

Heterosis and Gene Action among Single and Double-Cross Hybrids Performances in Cotton

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Abstract: The objective of present study was to estimate the magnitude of heterosis and gene action in different types of intra-specific crosses of *Gossypium barbadense* L. viz. single (A x B) and double (A x B) x (C x D) crosses. Significant or highly significant difference in most studied traits appeared due to different all genotypes (parents, single and double-cross hybrids). Mean performance of some single crosses was higher than the double-cross hybrids for most studied traits. The single-cross hybrid (Pima S₆ x Australian) and the double-cross hybrid (Pima S₆ x Australian) x (Karashanky x Giza 88) were the best mean performances for most studied traits. Some single and double-cross hybrids exhibited negative or positive and significant heterosis for most studied traits. However, the single-cross hybrid (Pima S₆ x Australian) and (Giza 85 x Giza 88) were showed desirable heterosis versus better-parent for most traits. The double-cross hybrids (Pima S₆ x Australian) x (Karashanky x Giza 88) and (Pima S₆ x Giza 88) x (Karashanky x Giza 85) were recorded positive heterosis versus better-parent and better-F₁ hybrid for most important studied traits, respectively. The heterosis over better-parents in all diallel crosses exhibited insignificant positive and desirable for all studied traits. While, the heterosis over mid-parents, Mid-F₁ hybrids, better-parent, better-F₁ hybrids and mid-parents and F₁ hybrids were desirable for some studied traits in all double-cross hybrids. In diallel crosses, both the additive and dominance genetic variances were presented in seed cotton yield/plant, lint cotton yield/plant and seed index traits, but additive genetic variance was lower in magnitude than dominance genetic variances for all studied traits. As for double-cross hybrids, additive x additive and additive x dominance genetic variances were observed and highest than the other types of epistatic genetic variances for all studied traits. Broad-sense heritability was high, but narrow-sense heritability was low for all the traits studied in single and double-cross hybrids. High and significant or highly significant correlation between mean performances and heterosis was observed for most studied traits in both single and double-cross hybrids.

Key words: Heterosis • Gene action • Heritability • Single and double-cross hybrids • Correlation between heterosis

INTRODUCTION

Several methods of making predictions of performance of double cross hybrids based on performance of single crosses were proposed. However, the most accurate prediction was found to be the mean value of the four non-parental single crosses [1]. A double cross hybrid results from the cross between two single crosses that are themselves the result of crosses between two selected inbred lines [2]. For successful double cross hybrid development, heterotic effects have to be maximized and the best results are expected when

four unrelated or diverse inbred lines are used. Although double cross hybrids show slightly higher variation in plant traits as compared to single crosses, which might affect the yield, the cost of seed production could be reduced because they are produced on single cross hybrids as parents, which produce more seeds compared to inbred parents, as in the case of single cross hybrids [3]. Synthesis of double-cross hybrids depends on the number of single-cross hybrids involved in the crosses; it can become unfeasible due to an increase in the number of single-cross hybrids used as genitors [4]. The breeding value of a line is a function of the additive gene action.

The additive genes are directly transported from the parents to the offspring are responsible for the resemblance between relatives and can be used to calculate inheritance [5]. Cheatham *et al.* [6] reported that Australian and wild cotton varieties have the genes to improve fiber quality and fertility; fineness and length primarily exhibit dominance genes effects, fiber percentage and fiber strength are controlled by additive genes effects; fiber yield and fiber elongation extension are controlled equally by additive and dominant gene effects, yield and fiber quality could be improved by using these varieties in the U.S.A breeding studies.

The term heterosis was coined by Shull [7]. Heterosis is the superiority of F_1 over the mean of the parents or over the better parent or over the standard check with respect to agriculturally useful traits [8]. The genetic causes involved in the expression of heterosis are dominance and nonallelic interactions [8]. The magnitude of heterosis can be maximized if the parents are genetically diverse from each other. Parents should differ for maximum number of yield influencing loci so that F_1 exhibits the dominance effect at as many of the yield influencing loci as possible. Exploiting heterosis is one of the methods to increase cotton yield. Kumar [9] stated that to maximize heterosis, there is a need for utilizing breeding programs aimed at constantly creating variability and increasing genetic diversity between populations that can further be exploited through selection for combining ability between such diverse populations. Also heterosis can be enhanced by increasing dominant gene action. It is difficult to precisely detect and manipulate the degree of dominant gene action while selecting based on phenotypic measurements, for high heterosis. However it is possible to create and improve heterotic populations against a tester or reciprocally develop diverse populations which differ for the alleles at a large number of yield influencing loci (showing dominance). Regarding previous studies on heterosis in cotton documented in numerous reviews, researches reported that different heterosis values obtained for yield and fiber quality properties [10]. Narrow sense heritability measures the extent of correspondence between breeding values and phenotypic values and expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of the population via selection [5, 11].

