Analysis of decision-making coefficients of three main fiber quality traits for upland cotton (*Gossypium hirsutum* L.)

Yongjun Mei · Wenming Hu · Shuli Fan · Meizhen Song · Chaoyou Pang · Shuxun Yu

Abstract The analysis of genetic correlations between fiber length (Len), strength (Str), micronaire, and 12 other traits was conducted using the additive (A)-dominance (D) genetic model, which considers genotype × environment interaction effects, in intra-specific upland cotton (*Gossypium hirsutum* L.) hybrids to effectively improve the quality of cotton cultivars in high planting density cases. Decision-making coefficients were computed based on the genetic correlation and path analysis of three fiber quality traits. The decision-making coefficient analysis of three fiber traits in cross breeding was beneficial for the improvement of Len by increasing the additive effects of Str and length of boll (LB) and decreasing lint percentage (LP), boll number of the top three fruit-bearing branches. The analysis was also beneficial for the improvement of Str and fiber fineness by increasing or decreasing the additive effects of other traits. Utilizing heterosis in hybrids was beneficial to the heterosis of Len by selecting the high dominance effects of number of nodes of the 1st fruit-bearing branch and LB and decreasing the dominance effects of diameter of boll (DB) and LP and for improving Str by increasing the dominance effects of DB and decreasing the dominance effects of number of fruit-bearing branches and number of nodes of the main stem (NNMS). Utilizing heterosis was also beneficial for improving fineness by increasing the dominance effects of LB, Str, and lint yield and decreasing the dominance effects of NNMS and Len.

Keywords Decision-making analysis · Fiber traits · Genetic correlation · Upland cotton

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Introduction

Cotton is one of the most important cultivated crops in the world. Higher fiber quality in upland cotton (*Gossypium hirsutum* L.) is increasingly demanded by the modern textile industry. Currently, few high yielding upland cotton cultivars have the fiber properties desired by the textile industry. Thus, the genetic enhancement of fiber traits is a primary task for most upland cotton breeders. Several studies have focused on general and specific combinations of parental lines and their hybrids (Meredith 1990; Tang et al. 1996).

Garcia del Moral et al. (1991) determined the direct and indirect effects of various plant characteristics on yield and yield components using path analysis in barley cultivars. Mixed linear model approaches have also been widely applied in cotton genetic studies (Wu et al. 1995; Tang et al. 1996; McCarty et al. 1998a, b, 2004a, b; Jenkins et al. 2007, 2009; Mei et al. 2007). Many researchers have applied correlation or path coefficients to improve targeted characters (Guler et al. 2001). Selection of the main fiber quality traits may be conducted by indirectly selecting the boll shape (Zhang and Mei 2004). However, path and correlation analyses can not identify which non-targeted characters mainly influence targeted characters. Because correlation coefficient r_{jy} has only related properties between non-target and target trait, but no decision properties, In addition, previous studies did not consider the relations among non-targeted characters when the targeted trait is improved.

Zhu (1993), Zhu and Weir (1994) reported an advanced correlation analysis that can be used to analyze the additive, dominance, and interaction effects between two main effects and environment. The net genetic effects on the resulting trait contributed by the phenotype value from a specific cause trait can be considered. Based on path analysis, Yuan et al. (2001) put forward the concept of a decision-making coefficient that can be used to compute the composite decision effect of specific non-targeted characters on targeted traits over the path (including direct and indirect decision effects). Compared with path, correlation, and multiple regression analyses, this proposed method could sort decision-making efficient from highest to lowest and then determine the decision-making and restrain characters of the target trait on a per order basis. Whereas decision-making coefficient has decision properties from nontarget trait on target trait (Because it come from decomposition of decision coefficient R^2). Yuan et al. (2001) only computed the phenotype decision-making coefficient and determined phenotype decision-making traits. Plant traits are composed of multiple genetic components, such as additive effects, dominance effects, and so on. Thus, Yuan's analysis only directed phenotype selection, not cross and heterosis breeding. Decision-making analysis is suitable for different genetic components combining genetic correlation analysis.

Xinjiang Province is the largest cotton production area in China. Because there are infrequent rainfall,

abundant sunlight, effective accumulated heat degree days, the average seed cotton yield is about 6,000 kg/ha. Low height (plant height: 80–100 cm), high density (270,000/ha) and film cover are main cultivation model. In the present work, the methods proposed by Zhu (1993), Zhu and Weir (1994), Yuan et al. (2001) were utilized to estimate the genetic correlation and genetic decision-making coefficients for selecting three fiber traits. The results will help determine the decision-making and restrain characteristics necessary for improving three main fiber traits in upland cotton.

Materials and methods

This research was carried out at the Agriculture Experimental Fields, Tarim University, Alar, Xin jiang Province, P.R. China from 2009 to 2010. Ten cultivars (Kelin 09-18B, ZH3-3, ZH4-5, 29-2, 267-9-1, 269-6-11, 328-5, 325-1-3, Ji You 768, and g3-2, which were early-medium cultivars) were selected as female parents, and 10 varieties (lines) (339-23-6, 338-1, 337-5-6, 246-6-24, 337-17-7, 246-6-5, 222-13-6, 223-23-7, 223-28-3, 223-14-5,) were selected as male parents (339-23-6, 338-1, 337-5-6, and 337-17-7 were early maturity varieties (lines), 222-13-6, 223-23-7, 223-28-3, and 223-14-5 were long fiber varieties (lines), and lines 246-6-24 and 246-6-5 were high lint percentage varieties (lines)). The incomplete diallel cross of F_1 crosses (10×10) and their parents were planted in a randomized complete block design with three replications every year. The length for each plot was 3.0 m, the width was 2.4 m, the widths of wide and narrow rows were 0.5 and 0.1 m, respectively, and the distance between plants was 0.1 m. Cotton seeds were sown with a thin film cover on 13 April every year. Standard production practices were followed in all environments. Seed cotton was harvested randomly from 20 plants in each plot. Standard culturing practices were followed throughout the growing season. Data were recorded on the following 15 traits: (1) number of nodes of the first fruit-bearing branch (NNFFB). (2) number of nodes of the main stem (NNMS), (3) number of fruit-bearing branches from bottom to top per plant (NFB), (4) length of boll from bottom to top(LB, cm), (5) diameter of boll at largest coarseness (DB, cm), (6) diameter of stem at cotyledonary trace (DS, cm), (7) plant height (PH, cm), (8) boll number of top three

fruit-bearing branches per plant (BNTTB), (9) total boll number per plant (TBN), (10) ball weight (BW, g), (11)lint percentage (LP, %), (12)lint yield per plant, (LY, g/p), (13) Upper half mean length (Len, mm), (14) fiber strength (Str, cN/tex), and (15) micronaire (Mic). NNFFB, NNMS, NFB, LB, DB, DS, PH, BNTTB and TBN were measured from 1st to 4th September; BW, LP, and LY were measured from 20 plants from 10th to 15th October. Three fiber traits were measured using a high volume instrument (HFT9000) in Cotton Research Institute, Chinese Academy of Agricultural Sciences, and considered as targeted traits in this experiment.

Statistical analysis

1 The AD genetic model (Zhu 1993), Zhu and Weir (1994), was employed to calculate the correlation of the genetic (QGAstation). Phenotype value y can be defined as

$$y = \mu + A + D + E + AE + DE + \varepsilon \qquad (1)$$

where μ = population mean, A = additive effects, $A \sim N(0, V_A)$, D = dominance effects, $D \sim N(0, V_D)$, E = environment effects, $E \sim N(0, V_E)$, AE = additive $\times$ environment interaction effects, $AE \sim N(0, V_{AE})$, DE = dominance $\times$ environment interaction effects, $DE \sim N(0, V_{DE})$, and ε = residual effects, $\varepsilon \sim N(0, V\varepsilon)$. Genetic correlation coefficients were estimated using the MINQUE(1) method. *Jackknifing* (cutting one genotype once) was used to approximate the standard errors of the estimated genetic parameters (Miller 1974; Zhu and Weir 1994). t test (two-tailed) was used to test the significance of the genetic parameters.

