

中美几个棉花品种育种应用价值研究

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摘要:用3个美国陆地棉品种为母本与2个中国品种配制6个杂交组合。5个亲本与其6个杂交组合F₂和F₃种植在美国密西西比州立大学农业试验站。利用加性-显性-加×加互作遗传模型(ADAA)进行数据分析。结果表明,除了加性和显性效应外,加×加互作效应控制大多数农艺性状和纤维性状。两个中国品种均可用于纤维克隆值的改良。品种CR110及Deltapine 90(DP90)在纤维长度和强度方面具有较好的一般配合力。与品种DP90的杂交组合可以在较晚世代用于产量的改良。杂交组合Stoneville 474(ST474)×CR110可用于在早期提高皮棉产量。除ST474×CR110之外,其它各组合均具有产量改良的潜力。组合Sure-Grow 747(SG747)×86-1在早期和晚期均比其它组合有较高的纤维强度。考虑到皮棉和纤维品质的基因型值,组合SG747×86-1可用于提高早期和晚期产量的改良且有好的纤维品质。

关键词:棉花;遗传模型;遗传效应;遗传改良

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Evaluating American and China Cotton Cultivars and Their Crosses for Improvement

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Abstract: The use of diverse elite cotton cultivars, *Gossypium hirsutum* L, in cotton breeding may lead to improvements of important traits. In this study, three American cultivars were used as female parents and crossed with two China cultivars. The five parents and six F₂ and F₃ hybrids were evaluated at Mississippi State University for three years. The additive, dominance, and additive × additive (ADAA) genetic models were used for data analysis. Variance components, genetic effects, and genotypic values were calculated. The results showed additive × additive epistatic effects were significant for most agronomic and fiber traits. China cultivars CR110 and 86-1 can be used as parents to improve fiber micronaire. CR110 and Deltapine 90 (DP90) were good combiners for fiber length and fiber strength. Genetic predictions showed that: 1) crosses with DP90 would improve lint yield in later generations, 2) the cross between CR110 and Stoneville 474 (ST474) can be used to increase lint yield at early generations but may not be good for selection at later generations, 3) all crosses except ST474 × CR110 provided the potential for yield improvement at later generations, 4) the cross between 86-1

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and Sure-Grow 747 (SG747) had higher fiber strength than the other crosses at both early and late generations, 5) considering genotypic values for lint yield and fiber traits, the cross SG747 × 86-1 can be used for yield improvement at early and late generations while fiber quality should remain acceptable. This study provides useful data on how diverse cultivars can be used to improve cotton yield and quality.

Key words: cotton; genetic model; genetic effects; genetic improvement

1 INTRODUCTION

Improving lint yield and fiber quality is an important objective for cotton breeders. To reach this goal, it is important to utilize genetic variability from diverse resources to limit vulnerability to pests and diseases, while providing useful variation that forms favorable genetic combinations. However, Van Esbroeck and Bowman^[1] observed that parental genetic diversity, as estimated by coefficient of parentage, was not imperative for cotton improvement. A review of research concerning the genetic properties of agronomic and fiber traits was provided by Meredith^[2]. Many recent agronomic and fiber trait studies focused on combining ability (genetic effects) by using inbred parents and their hybrids^[3-6]. These studies provided a good understanding of the genetic behavior of fiber traits in cotton. Because of the difficulty of producing enough F_1 seeds for experiments across different environments, F_2 -population seeds were often planted in the field experiments^[3-5, 7-8]. The data of F_2 and/or their parents were usually analyzed by ANOVA methods. However, such analyses may not be appropriate when large dominance effects exist or when data are unbalanced. Recently, mixed linear model approaches have been used in cotton to estimate genetic variances and to predict genetic effects^[6, 9-10]. However, many studies were based on additive-dominance (AD) and its GE genetic models^[3, 7-9, 11].

