



## **COMBINING ABILITY AND GENETIC COMPONENTS OF EGYPTIAN COTTON FOR EARLINESS, YIELD, AND FIBER QUALITY TRAITS**

**T.S.G. SALEM<sup>1</sup>, H.A. RABIE<sup>2</sup>, S.A.E. MOWAFY<sup>2</sup>, A.E.M. EISSA<sup>1</sup>  
and E. MANSOUR<sup>2\*</sup>**

<sup>1</sup> Cotton Research Institute, Agricultural Research Center, Giza, Egypt

<sup>2</sup> Agronomy Department, Faculty of Agriculture, Zagazig University, Zagazig, Egypt

\*Corresponding author email: sayed\_mansour\_84@yahoo.es

Email addresses of coauthors: tarekshaker84@yahoo.co.uk, eissa.anwar@yahoo.com, hassanrabie1000@yahoo.com, sabermowafy@yahoo.com

### **SUMMARY**

Cotton (*Gossypium barbadense*) is an important fiber crop that plays a major role in the economy and national income of many countries worldwide. Knowledge of combining ability and gene action in a population can help cotton breeders select potential parents and promising F<sub>1</sub> crosses and devise breeding strategies for developing high-yielding cultivars with desirable fiber quality traits. The aim of this study was to estimate the general combining ability (GCA) of six diverse cotton genotypes and the specific combining ability (SCA) of their F<sub>1</sub> crosses from half-diallel mating; to determine gene action and heritability for earliness characters, yield-related traits, and fiber quality parameters; to assess interrelationships among evaluated traits; and to classify the parents and their hybrids on the basis of earliness characters, yield and its related traits, and fiber quality parameters. Randomized complete block design with three replications was applied to evaluate the six parents and their 15 F<sub>1</sub> crosses at the Experimental Farm of Sids Research Station, Beni-Suef, Egypt. The obtained results revealed highly significant differences among parental genotypes and their F<sub>1</sub> crosses for all evaluated traits. Moreover, GCA and SCA effects were highly significant for all tested traits. The parental genotypes P5 and P6 exhibited good combining ability for increasing cotton yield and its related traits. In addition, the cross combinations P3 × P6, P4 × P5, P4 × P6, and P1 × P2 displayed positive SCA values for cotton yield and its contributing traits with the highest significance. Furthermore, the results revealed the significant contribution of additive and nonadditive gene actions to the inheritance of all the studied traits. Otherwise, the contribution of dominance effects to the components of genetic variance in the inheritance of the studied traits was higher than that of additive ones. Additionally, covariance–variance graphs revealed a high degree of genetic diversity for parents with different degrees of dominance and different distributions of dominant and recessive alleles in the parental genotypes for all evaluated traits.

**Keywords:** Cotton, combing ability, gene action, earliness, yield and its related traits, fiber quality, hierarchical clustering, principal components

**Key findings:** Dominance effects had higher contribution to the inheritance of earliness characters, yield-related traits, and quality parameters than additive ones. Different degrees of dominance and the different distributions of dominant and recessive alleles were exhibited by parental genotypes for all evaluated traits. Fiber length was positively associated with cotton yield and its contributing traits, whereas earliness characters had a negative association with cotton yield.

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## INTRODUCTION

Cotton (*Gossypium barbadense*) is one of the most important fiber and oil crops worldwide. It plays a major role in the economy and national income of cotton-producing countries. Globally, the highest producers of cotton are China, India, United States, Brazil, Pakistan, Turkey, and Australia (FAOSTAT, 2020). From 1965 to 2018, the cotton cultivation area in Egypt decreased from 800 thousand ha to 140 thousand ha, and cotton production declined from 1.48 million tons to 311 thousand tons (FAOSTAT, 2020). Therefore, great national efforts have been dedicated to increase cotton production through breeding programs. Accordingly, from 1965 to 2018, seed yield increased from 1856 kg/ha to 3296 kg/ha. Nevertheless, these efforts should be intensified to cope with the recent climate change that obstructs crop production (Mansour *et al.*, 2017a; 2018a,b; Migliore *et al.*, 2019; Gharib *et al.*, 2020; Mansour *et al.*, 2020).

Cotton has several uses: its fiber is one of the extremely acclaimed natural fibers; oil from its seed is used for human consumption; and feed

products for livestock are manufactured from its seeds, which are rich in protein (He *et al.*, 2013; Bellaloui *et al.*, 2015). Developing new high-yielding cotton cultivars with acceptable fiber quality characters is a major objective of all cotton breeders. The first step is selecting appropriate parents for producing crosses with potential heterosis (Kumar *et al.*, 2014; Mansour *et al.*, 2017b; 2018b; Hussain *et al.*, 2019; Gharib *et al.*, 2020; Mansour *et al.*, 2020). Diallel analysis is an effective biometric approach to identifying suitable parents and crosses through estimating general combining ability (GCA) and specific combining ability (SCA). GCA and SCA allow comparing the performance of investigated parents in different cross combinations. The genotypes that display high GCA reveal great capability to combine with other various genotypes and produce high-yielding progenies. By contrast, the genotypes that exhibit high SCA combine well only in certain crosses. Furthermore, high GCA reveals additive gene effects for the studied characters, and high SCA reveals nonadditive, dominant, and epistatic

effects (Başal and Turgut, 2003; Qu *et al.*, 2012; Mansour and Moustafa, 2016; Vasconcelos *et al.*, 2018). Additionally, diallel analysis enables breeders to detect the most efficient selection method through estimating the genetic nature of evaluated qualitative and quantitative characters (Hallauer and Miranda, 1988; Başal and Turgut, 2003; Salgotra *et al.*, 2009).

GCA and SCA are analyzed by using the Griffing (1956) method. The Hayman (1954 a, b) method is used to study gene action, genetic components, and the heritability of evaluated characters. The analyses of Griffing and Hayman provide rapid and general evidence for the genetic control of the tested parents and crosses in early generations. Likewise, the regression graph of covariance ( $W_r$ ) and variance ( $V_r$ ) of arrays provided by the Hayman method provides valuable information for cotton breeders given that the  $W_r$ - $V_r$  graph displays the average degree of the dominance of genes affecting the evaluated characters and the distribution of dominant and recessive alleles in the investigated parents (Jana, 1975; Syukur *et al.*, 2010).

The aims of this study were to estimate GCA and SCA in a half-diallel cross comprising six Egyptian cotton cultivars and their 15  $F_1$  hybrids and to determine genetic variance components and heritability for earliness, yield traits, and fiber quality traits. This study is an attempt to provide useful information for cotton breeding programs and to produce cotton crosses with diverse genetic backgrounds for enhancing cotton yield and fiber characteristics.

## MATERIAL AND METHODS

### Breeding materials and field experiments

The breeding materials used in this study were six diverse high-yielding and long staple *G. barbadense* genotypes, including two Egyptian commercial cultivars, two advanced lines in a cotton breeding program (in  $F_{10}$ ), and two exotic genotypes (American and Australian). The materials are described in Table 1. The seeds of these genotypes were obtained from the Cotton Breeding Section, Cotton Research Institute, Agriculture Research Center, Egypt. In the first season of 2016 (April 4), the six genotypes were grown in the Experimental Farm of Sids Research Station, Beni-Suef, Egypt (29° 04' N, 31° 05' E). The parents were crossed in all possible combinations in accordance with the 6 × 6 half-diallel mating system to produce 15  $F_1$  hybrids. In the second season of 2017 (April 5), the derived hybrids and their parents were sown in randomized complete blocks with three replications. Twenty-one entries were sown in single plots that included two ridges 4 m long with 80 cm spaces between ridges and 60 cm between hills. The hills were thinned at the seedling stage to retain one plant per hill and five plants per ridge. All recommended agronomic practices and inputs for cotton production, including hoeing; irrigation; phosphate, potassium, and nitrogen fertilizer application; and pest, disease, and weed control were performed uniformly to minimize environmental variability.

**Table 1.** Name, pedigree, and origin of the six cotton varieties used as parents in this study.

Codes	Genotype	Pedigree	Origin	Description
P1	Giza-90	Giza-83 × Dendra	Egypt	High-yielding, long staple, and high lint%
P2	Giza-95	(Giza-83 × [Giza-75 × 5844] × Giza-80)	Egypt	High-yielding, long staple, high lint%, and early maturity
P3	Australian	Unknown	Australia	Exotic short plant, long staple, medium lint%, and early maturity
P4	C.B58	Unknown	USA	Medium long staple, high lint%, and early maturity
P5	PL10	Giza-90 × C.B58	Egypt	High-yielding, long staple, high lint%, and early maturity
P6	PC10	([G83 × Giza-80] × Giza-89) × Australian	Egypt	Promising hybrid, high-yielding, long staple, high lint%, and early maturity

## Studied traits

### A. Earliness characters

The number of nodes to the first sympodial (fruiting) branch (NFSB) and days to first flower unfolding (DFFU) were counted from the sowing date. Days to the first opened boll (DFOB) were counted from the sowing date.

### B. Yield and its component traits

The number of opened bolls/plant (NOB/P) was averaged at 150 days after sowing from 10 plants of each plot. Boll weight/plant (BW/P, g) was measured as the average of 10 bolls from each plot. Seed yield/plant (SCY/P, g) was measured as the average of the harvested lint plus the seed from 10 plants of each plot. Lint yield (LCY/P, g) was measured as the average of lint obtained from 10 plants of each plot, and 100-seed weight (100-SW, g) was measured as the weight of 100 seeds that were taken randomly from each plot. Lint

percentage (L%) and lint index (LI) were calculated in accordance with the following equations:

$$L\% = \frac{\text{Lint yield (LCY/P)}}{\text{Seed yield (SCY/P)}} \times 100$$

$$LI = \frac{\text{Lint percentage (L\%)} \times 100 \text{ seed weight (100-SW)}}{100 - \text{Lint percentage (L\%)}} \times 100$$

### C. Fiber quality parameters

Fiber properties were recorded in the laboratories of Cotton Technology Research Division, Cotton Research Institute, Agriculture Research Center, Egypt, in accordance with the standard method of the American Society for Testing Materials Designation (American Society for Testing Materials, 1998) at 21 °C ± 1 °C and 65% ± 2% relative humidity.