2 In path analysis, the determination coefficient R^2 is defined as

$$R^2 = r_{1y}b_1^* + r_{2y}b_2^* + \cdots + r_{py}b_p^*$$
$$= \sum_{j=1}^{p} b_j^* \left(\sum_{k=1}^{p} r_{jk}b_k^* \right) = \sum_{j=1}^{p} (b_j^*)^2 + 2 \sum_{\substack{j=1 \\ j<k}}^{p} b_j^* r_{jk} b_k^* \qquad (2)$$

In this equation, the two indirect decision coefficients on trait y come from trait i through trait j and from trait j through trait i; thus, the indirect decision coefficients of trait j on trait y is $2b_j^* r_{jk} b_k^*$,

and the direct decision coefficients is $(b_j^*)^2$. Yuan et al. (2001) defined the sum of the indirect decision and direct decision coefficients as the decision-making coefficient R_j of trait j on trait y.

$$R_j = (b_j^*)^2 + 2 \sum_{j \neq k}^{p} b_j^* r_{jk} b_k^* \qquad (3)$$

where b_j^* and b_k^* are the direct path coefficients of the independent variables j and k, respectively, on the dependent variable y, p is the number of non-target traits, and r_{jk} is the correlation coefficient between traits j and k.

In path analysis, the correlation coefficient between traits j and y can be described as:

$$r_{jy} = b_j^* + \sum_{j \neq k}^{p} r_{jk}b_k^* \qquad (4)$$

$$\Rightarrow 2b_j^* \times r_{jy} = 2b_j^* \times (b_j^*) + 2 \sum_{j \neq k}^{p} b_j^* \times r_{jk} \times b_k^*$$

$$\Rightarrow 2 \times b_j^* \times r_{ky} - (b_j^*)^2 = (b_j^*)^2 + 2 \sum_{j \neq k}^{p} b_j^* \times r_{jk} \times b_k^* = R_{(j)} \qquad (5)$$

$$\Rightarrow R_{(j)} = 2 \times b_j^* \times r_{jy} - (b_j^*)^2. \qquad (6)$$

Using Equation (6), the decision-making coefficients can be easily calculated or the integrated decision coefficients of the each non-target traits on the target traits can be computed. Five steps were to calculate the decision-making coefficients of certain genetic components. First, the correlation coefficients of the genetic components of the 15 traits were calculated using QGAStation. Second, the correlation coefficients derived were converted into six square matrices of 15 $\times$ 15 corresponding to the additive, dominance, additive $\times$ environment, dominance $\times$ environment, genotype and phenotype correlation coefficients. Third, the inverse matrix of each square matrix on 14 non-target traits was calculated in Excel (MINVERSE function). Fourth, the inverse matrix of each square matrix on non-target traits was multiplied by the vector of the correlation coefficients between 14 non-target traits and 1 target trait to obtain direct path coefficient vectors of the non-target traits on the target

trait for certain genetic components (MMULT function). Finally, the decision-making coefficients (or the integrated decision coefficients of the non-target traits on the target trait) were calculated using Equation (6) for each genetic component. Steps 2–5 can be performed by hand in Excel.

The decision-making coefficient analysis showed that the decision-making traits are those traits that great improved the target trait as they increased, whereas the restriction traits are those traits that greatly reduced the target trait as they increased, and optional selecting traits, those traits with $R_{(i)}$ equal to or close to 0, that do not affect the target traits despite changes in the such traits.

Results

Phenotypic means for 15 traits of parents and F_1

From 2009 to 2010, similar behaviors were observed for all 15 traits between parents and F_1 crosses. All 15 traits exhibited large ranges and similar average in both years, only have slight difference. For instance, the maximum of the parents on Len, Str, LP, NNFFB, NNMS, NFB in 2009 was relatively higher than that of the parents in 2010; F_1 crosses exhibited relatively higher average on Len, Str and lower almost other traits compared with the corresponding traits of parents in same year. The average of F_1 on Len, Str, TBN, NNFFB, NNMS, NFB, DS, PH, BNTTB in 2009 were higher than those in 2010; The opposite results were observed on other traits (except for LB and DB). These results imply that heterosis and genetic interaction effects could be expected, such as genotype × environment interaction effects for these traits, Table 1.

Genetic variance analysis

The genetic variances of the 15 traits are listed in Table 2. The significant V_ε variances of all traits showed that they could be significantly influenced by other unidentified controlling factors. The relatively larger values of V_G and V_{GE} suggested that genotypic variation mainly controlled the performance of these traits, but improving planting conditions might have some effects to a certain extent.

Significant additive variances were detected for all traits except NFB and DS, with the largest proportion

of additive variances being observed for LP, Len, and DB in sequence, which was the main factor for their inheritance. For dominance variance, PH, BNTTB, TBN, BW, and LY were not significant. For V_{AE}, NNMS, NFB, LB, DS, PH, Len, Str, and Mic were highly significant, suggesting that differences in additive × environment were crucial for varying these traits and that improving planting conditions might have special selection effects. Highly significant dominance × environment variances for NFB, DS, PH, BNTTB, TBN, BW, LP, LY, Str, and Mic were observed, which implied that environmental conditions could affect the heterosis phenotypic behavior of these traits.

Genetic effect analysis for parents and crosses

Parent 19 exhibited a significant additive effect on three fiber traits (3.01 mm, 1.37 cN/tex, −0.28). Its offspring could have very good fiber but low LP (−2.32 %), NNFFB (−0.20), and PH (−2.65 mm) (Table 3). Parent 20 also demonstrated a significant additive effect on Len (1.71 mm), Str (0.57 cN/tex), and Mic (−0.26), as well as a highly significant additive effect on LY (1.14 g/p) and TBN (0.49). Parent 17 had a negative additive effect on LP (−1.36 %), LY (−1.34 %), Len (−1.34 mm), and Str (−1.15 cN/tex). Parents 16 and 14 showed a highly significant positive additive effect on LP (−2.61, 1.57 %) but a high impact on Len (−1.25, −1.49 mm).

As shown in Table 4, parents 5, 13, 18, 19, and 20 had a significant positive additive × environment effect on Len, which indicated that a longer fiber could be selected for their offspring in different years. Parent 18's Len, Str exhibited a significant positive additive × environment effect at 2 years, which showed that a high Len and Str could be selected for its offspring in different years. Other parents' offspring were found to have different but certain selection effects on Len, Str, and Mic in different years, because most of these parents' additive × environment effects significantly differed. In addition, the additive effects of these parents were negative or not significant, indicating that their offspring's selection effects differed on Len, Str, and Mic.

As shown in Table 5, the dominance effects of almost crosses were not significant or negative on Len and thus go against heterosis on Len. Significant higher dominance effects on Str were observed for

Table 1 Phenotypic means for 15 traits of parents and their F_1 over 2 years

Generation	Years	Len (mm)	Str (cN/tex)	Mic	TBN	BW (g)	LP (%)	LY (g/p)	NNFFB
Parents	2009	28.1	29.3	2.6	3.8	3.4	37.8	5.9	4.9
	Min	37.6	36.4	4.5	6.4	6.3	49.5	14.4	7.1
	Max	31.6	32.7	3.6	4.8	4.5	43.4	9.2	5.8
	Average								
F_1	2009	29.5	26.4	3.6	4.0	4.2	38.4	8.1	5.1
	Min	35.4	35.5	4.7	7.7	6.6	47.9	17.0	6.9
	Max								
	Average	31.0	32.2	4.0	5.6	4.9	44.7	12.3	5.9
Parents	2010	27.8	28.9	2.9	4.3	3.7	37.3	7.9	5.1
	Min	37.1	37.7	4.8	5.9	5.6	49.9	11.7	6.6
	Max	30.7	33.2	3.8	5.0	4.6	44.3	10.2	6.0
	Average								
F_1	2010	27.7	27.0	3.1	4.5	4.1	40.9	9.0	5.0
	Min	35.3	35.0	5.0	6.8	6.0	47.8	16.0	6.4
	Max	30.1	32.1	4.1	5.5	5.1	44.9	12.6	5.8
	Average								