Several recent studies of QTL mapping^[12-19] have provided evidence suggesting that epistasis may be an important genetic factor underlying complex traits. The detection of epistasis effects may provide more information that will further

our understanding of gene expression and interactions. Zhu^[20] developed an ADAA model for detecting additive, dominance, and additive × additive ($A \times A$) epistasis effects. This model requires three generations, parent, F_1 , and bulk F_2 . The mixed linear model approach not only allows the extensions of the use to other generations such as F_3 or F_4 , but also allows unbalanced data or unbalanced genetics design in different environments. The utilization of such models should aid breeders in the development of improved cultivars. McCarty et al^[21-22] reported that $A \times A$ epistatic effects were significant for most agronomic and fiber traits using F_2 and F_3 hybrids. Useful $A \times A$ epistatic effects could be used to improve fiber quality while remaining high yielding at both early and late generations.

In this research, three American cotton cultivars were crossed with two China cotton cultivars. The data collected from these hybrids with their parents at Mississippi State University in three years were analyzed by the mixed linear model approach. Genetic variance components, genetic effects, and genotypic values were evaluated.

2 MATERIALS AND METHODS

2.1 Plant Materials and Experimental Design

Three American cotton cultivars were used as female parents and were crossed to each of two cultivars from China. The two China parents were 1)86-1 and 2)CR110 and the three American parents were 3)'Deltapine 90' (DP90), 4)'Stoneville 474' (ST474), and 5)'Sure-Grow 747' (SG747). Crosses and subsequent evaluations were conducted at the Plant Science Research Center, Mississippi State, MS (33.4 N, 88.8 W). F_1 seeds were sent to a winter nursery

to produce the F_2 . Five parents and six F_2 hybrids were grown in 2001 and 2002. Seeds were harvested from the 2002 test (F_2 - bulks), and the resulting F_3 -bulk populations, F_2 s, and parents were grown in 2003.

The experimental design was a randomized complete block with four replicates in 2001 and 2002 and six replicates in 2003. Plot size each year was a single row 12-m in length with row spacing of 0.97-m. The planting was a two-planted/one-skip row pattern. The stand density consisted of single plants spaced approximately 10 centimeters apart. The soil type was a Leeper silty clay loam. Standard production practices were followed each year.

A 25-boll, hand-harvested sample was collected from each plot prior to machine harvest. These samples were weighed and ginned on a laboratory 10-saw gin to determine boll weight, lint percentage and provide lint samples for fiber analysis. Lint samples were sent to STARLAB Inc., Knoxville, TN for determination of micronaire, elongation (E1), fiber strength (T1), and 2.5 % span length (SL2.5). Fiber measurements were conducted by single instrument. The plots were harvested with a mechanical picker, then the seed cotton was weighed and the data were used to calculate lint yields.

2.2 Genetic Models and Analysis Methods

LSD (least significance difference) multiple comparisons were conducted between generations for each of three years (parent and F_2 for 2001 and 2002, parents, F_2 , and F_3 for 2003) (Table 1). LSD multiple comparisons were also conducted among genotypes for each year (Table 2).

An additive-dominance additive additive (ADAA) and genotype by environment interaction genetic model was employed for data analysis^[20-23].

The mixed linear models were as follows:

Parents:

$$y_{hijk(P)} = \mu + E_h + 2A_i + D_{ii} + 4AA_{ii} + 2AE_{hi} + DE_{hii} + 4AAE_{hii} + B_{k(h)} + e_{hik}$$

F_2 :

$$y_{hijk(F_2)} = \mu + E_h + (A_i + A_j) + \frac{1}{4}D_{ii} + \frac{1}{4}D_{jj} + \frac{1}{2}D_{ij} + (AA_{ii} + AA_{jj} + 2AA_{ij}) + (AE_{hi} + AE_{hj}) + \frac{1}{4}DE_{hii} + \frac{1}{4}DE_{hjj} + \frac{1}{2}DE_{hij} + (AAE_{hii} + AAE_{hjj} + 2AAE_{hij}) + B_{k(h)} + e_{hijk}$$

F_3 :

$$y_{hijk(F_3)} = \mu + E_h + (A_i + A_j) + \frac{3}{8}D_{ii} + \frac{3}{8}D_{jj} + \frac{1}{4}D_{ij} + (AA_{ii} + AA_{jj} + 2AA_{ij}) + (AE_{hi} + AE_{hj}) + \frac{3}{8}DE_{hii} + \frac{3}{8}DE_{hjj} + \frac{1}{4}DE_{hij} + (AAE_{hii} + AAE_{hjj} + 2AAE_{hij}) + B_{k(h)} + e_{hijk}$$