Micronaire reading (MR) was used to express fiber fineness. Fiber strength (FS) was measured by using a Pressley instrument at zero gauge (g/tex). Fiber strength is closely related to yarn and fabric strength and spinning efficiency. Fiber length at

2.5% (FL, mm) was estimated as the space in mm spanned by 2.5% of the fibers as recorded on a digital fibrograph. Uniformity ratio (UR%) was calculated in accordance with the following equation:

$$\text{UR\%} = \frac{50\% \text{ span length}}{2.5\% \text{ span length}} \times 100$$

### Statistical analysis

Analysis of variance was performed in accordance with Steel and Torrie (1980). Least significant difference (LSD) was calculated by using R statistical software version 3.6.1. Genetic analyses involved the Griffing (1956) method 2, model 1, as outlined by Singh and Chaudhary (1985). Additionally, the approach of Hayman (1954a,b) was used to estimate the genetic components of variation for additive and dominance variances. The same approach has been characterized by Mather and Jinks (1982). Hierarchical cluster and principal component analyses were applied with R statistical software, library factextra (Kassambara and Mundt, 2017).

## RESULTS AND DISCUSSION

### Analysis of variance

The analysis of variance for evaluated traits, namely, earliness characters, yield and its related traits, and fiber quality parameters is shown in Table 2. The investigated genotypes exhibited highly significant differences in all studied traits. Furthermore, dividing the genotypic variance into parents, crosses, and parent vs. crosses revealed that the variance due

to parents, as well as crosses, were highly significant for all investigated traits. Significant differences were observed among parents and their F<sub>1</sub> crosses for most studied traits. The obtained results indicated the presence of genetic variability in the used parental genotypes. In addition, the traits followed different patterns in each genotype. Therefore, these parents and their crosses could be exploited further in cotton breeding programs for improving earliness characters, yield and its contributing traits, and fiber quality parameters. Similarly, significant variance has been previously reported between cotton parents and their crosses (Khalifa *et al.*, 2016; Nazmey *et al.*, 2018; Taha *et al.*, 2018; Chaudhary *et al.*, 2019; El-Aref *et al.*, 2019).

The variance due to GCA and SCA was estimated and presented in Table 2. The variance of GCA and SCA was highly significant for all evaluated traits, indicating that additive and nonadditive gene actions contributed significantly to the inheritance of the studied traits and the selection of transgressive genotypes through cotton breeding programs. However, for most traits, the variance due to SCA was greater than that due to GCA and the ratio of GCA/SCA was less than 1, indicating the importance of nonadditive gene action in the inheritance of these traits. Accordingly, selection should be postponed to advanced generations because selection in early generations could be useless. The significance of additive and nonadditive gene action with more pronounced nonadditive effect in the heredity of cotton traits has been reported previously by numerous authors (Karademir and Gencer, 2010; Amein *et al.*, 2013;

**Table 2.** Mean squares of evaluated traits, namely, earliness traits, fiber quality, and yield and its contributing traits for the six cotton genotypes and their 15 F<sub>1</sub> crosses.

Source of variation	d.f.	Yield and its contributing traits						
		NOB/P	BW/P	SCY/P	LCY/P	L%	100-SW	LI
Replications	2	1.44 <sup>NS</sup>	0.01 <sup>NS</sup>	0.10 <sup>NS</sup>	0.11 <sup>NS</sup>	0.02 <sup>NS</sup>	0.05 <sup>NS</sup>	0.04 <sup>NS</sup>
Genotypes	20	24.42 <sup>**</sup>	0.11 <sup>**</sup>	310.45 <sup>**</sup>	71.67 <sup>**</sup>	1.98 <sup>**</sup>	1.49 <sup>**</sup>	0.77 <sup>**</sup>
Parents (P)	5	23.14 <sup>**</sup>	0.15 <sup>**</sup>	183.35 <sup>**</sup>	61.98 <sup>**</sup>	3.46 <sup>**</sup>	1.13 <sup>**</sup>	0.82 <sup>**</sup>
Crosses (C)	14	26.61 <sup>**</sup>	0.06 <sup>**</sup>	276.13 <sup>**</sup>	52.11 <sup>**</sup>	0.95 <sup>**</sup>	1.63 <sup>**</sup>	0.81 <sup>**</sup>
P vs. C	1	0.22 <sup>*</sup>	0.58 <sup>**</sup>	1426.36 <sup>**</sup>	394.04 <sup>**</sup>	9.04 <sup>**</sup>	1.28 <sup>**</sup>	0.01 <sup>NS</sup>
GCA	5	29.38 <sup>**</sup>	0.13 <sup>**</sup>	165.87 <sup>**</sup>	38.78 <sup>**</sup>	2.48 <sup>**</sup>	0.36 <sup>**</sup>	0.36 <sup>**</sup>
SCA	15	22.77 <sup>**</sup>	0.10 <sup>**</sup>	358.64 <sup>**</sup>	82.63 <sup>**</sup>	1.82 <sup>**</sup>	1.86 <sup>**</sup>	0.91 <sup>**</sup>
Error	40	0.82	0.02	0.38	0.33	0.15	0.06	0.04
Total	62	8.45	0.04	100.39	23.34	0.74	0.52	0.28
$\sigma^2$ GCA / $\sigma^2$ SCA		0.16	0.15	0.06	0.06	0.17	0.02	0.05

Source of variation	d.f.	Earliness traits				Fiber quality traits			
		NFSB	DFFU	DFOB	MR	FS	FL	UR	
Replications	2	0.26 <sup>NS</sup>	0.06 <sup>NS</sup>	0.14 <sup>NS</sup>	0.02 <sup>NS</sup>	0.01 <sup>NS</sup>	0.34 <sup>NS</sup>	0.38 <sup>NS</sup>	
Genotypes	20	0.94 <sup>**</sup>	5.48 <sup>**</sup>	44.48 <sup>**</sup>	0.11 <sup>**</sup>	0.21 <sup>**</sup>	1.80 <sup>**</sup>	3.23 <sup>**</sup>	
Parents (P)	5	0.67 <sup>**</sup>	16.90 <sup>**</sup>	47.53 <sup>**</sup>	0.13 <sup>**</sup>	0.18 <sup>**</sup>	1.64 <sup>**</sup>	1.96 <sup>**</sup>	
Crosses (C)	14	0.68 <sup>**</sup>	1.66 <sup>**</sup>	38.52 <sup>**</sup>	0.11 <sup>**</sup>	0.24 <sup>**</sup>	1.70 <sup>**</sup>	3.75 <sup>**</sup>	
P vs. C	1	5.83 <sup>**</sup>	1.86 <sup>**</sup>	112.65 <sup>**</sup>	0.01 <sup>NS</sup>	0.01 <sup>NS</sup>	3.95 <sup>**</sup>	2.32 <sup>*</sup>	
GCA	5	0.52 <sup>**</sup>	9.22 <sup>**</sup>	30.65 <sup>**</sup>	0.09 <sup>**</sup>	0.14 <sup>**</sup>	1.67 <sup>**</sup>	3.61 <sup>**</sup>	
SCA	15	1.08 <sup>**</sup>	4.24 <sup>**</sup>	49.09 <sup>**</sup>	0.12 <sup>**</sup>	0.24 <sup>**</sup>	1.84 <sup>**</sup>	3.10 <sup>**</sup>	
Error	40	0.06	0.09	0.17	0.01	0.02	0.15	0.33	
Total	62	0.35	1.83	14.46	0.04	0.08	0.69	1.26	
$\sigma^2$ GCA / $\sigma^2$ SCA		0.06	0.28	0.08	0.09	0.07	0.11	0.15	

df is degrees of freedom, NS is not significant, \* is significant at *P*-value < 0.05 and \*\* is highly significant at *P*-value < 0.01. NOB/P is number of opened bolls per plant, BW/P is boll weight per plant (g), SCY/P is seed yield per plant (g), LCY/P is lint yield per plant (g), L% is lint percentage, 100-SW is 100-seed weight (g), LI is lint index, NFSB is number of nodes to first sympodial branch, DFFU is days to first flower unfolding, DFOB is days to the first opened boll, MR is micronaire reading, FS is fiber strength (g/tex), FL is fiber length at 2.5% (mm) and UR is uniformity ratio (%).

**Table 3.** Mean performance of the evaluated 14 traits for six cotton genotypes and their 15 F<sub>1</sub> crosses.

Genotypes	Yield and its contributing traits						Earliness traits				Fiber quality traits			
	NOB/P	BW/P	SCY/P	LCY/P	L%	100-SW	LI	NFSB	DFFU	DFOB	MR	FS	FL	UR
P1	50.43	2.94	148.23	57.15	38.56	9.93	6.23	6.87	64.80	120.33	4.13	10.10	31.20	85.00
P2	51.67	3.09	159.35	65.79	41.29	9.50	6.68	6.70	58.73	114.10	4.20	10.03	30.23	83.93
P3	50.25	2.82	141.53	56.23	39.73	10.57	6.97	6.87	61.47	113.60	4.30	10.40	31.87	83.97
P4	46.30	3.29	152.33	60.43	39.67	9.02	5.93	6.70	63.43	119.53	3.87	9.70	30.20	83.30
P5	49.81	3.28	163.47	67.46	41.27	10.17	7.14	7.83	63.20	116.87	4.33	10.00	31.30	85.47
P6	54.87	2.77	151.98	60.05	39.51	9.10	5.94	6.50	65.10	123.97	3.87	10.30	31.83	83.87
P1 × P2	51.19	3.25	166.19	69.13	41.60	10.10	7.19	6.73	62.77	115.07	4.00	9.70	32.30	83.40
P1 × P3	45.16	3.44	155.35	63.63	40.96	8.87	6.15	6.43	62.70	125.00	4.00	10.13	32.83	85.33
P1 × P4	51.03	3.16	161.38	66.41	41.15	8.63	6.04	6.73	62.23	114.23	4.00	9.90	31.23	84.37
P1 × P5	53.92	3.07	165.18	65.88	39.88	8.73	5.79	6.43	62.60	113.53	4.37	10.30	31.17	85.07
P1 × P6	50.50	3.29	166.08	66.60	40.10	10.57	7.07	6.77	63.37	116.43	3.90	9.83	31.97	84.33
P2 × P3	51.43	3.04	156.33	64.02	40.95	10.41	7.22	6.97	62.10	120.80	3.93	9.97	31.60	83.43
P2 × P4	47.09	3.13	147.20	60.88	41.36	8.57	6.05	6.57	64.83	114.17	3.97	10.03	31.73	83.27
P2 × P5	50.23	3.19	160.36	65.43	40.81	9.53	6.58	5.73	63.47	114.53	4.40	10.23	31.07	85.63
P2 × P6	50.93	3.21	163.36	66.47	40.69	9.21	6.32	5.47	62.87	113.47	4.20	10.33	31.37	86.27
P3 × P4	47.49	3.29	156.01	61.92	39.69	9.44	6.21	6.20	63.80	117.07	4.30	10.60	31.70	86.10
P3 × P5	49.40	3.31	163.65	67.05	40.97	8.71	6.05	5.60	62.87	112.43	3.83	9.77	32.23	85.80
P3 × P6	57.53	3.13	180.07	74.76	41.52	9.34	6.64	6.13	63.60	113.17	4.03	9.97	32.00	83.70
P4 × P5	50.59	3.60	182.01	74.94	41.17	10.37	7.26	5.90	63.57	112.83	4.17	10.03	32.70	83.53
P4 × P6	52.20	3.33	173.56	70.63	40.70	10.03	6.88	5.67	64.13	112.43	4.37	9.87	31.20	83.90
P5 × P6	47.67	3.22	153.49	63.08	41.09	8.47	5.91	6.23	62.63	111.43	4.33	10.63	29.80	86.07
LSD <sub>0.05</sub>	1.49	0.09	1.01	0.95	0.64	0.41	0.33	0.41	0.49	0.69	0.15	0.25	0.63	0.94
LSD <sub>0.01</sub>	2.00	0.12	1.35	1.27	0.86	0.55	0.44	0.56	0.66	0.92	0.20	0.34	0.85	1.26