Generation	Years	NNMS	NFB	LB (cm)	DB (cm)	DS (cm)	PH (cm)	BNTTB
Parents	2009	10.6	5.7	3.9	2.8	0.9	62.1	1.2
	Min	15.3	8.2	5.5	3.6	1.3	83.9	2.7
	Max	13.2	7.4	4.8	3.2	1.1	73.5	2.0
	Average							
F_1	2009	11.8	6.7	4.4	2.9	0.9	62.0	1.5
	Min	15.0	8.1	5.3	3.6	1.5	84.4	3.3
	Max	13.5	7.6	4.9	3.3	1.2	74.3	2.4
	Average							
Parents	2010	10.4	5.3	4.0	2.9	1.1	41.4	1.3
	Min							
	Max	14.7	8.1	5.3	3.7	1.4	79.7	3.1
	Average	13.2	7.3	4.7	3.3	1.2	70.6	2.3
F_1	2010	11.2	6.2	4.4	3.1	0.9	64.6	1.4
	Min							
	Max	14.3	7.9	5.3	3.5	1.3	79.8	3.4
	Average	13.1	7.3	4.9	3.3	1.1	74.0	2.1

crosses 3 × 15 (1.96 cN/tex), 2 × 13 (1.67 cN/tex), 4 × 11 (1.37 cN/tex), and 4 × 12 (1.06 cN/tex), which showed that these dominance effects can improve heterosis on Str for these crosses. Significant higher negative dominance effects on Mic were also detected for crosses 1 × 11 (−0.51) and 5 × 14 (−0.14), which demonstrated that dominance effects can improve heterosis on fineness for these crosses.

Significant negative larger dominance × environment effects on Mic for cross 6 × 20 (−0.40, −0.44; Table 6) as well as positive dominance × environment effects for crosses 3 × 15 (0.40, 0.33) and 3 × 17 (0.42, 0.59) were observed, which indicated that positive and negative heterosis might be displayed for these two crosses respectively. The analytical results obtained for the additive and additive × environment effects of other parents as well as for the

Table 2 Genetic variance of fifteen traits

Parameter	NNFFB	NNMS	NFB	LB	DB	DS	PH	BNTTB	BW	TBN	LP	LY	Len	Str	Mic
V_A	0.07**	0.17**	0.00	0.03**	0.012**	0.00	1.59**	0.02**	0.10**	0.12**	2.85**	1.48**	2.49**	0.86**	0.06**
V_D	0.03**	0.15**	0.33**	0.02**	0.002**	0.001**	0.00	0.00	0.00	0.00	0.39**	0.34	0.44**	0.93**	0.08**
V_{AE}	0.00	0.09**	0.10**	0.01**	0.00	0.012*	16.47**	0.00	0.00	0.00	0.00	0.00	0.02**	0.62**	0.03**
V_{DE}	0.00	0.00	0.14**	0.00	0.00	0.013**	29.73**	0.17**	0.12**	0.58**	1.05**	5.93**	0.00	1.05**	0.08**
V_ε	0.21**	1.15**	0.31**	0.06*	0.012**	0.014**	5.58**	0.09**	0.22**	0.18**	0.25**	0.32**	1.37**	0.49**	0.09**
V_P	0.30+	1.55+	0.88**	0.11**	0.026*	0.039+	53.57*	0.27*	0.44**	0.87*	4.54**	8.07*	4.32**	3.94**	0.34**

Significance at [+] 0.1, [*] 0.05, [**] 0.01 level, respectively

dominance and dominance $\times$ environment effects of other crosses are reported in Tables 3–7.

Genetic correlation between three fiber quality traits and other traits

Genetic correlations were analyzed using QGAStation software to understand the relationship between fiber traits and other traits. Table 7 shows the genetic correlation between the three targeted fiber quality traits and other traits. The dominance $\times$ environment interaction variance of Len was 0; thus, the r_{DE} between Len and other traits is not discussed in this study. Significantly positive additive correlations were observed between Len and LB ($r_A = 0.75$), DB ($r_A = 0.43$), BNTTN ($r_A = 1.00$), TBN ($r_A = 0.68$), LY ($r_A = 0.35$), and Str ($r_A = 0.95$). In contrast, significantly negative additive relationships were observed between Len and NNFFB ($r_A = -0.78$), NNMS ($r_A = -0.62$), PH ($r_A = -1.00$), LP ($r_A = -0.54$), and Mic ($r_A = -0.80$). The above relationships indicate that the varieties have high Len and high LB, DB, BNTTB, TBN, LY, and Str but low NNFFB, NNMS, PH, LP, and Mic.

Significantly positive dominance correlations were observed between Len and NNFFB ($r_D = 0.43$), DB ($r_D = 0.21$), and Str ($r_D = 0.56$), whereas significantly negative dominance relationships were observed between Len and NNMS ($r_D = -0.55$), LP ($r_D = -0.54$), LY ($r_D = -1.00$), and Mic ($r_D = -0.70$). The above relationships indicate that these crosses may have high dominance effects on Len and high NNFFB, DB, and Str but low NNMS, LP, LY, and Mic.

Significantly positive additive $\times$ environment relationships were observed between Len and LB ($r_{AE} = 0.40$) and Str ($r_{AE} = 1.00$), whereas significantly negative additive $\times$ environment relationships were observed between Len and NNMS ($r_{AE} = -1.00$), NFB ($r_{AE} = -1.00$), and Mic ($r_{AE} = -0.76$). No significant additive $\times$ environment correlations were observed between Len and other traits, indicating that Len can be selected with high LB and Str but low NNMS, NFB, and Mic in certain environments.

Significant genotype correlations between Len and other traits showed that the high genotype for Len had high LB, DB, DS, BNTTB, TBN, and Str but low NNFFB, NNMS, PH, LP, and Mic in the phenotype value. Significant phenotype correlations between Len and other traits showed that the high phenotype value