Where, A_i (or A_j) is additive effect from parent i (or j); D_{ii} , D_{jj} or D_{ij} is the dominance effect; AA_{ii} , AA_{jj} , or AA_{ij} is the additive \times additive ($A \times A$) epistatic effect; AE_{hi} (or AE_{hj}) is additive by environment interaction effect; DE_{hii} , DE_{HJJ} or DE_{hij} is the dominance by environment interaction effect; AAE_{hii} , AAE_{hjj} , or AAE_{hij} is the AA by environment interaction effect; $B_{k(h)}$ is the block effect with $B_{k(h)} \sim N(0, \sigma_B^2)$; e_{hijk} is the random error with $e_{hijk} \sim N(0, \sigma_e^2)$.

There were only five parents used in this study; thus, typically these genetic effects should be assumed to be fixed. Since the ADAA model is complicated and the genetic design is unbalanced in this study and since we are interested in both genetic effects and genetic variation, a mixed linear model approach, minimum norm quadratic unbiased estimation (MINQUE) was used to estimate genetic variance components based on this ADAA model. The prediction equations for parents and hybrids are referenced from McCarty et al^[22]. The Jackknifing over blocks within environments was used to estimate standard errors of variance, and the predicted effects^[24]. The degrees of freedom were 13 and approximate t-tests were used for each parameter. Narrow-sense heritability across environments was defined as $h_N^2 = (V_A + V_{AA})/V_P$,

while broad-sense heritability across environments was defined as $h_B^2 = (V_A + V_{AA} + V_D) / V_P^{[25]}$. The data set was analyzed by our computer program written in C++.

3 RESULTS

3.1 Phenotypic data analysis

On average, F_2 hybrids had greater boll weight than parents (Table 1) for each of three years. In addition, F_3 hybrids did not differ from F_2 but they differed from their parents for boll weight in 2003. This is indicative of epistatic effects controlling this trait. F_2 hybrids generally had lower lint percentage than their parents in all three years, while the F_3 hybrids were not different from their F_2 . This also suggested epistatic effects for lint percentage. F_2 hybrids were not different from their parents for lint yield and fiber length in 2001 or 2002, while they were different in 2003. This is indicative of genotype by environment interaction ($G \times E$) effects controlling lint yield. The similar evidence of $G \times E$ could also be observed for other traits.

The mean values for each parent, F_2 , and F_3 (only in 2003) for each of three years are given in Table 2. Most F_2 hybrids had numerically greater boll weight and lower lint percentage

than their better parents in each of three years (Table 2). Averaged overall there was no difference for lint yield between parents and F_2 hybrids in 2001 and 2002 (Table 1); however, some F_2 hybrids with high positive heterosis and negative heterosis were observed in 2001 and 2002 (Table 2). For example, the cross 86-1 \times SG747 had very strong heterosis and the crosses DP90 \times 86-1 and ST474 \times CR110 had very negative heterosis in 2001. The crosses SG747 \times 86-1 and DP \times CR86-1 had very high heterosis for lint yield in 2002. All F_2 hybrids and all F_3 hybrids except ST474 \times CR110 had better parent heterosis for lint yield in 2003. The F_3 yield did not decrease from its corresponding F_2 except the cross ST474 \times CR110, for which F_3 yielded less lint than its F_2 hybrid in 2003; indicating positive heterozygous dominance effects between parents CR110 and ST474 and epistatic effects in other crosses.

In summary, the phenotypic data (Tables 1 and 2) provide evidence of epistatic effects and $G \times E$ interaction effects controlling these traits. Thus using the ADAA model to further analyze the data will provide additional insight for this study.

Table 1 Mean values for parents, F_2 s, and F_3 s for agronomic and fiber traits for three years.