NOB/P is number of opened bolls per plant, BW/P is boll weight per plant (g), SCY/P is seed yield per plant (g), LCY/P is lint yield per plant (g), L% is lint percentage, 100-SW is 100-seed weight (g), LI is lint index, NFSB is number of nodes to first sympodial branch, DFFU is days to first flower unfold, DFOB is days to first opened boll, MR is micronaire reading, FS is fiber strength (g/tex), FL is fiber length at 2.5% (mm) and UR is uniformity ratio (%).

Hamoud, 2014; Khalifa *et al.*, 2016; Ekinci and Basbag, 2018; Taha *et al.*, 2018; Chaudhary *et al.*, 2019).

### **Mean performance of parents and F<sub>1</sub> crosses**

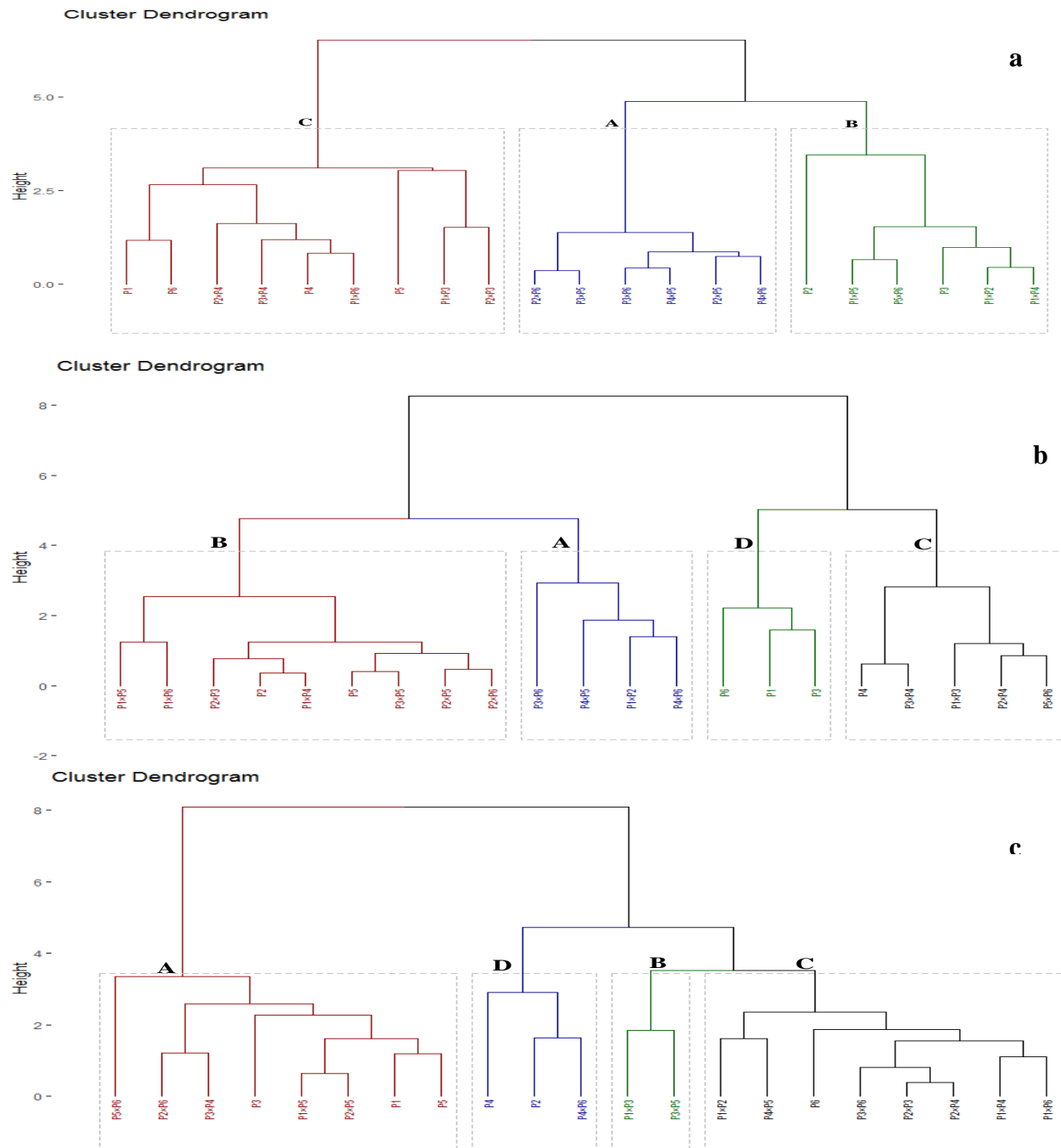
The mean performances of the used parental cotton genotypes and their 15 F<sub>1</sub> crosses for the investigated traits are displayed in Table 3. The parents and their hybrids exhibited significant difference in earliness characters, fiber quality parameters, and yield and its related traits. Notably, the parents P2 and P3 exhibited the lowest values of NFSB, DFFU, and DFOB. These traits indicated their earliness compared with the other parents. Furthermore, P5 and P2 surpassed the other parents for BW/P, SCY/P, LCY/P, L%, LI, NFSB, MR, and UR%. Accordingly, these genotypes could be considered as good parents for increasing cotton yield and its attributes in breeding programs. By contrast, P1, P3, P4, and P6 displayed the lowest values for NOB/P, BW/P, SCY/P, LCY/P, LI, NFSB, and DFOB (Table 3). Moreover, P4 exhibited the lowest value for 100-SW, LI, MR, FS, FL, and UR%. The performance of F<sub>1</sub> cross hybrids in all evaluated traits was better than that of the parents (Table 3). Particularly, the hybrids P3 × P6, P4 × P5, P4 × P6, and P1 × P2 surpassed the parents and the other hybrids in NOB/P, BW/P, SCY/P, LCY/P, L%, 100-SW, LI, and FL. The hybrids P2 × P4, P5 × P6, P1 × P3, and P3 × P4 displayed the lowest yield and its contributing traits. The obtained results were in accordance with the findings of previous studies that demonstrated significant genetic differences for earliness characters,

yield and its related traits, and fiber quality parameters (Khan and Hassan, 2011; Khalifa *et al.*, 2016; Nazmey *et al.*, 2018; El-Aref *et al.*, 2019).

### **Genotypic classification according to performance**

The parents and their F<sub>1</sub> crosses were classified by using hierarchical clustering into three groups on the basis of earliness characters (Figure 1a). Group A included six hybrids that presented the lowest values of NFSB, DFFU, and DFOB. Accordingly, these hybrids could be characterized as early in flowering. Group B comprised two parents and four hybrids that displayed intermediate values and consequently could be characterized as intermediate in their flowering. Group C contained four parents and five hybrids that possessed the highest values of earliness characters; therefore, they could be characterized as late in flowering. The parents and their F<sub>1</sub> crosses were classified into four groups (Figure 1b) in accordance with yield and its contributing traits. Group A included four hybrids that presented the highest yield traits; therefore, these hybrids could be considered as very high-yielding genotypes. Group B comprised two parents and seven hybrids that displayed high yield values. Accordingly, they could be considered as high-yielding genotypes. Group C contained one parent and four hybrids that exhibited intermediate values of cotton yield and its related traits. Finally, Group D included three parents that presented the lowest yield values. These parents could be considered as low-yielding genotypes. Furthermore, the evaluated parents and their F<sub>1</sub> crosses were classified





**Figure 1.** Dendrogram of phenotypic distances among 21 cotton genotypes (six parents and 15 hybrids) based on earliness characters (a), yield-related traits (b), and fiber quality traits (c).

**Table 4.** Estimates of the general combining ability (GCA) effects of six cotton genotypes for the investigated traits.