Table 3 Additive effects of 20 parents on 15 traits

Parents	NNFFB	NNMS	NFB	LB (cm)	DB (cm)	DS (cm)	PH (cm)	BNTTB	TBN	BW (g)	LP (%)	LY (g/p)	Len (mm)	Str (cN/tex)	Mic
1	0.09*	0.06	0.00	0.01	-0.10**	0.00	-0.20	0.01	0.04	-0.30+	-1.36*	-0.83	-0.44	0.62*	0.16**
2	0.00	0.23	0.00	0.00	-0.07*	0.00	0.07	0.03	0.22+	-0.21	0.28	-0.01	0.20	0.08	-0.08
3	-0.07	-0.03	0.00	-0.12	0.09*	0.00	0.41	0.08	0.54+	0.56**	0.25	2.65**	-0.62+	-0.75+	0.29*
4	0.22+	0.33*	0.00	0.01	-0.06*	0.00	0.14	-0.02	-0.09	0.32+	1.07**	0.78+	-0.67*	-0.72	0.07*
5	0.01	-0.14	0.00	0.02	0.05	0.00	0.77	-0.05	0.15	0.09	0.49	0.62	0.74+	0.81	0.31**
6	0.32**	0.50**	0.00	0.10+	-0.10*	0.00	0.89	0.07	-0.07	-0.28**	-0.36	-0.78*	-0.93**	-0.10	0.20+
7	-0.23+	0.09	0.00	0.10+	-0.03	0.00	-0.10	-0.04	0.06	0.17	-0.97+	0.29	0.18	-0.05	0.01
8	0.37**	0.20	0.00	-0.04	-0.08*	0.00	-0.13	0.11	-0.10	-0.16+	1.16**	-0.29	-0.47**	-0.73*	-0.05
9	-0.03	0.14	0.00	0.09	-0.06*	0.00	-0.02	-0.08	0.04	0.14*	-1.58*	0.00	0.08	-0.06	-0.06
10	-0.05	-0.08	0.00	0.05	-0.07+	0.00	1.14	-0.01	0.17	-0.33*	-0.19	-0.49	-0.06	-0.56	-0.09+
11	-0.22**	-0.53*	0.00	0.07	0.05*	0.00	-0.45	0.00	-0.15	-0.01	0.88**	-0.21	-0.34	0.09	-0.08
12	-0.17+	-0.27	0.00	-0.06+	0.06*	0.00	-0.13	0.12*	-0.19	0.08	-0.04	-0.25	-0.57**	-0.21	0.07+
13	-0.22**	0.09	0.00	0.03	0.07	0.00	0.22	0.02	-0.11	-0.10	-0.81	-0.62	1.25	0.37	-0.20*
14	0.04	0.31*	0.00	-0.24*	0.11*	0.00	0.89	-0.10	-0.36*	-0.07	1.57**	-0.67	-1.49**	-0.87	0.01
15	0.09	0.35+	0.00	-0.25+	0.01	0.00	1.16	-0.10	-0.14	-0.20	0.83*	-0.57+	-0.16	0.57	0.07**
16	0.18+	-0.12	0.00	-0.19**	0.07	0.00	0.02	-0.11	-0.26*	0.03	2.61**	0.06	-1.25**	0.11	0.08
17	0.15	-0.18+	0.00	0.04	-0.11**	0.00	-0.49	-0.20*	-0.41+	-0.06	-1.36*	-1.26+	-1.34**	-1.15*	0.02
18	-0.10	-0.01	0.00	0.17*	0.07	0.00	0.01	0.09	0.17*	0.00	0.09	0.36	1.16*	0.61	-0.21
19	-0.20**	-0.55+	0.00	0.14+	0.11**	0.00	-2.65*	0.14*	0.02	0.23	-2.32*	0.08	3.01**	1.37*	-0.28+
20	-0.17*	-0.39	0.00	0.07	0.02+	0.00	-1.57*	0.05	0.49**	0.09+	-0.22	1.14**	1.71+	0.57*	-0.26*

Significance at + 0.1, * 0.05, ** 0.01 level, respectively

Table 4 Additive × environment interaction effects of parents on eight traits

Parents	NNMS		NFB		LB (cm)		DS (cm)		PH (cm)		Len (mm)		Str (cN/tex)		Mic	
	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010
1	0.00	0.04	0.05	−0.06	0.05	−0.04	−0.01	0.02	−2.8	2.32[+]	0.02	−0.08*	0.10	0.48[+]	0.08	0.07
2	0.14	0.04	0.08	0.13	−0.03	0.03	−0.01	0.01	−1.79	1.96	−0.02*	0.05*	0.46	−0.38	0.18*	−0.25[+]
3	0.17	−0.2	0.25	−0.23	−0.03	−0.06	0.01	0.00	1.19	−0.20	−0.03	−0.05[+]	−0.39	−0.31*	0.07	0.20
4	0.19	0.06	0.19	−0.05	0.02	−0.01	0.00	−0.02	0.49	−0.14	0.01	−0.09*	−0.39	−0.28	−0.02	0.09
5	−0.37	0.27	−0.33	0.2	−0.01	0.02	0.07*	−0.02[+]	0.7	1.17	0.04[+]	0.06[+]	0.67**	0.09	0.03	0.26[+]
6	0.36	0.01	0.35	−0.13	0.07	0.00	0.05*	−0.05*	2.15	0.01	−0.08[+]	−0.05*	−0.22	0.13	−0.04	0.23[+]
7	−0.11	0.18	−0.08	0.33	−0.01	0.07[+]	−0.03	0.02	−3.21*	2.96*	0.00	0.03	0.12	−0.17	0.06	−0.05
8	−0.12	0.26	−0.36	0.27	−0.04	0.02	−0.07	0.03	−4.52*	4.20*	−0.08[+]	0.02	−1.09*	0.40	−0.09	0.04
9	0.29[+]	−0.18[+]	0.16	−0.02	0.12*	−0.05*	0.08**	−0.07*	4.34**	−4.38**	−0.06[+]	0.07*	−0.42**	0.37*	0.01	−0.07
10	0.10*	−0.16*	0.06	−0.09	−0.02	0.06	−0.05[+]	0.11[+]	2.30[+]	0.45	0.07[+]	−0.08*	0.96**	−1.49*	0.10[+]	−0.19[+]
11	0.03	−0.42*	0.12[+]	−0.44[+]	−0.02	0.07	−0.01	0.02	−0.21	−0.88	−0.09*	0.04*	−0.07	0.16	−0.06	−0.01
12	−0.32	0.11	−0.23	0.11	−0.01	−0.03	−0.02	0.04	−2.52	2.20	−0.06[+]	−0.01*	−0.18	−0.01	0.12	−0.06
13	−0.31	0.37*	−0.22	0.45*	−0.01	0.03[+]	−0.09*	0.10*	−3.06*	3.60*	0.14[+]	0.03**	0.60	−0.25	−0.07	−0.11
14	0.04	0.19	0.07	0.17	−0.19	0.02	0.15[+]	−0.34	3.12[+]	−0.98	−0.11[+]	−0.09	−0.46[+]	−0.36	0.09	−0.08
15	0.25	0.01	0.18	0.07	−0.06	−0.11	−0.02	0.04	1.70	1.11	−0.09[+]	0.07[+]	−0.38	0.92**	0.06	0.01
16	0.02	−0.12	0.07	−0.30	−0.12*	−0.02	−0.09*	0.07*	1.95	−1.90	−0.13[+]	−0.03*	−0.58*	0.68*	0.20	−0.13
17	0.07[+]	−0.21[+]	−0.06	−0.21[+]	0.10	−0.07	0.05[+]	−0.03[+]	1.95*	−3.13*	−0.05[+]	−0.13*	−0.25	−0.82*	−00.17	0.18
18	−0.01	−0.33	0.06	−0.34	0.12[+]	0.09[+]	0.00	0.04	0.03	−9.17**	0.15[+]	0.20*	0.57[+]	1.00**	−00.20	−0.11
19	−0.08	0.07	0.00	0.15	0.00	−0.01	0.00	0.00	2.77[+]	0.80	0.19[+]	0.03**	0.28	−0.14	−00.15	−0.03
20	−0.36	0.15	−0.37	0.35*	0.06	0.02	−0.01	0.02	−4.59	2.85	0.20*	0.31*	0.67	0.57	−00.21	0.23