Year	Gen	boll weight	lint percentage	lint yield	MIC	2.5% span	elongation	fiber strength
		/g	/%	/(lb \cdot acre ⁻¹)		length/mm	/%	/(kNm \cdot kg ⁻¹)
2001	P	5.33	40.68	1411	4.87	28.33	6.99	186.90
	F_2	5.71	39.86	1326	4.66	28.52	6.83	194.27
	LSD _{0.05}	0.13	0.43	NS	0.11	NS	NS	5.39
2002	P	5.42	43.28	1378	4.78	28.66	7.95	184.20
	F_2	5.68	42.27	1551	4.58	28.86	7.34	184.02
	LSD _{0.05}	0.14	0.42	NS	0.10	NS	0.46	NS
2003	P	5.63	40.17	1333	4.62	28.69	8.66	199.26
	F_2	5.71	39.88	1601	4.45	28.98	8.47	207.08
	F_3	5.81	39.95	1583	4.46	28.95	8.29	205.92
	LSD _{0.05}	0.11	NS	87	0.10	0.30	0.32	3.51

Table 2 Mean values for each parent, F₂, and F₃ for agronomic and fiber traits in three years

Year	Genotype	Gen	boll weight /g	lint percentage /%	lint yield /($\text{lb} \cdot \text{acre}^{-1}$)	MIC	2.5% span length /mm	elongation /%	fiber strength /($\text{kNm} \cdot \text{kg}^{-1}$)
2001	86-1	0	5.05	40.55	1351	4.55	27.88	7.19	184.5
	CR110	0	4.81	40.00	890	3.88	28.51	6.56	183.75
	DP90	0	5.52	39.99	1699	5.25	28.51	6.31	195.88
	ST474	0	5.52	41.49	1778	5.45	28.13	7.25	187.88
	SG747	0	5.73	41.38	1336	5.23	28.61	7.66	182.50
	DP90×86-1	2	5.58	40.43	1142	4.70	28.38	6.75	188.38
	ST474×86-1	2	5.58	40.91	1515	4.90	28.51	6.81	192.13
	SG747×86-1	2	5.72	39.94	1582	4.88	28.19	7.69	175.88
	DP90×CR110	2	5.84	38.41	1374	4.38	28.70	6.44	212.38
	ST474×CR110	2	5.72	39.87	1220	4.45	28.51	6.38	201.88
	SG747×CR110	2	5.83	39.62	1124	4.65	28.83	6.94	195.00
	LSD _{0.05}			0.31	1.03	374	0.26	0.53	0.72
2002	86-1	0	5.27	43.45	1195	4.45	28.19	8.13	178.38
	CR110	0	5.63	41.16	1308	4.23	28.83	8.06	185.38
	DP90	0	5.56	42.17	1602	4.90	28.83	6.88	204.38
	ST474	0	5.12	44.90	1284	5.20	28.32	7.63	180.75
	SG747	0	5.54	44.70	1502	5.13	29.11	9.06	172.13
	DP90×86-1	2	5.56	42.90	1515	4.53	28.83	7.13	187.25
	ST474×86-1	2	5.89	43.33	1400	4.80	28.70	7.25	180.63
	SG747×86-1	2	5.53	42.39	1735	4.63	28.58	8.06	173.88
	DP90×CR110	2	5.52	41.76	1766	4.30	29.46	6.44	193.88
	ST474×CR110	2	5.63	42.54	1266	4.68	28.45	6.50	188.38
	SG747×CR110	2	5.96	40.69	1624	4.58	29.15	8.69	180.13
	LSD _{0.05}			0.34	1.00	415	0.24	0.74	1.11
2003	86-1	0	5.54	39.50	1336	4.17	28.22	9.08	191.00
	CR110	0	6.23	40.33	1182	4.38	29.29	7.63	212.92
	DP90	0	5.18	39.09	1133	4.74	28.99	7.77	218.79
	ST474	0	5.40	41.24	1612	4.91	28.43	8.88	193.79
	SG747	0	5.80	40.72	1401	4.88	28.54	9.96	179.79
	DP90×86-1	2	5.50	39.47	1416	4.52	28.68	8.96	203.42
	ST474×86-1	2	5.75	41.25	1739	4.57	28.60	8.83	200.75
	SG747×86-1	2	5.57	39.50	1572	4.45	28.51	9.17	190.17
	DP90×CR110	2	5.59	39.01	1499	4.25	29.80	7.75	226.67
	ST474×CR110	2	5.90	39.80	1820	4.48	28.70	7.75	216.58
	SG747×CR110	2	5.96	40.27	1563	4.43	29.59	8.38	204.92
	DP90×86-1	3	5.81	40.21	1609	4.53	28.96	8.71	202.83
	ST474×86-1	3	5.80	41.75	1624	4.55	28.43	8.04	203.92
	SG747×86-1	3	5.61	39.58	1513	4.45	28.70	9.50	190.50
	DP90×CR110	3	5.62	39.30	1587	4.40	29.57	7.54	216.42
	ST474×CR110	3	5.94	39.04	1509	4.28	28.79	7.46	212.83
SG747×CR110	3	6.10	39.82	1653	4.52	29.23	8.50	209.00	
LSD _{0.05}			0.28	1.07	213	0.25	0.73	0.79	8.57