Parents	Yield and its contributing traits						
	NOB/P	BW/P	SCY/P	LCY/P	L%	100-SW	LI
P1	-0.07 <sup>NS</sup>	-0.02 <sup>NS</sup>	-1.47 <sup>**</sup>	-1.25 <sup>**</sup>	-0.43 <sup>**</sup>	0.04 <sup>NS</sup>	-0.09 <sup>NS</sup>
P2	0.12 <sup>NS</sup>	-0.04 <sup>*</sup>	-1.28 <sup>**</sup>	0.19 <sup>NS</sup>	0.47 <sup>**</sup>	0.05 <sup>NS</sup>	0.16 <sup>*</sup>
P3	-0.22 <sup>NS</sup>	-0.05 <sup>**</sup>	-3.49 <sup>**</sup>	-1.52 <sup>**</sup>	-0.08 <sup>NS</sup>	0.19 <sup>*</sup>	0.10 <sup>NS</sup>
P4	-1.53 <sup>**</sup>	0.10 <sup>**</sup>	0.31 <sup>NS</sup>	-0.04 <sup>NS</sup>	-0.10 <sup>NS</sup>	-0.17 <sup>*</sup>	-0.14 <sup>*</sup>
P5	-0.22 <sup>NS</sup>	0.08 <sup>**</sup>	3.66 <sup>**</sup>	1.91 <sup>**</sup>	0.28 <sup>*</sup>	-0.03 <sup>NS</sup>	0.06 <sup>NS</sup>
P6	1.92 <sup>**</sup>	-0.07 <sup>**</sup>	2.27 <sup>**</sup>	0.71 <sup>**</sup>	-0.14 <sup>NS</sup>	-0.08 <sup>NS</sup>	-0.09 <sup>NS</sup>
S.E. (gi)	0.26	0.02	0.18	0.17	0.11	0.07	0.06

Parents	Earliness traits			Fiber quality traits			
	NFSB	DFFU	DFOB	MR	FS	FL	UR
P1	0.23 <sup>**</sup>	0.23 <sup>*</sup>	1.66 <sup>**</sup>	-0.04 <sup>NS</sup>	-0.07 <sup>NS</sup>	0.17 <sup>NS</sup>	0.07 <sup>NS</sup>
P2	-0.02 <sup>NS</sup>	-0.99 <sup>**</sup>	-0.68 <sup>**</sup>	0.01 <sup>NS</sup>	-0.03 <sup>NS</sup>	-0.25 <sup>*</sup>	-0.26 <sup>NS</sup>
P3	0.01 <sup>NS</sup>	-0.43 <sup>**</sup>	0.50 <sup>**</sup>	-0.02 <sup>NS</sup>	0.08 <sup>NS</sup>	0.45 <sup>**</sup>	0.05 <sup>NS</sup>
P4	-0.07 <sup>NS</sup>	0.50 <sup>**</sup>	-0.23 <sup>NS</sup>	-0.04 <sup>NS</sup>	-0.10 <sup>*</sup>	-0.19 <sup>NS</sup>	-0.52 <sup>**</sup>
P5	0.07 <sup>NS</sup>	0.01 <sup>NS</sup>	-1.65 <sup>**</sup>	0.12 <sup>**</sup>	0.04 <sup>NS</sup>	-0.12 <sup>NS</sup>	0.64 <sup>**</sup>
P6	-0.22 <sup>**</sup>	0.67 <sup>**</sup>	0.40 <sup>**</sup>	-0.03 <sup>NS</sup>	0.08 <sup>NS</sup>	-0.06 <sup>NS</sup>	0.01 <sup>NS</sup>
S.E. (gi)	0.07	0.09	0.12	0.03	0.04	0.11	0.16

NS is not significant, \* is significant at  $P$ -value < 0.05 and \*\* is highly significant at  $P$ -value < 0.01. NOB/P is the number of opened bolls per plant, BW/P is boll weight per plant (g), SCY/P is seed yield per plant (g), LCY/P is lint yield per plant (g), L% is lint percentage, 100-SW is 100-seed weight (g), LI is lint index, NFSB is number of nodes to first sympodial branch, DFFU is days to first flower unfolding, DFOB is days to the first opened boll, MR is micronaire reading, FS is fiber strength (g/tex), FL is fiber length at 2.5% (mm) and UR is uniformity ratio (%).

into four groups (Figure 1c) in terms of fiber quality parameters. Group A included three parents and five hybrids that presented the highest values of fiber quality parameters; therefore, these genotypes could be considered as having very high fiber quality. Group B comprised two hybrids that displayed high values. Accordingly, they could be considered as high-quality genotypes. Group C contained one parent and seven hybrids that exhibited intermediate fiber quality values. Finally, group D included two parents and one hybrid that presented the lowest quality values. These genotypes could be considered as low-quality ones. Previous studies have used

hierarchical clustering to classify cotton genotypes in accordance with performance (Araújo *et al.*, 2014; Iqbal *et al.*, 2015; Kaleri *et al.*, 2015; Jarwar *et al.*, 2019).

### GCA and SCA effects

The GCA effect of the investigated parental genotypes was estimated for the evaluated traits to distinguish the best parents and good combiners for producing transgressive phenotypes (Table 4). Negative GCA effects are desirable for earliness characters, whereas positive effects are desirable for yield and its related traits and for fiber quality parameters. The obtained

**Table 5.** Estimates of the specific combining ability (SCA) effects of the 15 crosses for the studied traits.

Crosses	Yield and its contributing traits						
	NOB/P	BW/P	SCY/P	LCY/P	L%	100-SW	LI
P1 × P2	0.68 <sup>NS</sup>	0.12 <sup>**</sup>	8.59 <sup>**</sup>	5.05 <sup>**</sup>	0.95 <sup>**</sup>	0.52 <sup>**</sup>	0.63 <sup>NS</sup>
P1 × P3	-5.02 <sup>**</sup>	0.34 <sup>**</sup>	-0.03 <sup>NS</sup>	1.26 <sup>**</sup>	0.87 <sup>**</sup>	-0.85 <sup>**</sup>	-0.34 <sup>NS</sup>
P1 × P4	2.17 <sup>**</sup>	-0.10 <sup>**</sup>	2.20 <sup>**</sup>	2.56 <sup>**</sup>	1.07 <sup>**</sup>	-0.73 <sup>**</sup>	-0.22 <sup>NS</sup>
P1 × P5	3.75 <sup>**</sup>	-0.18 <sup>**</sup>	2.65 <sup>**</sup>	0.08 <sup>NS</sup>	-0.57 <sup>*</sup>	-0.76 <sup>**</sup>	-0.66 <sup>**</sup>
P1 × P6	-1.81 <sup>**</sup>	0.20 <sup>**</sup>	4.94 <sup>**</sup>	2.01 <sup>**</sup>	0.06 <sup>NS</sup>	1.11 <sup>**</sup>	0.76 <sup>**</sup>
P2 × P3	1.06 <sup>*</sup>	-0.05 <sup>NS</sup>	0.76 <sup>*</sup>	0.21 <sup>NS</sup>	-0.04 <sup>NS</sup>	0.69 <sup>**</sup>	0.47 <sup>**</sup>
P2 × P4	-1.96 <sup>**</sup>	-0.12 <sup>**</sup>	-12.17 <sup>**</sup>	-4.41 <sup>**</sup>	0.39 <sup>NS</sup>	-0.80 <sup>**</sup>	-0.46 <sup>*</sup>
P2 × P5	-0.13 <sup>NS</sup>	-0.04 <sup>NS</sup>	-2.36 <sup>**</sup>	-1.81 <sup>**</sup>	-0.55 <sup>*</sup>	0.03 <sup>NS</sup>	-0.13 <sup>**</sup>
P2 × P6	-1.57 <sup>**</sup>	0.13 <sup>**</sup>	2.03 <sup>**</sup>	0.43 <sup>NS</sup>	-0.25 <sup>NS</sup>	-0.26 <sup>NS</sup>	-0.25 <sup>NS</sup>
P3 × P4	-1.23 <sup>*</sup>	0.06 <sup>NS</sup>	-1.15 <sup>**</sup>	-1.66 <sup>**</sup>	-0.73 <sup>**</sup>	-0.07 <sup>NS</sup>	-0.24 <sup>**</sup>
P3 × P5	-0.62 <sup>NS</sup>	0.10 <sup>**</sup>	3.14 <sup>**</sup>	1.51 <sup>**</sup>	0.17 <sup>NS</sup>	-0.93 <sup>**</sup>	-0.60 <sup>**</sup>
P3 × P6	5.37 <sup>**</sup>	0.07 <sup>*</sup>	20.95 <sup>**</sup>	10.43 <sup>**</sup>	1.14 <sup>**</sup>	-0.26 <sup>NS</sup>	0.14 <sup>NS</sup>
P4 × P5	1.88 <sup>**</sup>	0.23 <sup>**</sup>	17.70 <sup>**</sup>	7.93 <sup>**</sup>	0.39 <sup>NS</sup>	1.08 <sup>**</sup>	0.85 <sup>NS</sup>
P4 × P6	1.35 <sup>*</sup>	0.11 <sup>**</sup>	10.65 <sup>**</sup>	4.83 <sup>**</sup>	0.33 <sup>NS</sup>	0.78 <sup>**</sup>	0.62 <sup>**</sup>
P5 × P6	-4.48 <sup>**</sup>	0.02 <sup>NS</sup>	-12.77 <sup>**</sup>	-4.68 <sup>**</sup>	0.35 <sup>NS</sup>	-0.91 <sup>**</sup>	-0.54 <sup>*</sup>
S.E. (sij)	0.52	0.03	0.35	0.33	0.23	0.14	0.11

