18.1	25.5	52.0	3.4	1.6	17.6	22.6
		(.)	1.3	4.1		3.5	3.8	0.5	8.8	
E ₁ , %	7.4	9.5	17.8	9.5	36.8	38.1	9.5	2.0	13.6	25.1
		1.2	1.8	3.7		4.1	3.8	0.1	7.8	
Micronaire	4.45	3.8	31.5	38.6	73.9	16.1	1.1	2.0	6.9	10.0
		0.7	1.7	4.2		5.2	2.0	1.9	4.9	
Yarn tenacity	132	6.3	11.4	25.5	43.2	39.3	5.9	3.3	8.2	17.4
		0.9	1.4	4.2		3.7	4.0	2.5	5.7	
High Volume Instrument Samples										
UHM, mm	29.4	2.4	15.8	37.6	55.8	36.3	0.0	2.7	5.1	7.8
		0.3	1.4	4.0		6.2	1.2	1.1	2.3	
Unif. Ratio, %	83.5	6.2	19.0	53.4	78.6	14.7	0.8	2.1	3.7	6.6
		0.8	1.2	4.1		5.7	1.2	2.4	2.4	
Strength	31.5	3.3	4.9	30.7	38.9	47.9	0.3	2.0	11.0	13.3
		0.2	1.0	4.3		3.6	3.9	3.1	5.0	
Elongation	8.0	38.1	1.0	354	74.5	20.7	0.3	2.2	2.4	4.9
		1.5	0.2	4.2		6.6	1.4	4.4	3.5	
Micronaire	4.49	5.6	31.2	38.1	74.9	17.7	0.0	1.2	6.2	7.4
		0.8	1.7	4.1		1.4	1.4	0.8	5.6	
Rd	71.7	4.5	48.9	41.1	94.5	3.6	0	0.1	1.8	1.9
		0.7	1.8	4.1		5.8	(.)	0.2	2.9	
+b	8.14	0	47.8	38.5	86.3	9.2	0.8	0.6	3.1	4.5
		(.)	1.9	4.5		5.4	1.6	0.6	2.8	

^z estimated “t” value is given directly under its respective variance.

t estimated by variance component divided by standard error. t values for 40, and 100 + df are 2.02 and 1.98, respectively for 0.05 probability levels and 2.70 and 2.62, respectively for 40 and 100 + df at the 0.01 probability level.

Table 6. Gossypol trait means and their variance components expressed as a percent of the total variance.

Gossypol trait	Mean	Environmental				Genotype Total	Genotypic X Environment			
		Year (Y)	Loc (L)	YL	Total %	(G)	GY	GL	GYL	Total %
Plus (+), %	0.77	8.3	3.8	28.7	40.8	47.0	1.0	3.6	7.5	12.1
		1.1 ^z	0.7	4.0		6.7	1.4	3.1	6.2	
Minus (-), %	0.54	12.7	8.6	39.9	61.2	29.0	0.7	2.7	6.4	9.8
		1.2	0.9	4.0		6.6	1.2	2.4	5.5	
Total, %	1.31	11.2	6.4	36.0	53.6	35.6	0.9	3.0	7.0	10.9
		1.2	0.9	4.0		6.7	1.4	2.7	6.0	
+ % of Total, %	0.59	0.8	3.4	12.6	16.8	72.2	0.0	2.0	9.1	11.1
		0.5	1.1	4.0		7.0	(.)	1.7	7.3	

^z estimated “t” value is given directly under its respective variance.

t estimated by variance component divided by standard error. t values for 40, and 100 + df are 2.02 and 1.98, respectively for 0.05 probability levels and 2.70 and 2.62, respectively for 40 and 100 + df at the 0.01 probability level.

The contributions of G to the total variances for all four yield traits reported in Table 4 were much lower than those associated with E. Yield G estimates were highly significant for all yield traits except N yield. GE interactions ranged from 7.8 to 8.9% for the four yield traits. The size of these GE interaction variances relative to G variances suggests that regionalization is still needed for cotton yield studies.