3.2 Variance components and heritability

The proportions of each variance component to its phenotypic variance for all traits are summarized in Table 3. No additive, dominance, or $A \times E$ effects were detected for boll weight, while $A \times A$, $AA \times E$, and $D \times E$ effects were important for boll weight. Additive, dominance, and $A \times A$ epistatic effects were significant for lint percentage, while only $AA \times E$ interactions effects were significant for this trait. Strong dominance effects and $D \times E$ effects contributed 35% and 41% to total variance for lint yield. $A \times A$ epistatic effects were also detected for lint yield. Additive effects were significant for all fiber traits and dominance effects were only significant for fiber strength. $A \times A$ epistatic and $A \times E$ interactions effects were significant for all fi-

ber traits except fiber strength. No $D \times E$ effects were detected for fiber traits except elongation (54%), while $AA \times E$ effects were significant for all fiber traits except elongation. In summary, the epistatic effects were significant for all traits when both $A \times A$ and $AA \times E$ effects were considered. $G \times E$ interaction effects were large for boll weight (69%), lint yield (48%), and elongation (57%), indicating that the selection for these traits needs to be done in multiple environments.

Narrow sense heritability for boll weight and lint yield was low, indicating that selection needs to be conducted at late generation, while selection for lint percentage and micronaire may start at early generation using these crosses.

Table 3 Estimated proportions of variance components to phenotypic variance for agronomic and fiber traits

	boll weight	lint percentage	lint yield	MIC	2.5% span length	elongation	fiber strength
VA/VP	0.00	0.10*	0.00	0.36**	0.25**	0.14**	0.20**
VD/VP	0.00	0.18**	0.35**	0.00	0.00	0.00	0.55**
VAA/VP	0.17**	0.22**	0.06*	0.13**	0.09*	0.10**	0.00
VAE/VP	0.00	0.00	0.03	0.12**	0.14*	0.03*	0.00
VDE/VP	0.58**	0.00	0.41**	0.00	0.00	0.54**	0.00
VAAE/VP	0.11**	0.22**	0.04	0.09**	0.15**	0.00	0.08*
V _e /VP	0.14**	0.28**	0.12**	0.30**	0.37**	0.18**	0.18**

Note: *, ** significant at probability levels of 0.05 and 0.01, respectively.

3.3 Predicted genetic effects

Additive and $A \times A$ epistatic effects are two important types of genetic effects for selection. The results are summarized in Tables 4 and 5. CR110 will decrease lint percentage if it is used as a parent and ST474 can be used as a parent to increase lint percentage (Table 4). Both cultivars from China can be used as parents to improve (decrease) fiber fineness, while two American cultivars, ST474 and SG747, will increase fiber micronaire if they are used as parents. Cultivar 86-1 and ST474 will decrease fiber length if they are used as parents, while CR110 and DP90 are good combiners for fiber length improvement. Cultivars 86-1 and SG747 are two

poor combiners while CR110 and DP90 are good combiners for fiber strength.

Additive and $A \times A$ effects are heritable to the offspring progenies. All homozygous $A \times A$ epistatic effects for boll weight except cultivar SG747 were negative and significant (Table 5). Heterozygous $A \times A$ effects between 86-1 and ST474, CR110 and ST474, and CR110 and SG747 were positive and significant. The results explained why most F_2 and F_3 hybrids had greater boll weight than their parents. $A \times A$ effects for lint percentage for cultivars ST474 and SG747 were positive and significant, indicating that both parents could be used to improve lint percentage. The cross ST474 \times 86-1 could be

used to keep high lint percentage either in early and late generations as shown in Table 6 from the predicted genotypic values. The crosses with DP90 as one parent should improve lint yield in later generation (see predicted yield values for crosses DP90 × 86-1 and DP90 × CR110 at F₆).