Crosses	Earliness traits				Fiber quality traits		
	NFSB	DFFU	DFOB	MR	FS	FL	UR
P1 × P2	0.09 <sup>NS</sup>	0.47 <sup>**</sup>	-1.86 <sup>**</sup>	-0.09 <sup>NS</sup>	-0.28 <sup>**</sup>	0.87 <sup>**</sup>	-0.98 <sup>**</sup>
P1 × P3	-0.23 <sup>NS</sup>	-0.16 <sup>NS</sup>	6.89 <sup>**</sup>	-0.06 <sup>NS</sup>	0.04 <sup>NS</sup>	0.71 <sup>**</sup>	0.65 <sup>NS</sup>
P1 × P4	0.14 <sup>NS</sup>	-1.56 <sup>**</sup>	-3.14 <sup>**</sup>	-0.04 <sup>NS</sup>	-0.02 <sup>NS</sup>	-0.25 <sup>NS</sup>	0.25 <sup>NS</sup>
P1 × P5	-0.29 <sup>*</sup>	-0.70 <sup>**</sup>	-2.43 <sup>**</sup>	0.17 <sup>**</sup>	0.24 <sup>*</sup>	-0.39 <sup>NS</sup>	-0.21 <sup>NS</sup>
P1 × P6	0.33 <sup>*</sup>	-0.60 <sup>**</sup>	-1.58 <sup>**</sup>	-0.15 <sup>**</sup>	-0.26 <sup>**</sup>	0.36 <sup>NS</sup>	-0.31 <sup>NS</sup>
P2 × P3	0.55 <sup>**</sup>	0.46 <sup>*</sup>	5.03 <sup>**</sup>	-0.18 <sup>**</sup>	-0.16 <sup>NS</sup>	-0.10 <sup>NS</sup>	-0.92 <sup>**</sup>
P2 × P4	0.22 <sup>NS</sup>	2.26 <sup>**</sup>	-0.87 <sup>**</sup>	-0.12 <sup>*</sup>	0.08 <sup>NS</sup>	0.67 <sup>**</sup>	-0.52 <sup>NS</sup>
P2 × P5	-0.75 <sup>**</sup>	1.38 <sup>**</sup>	0.91 <sup>**</sup>	0.16 <sup>**</sup>	0.14 <sup>NS</sup>	-0.07 <sup>NS</sup>	0.69 <sup>*</sup>
P2 × P6	-0.73 <sup>**</sup>	0.12 <sup>NS</sup>	-2.21 <sup>**</sup>	0.11 <sup>NS</sup>	0.20 <sup>*</sup>	0.18 <sup>NS</sup>	1.95 <sup>**</sup>
P3 × P4	-0.17 <sup>NS</sup>	0.67 <sup>**</sup>	0.85 <sup>**</sup>	0.24 <sup>**</sup>	0.53 <sup>**</sup>	-0.06 <sup>NS</sup>	2.01 <sup>**</sup>
P3 × P5	-0.91 <sup>**</sup>	0.22 <sup>NS</sup>	-2.37 <sup>**</sup>	-0.39 <sup>**</sup>	-0.44 <sup>**</sup>	0.40 <sup>NS</sup>	0.55 <sup>NS</sup>
P3 × P6	-0.09 <sup>NS</sup>	0.30 <sup>NS</sup>	-3.69 <sup>**</sup>	-0.04 <sup>NS</sup>	-0.28 <sup>**</sup>	0.11 <sup>NS</sup>	-0.92 <sup>**</sup>
P4 × P5	-0.53 <sup>**</sup>	-0.01 <sup>NS</sup>	-1.24 <sup>**</sup>	-0.03 <sup>NS</sup>	0.01 <sup>NS</sup>	1.51 <sup>**</sup>	-1.15 <sup>**</sup>
P4 × P6	-0.48 <sup>**</sup>	-0.10 <sup>NS</sup>	-3.69 <sup>**</sup>	0.32 <sup>**</sup>	-0.20 <sup>*</sup>	-0.04 <sup>NS</sup>	-0.15 <sup>NS</sup>
P5 × P6	-0.05 <sup>NS</sup>	-1.11 <sup>**</sup>	-3.27 <sup>**</sup>	0.13 <sup>*</sup>	0.42 <sup>**</sup>	-1.52 <sup>**</sup>	0.86 <sup>*</sup>
S.E. (sij)	0.15	0.17	0.24	0.05	0.09	0.22	0.33

NS is not significant, \* is significant at  $P$ -value < 0.05 and \*\* is highly significant at  $P$ -value < 0.01.

NOB/P is number of opened bolls per plant, BW/P is boll weight per plant (g), SCY/P is seed yield per plant (g), LCY/P is lint yield per plant (g), L% is lint percentage, 100-SW is 100-seed weight (g), LI is lint index, NFSB is the number of nodes to first sympodial branch, DFFU is days to first flower unfolding, DFOB is days to the first opened boll, MR is micronaire reading, FS is fiber strength (g/tex), FL is fiber length at 2.5% (mm) and UR is uniformity ratio (%).

results showed that P2 presented good combining ability for reducing DFFU and DFOB. Moreover, P3 could be considered as a good combiner for reducing DFFU, P5 for reducing DFOB,

and P6 for reducing NFSB. In terms of yield-contributing traits and fiber quality, P5 displayed good combining ability for increasing BW/P, SCY/P, LCY/P, L%, MR, and UR%. Moreover,

P6 was a good combiner for increasing NOB/P, SCY/P, and LCY/P. Accordingly, these genotypes could be used for further developing segregating populations in cotton breeding programs. Furthermore, SCA effects were estimated for identifying the best cross combinations for further exploitation in cotton breeding. Significant effects were found for several crosses in each trait, indicating the presence of nonadditive (dominance and epistasis) gene action (Table 5). The crosses P1 × P4, P1 × P5, P1 × P6, P2 × P6, P3 × P5, P3 × P6, P4 × P6, and P5 × P6 exhibited the highest significantly negative SCA effects for earliness characters and reducing NFSB, DFFU, and DFOB. Conversely, the highest significantly positive SCA values for cotton yield and its contributing traits were assigned to P3 × P6, P4 × P5, P4 × P6, and P1 × P2. Likewise, P2 × P5, P2 × P6, P3 × P4, P1 × P5, and P5 × P6 exhibited the highest significantly additive ones. Moreover, the average degree of dominance  $(H1/D)^{1/2}$  was positive and higher than unity for all evaluated traits, emphasizing the presence of over-dominance gene effects for these traits. The dominance effects for these traits indicated that selection in early generations might not be useful and should be delayed to advanced generations. The relative frequency of dominant to recessive alleles in the genotypes (F) was positive and insignificant for most evaluated traits. This result indicated the presence of dominant alleles more than that of recessive ones in the used parents, as well as the important role of dominant genes for the evaluated traits (Table 6). This result corresponded with the proportion of dominance and recessive genes (KD/KR) in the parents exceeding the

positive SCA values for fiber quality parameters. The obtained results were in harmony with the results of previous studies that used GCA and SCA to identify good combiners and good cross combinations (Amein *et al.*, 2013; Hamoud, 2014; Kumar *et al.*, 2014; Khalifa *et al.*, 2016; Ekinci and Basbag, 2018; Taha *et al.*, 2018; Chaudhary *et al.*, 2019).

### Components of genetic variance

The components of genetic variance for evaluated traits are shown in Table 6. The additive component (D) was significant for all studied traits, except for SCY/P, 100-SW, NFSB, FL, and UR%. Furthermore, the dominance components (H1 and H2) were positive and significant for all evaluated traits. In addition, the H1 value was greater than D, suggesting that the contribution of the over-dominance effects in the inheritance of these traits was higher than that of unity and that the dominant genes were more frequent than recessive ones for all evaluated traits. Likewise, this result was reinforced by the assessments of the  $H_2/4H_1$  ratio, which was lower than 0.25 for all investigated characters, proving the dissimilar distribution of positive and negative alleles among the used parents. The environmental component (E) was not significant for all evaluated traits, revealing the lower importance of environmental factors in the expression of these traits. Narrow-sense heritability is very important for cotton breeders given that phenotypic selection efficiency depends on its value. It was assessed for studied traits and varied from low to moderate (2.69% to 29.66%). Its low values were due to the excess of the dominance effect.

**Table 6.** Components of genetic variance for the evaluated cotton characters.

Components	Yield and its contributing traits						
	BWP	NOB/P	SCY/P	LCYP	L%	100-SW	LI
D	0.05**	7.43*	60.99 <sup>NS</sup>	20.55*	1.11**	0.36 <sup>NS</sup>	0.26**
H <sub>1</sub>	0.12**	30.05**	450.85**	101.84**	2.14**	2.55**	1.29**
H <sub>2</sub>	0.11**	29.34**	399.3**	88.83**	1.81**	2.22**	1.08**
F	0.05 <sup>NS</sup>	4.05 <sup>NS</sup>	83.19 <sup>NS</sup>	28.59 <sup>NS</sup>	1.20**	0.65 <sup>NS</sup>	0.43 <sup>NS</sup>
h <sup>2</sup>	0.12**	-0.11 <sup>NS</sup>	308.1**	85.07**	1.93**	0.27 <sup>NS</sup>	-0.01 <sup>NS</sup>
E	0.01 <sup>NS</sup>	0.28 <sup>NS</sup>	0.12 <sup>NS</sup>	0.11 <sup>NS</sup>	0.05 <sup>NS</sup>	0.02 <sup>NS</sup>	0.01 <sup>NS</sup>
(H <sub>1</sub> /D) <sup>1/2</sup>	1.58	2.01	2.72	2.23	1.39	2.67	2.22
H <sub>2</sub> /4H <sub>1</sub>	0.21	0.24	0.22	0.22	0.21	0.22	0.21
KD/KR	1.99	1.31	1.67	1.91	2.28	2.04	2.18
H <sup>2</sup> /H <sub>2</sub>	1.17	-0.01	0.77	0.96	1.07	0.12	-0.01
H (n.s)	22.62	21.16	12.81	10.01	19.58	2.69	6.25