Significance at [+] 0.1, * 0.05, ** 0.01 level, respectively

Table 5 Dominance effects of part crosses on 11 traits

Crosses	NNFFB	NNMS	NFB	LB (cm)	DB (cm)	DS (cm)	LP (%)	LY (g)	Len (mm)	Str (cN/tex)	Mic
1×11	−0.02	−0.25	−0.32	0.05	0.03+	−0.04	−0.13	−0.34	0.51	−0.19	−0.51*
1×12	0.08	0.66	0.79+	0.29*	0.02	0.03	0.53	−0.07	−0.82*	0.63+	0.01
1×7	0.07	0.45	0.51	0.13	0.01	0.00	0.08	0.77+	−1.08*	−0.59*	0.57*
1×18	−0.04	0.16	0.28	0.19*	0.02	0.00	1.02+	0.65+	−0.70*	0.01	0.55*
2×13	−0.38+	−0.06	0.51	−0.07*	0.02	0.00	−0.75+	−0.29	0.23	1.67*	0.14
2×15	−0.08	−0.31	−0.3	−0.06	0.01	−0.02	0.33	0.87+	0.10	−0.39	0.20*
2×16	0.19+	−0.01	−0.31	−0.05	0.02	−0.03	−0.43	−0.16	0.19	−0.52	−0.19
2×17	−0.12	−0.34	−0.29	0.01	−0.13	−0.01	0.29+	−0.15	−1.20+	−1.54*	−0.05
3×11	0.19	0.10	−0.15	−0.05	−0.04	0.05	−0.89+	−0.16+	0.63	0.79*	0.02
3×13	−0.19	0.13	0.48	0.01	0.07	0.01	1.16	1.15+	0.37	0.47	0.22
3×15	0.07	−0.50	−0.81+	0.06	0.03	−0.03	0.58	0.44+	0.05	1.96*	−0.03
3×16	−0.10+	0.73+	1.17*	−0.19+	0.00	0.02	0.84	1.07+	−0.27	−0.13	0.10
3×17	−0.26+	−0.28	0.01	−0.26*	−0.02	−0.03	0.09	1.01*	−1.06+	−0.75	0.83*
3×18	0.18+	−0.07	−0.37	0.00	−0.05+	0.00	−0.78+	−0.56*	−0.99+	−0.89+	0.20+
4×11	0.28+	0.05	−0.37	−0.08	0.02	−0.02	0.79+	0.06	0.47	1.37+	0.12
4×12	0.20+	−0.44	−0.92*	0.11	0.00	−0.01	0.11	0.16	−0.23	1.06*	0.43*
4×18	0.01	0.32	0.44	−0.10+	−0.01	0.02	0.82	0.96+	−0.39	−2.36	−0.07
5×14	−0.02	−0.03	−0.02	−0.15	−0.07+	0.00	−0.48+	−0.15	0.03	−0.23	−0.14+
5×19	−0.11	0.80+	1.28*	0.10	0.05	0.05	0.27	1.38+	0.91+	−0.33*	0.56*
6×20	0.02	0.56+	0.75*	−0.07*	0.01	−0.02	0.84+	0.10	−1.14+	−2.03*	0.04
7×14	0.08	0.29	0.28	0.05	0.01	0.01	−0.12	0.05	−0.11	0.23	−0.13
8×11	−0.12	−0.59+	−0.63	0.23*	0.01	0.00	0.15	−0.18+	0.12	0.68*	0.06+

Significance at $^+$ 0.1, * 0.05, respectively

for Len had high NNFFB, NNMS, NFB, LB, DS, BNTTB, TBN, Str and low DB, PH, BW, LY and Mic in the phenotype value.

The genetic main effect relationship between Str and other traits was close to that of Len and other traits; only the size order showed slight differences (except between Str and NNFFB, Str and NFB, Str and Mic on dominance effect). Significant additive × environment interaction correlations were observed between Str and NFB ($r_{AE} = -0.50$), DS ($r_{AE} = -0.03$), PH ($r_{AE} = -0.15$), and Len ($r_{AE} = 1.00$). These results reveal that selecting materials for Str with high NFB, DS, and PH is difficult in certain environments but obtaining materials with long fibers is relatively easy. Significant dominance × environment interaction correlations between Str and NFB ($r_{DE} = 0.62$), BW ($r_{DE} = 0.27$), LY ($r_{DE} = 0.50$), and Mic ($r_{DE} = -0.04$) revealed that Str may have heterosis with low Mic but high NFB, BW, and LY under certain conditions.

The signs of significant genetic components correlation coefficients were almost opposite between Mic and other traits, compared with the genetic correlation between Str and other traits, suggesting that fineness can be simultaneously improved with difficulty with LP ($r_A = 0.31$) in certain environments; Fineness was improved with Len ($r_{AE} = -0.76$) and PH ($r_{AE} = -0.59$) synchronously during cross breeding. Significant dominance correlations also existed in Mic and LP ($r_D = 0.74$). In addition, fineness may have heterosis with low Str ($r_{DE} = -0.04$) and high DS ($r_{DE} = 0.43$), PH ($r_{DE} = 0.63$), BNTTB ($r_{DE} = 0.62$), TBN ($r_{DE} = 0.29$), and LY ($r_{DE} = 0.28$) in certain environments. Significant genotypic and phenotypic correlations existed between Mic and other several traits, showing that these varieties have little Mic with long bolls and fibers but low NNFFB, NNMS, PH, and LP in the genotype and phenotype value.

Decision-making analysis on length

The decision-making coefficients from other traits on the three main fiber Len, Str and Mic are listed in

Table 6 Dominance × environment interaction effects of part crosses on 10 traits

Crosses	NNFFB		DS (cm)		PH (cm)		NFB		TBN	
	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010
1 × 11	−0.68	0.13	−0.09	0.02	−4.46[+]	−2.87*	−0.37	−0.21	0.04	−0.46
1 × 12	0.59	0.44	−0.03	0.08[+]	−2.17*	2.89	−0.10	0.83	0.80[+]	0.53
1 × 17	0.32[+]	−0.20	−0.06	−0.02	4.05*	3.97	−0.38	−0.49*	2.64[+]	−0.37[+]
1 × 18	−0.28	0.50	0.00	0.12*	1.97*	4.78*	0.38[+]	−0.10	−0.18	0.98
2 × 13	−0.14	−0.39	−0.13[+]	−0.11*	−1.34	2.33	0.18	−0.32*	−1.22[+]	−0.46*
2 × 15	−0.56	−0.61	−0.03	−0.18*	−10.70[+]	−10.68*	0.26[+]	−0.07	0.59[+]	−1.15[+]
2 × 16	0.37	0.68	0.16*	0.19[+]	5.62[+]	7.84	0.35	0.23	0.64[+]	0.85
2 × 17	0.65	−0.25	0.28[+]	0.10	3.06	−0.15	1.02[+]	1.23	2.06	−0.08
3 × 11	0.35	−0.16	−0.08[+]	−0.14[+]	7.47[+]	−4.59*	0.38	−0.91[+]	−0.02	1.11
3 × 13	0.25	0.07*	0.17*	−0.02	8.84*	2.77	0.85[+]	0.29	0.71[+]	0.44
3 × 15	−0.48	0.30	0.09	0.12[+]	4.28	8.36*	−0.23	−0.51[+]	0.93[+]	−0.05
3 × 16	−0.3	−0.31	0.09	−0.05	1.34+	−6.81	0.26	0.03+	0.67+	−1.26+
3 × 17	−0.13	−0.14	0.03[+]	0.04*	1.44*	3.56[+]	0.45[+]	0.00	−0.55	1.00[+]
3 × 18	0.30	−0.13	0.11*	−0.02	1.93	6.91*	0.22	−0.32	0.51*	−0.04
4 × 11	0.55	−0.03	0.06*	−0.09*	5.00[+]	1.06	0.23	0.17	−0.07	0.16
4 × 12	0.48	0.32	0.14*	−0.09*	5.75*	1.86	0.33*	−0.34	0.54*	−0.66[+]
4 × 18	0.20	0.22	−0.43[+]	−0.01	−1.56	1.74	−0.40[+]	−0.19	−0.10	0.41
5 × 14	0.02	−0.03	0.05	−0.13*	−0.18*	−9.55[+]	−0.26[+]	−0.61[+]	−0.44[+]	−0.34[+]
5 × 19	−0.42	−0.66	0.09*	0.04	−10.92*	−1.92[+]	0.48	−0.06*	0.47[+]	0.36
6 × 20	0.13[+]	−0.14	−0.21[+]	0.22[+]	−1.62	0.99	−0.24	0.52[+]	−0.94	−0.21