The cross ST474 × CR110 can be used to increase lint yield at early generations but provides poor potential for selection at late generation because of positive heterozygous dominance (data not shown) effect between these two parents.

Table 4 Additive effects for agronomic and fiber traits

	lint percentage /%	MIC	2.5% span length/mm	elongation /%	fiber strength /(kNm · kg ⁻¹)
86-1	0.14	-0.08**	-0.43*	0.22	-5.97**
CR110	-0.52 ⁺	-0.27**	0.40 ⁺	-0.35 ⁺	6.18**
DP90	-0.16	0.03	0.25 ⁺	-0.30 ⁺	5.81**
ST474	0.48 ⁺	0.18**	-0.35*	-0.17	0.34
SG747	0.04	0.14**	0.07	0.58*	-6.60**

Note: +, *, and ** significant levels at 0.10, 0.05, and 0.01, respectively.

Table 5 A × A epistatic effects for agronomic and fiber traits

	boll weight	lint percentage	lint yield	MIC	2.5% span length	elongation
86-1 × 86-1	-0.18**	-0.09	-18	-0.04 ⁺	-0.31	0.21*
CR110 × CR110	-0.09**	0.15	-161	-0.07**	0.07 ⁺	0.07
DP90 × DP90	-0.13**	-0.20*	400*	0.05	-0.02	-0.05
ST474 × ST474	-0.13**	0.44*	-559*	0.12*	-0.20 ⁺	0.28**
SG747 × SG747	-0.04	0.49*	61	0.07 ⁺	0.01	0.21**
DP90 × 86-1	0.13	0.33 ⁺	-553 ⁺	-0.02	0.14	-0.02
ST474 × 86-1	0.15**	0.43**	332 ⁺	0.02	0.03	-0.34**
SG747 × 86-1	0.00	-0.32	248	-0.01	-0.05	0.22
DP90 × CR110	0.02	-0.26	-236*	-0.05	0.22	-0.27*
ST474 × CR110	0.10**	-0.45*	808 ⁺	-0.09 ⁺	-0.03	-0.43*
SG747 × CR110	0.18**	-0.54*	-321*	0.01	0.12	0.11

Note: +, *, and ** significant levels at 0.10, 0.05, and 0.01, respectively.

3.4 Predicted genotypic values at F₂ and F₆

Predicted genotypic values at F₂ and F₆ under no selective pressure may provide the information for F₂ heterosis utilization and pure line selection at late generations. The results are summarized in Table 6. Three F₂ hybrids (ST474 × 86-1, SG747 × 86-1, and ST474 × CR110) had better-parent heterosis for lint yield. Five F₂ hybrids (ST474 × 86-1, SG747 × 86-1, DP90 × CR110, ST474 × CR110, and SG747 × CR110) had at least 20% middle-parent heterosis for lint yield (33.2%, 34.8%, 24.4%, 46.5%, and 21.0% respectively) (Table 6). Thus, yield heterosis can be used from hybrid ST474 × CR110 at F₁ and F₂. All crosses

except ST474 × CR110 provide the potentials for yield improvement at later generation. All crosses at F₂ and F₆ had greater boll weight than mid-parent and both heterosis and pure lines with larger bolls than parents can be expected. Slightly lower lint percentage for crosses SG747 × 86-1, DP90 × CR110, ST474 × CR110, SG747 × CR110 would be expected at both early and late generations; while the other two crosses could have slightly higher lint percentage at both early and late generation. The cross SG747 × 86-1 had higher fiber strength than the other crosses at both early and late generations. Considering genotypic values for lint yield and fiber traits, the cross SG747 × 86-1 can be used for

yield improvement at early and late generations while fiber quality remains acceptable.

Table 6 Predicted F_2 and F_6 genotypic values for agronomic and fiber traits.