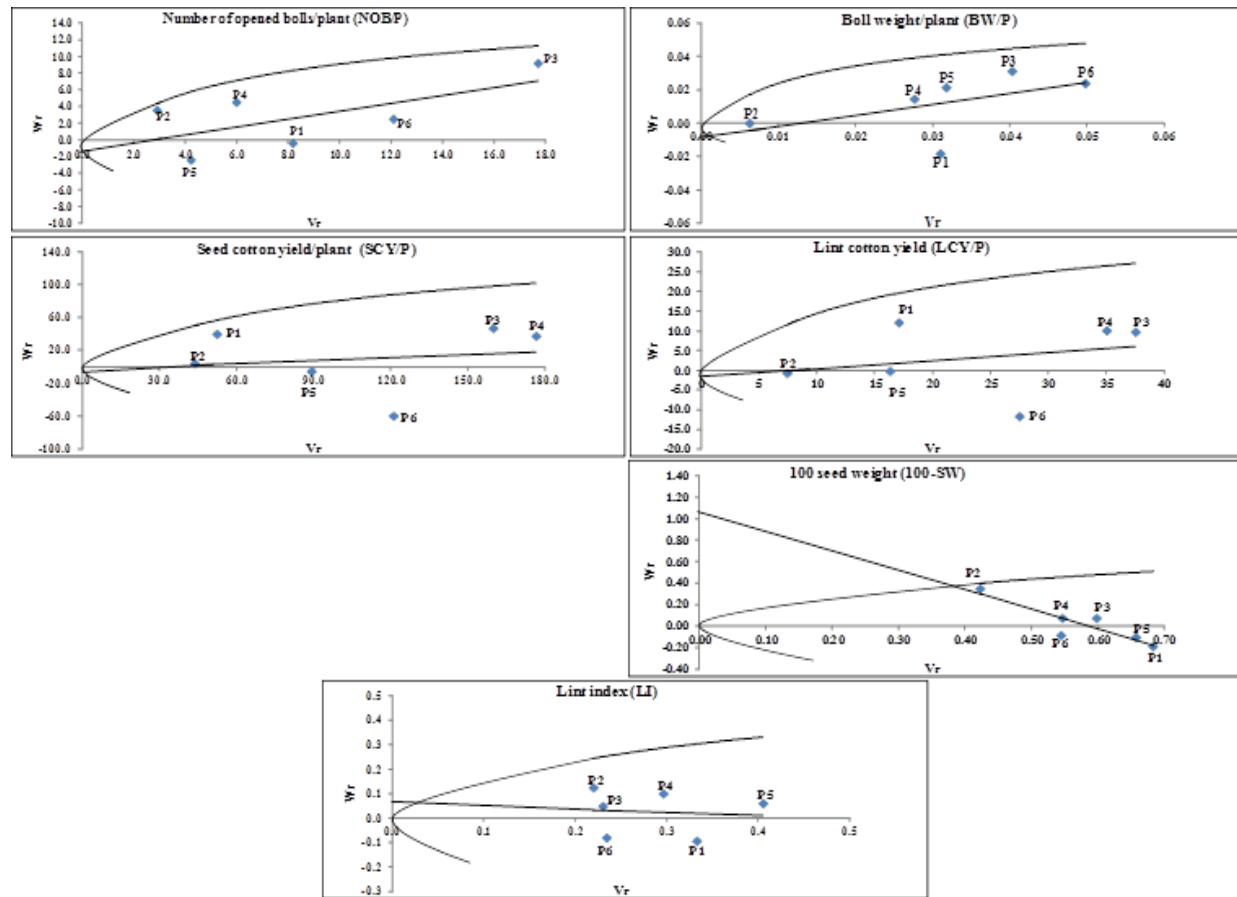
Components	Earliness traits			Fiber quality traits			
	NFSB	DFFU	DFOB	MR	FS	FL	UR
D	0.20 <sup>NS</sup>	5.6**	15.79*	0.04**	0.05*	0.49 <sup>NS</sup>	0.55 <sup>NS</sup>
H <sub>1</sub>	1.31**	6.95**	73.91**	0.17**	0.32**	2.42**	3.89**
H <sub>2</sub>	1.01**	4.08*	48.38**	0.13**	0.28**	1.95*	3.71**
F	0.39 <sup>NS</sup>	7.59**	33.42*	0.07 <sup>NS</sup>	0.07 <sup>NS</sup>	0.66 <sup>NS</sup>	0.12 <sup>NS</sup>
H <sup>2</sup>	1.25**	0.38 <sup>NS</sup>	24.31*	-0.01 <sup>NS</sup>	-0.01 <sup>NS</sup>	0.82 <sup>NS</sup>	0.44 <sup>NS</sup>
E	0.02 <sup>NS</sup>	0.03 <sup>NS</sup>	0.06 <sup>NS</sup>	0.01 <sup>NS</sup>	0.01 <sup>NS</sup>	0.05 <sup>NS</sup>	0.11 <sup>NS</sup>
(H <sub>1</sub> /D) <sup>1/2</sup>	2.57	1.11	2.16	2.09	2.45	2.22	2.67
H <sub>2</sub> /4H <sub>1</sub>	0.19	0.15	0.16	0.19	0.22	0.20	0.24
KD/KR	2.23	4.11	2.91	2.35	1.75	1.87	1.08
h <sup>2</sup> /H <sub>2</sub>	1.23	0.09	0.50	-0.01	-0.01	0.42	0.12
h (n.s)	17.18	29.66	24.53	17.29	10.87	21.43	22.78

NS is not significant, \* is significant at  $P$ -value < 0.05 and \*\* is highly significant at  $P$ -value < 0.01. NOB/P is the number of opened bolls per plant, BW/P is boll weight per plant (g), SCY/P is seed yield per plant (g), LCY/P is lint yield per plant (g), L% is lint percentage, 100-SW is 100-seed weight (g), LI is lint index, NFSB is the number of nodes to the first sympodial branch, DFFU is days to the first flower unfolding, DFOB is days to the first opened boll, MR is micronaire reading, FS is fiber strength (g/tex), FL is fiber length at 2.5% (mm) and UR is uniformity ratio (%).

Various researchers have analyzed genetic components for cotton traits and demonstrated the significance of additive and nonadditive components in the heredity of evaluated traits with increased incidence for dominance genetic effects (Aguado *et al.*, 2008; Ali and Awan, 2009; Mohamed *et al.*, 2009; Khan and Hassan, 2011).

### Wr-Vr graph

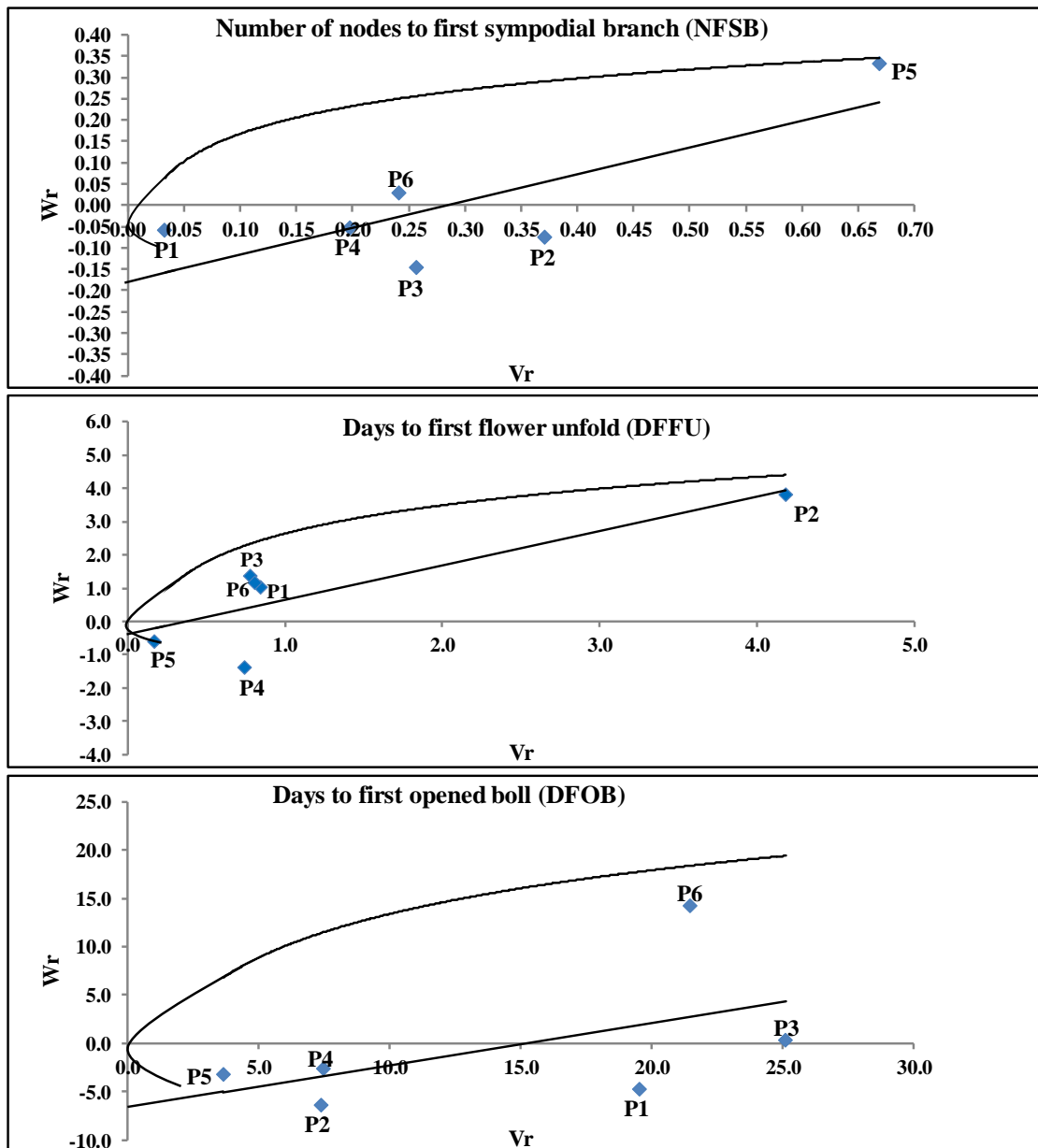
Wr-Vr regression graphs were estimated for further elucidating the genetic nature of parental variation. The graphs for earliness characters, yield and its related traits, and fiber quality parameters are presented in Figures 2 to 4. The regression line



**Figure 2.** Wr–Vr graphs for cotton yield and its contributing traits in parental cotton genotypes.

passed below the origin in all studied traits, except for 100-SW, LI, MR, FL, and UR%. For these traits, the line passed above the origin, whereas for FS, the lines passed through the origin. This pattern revealed the presence of complete dominance gene effects in the inheritance of FS, partial dominance for 100-SW, LI, MR, FL, and UR%, and over-dominance for the remaining traits. The distribution of parents along the regression line revealed that P2 possessed the maximum number of dominant alleles for cotton yield and its contributing traits (Figure 2). Otherwise, P3 carried the maximum number of recessive alleles for NOB/P and LCY/P; P6 for

BW/P; P4 for SCY/P; P5 for LI; and P1 for 100-SW. Similarly, P1 carried dominant alleles for NFSB, whereas P5 carried dominant alleles for DFFU and DFOB (Figure 3). P5 carried the maximum number of recessive alleles for NFSB, P2 for DFFU, and P3 for DFOB. Furthermore, P1 possessed the maximum number of dominant alleles for MR, FS, and UR%, whereas P3 had the maximum number of dominant alleles for FL (Figure 3). P5 carried the maximum number of recessive alleles for MR and FL, P6 for FS, and P2 for UR%. Numerous studies presented similar results for the Wr–Vr regression graphs of cotton yield and its contributing traits (Mohamed *et al.*,