Fiber Traits. The two fiber length measurements give almost identical means. The BG 2.5% SL average length was 29.5 and the HVI UHM was 29.4 (Table 5). Two fiber length traits measured to aid in describing fiber length distribution were 50% SL and uniformity index. The 50% SL from the BG fiber array is the length at the distribution point that separates the longest and shortest 50% of the fibers. The uniformity ratio is the ratio of mean fiber length and UHM length. The E, G, and GE components for 50% were 67.7, 22.0, and 10.4%, respectively. Uniformity ratio's E, G, and GE were 78.6, 14.7, and 6.6%, respectively. These two length measurements are useful in describing fiber length distributions. Their E, G, and GE profiles also were similar. Average micronaire means were 4.45 and 4.49 for BG and HVI, respectively, and their variance components for E, G, and GE follow similar patterns. The two measures of fiber bundle strength have different units of measure and therefore means of fiber bundle strength were different. However, the distribution of the variances for both across E, G, and GE was similar. The variability results for fiber elongation before break was not consistent. Elongation means were 7.4 for BG and 8.0 for HVI. This difference in variance distribution was expected because there are no standards established for setting HVI machinery for elongation. The only way that HVI elongation values can be compared is if all samples are measured on the same machine by the same technician, and even then the data would be questionable if taken over any extended period of time. Elongation values are seldom given priorities in breeding, probably because the USA marketing system does not assign priorities and discounts based on elongation.

The influence of E on fiber traits was variable with E being 94.5 and 86.3% for the two colorimeter traits, Rd and +b, respectively, and the lowest variation attributable to E was 25.5% for BG fiber strength. The G estimates among fiber traits ranged from 52% for BG strength, as expected, to 3.6% for Rd. The two systems identified similar G contributions to strength at 52.0 and 47.9%, respectively for BG and HVI, and

to micronaire, which were 16.1 and 17.7% of total variance components, BG and HVI, respectively. In general, Y-L variances were high for all traits, similar to those contributions for yield traits. In contrast to lint yield, however, most fiber traits had large G/GE ratios suggesting that these fiber traits can be expected to, in general, have strong rank-order comparisons across a broad range of environments. Thus, the need for regionalization is less for fiber traits than that for yield. Usually lint yield GE determines specific regionalization when yield and fiber quality both are measured. However, the number of field replications for yield is twice that for fiber traits. These data suggest that the number of locations from which fiber data are collected could be reduced.

Gossypol/Seed. Cotton seeds might increase in importance due to worldwide need for more food and feed, which might concomitantly mandate a higher priority on breeding and genetic research. The primary problem with cotton seed for human and animal consumption is gossypol. Gossypol determination is made by establishing the amount of + and - isomers whose total is reported as 'total gossypol.' Stipanovic et al. (2005) indicated that of the two isomers, the - isomer is the most biologically active. McMichael (1960) determined that two alleles, (G_2 , G_3), could determine the presence or absence of gossypol in the plant and seed. Lee et al. (1968) determined that the $gl_2 gl_2$, G_2 , G_3 would result in a 76% reduction in seed gossypol. Relative to the research on yield, there has been little research on the GE of gossypol and its two isomers. Both Percy et al. (1996) and Stipanovic et al. (2005) reported considerable genetic variability in total gossypol and its two isomers.

Variance distributions for +, -, and total gossypol (Table 6) follow a pattern similar to that for yield components and fiber traits (Tables 4 and 5). The average E, G, and GE of all three gossypol traits, +, -, and total is 51.9, 37.2, and 11.1%, respectively. All three traits are greatly influenced by E, with E being 53.6% for total gossypol. However, the E contribution of +% of total gossypol is the least (16.9%) of any of the 26 traits and its G variance component is 72.2%, the highest of any of the 26 traits. Stipanovic et al. (2005) indicated the importance of decreasing - gossypol and increasing the + gossypol in enabling the escalation of the amount of cottonseed that could be safely used in animal rations. Considerable genetic variation in *G barbadense* L. for the + and - isomers has been reported by Percy et al. (1996) and Stipanovic et al. (2005). This study

suggests that if the + and – percent of total gossypol are as E stable in all populations as indicated in these studies, that selection could be effective in a small number of environments, perhaps as few as one. Selection can be practiced in two stages. First, a large number of genotypes segregating for + and –% contributions could be selected in one environment followed by evaluations the following year in broader environments.

SUMMARY

Despite many changes in breeding, the variances due to E, G, and GE have changed little during the last 50 yr. Yield is influenced mostly by E and its G and GE sources of variability are approximately equivalent. The need for regionalization for lint yield evaluation still exists. Yield components and fiber quality traits were not as influenced by E and GE over the years, locations, and G in this study. These data support the concept of identifying optimum testing environments that best represent target-growing environments to best discriminate breeding line and/or cultivar yield performance (Campbell and Jones, 2005). Oil yield and oil% have similar E, G, and GE components as lint yield and lint percent. The most stable trait was the percent + isomer of the total gossypol content, with E = 17%. It also had the highest G contribution, 72% of total variability.

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DISCLAIMER

Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the US Department of Agriculture.

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