Gen	Cross	boll weight/g	lint percentage/%	lint yield /($\text{lb} \cdot \text{acre}^{-1}$)	MIC	2.5% span length/mm	elongation /%	fiber strength /($\text{kNm} \cdot \text{kg}^{-1}$)
F_2	DP90×86-1	5.68	40.84	1202	4.51	28.81	7.56	197.69
	ST474×86-1	5.72	42.47	1577	4.83	27.43	7.39	187.16
	SG747×86-1	5.50	40.75	1691	4.63	28.18	9.20	208.43
	DP90×CR110	5.54	39.37	1557	4.40	29.79	6.34	201.27
	ST474×CR110	5.72	40.45	1503	4.21	28.85	6.50	197.20
	SG747×CR110	5.96	39.67	1327	4.53	29.45	8.25	183.82
F_6	DP90×86-1	5.68	41.33	1550	4.34	28.38	7.56	192.53
	ST474×86-1	5.72	42.69	1286	4.87	27.49	7.39	190.76
	SG747×86-1	5.50	40.71	1585	4.59	27.95	9.20	212.07
	DP90×CR110	5.54	39.19	1724	4.05	30.07	6.34	172.73
	ST474×CR110	5.72	39.96	956	4.41	28.97	6.50	184.51
	SG747×CR110	5.96	39.28	1454	4.40	29.84	8.25	189.58

4 DISCUSSION

4.1 Use of diverse resources in cotton breeding

It is commonly believed that the use of widely diverse genetic resources could provide favorable combinations in breeding programs. The elite cultivars from different regions or countries may provide favorable gene combinations to improve agronomic traits.

4.2 Epistatic effects

In this study, we observed that epistasis is an important genetic phenomenon for agronomic and fiber traits in upland cotton. Many studies have reported epistatic effects controlling many quantitative traits in upland cotton^[19,21-23,26-27]. $A \times A$ epistatic effects provide desirable heterosis for lint yield and fiber quality while also providing the potential for inbred line selection at late generations^[21-22,26]. In this study, two crosses provide a contrast. The cross ST474 × CR110 should have strong heterosis for lint yield at early generation but should quickly depress yield due to large inbreeding depression; whereas, the cross SG747 × 86-1 should provide good yield and fiber quality for hybrids as well as for pure lines at later generations.

4.3 The use of mixed linear model approach

In some genetic experiments, the data sets

are unbalanced and the genetic design may be balanced and/or unbalanced. In this study the genotypes and the number of replicates in the first two years were different from those in the third year. The number of check lines in some experiments varied. On the other hand, the ADA model for parent, F_2 , or F_3 in this study may contain coefficients with values other than zero and one. The mixed linear model approaches provide more flexibility than ANOVA models and general linear models in at least three ways: (1) they can be used to analyze unbalanced data or unequal genetic designs; (2) they can be used to analyze complicated genetic models; and (3) they can be used to estimate variance components and predict genetic effects simultaneously.

References:

- [1] VAN ESBROECK G, Bowman D T. Cotton germplasm diversity and its importance to cultivar development[J]. *J Cotton Science*, 1998(2): 121-129.
- [2] MEREDITH W R Jr. Quantitative genetics[A]. KOHEL R J, Lewis C F. Cotton[C]. Madison, WI: Am Society of Agronomy, 1984. 131-150.
- [3] MEREDITH W R Jr. Yield and fiber-quality potential for second generation hybrids [J]. *Crop Sci*, 1990,30:1045-1048.