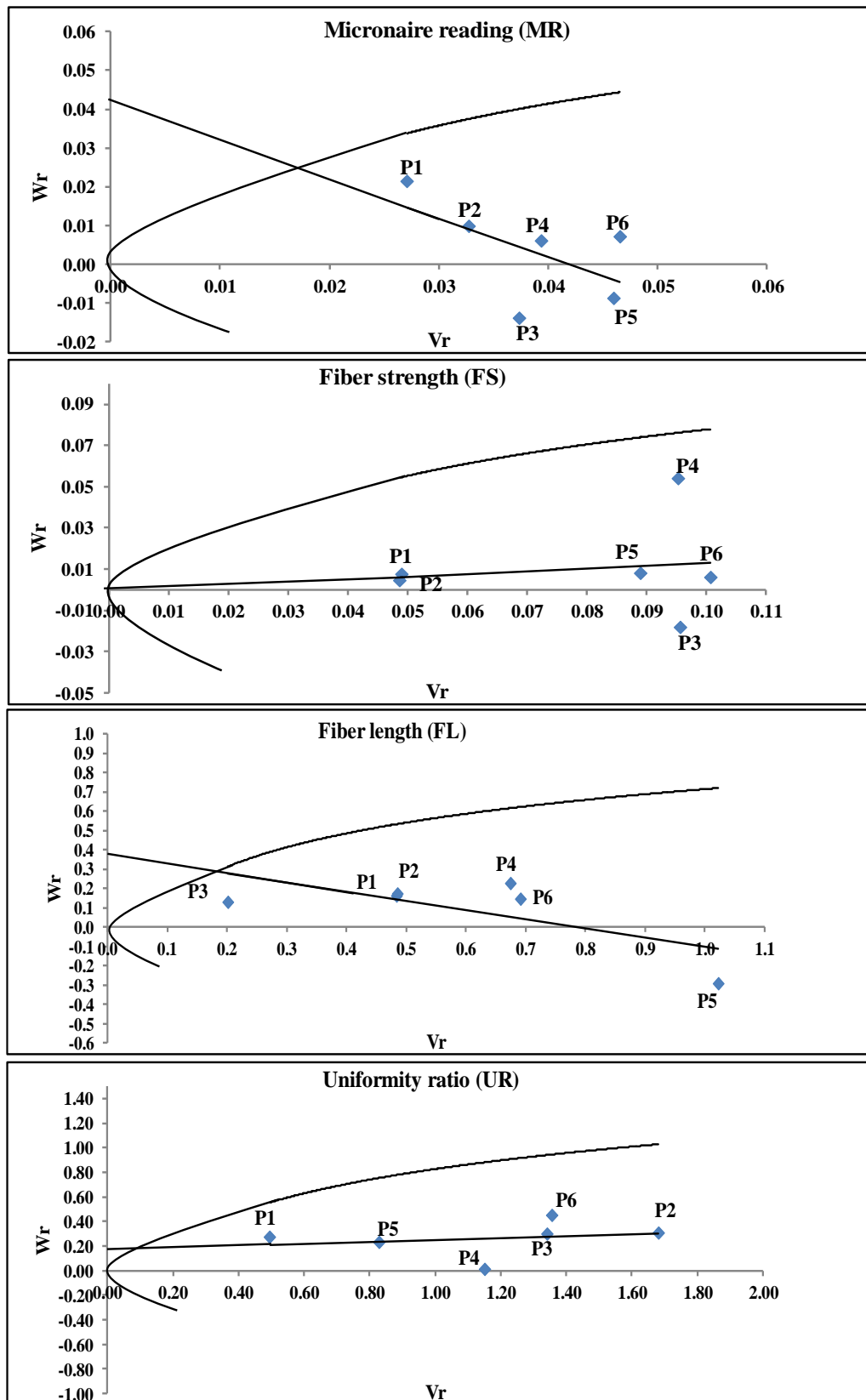
**Figure 3.**  $W_r$ - $V_r$  graphs for the earliness traits of parental cotton genotypes.

2009; Nabi *et al.*, 2010; Channa *et al.*, 2013; Latif *et al.*, 2014; Shah *et al.*, 2014; Mahdy *et al.*, 2018).

### Interrelationship among evaluated traits

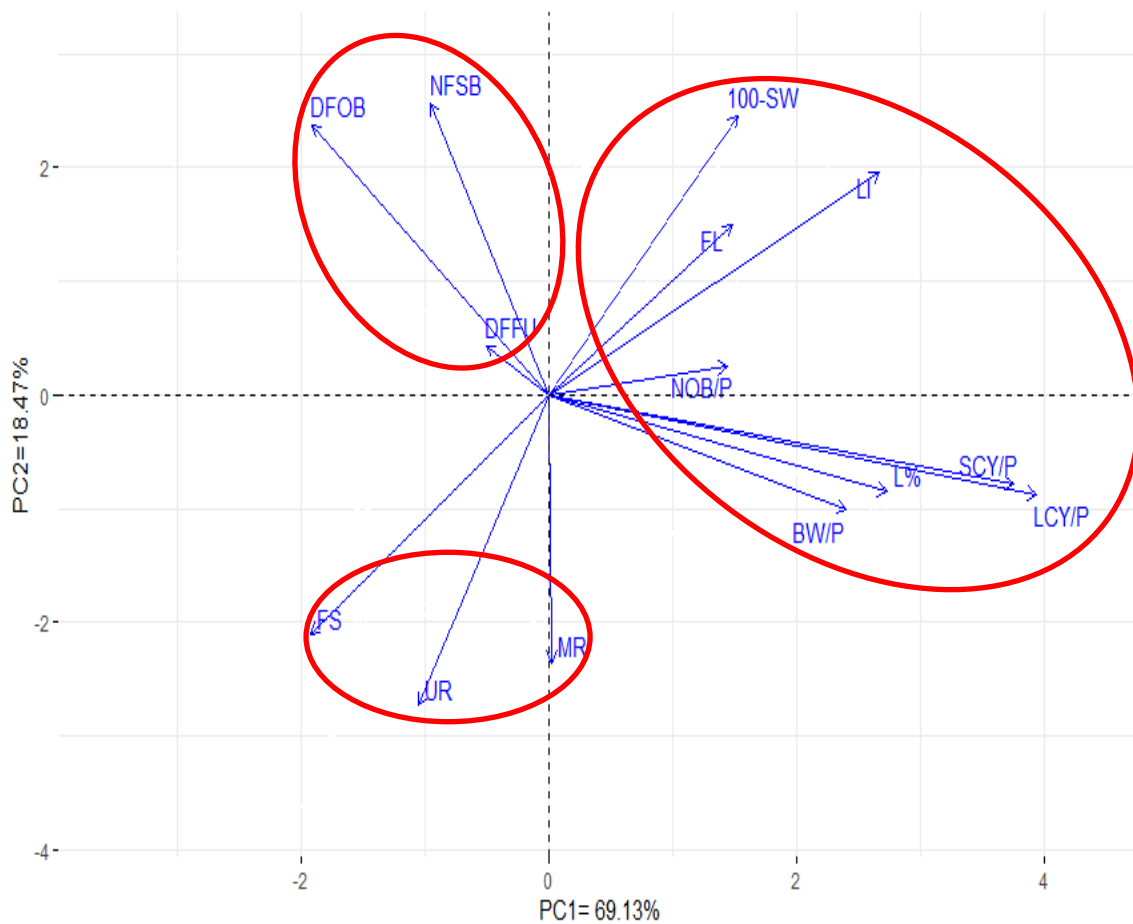
The relationship among the tested traits, namely, earliness characters,

yield and its related traits, and fiber quality parameters was estimated by using principal components. This interrelationship could provide useful information for screening cotton genotypes and breeding programs. The biplot of principal components is an appropriate statistical tool for presenting the interrelationship among



**Figure 4.**  $W_r$ - $V_r$  graphs for the fiber quality traits of parental cotton genotypes.





**Figure 5.** Biplot of cotton genotypes (parents and hybrids) and evaluated characters; number of opened bolls per plant (NOB/P), boll weight per plant (BW/P, g), seed yield per plant (SCY/P, g), lint yield per plant (LCY/P, g), lint percentage (L%), 100-seed weight (100-SW, g), lint index (LI), the number of nodes to the first sympodial branch (NFSB), days to the first flower unfolding (DFFU), days to the first opened boll (DFOB), micronaire reading (MR), fiber strength (FS, g/tex), fiber length at 2.5% (FL, mm) and uniformity ratio (UR,%).

evaluated traits. The first two principal components presented most of variability of approximately 87.6% (69.13% by PC1 and 18.47% by PC2). Consequently, they were used to construct the biplot (Figure 5). The traits characterized by parallel or adjacent vectors present strong positive relationships, whereas vectors

that are positioned closely opposite (at 180°) exhibit highly negative relationships. The evaluated traits could be divided into three groups. The first group included cotton yield and its contributing traits (NOB/P, BW/P, SCY/P, LCY/P, L%, 100-SW, and LI) and FL. The second group comprised earliness characters (NFSB,

DFFU. and DFOB). Finally, the third group contained MR, FS, and UR%. These obtained results showed that FL was positively associated with cotton yield and its contributing traits. Consequently, the high values of the contributing traits provided additional FL. By contrast, the earliness characters had a negative association with cotton yield and its contributing traits. Previous researchers used the biplot of principal components to display the interrelationships among cotton traits (Noorka *et al.*, 2011; Shakeel *et al.*, 2015; Javed *et al.*, 2017; Jarwar *et al.*, 2019; Rathinavel, 2019).

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## REFERENCES

- Abaza GSM, Awaad HA, Attia ZM, Abdel-lateif KS, Gomaa MA, Abaza SMSM Mansour E (2020). Inducing potential mutants in bread wheat using different doses of certain physical and chemical mutagens. *Plant Breed. Biotechnol.* 8: 252-264.
- Aguado A, De-Los Santos B, Blanco C, Romero F (2008). Study of gene effects for cotton yield and *Verticillium* wilt tolerance in cotton plant (*G. hirsutum* L.). *Field Crops Res.* 107(1): 78-86.
- Ali MA, Awan SI (2009). Inheritance pattern of seed and lint traits in cotton (*G. hirsutum*). *Int. J. Agric. Biol.* 11(1): 44-48.
- Amein MMM, Masri MI, Abd El-Bary AMR, Attia SS (2013). Combining ability and heterosis for yield and fiber quality traits in cotton (*G. Barbadosense* L.). *Egyptian J. Plant Breed.* 203(1133): 1-14.
- American Society for Testing Materials ASTM (1998). D.4605 and 3818-3898, Vol. 7. No. 1 Easton, MD, USA.
- Araújo LFD, Almeida WS, Bertini CHCM., Neto V, das Chagas F, Bleicher E (2014). The use of different clustering methods in the evaluation of genetic diversity in upland cotton. *Rev. Cienc. Agron.* 45(2): 312-318.
- Başal H, Turgut I (2003). Heterosis and combining ability for yield components and fiber quality parameters in a half diallel cotton (*G. hirsutum* L.) population. *Turk. J. Agric. For.* 27(4): 207-212.
- Bellaloui N, Stetina SR, Turley RB (2015). Cottonseed protein, oil, and mineral status in near-isogenic *G. hirsutum* cotton lines expressing fuzzy/linted and fuzzless/linted seed phenotypes under field conditions. *Front. Plant Sci.* 6, Article 137.
- Channa SA, Baloch AW, Baloch MJ, Ahmad I, Wasila H (2013). Genetic analysis of fiber characters of upland cotton (*G. hirsutum* L.). *Glob. J. Biodivers. Sci. Manag.* 3(2): 264-268.
- Chaudhary MT, Majeed S, Shakeel A, Du-Yinhua J, Xiongming MTA (2019). Estimation of heterosis and combining ability for some quantitative parameters in *G. hirsutum*. *Int. J. Biosci.* 15(2): 166-173.
- Ekinci R, Basbag S (2018). Combining ability analysis and heterotic effects for cotton fiber quality traits. *Ekin J. Crop Breed Genet.* 4(2): 20-25.
- El-Aref KA, Zaher AE, Haridy MH, Shrmokh HM (2019). Genetic analysis for diallel crosses on Egyptian cotton (*G. barbadense* L.). *Assiut J. Agric. Sci.* 50(3): 1-15.
- FAOSTAT (2020). Food and Agriculture Organization of the United Nations.