The present investigation was undertaken to obtain information on heterosis, gene action and heritability to identify useful parents, single and double-cross hybrids

and correlate the means with heterosis in single and double-cross hybrids for yield, yield components and fiber quality traits.

MATERIALS AND METHODS

The present experiment was conducted during three seasons. The first (2009) and second (2010) seasons were conducted at Experimental Farm of the Agronomy Department, Faculty of Agriculture, Al-Azhar University, Nasr City, Cairo, Egypt, while the third (2011) season was sown in the site of Experimentation at Messir-Sakha-Kafr El-Sheikh, Egypt. The five parents namely, Pima S₆, Australian, Karashanky, Giza 85 and Giza 88 were planted and crossed using a half diallel mating design during 2009 season to develop ten F_1 's crosses. During 2010 season, the single crosses were sown and crossed to produce double-cross hybrids with the restriction that no parent should appear more than once in the same double cross combinations to obtain fifteen double-cross hybrids [number of double-cross hybrids = $n(n-1)(n-2)(n-3)/8$, where, n: is the number of parental varieties]. Crossing was done by following the conventional hand emasculation and pollination method developed. Five parents, ten single and fifteen double-cross hybrids were planted in a randomized complete block design with three replications during 2011 season. Each replication contained 30 plots. Each plot contained three rows. Each row was 4 m long and 0.60 m wide. Hills were spaced at 0.40 m and thinned at one plant per hill. Observations were recorded for seed cotton yield/plant (S.C.Y. /P. g), lint cotton yield/plant (L.C.Y. /P. g), boll weight (B.W. g), lint percentage (L. %), number of bolls/plant (No. B. /P.), seed index (S.I. g), lint index (L.I. g), 2.5% span length (2.5% S.L.), fiber fineness (F.F.), fiber strength (F.S.) and uniformity ratio (U.R. %) traits. Recommended cultural practices were carried out and the crop was grown under uniform field conditions to minimize environmental variations to the maximum possible extent.

Statistical Analysis: Data were subjected to analysis of variance technique as outlined by Cochran and Cox [12] to test the null hypothesis of no differences between various F_1 populations and their parental line means. The data of all the parameters on ten single hybrids and five parental genotypes were further subjected to the gene action according to Griffing's [13] Method-II and the double-cross hybrids are then analyzed according to Rawlings and Cockerham [14] as outlined by Singh and Chaudhary [15].

RESULTS AND DISCUSSION

Mean Performance: Mean performance was considered as the first important selection index in the choice of parents and the parents with high mean performance will result in superior hybrids. The mean performances of the parents, single and Double-cross hybrids were estimated from the data of one year (2011) for yield, yield components and fiber quality traits and presented in Table 1. The mean performances values of parents, single and double-cross hybrids displayed significant or highly significant differences for seed cotton yield/plant, lint cotton yield/plant, boll weight, number of bolls/plant, seed index and 2.5% span length traits. In respect to, the mean values of all genotypes were insignificantly differed for other studied traits. In general, significant differences were recorded between means when compared with the L.S.D. values. The highest mean performances were found for the parents Pima S₆, Australian and Karashanky for yield and yield components traits. On the contrary, the Egyptian parents Giza 85 and Giza 88 had the best fiber quality traits. The single cross hybrids P₁ x P₂ exhibited best mean values and excelled other genotypes for the traits i.e. seed cotton yield/plant (96.57 g), lint cotton yield/plant (39.20 g), number of bolls/plant (33.47) and seed index (9.56 g). The maximum lint percentage (41.50 %), lint index (7.04 g) and 2.5% span length (33.70 mm) traits were produced by single-cross hybrid P₁ x P₃. The best boll weight (2.97 g) and uniformity ratio (88.23) produced by single-cross hybrid P₃ x P₅. The single-cross hybrid P₂ x P₃ manifested greatest mean values for fiber strength (10.50). While, trait fiber fineness (3.97) was exhibited by single-cross hybrids P₁ x P₃ and P₄ x P₅. Generally, these data indicated that, the superiority of some single crosses, with respect to their corresponding parents. These view points were kept in mind while selecting these single crosses as diverse F₁ base populations for initiating reciprocal selection for combining ability. The mean of some crosses derived F₁s were highly superior over double cross base. The means of 15 double-cross hybrids elicited that, the crosses (P₁ x P₂) x (P₃ x P₅) for seed cotton yield/plant (87.32 g), lint cotton yield/plant (33.52 g) and uniformity ratio (89.27%) traits, (P₁ x P₂) x (P₄ x P₅) for boll weight (3.14 g) and fiber strength (10.50), (P₁ x P₂) x (P₃ x P₄) for lint percentage (41.31 %), (P₂ x P₃) x (P₃ x P₄) for number of boll/plant (30.53), (P₁ x P₄) x (P₂ x P₅) for seed index (9.74 g) and fiber fineness (3.67), (P₂ x P₄) x (P₃ x P₅) for lint index (6.97 g) and (P₁ x P₅) x (P₃ x P₄) for 2.5% span length (34.63 mm) were recorded the best mean performances. The highest combinations indicating that importance of