- [4] TANG B, Jenkins J N, McCarty J C, et al. F₂ hybrids of host plant germplasm and cotton cultivars; I. Heterosis and combining ability for lint yield and yield components[J]. *Crop Sci*, 1993a, 33:700-705.
- [5] TANG B, Jenkins J N, McCarty J C, et al. F₂ hybrids of host plant germplasm and cotton cultivars; II. Heterosis and combining ability for fiber properties [J]. *Crop Sci*, 1993b, 33:706-710.
- [6] WU J, Zhu J, Xu F, et al. Analysis of genetic effect 5 (environment interactions for yield traits in upland cotton[J]. *Heredita*, 1995, 17(5):1-4.
- [7] SHOEMAKER D B. Genetic analyses of agronomic traits of selected American and Australian cotton genotypes and their F₂ hybrids[D]. Mississippi State Univ. 2000.
- [8] CHEATHAM C L. Genetics and combining ability of yield and fiber properties associated with selected American and Australian cotton genotypes[D]. Mississippi State Univ. 2001.
- [9] TANG B, Jenkins J N, Watson C E, et al. Evaluation of genetic variances, heritabilities, and correlations for yield and fiber traits among cotton F₂ hybrid populations[J]. *Euphytica*, 1996, 91:315-322.
- [10] McCARTY J C, Jenkins J N Jr, Zhu J. Introgression of day-neutral genes in primitive cotton accessions; I. Genetic variances and correlations [J]. *Crop Sci*, 1998, 38:1425-1428.
- [11] CHEATHAM C L, Jenkins J N, McCarty J C Jr, et al. Genetic variance and combining ability of crosses of American cultivars, Australian cultivars, and wild cottons[J]. *J Cotton Science*, 2003, 7: 16-22.
- [12] DOEBLEY J, Stec A, Gustus C. Teosinte branched1 and the origin of maize; Evidence for epistasis and evolution of dominance[J]. *Genetics*, 1995, 141:333-346.
- [13] LARK K G, Chase K, Adler F, et al. Interaction between quantitative trait loci in soybean in which trait variation at one locus is conditional upon a specific allele at another[J]. *Proc Natl Acad Sci USA*, 1995, 92:4656-4660.
- [14] LI Z K, Priston S R M, Park W D, et al. Epistasis for three grain yield components in rice (*Oryza sativa* L.)[J]. *Genetics*, 1997, 145:453-465.
- [15] ESHED Y, Zamir D. Less-than-additive interaction of QTL in tomato [J]. *Genetics*, 1996, 143:1807-1817.
- [16] CAO G, Zhu J, He C, et al. Impact of epistasis and QTL×environment interaction on developmental behavior of plant height in rice (*Oryza sativa* L.)[J]. *Theor Appl Genet*, 2001, 103:153-160.
- [17] LIAO C Y, Wu P, Hu B, et al. Effects of genetic background and environment on QTLs and epistasis for rice (*Oryza sativa* L.) panicle number[J]. *Theor Appl Genet*, 2001, 103:104-111.
- [18] LEE S H, Park K Y, Lee H S, et al. Genetic mapping of QTLs conditioning soybean sprout yield and quality[J]. *Theor Appl Genet*, 2001, 103: 702-709.
- [19] WU JIXIANG. Genetic variation, conditional analysis, and QTL mapping for agronomic and fiber traits in upland cotton[D]. Mississippi State Univ. 2003.
- [20] ZHU J. General genetic models and new analysis methods for quantitative traits [J]. *J of Zhejiang Agricultural Univ*, 1994, 20(6):551-559.
- [21] McCARTY J C Jr, Jenkins J N, Wu J. Primitive accession germplasm by cultivar crosses as sources for cotton improvement I: Phenotypic values and variance components [J]. *Crop Sci*, 2004, 44: 1226-1230.
- [22] McCARTY J C Jr, Jenkins J N, Wu J. Primitive accession germplasm by cultivar crosses as sources for cotton improvement II: Genetic effects and genotype values[J]. *Crop Sci*, 2004, 44: 1231-1235.
- [23] XU Z C, Zhu J. A new approach for predicting heterosis based on an additive, dominance and additive × additive model with environment interaction[J]. *Heredity*, 1999, 82: 510-517.
- [24] MILLER R G. The Jackknife- a review[J]. *Biometrika*, 1974, 61:1-15.
- [25] ZHU J. Analytical methods for genetic models[M]. Beijing, China: Press of China Agriculture, 1998.
- [26] McCARTY J C Jr, Jenkins J N, Wu J. Use of primitive accessions of cotton as sources of genes for improving yield components and fiber properties[J]. *Mississippi Agric and Forestry Exp Stn Bull*, 2003: 1130.
- [27] SAHA S, Wu J, Jenkins J N, et al. Association of agronomic and fiber traits with specific Pima 3-79 chromosomes in a TM-1 Background[J]. *J Cotton Sci*, 2004 (in press). ●