- Statistical database (accessed 10 June 2020).
- Gharib, MAAH, Qabil N, Salem AH, Ali MMA, Awaad HA, Mansour E (2020). Characterization of wheat landraces and commercial cultivars based on morpho-phenological and agronomic traits. *Cereal Res. Commun.* 1-11.
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* 9: 463-493.
- Hallauer A, Miranda J (1988). Quantitative Genetics in Maize Breeding. Iowa State University Press. Ames, IA.
- Hamoud HME (2014). Use of biplot approach for genetic analysis of yield and related traits in cotton (*G. barbadense*). *J. Plant Prod.* 5(1): 135-145.
- Hayman B (1954a). The analysis of variance of diallel tables. *Biometrics* 10: 235-244.
- Hayman B (1954b). The theory and analysis of diallel crosses. *Genet.* 39: 789-809.
- He Z, Shankle M, Zhang H, Way TR, Tewolde H, Uchimiya M (2013). Mineral composition of cottonseed is affected by fertilization management practices. *Agron. J.* 105(2): 341-350.
- Hussain A, Zafar ZU, Athar HUR, Farooq J, Ahmad S, Nazeer W (2019). Assessing gene action for hypoxia tolerance in cotton (*G. hirsutum* L.). *Agron. Mesoam.* 30(1): 51-62.
- Iqbal MA, Ammad A, Zafar Y (2015). Characterization of indigenous *G. arboreum* L. Genotypes for various fiber quality traits. *Pak. J. Bot.* 47(6): 2347-2354.
- Jana S (1975). Genetic analysis by means of diallel graph. *Heredity* 35: 1-19.
- Jarwar AH, Wang X, Iqbal MS, Sarfraz Z, Wang L, Ma Q, Shuli F (2019). Genetic divergence on the basis of principal component, correlation and cluster analysis of yield and quality traits in cotton cultivars. *Pak. J. Bot.* 51(3): 1143-1148.
- Javed M, Hussain SB, Baber M (2017). Assessment of genetic diversity of cotton genotypes for various economic traits against cotton leaf curl disease (CLCuD). *Genet. Mol. Res.* 16(1): 1-12.
- Kaleri AA, Rajput SY, Kaleri GA, Kaleri MK, Marri JA (2015). Analysis of genetic diversity in genetically modified and non-modified cotton (*G. hirsutum* L.) genotypes. *J. Agric. Vet. Sci.* 8(12): 70-76.
- Karademir E, Gencer O (2010). Combining ability and heterosis for yield and fiber quality properties in cotton (*G. hirsutum* L.) obtained by half diallel mating design. *Not. Bot. Horti Agrobot. Cluj Napoca.* 38(1): 222-227.
- Kassambara A, Mundt F (2017). Package 'factoextra'. Extract and visualize the results of multivariate data analyses. Available online: <https://CRAN.R-project.org/package=factoextra> (accessed on 15 June 2020).
- Khalifa HS, Said SRN, Eissa AEM (2016). Diallel analysis on some Egyptian cotton genotypes for earliness, yield components and some fiber traits. *Egyptian J. Plant Breed.* 20(1): 11-25.
- Khan NU, Hassan G (2011). Genetic effects on morphological and yield traits in cotton (*G. hirsutum* L.). *Span. J. Agric. Res.* 9(2): 460-472.
- Kumar KS, Ashokkumar K, Ravikesavan R (2014). Genetic effects of combining ability studies for yield and fiber quality traits in diallel crosses of upland cotton (*G. hirsutum* L.). *Afr. J. Biotechnol.* 13(1): 119-126.
- Latif A, Ahmad T, Hayat S, Sarwar G, Ehsan MZ, Raza MM, Sarwar M, Khan IA (2014). Genetics of yield and some yield contributing traits in upland cotton (*G. hirsutum* L.). *J. Plant Breed. Crop Sci.* 6: 57-63.
- Mahdy EES, Ahmed AAE, Abdel-Zaher GH, Sayed MA, Husein MG (2018). Genetic analysis of earliness and lint yield under normal and late

- sowing dates in Egyptian cotton. *Egyptian J. Agron.* 40(1): 31-44.
- Mansour E, Abdul-Hamid MI, Yasin MT, Qabil N, Attia A (2017a). Identifying drought-tolerant genotypes of barley and their responses to various irrigation levels in a Mediterranean environment. *Agric. Water Manag.* 194: 58-67.
- Mansour E, Merwad A, Yasin M, Abdul-Hamid M, El-Sobky E, Oraby H (2017b). Nitrogen use efficiency in spring wheat: Genotypic variation and grain yield response under sandy soil conditions. *J. Agric. Sci.* 155, 1407-1423.
- Mansour E, Moustafa ES (2016). Estimation of combining ability and gene action for yield contributing traits in spring barley under normal and salinity conditions. *Egyptian J. Agron.* 38(3): 431-483.
- Mansour E, Moustafa ES, El-Naggar NZ, Abdelsalam A, Igartua E (2018a). Grain yield stability of high-yielding barley genotypes under Egyptian conditions for enhancing resilience to climate change. *Crop Pasture Sci.* 69(7): 681-690.
- Mansour E, Moustafa ES, Qabil N, Abdelsalam A, Wafa HA, El Kenawy A, Casas AM, Igartua E (2018b). Assessing different barley growth habits under Egyptian conditions for enhancing resilience to climate change. *Field Crops Res.* 224: 67-75.
- Mansour E, Moustafa ESA, Desoky EM, Ali MMA, Yasin MAT, Attia A, Alsuhaibani N, Tahir MU, El-Hendawy S (2020). Multidimensional evaluation for detecting salt tolerance of bread wheat genotypes under actual saline field growing conditions. *Plants* 9: Article 1324.
- Mather K, Jinks JL (1982). Biometrical genetics, 3<sup>rd</sup> ed. Chapman and Hall Ltd, London, UK.
- Migliore G, Zinnanti C, Schimmenti E, Borsellino V, Schifani G, Di, Franco CP, Ascuito A (2019). A Ricardian analysis of the impact of climate change on permanent crops in a Mediterranean region. *New Medit.* 18(1):41-52
- Mohamed GI, Abd-El-Halem SHM, and Ibrahim EMA (2009). A genetic analysis of yield and its components of Egyptian cotton (*G. barbadense* L.) under divergent environments. *Am. Eur. J. Agric. Environ. Sci.* 5(1): 5-13.
- Nabi G, Azhar FM, Khan AA (2010). Genetic mechanisms controlling variation for salinity tolerance in upland cotton at plant maturity. *Int. J. Agric. Biol.* 12: 521-526.
- Nazmey MNA, Eissa AEM, Yehia WMB (2010). Genetical analysis for F<sub>1</sub> and F<sub>2</sub> generation in some Egyptian cotton crosses (*G. barbadense* L.). *J. Agric. Chem. Biotechnol.* (6): 341-350.
- Noorka IR, Shahid SA, Rouf S (2011). Principal component analysis for soil conservation tillage vs conventional tillage in semi-arid region of Punjab Province of Pakistan. *Iran J. Earth Sci.* 3(1): 20-24.
- Qu Z, Li L, Luo J, Wang P, Yu S, Mou T, Zheng X, Hu Z. (2012). QTL mapping of combining ability and heterosis of agronomic traits in rice backcross recombinant inbred lines and hybrid crosses. *PLoS One* 7(1): Article e28463.
- Rathinavel K (2019). Agro-morphological Characterization and Genetic Diversity Analysis of Cotton Germplasm (*G. hirsutum* L.). *Int. J. Curr. Microbiol. Appl. Sci.* 8(2): 2039-2057.
- Salgotra RK, Gupta BB, Singh P (2009). Combining ability studies for yield and yield components in Basmati rice. *ORYZA - Int. J. Rice* 46(1): 12-16.
- Shah SAS, Akhtar LH, Minhas R, Bukhari MS, Shah SSM, Azhar FM (2014). Genetic control of yield and yield related traits in selected upland cotton varieties of Pakistan. *J.*

- Agric. Sci. Sri Lanka* 9(3): 129-138.
- Shakeel A, Talib I, Rashid M, Saeed A, Ziaf K, Saleem MF (2015). Genetic diversity among upland cotton genotypes for quality and yield related traits. *Pak. J. Agric. Sci.* 52: 73-77.
- Singh RK, Chaudhary BD (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers Ludhiana New Delhi. pp. 102-164.
- Steel RGD, Torrie JH (1980). Principles and procedures of statistics, a biological approach, 2<sup>nd</sup> ed. McGraw Hill, Inc, New York.
- Syukur M, Sujiprihati S, Yuniarti R (2010). Analysis using Hayman method to study genetic parameters of yield components in pepper (*Capsicum annuum* L.). *HAYATI J. Biosci.* 17: 183-188.
- Taha EM, El-Karamity AE, Eissa AEM, Asaad MR (2018). Heterosis and combining ability of some Egyptian cotton genotypes. *El-Minia J. Agric. Res. Dev.* 38(1): 1-61.
- Vasconcelos UAA, Cavalcanti JJV, Farias FJC, Vasconcelos WS, Santos RCD (2018). Diallel analysis in cotton (*G. hirsutum* L.) for water stress tolerance. *Crop Breed. Appl. Biotechnol.* 18(1): 24-30.