Crosses	BW (g)		LP (%)		LY (g)		Str		Mic	
	2009	2010	2009	2010	2009	2010	2009	2010	2009	2010
1 × 11	0.02[+]	0.24+	−1.04[+]	−1.75*	−0.40	−0.59	1.2	0.72[+]	0.11	−0.13[+]
1 × 12	0.11	0.19	1.36[+]	0.34	2.98[+]	2.11	0.31*	−0.51	−0.21*	0.45[+]
1 × 17	0.11	−0.62	1.10*	1.08	6.70*	−2.69*	0.72*	−0.27**	0.60*	0.31
1 × 18	−0.34	0.45	−1.41[+]	−1.86*	−2.23[+]	3.30*	−1.08[+]	1.13[+]	0.25*	−0.02
2 × 13	0.40	−0.72	0.27	1.59*	−1.49	−3.23*	1.93[+]	−1.62*	−0.44*	0.20*
2 × 15	−0.35	0.02	−0.99*	−0.22	−0.3	−2.42	0.74	0.23	0.23	−0.50*
2 × 16	0.17	−0.04	1.37[+]	0.23	2.55	1.69[+]	−3.87[+]	−0.5	0.05*	−0.26*
2 × 17	0.51	0.29	−0.8	−0.87	6.54[+]	0.56	−0.13	0.51	0.55*	0.10
3 × 11	−0.14	−0.20	1.67[+]	0.92	−0.20	2.17	−2.19[+]	−0.22	0.10	−0.24*
3 × 13	−0.32	0.03	1.63*	2.08[+]	0.85	2.16[+]	−0.44	1.18	0.00	−0.14[+]
3 × 15	0.21*	0.29	0.51	0.17	2.92*	1.3	1.56[+]	−0.47	0.40*	0.33*
3 × 16	0.07	0.25	−0.49	−0.93+	1.31+	−2.65*	0.69	−1.63	−0.04	0.42
3 × 17	−0.16	−0.27	−0.55	1.15	−1.92	1.74[+]	0.38	−0.27*	0.42*	0.59*
3 × 18	−0.02	0.15	−0.71	1.20[+]	0.74[+]	0.92	0.26[+]	0.54	−0.45*	0.30
4 × 11	−0.05	0.20	0.29[+]	0.12	−0.34	1.29	−0.27*	1.01[+]	0.13*	−0.14*
4 × 12	0.19[+]	0.01	−0.24	1.29[+]	1.77*	−1.04[+]	0.01	−0.28	0.03	0.13
4 × 18	0.19	−0.03	−0.08	−0.16	0.36*	0.61	1.12+	−0.28	0.13*	−0.06
5 × 14	0.11	0.18	−0.43[+]	−1.86[+]	−0.85	−0.64	0.32	0.72[+]	0.08*	−0.16
5 × 19	0.18	−0.07[+]	−2.23*	0.11	0.86[+]	0.64	1.13	0.32	−0.19	−0.03[+]
6 × 20	−0.11	−0.20[+]	−0.02	0.07	−2.34	−1.06[+]	−0.39	−2.95[+]	−0.40*	−0.44*

Significance at [+] 0.1, * 0.05, ** 0.01 level, respectively

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Table 7 Genetic correlation coefficients between fiber length, strength, micronaire, and other traits

Parameter	NNFFB	NNMS	NFB	LB	DB	DS	PH	BNTTB	TBN	BW	LP	LY	Len	Str	Mic
Fiber length															
r_A	-0.78**	-0.62**	0.00	0.75**	0.43**	0.00	-1.00*	1.00**	0.68*	0.27	-0.54**	0.35*	–	0.95**	-0.80**
r_D	0.43**	-0.55*	-0.49	-0.32	0.21**	1.00	0.00	0.00	0.00	0.00	-0.54**	-1.00*	–	0.56**	-0.70+
r_{AE}	0.00	-1.00*	-1.00*	0.40+	0.00	-0.44	-0.79	0.00	0.00	0.00	0.00	0.00	–	1.00*	-0.76*
r_{DE}	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	–	0.00	0.00
r_G	-0.31**	-0.24*	-0.13	0.28**	0.28*	0.16+	-0.34+	0.13*	0.15*	0.10	-0.41**	0.09	–	0.62**	-0.47**
r_P	0.33**	0.54**	0.33**	1.00**	-0.16**	0.28**	-0.16+	0.81**	0.48**	-0.48**	-0.34	0.06	–	0.58*	-0.52**
Fiber strength															
r_A	-0.71*	-0.32+	0.00	0.60**	0.63**	0.00	-1.00**	1.00**	0.65*	0.07	-0.40**	0.28*	0.95**	–	-0.69
r_D	-0.37+	-0.95+	-0.53*	-0.02	0.48*	0.12	0.00	0.00	0.00	0.00	-0.21**	-1.00*	0.56**	–	0.00
r_{AE}	0.00	-0.66	-0.50**	-0.21	0.00	-0.03*	-0.15**	0.00	0.00	0.00	0.00	0.00	1.00*	–	0.32
r_{DE}	0.00	0.00	0.00	0.00	0.00	-0.09	0.19	0.52	0.62*	0.27**	0.04	0.50**	0.00	–	-0.04*
r_G	-0.15*	-0.21	-0.19	0.14	0.23*	0.07	-0.29+	0.04	0.11	0.03	-0.25	0.05	0.62**	–	-0.14+
r_P	0.16	0.12**	0.03*	0.57**	0.05	0.14*	-0.17	0.39**	0.27*	-0.26**	-0.18	0.03	0.58**	–	-0.12
Micronaire															
r_A	0.81*	0.65	0.00	-0.51**	-0.09	0.00	1.00*	-0.64	-0.42	-0.10	0.31*	-0.12*	-0.80**	-0.69	–
r_D	-0.08	0.45	0.33	-0.06	0.11	-0.64	0.00	0.00	0.00	0.00	0.74+	1.00*	-0.70+	0.00	–
r_{AE}	0.00	-0.01	-0.22*	-1.00*	0.00	-0.52	-0.59**	0.00	0.00	0.00	0.00	0.00	-0.76*	0.32	–
r_{DE}	0.00	0.00	0.46	0.00	0.00	0.43+	0.63**	0.62**	0.29+	0.22	0.22	0.28*	0.00	-0.04*	–
r_G	0.14**	0.18*	0.16	-0.24**	-0.11	0.00	0.32*	0.01	0.19	0.17	0.27**	0.28	-0.47**	-0.14+	–
r_P	0.13**	0.38**	0.27	-0.27*	-0.08	0.05	0.39**	0.14	0.19	0.31	0.30**	0.30	-0.52**	-0.12	–

Significance at $^+$ 0.1, * 0.05, ** 0.01 level, respectively. r_A additive correlation coefficient; r_D dominance correlation coefficient; r_{AE} additive × environment interaction correlation coefficient; r_{DE} dominance × environment × environment correlation coefficient; r_G genotype correlation coefficient; r_P phenotype correlation coefficient

Table 8. The order of decision-making coefficients from all additive effects of other traits to those of Len were Str ($R_{(A)} = 0.87$) > LB ($R_{(A)} = 0.43$) > TBN ($R_{(A)} = 0.27$) > NNFFB ($R_{(A)} = 0.12$) > PH ($R_{(A)} = 0.11$) > BW ($R_{(A)} = 0.07$) > Mic ($R_{(A)} = 0.07$) > NNMS ($R_{(A)} = 0.01$) > DB ($R_{(A)} = -0.11$) > LY ($R_{(A)} = -0.13$) > BNTTB ($R_{(A)} = -0.21$) > LP ($R_{(A)} = -0.53$). This result indicates that additive effects of Str and LB may increase the length of hybrid offspring and attain the best effects when they are enhanced. In contrast, high LP and BNTTB on additive effects (the orders of the two decision-making coefficients are 12th and 11th, respectively) can decrease additive effects on Len. This result shows that Str and LB are the main decision-making traits of additive effects on Len, whereas LP and BNTTB are the main restricting traits.

The results of the additive effect of parents and the decision-making coefficients analysis (Table 3 and 4) revealed that parents 19 (1.37 cN/tex) and 20 (0.57 cN/tex) on Str, parent 19 on LP (-2.32 %), as well as parents 18 (0.17 cm) and 19 (0.14 cm) on LB can increase the additive effects of fiber Len for their offspring. This does not hold for parent 19, which was determined to have high BNTTB (0.14).

Table 8 shows that the main decision-making traits of enhancing dominance effects for Len were NNFFB ($R_{(D)} = 0.03$) and LB ($R_{(D)} = 0.03$). The main restraining traits were DB ($R_{(D)} = -20.11$) and LP ($R_{(D)} = -7.29$); arbitrary selected traits include NNMS ($R_{(D)} = 0.00$), and LY ($R_{(D)} = 0.00$). These dominance effects were 0 on PH, BNTTB, TBN, BW, thus there was not effect on dominance effects of Len.

As shown in Table 5, the dominance effects of crosses 5 × 14 (-0.07^+) and 3 × 18 (-0.05^+) on DB as well as those of crosses 3 × 11, 3 × 18, and 2 × 13 on LP all avail the dominance effects of Len. By contrast, the dominance effects of DB for 1 × 11 (0.03^+), 1 × 18, 4 × 11, and 6 × 20 on LP go against those of Len. As all effects with 0 (or genetic component variance being 0) cannot influence the genetic component effect of target traits, their decision-making coefficients were not analyzed in this study.

All additive × environment $R_{(AE)}$ values were less than 0; thus, the main restraining traits of the additive × environment decision-making coefficients of the other traits on Len were DS [$R_{(AE)} = -637.96$] and Str [$R_{(AE)} = -183.15$]. This suggests that reductions in the additive × environment effects of these traits may increase those of Len in offspring under certain environments.

The largest decision-making coefficients ($R_{(P)}$) on the phenotype and genotype of Len were Str and BNTTB. The smallest decision-making coefficients were Mic on the phenotype ($R_{(i)} = -0.39$) and DB ($R_{(i)} = -0.18$) on the genotype of Len. Therefore, the decision-making traits of the phenotype and genotype for Len were Str and BNTTB; the restraining traits were Mic on the phenotype value and DB on the genotype value. These results indicate that selecting high Str and BNTTB on the phenotype and genotype can yield significant improvements in the phenotype and genotype values of Len. In addition, decreasing the phenotype value of Mic can improve the phenotype value of Len and increase fineness.

Decision-making analysis on fiber strength

Among all of the additive decision-making coefficients to Str, Len was the largest ($R_{(A)} = 0.77$), followed by BNTTB ($R_{(A)} = 0.23$) (Table 8). The smallest coefficients were LB ($R_{(A)} = -0.83$) and TBN ($R_{(A)} = -0.52$). These data indicate that increasing the additive effects of Len and BNTTB and decreasing the additive effects of LB and TBN can improve the Str of hybrid offspring and that fiber Len should be increased by selecting Len for the offspring of parents 18, 19 and 20 as well as a short boll and less TBN for the offspring of parents 14 and 17 (Table 3).

The main decision-making trait that affected the dominance effects of Str was DB ($R_{(D)} = 0.16$); the main restraining traits were NFB ($R_{(D)} = -13.97$) and NNMS ($R_{(D)} = -8.43$). These results show that positively selecting DB and negatively selecting NFB and NNMS may improve the Str of hybrids due to dominance correlations. In addition, the dominance of crosses 4 × 12 (-0.92) and 3 × 15 (-0.81) on NFB as well as that of cross 8 × 11 (-0.59) on NNMS can improve the dominance of Str for these crosses (Table 5).

The main decision-making trait that affected the additive × environment interaction effects of Str was Len ($R_{(AE)} = 0.41$), whereas the main restraining traits were PH ($R_{(AE)} = -0.47$) and DS ($R_{(AE)} = -0.40$). These results indicate that enhancing the additive effect of Len and decreasing the additive effect of PH and DS can improve the Str of offspring under certain conditions.

The main decision-making trait that affected dominance × environment interaction effects of Str was NFB ($R_{(DE)} = 0.18$), whereas the main restraining traits were LY ($R_{(DE)} = -1.63$) and TBN ($R_{(DE)} = -1.52$). These findings reveal that the dominance × environment interaction correlation among traits was beneficial for the improvement of heterosis of Str when high dominance effects of NFB are selected and LY and TBN are selected in the negative direction under certain conditions.

Table 8 shows that selecting high phenotype and genotype values of Len and low Mic is beneficial for Len. In addition, selecting high genotype values of LB might yields favorable effects.

Decision-making analysis on micronaire

Within certain ranges, the smaller the Mic, the better the fineness of offspring; thus, smaller decision-making coefficients and restraining effects will result in improved fiber fineness. Decision-making coefficients of various genetic components on Mic are listed in Table 8. The main decision-making traits that affect the additive effects of Mic are Str ($R_{(A)} = -4.86$) and LB ($R_{(A)} = -2.37$), whereas the main restraining traits are Len ($R_{(A)} = 0.78$) and PH ($R_{(A)} = 0.30$). Therefore, selecting positively high additive effects of Str and LB and negatively high additive effects of Len and PH were beneficial for improving the fiber fineness of the hybrid progeny. Thus, based on Table 3, high Str, long boll, and low PH should be selected for the offspring of parent 19, high Str and low PH should be selected for those of parent 20, and short Len should be selected for those of parents 14 and 17.

Table 8 shows that the main decision-making traits that affect the dominance effects of Mic are LB ($R_{(D)} = -4.12$), Str ($R_{(D)} = -4.11$), and NFB ($R_{(D)} = -3.21$), whereas the main restraining traits are NNMS ($R_{(D)} = 0.39$) and Len ($R_{(D)} = 0.28$). This result indicates that selecting low dominance effects on LB, Str, and NFB and high dominance effects on NNMS and Len would be beneficial for enhancing the heterosis of fiber fineness. The results also suggest that the dominance of crosses may improve the dominance of fineness for 1 × 12 (0.29 mm) and 8 × 11 (0.23 mm) on LB, 3 × 15 (1.96 cN/tex) and 4 × 11 (1.37 cN/tex) on Str, 5 × 19 (1.28) and 3 × 16 (1.17) on NFB, 8 × 11 (−0.59) on NNMS, as well as 2 × 17 (−1.20) and 6 × 20 (−1.14) on Len.

For additive × environment interaction effects on Mic, Str ($R_{(i)} = -7.82$), NFB ($R_{(i)} = -2.54$), and PH ($R_{(i)} = -2.34$) have decision-making effects, whereas Len ($R_{(i)} = 0.85$) had a restraining effect on improving fiber fineness in certain environments.

The decision-making traitts for the dominance × environment interaction effects of Mic are LY ($R_{(i)} = -1.04$), BW ($R_{(i)} = -0.27$), DS ($R_{(i)} = -0.12$). Str ($R_{(i)} = 0.24$) is a restraining trait revealed their usefulness for improving heterosis on fiber fineness by increasing LY, BW, and DS and decreasing the dominance × environment interaction effects of Str.

The main decision-making traits that influences the phenotypic value of Mic is Len ($R_{(i)} = -0.99$), and followed by PH ($R_{(i)} = -0.17$); the restraining trait is Str ($R_{(i)} = 0.47$). This result shows that enhancing the phenotypic value of Len and PH and decreasing the phenotypic value of Str should decrease the phenotypic value of Mic and improve fiber fineness. The main decision-making traits that affect genotypic values are Len ($R_{(i)} = -0.78$) and LB ($R_{(i)} = -0.31$), whereas the main restraining trait is Str ($R_{(i)} = 0.51$).

Discussion

Garcia del Moral et al. (1991) and Guler et al. (2001) investigated the direct and indirect effects of non-target traits on target traits using path analysis, which revealed internal relationships among the traits. However, this method is not performed in breeding due to the direct and multiple indirect effects involved (i.e., some effects might be positive, whereas others might be negative).

Correlation analysis can be used to illustrate the size and property of correlation among traits. However, indirect selection in breeding is also difficult in breeding practice because of neglect in the correlation among non-target traits and the lack of an effective method with which to unify the same genetic effects of different traits (Galanopoulou-Sendouca and Roupakias 1999; Mccarty et al. 2008). Modern molecular biology and quantitative genetics reveal that QTL has various effects, such as additive and dominance effects, among others (Shen et al. 2006; Jiao et al. 2010). Its complex correlativity makes the genetic relationship among characters much more difficult to

Table 8 Decision-making coefficients (R_i) of the genetic components of other characters to fiber length, strength, and micronaire individual and order from maximum to minimum for $R_{(i)}$

Traits	Length										Strength											
	A		D		AE		P		G		A		D		AE		DE		P		G	
	R_A	Order	R_D	Order	R_{AE}	Order	R_P	Order	R_G	Order	R_A	Order	R_D	Order	R_{AE}	Order	R_{DE}	Order	R_P	Order	R_G	Order
NNFFB	0.12	4	0.03	1	–	–	0.11	5	0.13	3	−0.19	11	−0.68	6	–	–	–	–	−0.02	13	0.01	5
NNMS	0.01	8	0.00	4	0.00	1	0.12	4	0.01	12	−0.01	7	−8.43	9	−0.09	3	–	–	−0.01	11	−0.03	11
NFB	–	–	0.01	3	0.00	1	0.00	9	0.01	11	0.00	6	−13.97	10	0.04	2	0.18	1	0.02	4	0.00	8
LB	0.43	2	0.03	2	0.00	1	−0.12	11	0.05	5	−0.83	13	−0.99	8	−0.12	4	–	–	0.00	8	0.13	2
DB	−0.11	9	−20.11	9	–	–	−0.18	13	−0.01	14	0.17	3	0.16	1	–	–	–	–	0.05	3	0.00	7
DS	–	–	−0.04	5	−637.96	5	0.06	6	0.02	8	0.00	6	−0.08	2	−0.40	6	−0.15	5	0.00	7	0.00	10
PH	0.11	5	–	–	−98.13	2	0.17	3	0.02	10	−0.15	9	–	–	−0.47	7	−0.08	4	0.06	2	0.03	4
BNTTB	−0.21	11	–	–	–	–	0.27	2	0.20	2	0.23	2	–	–	–	–	−0.22	7	−0.01	10	−0.03	13
TBN	0.27	3	–	–	–	–	−0.17	12	0.00	13	−0.52	12	–	–	–	–	−1.52	8	0.01	6	0.01	6
BW	0.07	6	–	–	–	–	0.01	8	0.03	6	−0.19	10	–	–	–	–	−0.18	6	−0.01	12	0.05	3
LP	−0.53	12	−7.29	8	–	–	−0.11	10	0.06	4	0.15	4	−0.41	4	–	–	0.00	2	0.01	5	−0.03	12
LY	−0.13	10	0.00	10	–	–	0.05	7	0.02	9	0.07	5	−0.83	7	–	–	−1.63	9	0.00	9	0.00	9
Len							0.33	1	0.36	1	0.77	1	−0.43	5	0.41	1	–	–	0.39	1	0.33	1
Str	0.87	1	−0.82	7	−183.15	4																
Mic	0.02	7	−0.65	6	−111.09	3	−0.39	14	0.02	7	−0.03	8	−0.13	3	−0.34	5	−0.01	3	−0.14	14	−0.18	14

Traits	Micronaire											
	A		D		AE		DE		P		G	
	R_A	Order	R_D	Order	R_{AE}	Order	R_{AE}	Order	R_P	Order	R_G	Order
NNFFB	0.23	3	−0.85		–	–	–	–	0.00	5	−0.02	9
NNMS	−0.40	9	0.39		−1.79	4	–	–	0.00	6	0.01	5
NFB	–	–	−3.21		−2.54	6	0.05	2	0.02	2	−0.07	10
LB	−2.37	11	−4.12		−0.85	3	–	–	−0.06	11	−0.31	13
DB	−0.02	7	−0.23		–	–	–	–	−0.09	12	0.00	7
DS	–	–	0.01		−0.76	2	−0.12	7	0.00	8	0.01	6
PH	0.30	2	–		−2.34	5	−0.08	5	−0.17	13	−0.13	11
BNTTB	0.10	5	–		–	–	−0.04	3	0.00	7	0.06	2
TBN	−1.20	10	–		–	–	−0.09	6	0.01	3	0.03	3
BW	−0.18	8	–		–	–	−0.27	8	−0.01	9	−0.19	12
LP	0.11	4	−2.55		–	–	−0.05	4	0.01	4	0.03	4
LY	0.07	6	0.25		–	–	−1.04	9	−0.02	10	0.00	8

Table 8 continued

Traits	Micronaire													
	A		D		AE		DE		P		G	
	R_A	Order	R_D	Order	R_{AE}	Order	R_{AE}	Order	R_P	Order	R_G	Order
Len	0.78	1	0.28	2	0.85	1	–	–	−0.99	14	−0.78	14
Str	−4.86	12	−4.11	9	−7.82	7	0.24	1	0.47	1	0.51	1

"–" indicates that the variance of different genetic components is 0; therefore, these traits are not used in the analysis

select than non-target traits. Selection of one trait will influences the selection of other non-target traits, as well as the target trait itself, in the process of improving targeted traits. The decision-making coefficients put forward by Yuan et al. (2001) based on path analysis can compute synthetic decision actions from non-target traits to target traits and determine the decision-making, restraining, and optional selecting traits; the selection direction of non-target traits to target traits can also be achieved by these coefficients. For instance, in this study, phenotype correlation coefficients between Len and LB, TBN were 1.00[**] and 0.48[**] (Table 7), whereas the phenotype decision-making coefficients of LB and TBN on Len was −0.12 and −0.17 (Table 8). This result clearly suggests that LB and TBN have restraining on Len. Whereas this result accords with the practice of breeding practices. Thus, larger discrepancies may exist when correlation coefficients are used as indirect selection criteria. In contrast, decision-making coefficient analysis can be used to compute the size of synthetic decision effect of various non-target traits to target traits and determine the orientation of every non-target trait on the target characteristic, thereby enhancing the selection effect.

Decision-making coefficients may be positive or negative (Yuan et al. 2001). Different targets require different directions; thus, selection of the direction of non-target traits may also vary. For example, in this study, the high additive effects of Str are desirable for Len when the targeted trait is Len. This result shows that if a high target trait is required by researchers, the decision-making of non-targeted traits on target traits should be better than 0 ($R_{(i)} > 0$) and the character value of the non-targeted trait should be increased. In addition, selecting one or several high values with the largest decision-making coefficients results in the best selection effects. If the decision-making coefficient is less than 0 ($R_{(i)} < 0$), the non-target trait should be decreased. If a low target trait is required by researchers, the decision-making coefficient of non-targeted traits on target traits should be less than 0 ($R_{(i)} < 0$) and the character value of the non-targeted trait should be increased.

Decision-making coefficients of different genetic components can be used for directing different types breeding. Aside from the various decision-making coefficients mentioned above, additive decision-making coefficients and decision-making coefficients of

A × A epistatic effects can be used for guiding cross breeding. Decision-making coefficients of other genetic components, such as dominance and dominance × environment interaction effects can still be applied to analyze the dominance decision-making coefficients of heterosis. The genetic decision-making coefficient analysis is different from conditional variance analysis, which can analyze the contribution of the different genetic component from the phenotype value of the cause trait to the result trait. The two methods are quite different from each other in this regard, and the results they yield are slightly different (Zhu 1995; Mei et al. 2007; Wu et al. 2008). Condition analysis usually calculates the effects of the phenotype value of one non-target trait on different genetic components of one target trait well. However, if multiple non-target traits on one target trait were to be analyzed, the results might not be explained well. In addition, additive effects do not change with increasing generation, whereas dominance and dominance × environment effects gradually approach 0. Therefore, the phenotype of non-target traits might change with increasing generation, as with the contribution of additive effects. In conclusion, the decision-making analysis is a better method in cross and heterosis breeding. Our study aim is to confirm decision-making and restrict traits of three main fiber quality traits for upland cotton.

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