low and average parents in the exploitation of heterosis for studied traits. The results exhibited some parents, single cross hybrids and double-cross hybrids were superiority than grand means for studied traits. There were relatively large variations in all genotypes for these traits. Since the double cross was revealing high potentiality it could be an indication of differences in the dominant favourable alleles distributed among the two single cross parents are different. In the present study it was proposed to use the actual double cross performance as an indicator of genetic diversity existing between the concerned single crosses. Consequently, the parents involved in the previous combinations should be used in improving yield and its components and the best crosses should be used in initiated the breeding program. The double cross hybrids exhibited wider variability for seed cotton yield indicating the presence of variability for combining ability among the parents (parents and single cross hybrids).

Heterosis: When the F₁ hybrids were compared with their parental means, the crosses were found to have higher values generally and in some cases they surpassed their better-parent revealing positive heterosis for most studied traits. Among the heterosis values of derived F₁ (single and double-cross hybrids) over mid-parents and better-parent, majority of the F₁s registered insignificant or significant and negative or positive heterosis for all studied traits.

Diallel Crosses:

Heterosis Versus Mid-and Better-Parents: The Heterosis versus mid-and better-parents values estimated for studied traits in a half diallel mating design are presented in Tables 2 and 3, respectively. Derived F₁s P₁ x P₂, P₁ x P₄ and P₄ x P₅ exhibited significant or highly significant positive heterosis relative to mid-parents for seed cotton yield/plant, lint cotton yield/plant and number of bolls/plant traits. The cross P₁ x P₃ had significant or highly significant positive heterosis relative to mid-parents for lint index, 2.5% span length and uniformity ratio traits. The cross P₃ x P₅ was significant positive heterosis relative to mid-parents for seed index and uniformity ratio traits. The cross P₁ x P₄ showed highly significant negative (useful) heterosis relative to mid-parents for fiber fineness. However, boll weight, lint percentage and fiber strength traits were significant negative or insignificant (positive and negative) heterosis relative to mid-parents. As for heterosis versus better-parent, the cross P₁ x P₂ displayed significant and

Table 1: The means performance of the parents, single and double-cross hybrids for studied traits in cotton (*Gossypium barbadense* L.).

Genotypes	Traits										
	S.C.Y./P(g)	L.C.Y/P (g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
Parents											
Pima S6 (P1)	67.62	26.97	3.15	40.01	21.57	9.27	5.81	29.80	4.20	10.07	83.73
Australian (P2)	79.95	32.61	3.01	40.90	26.70	8.81	6.14	31.97	4.47	10.23	85.23
Karashanky (P3)	62.53	25.03	2.80	40.30	22.44	9.12	6.24	29.70	4.13	9.90	84.67
Giza 85 (P4)	66.20	25.35	2.84	38.28	23.44	8.66	5.37	32.60	4.17	9.93	86.37
Giza 88 (P5)	57.90	22.26	2.75	38.39	21.16	8.31	5.58	34.03	4.03	10.57	85.73
Grand Mean	66.84	26.45	2.91	39.57	23.06	8.83	5.83	31.62	4.20	10.14	85.15
Single Hybrids											
P1 x P2	96.57	39.20	2.89	40.69	33.47	9.56	6.55	32.73	4.10	9.87	86.17
P1 x P3	76.55	31.07	2.93	41.50	26.23	9.55	7.04	33.70	3.97	9.97	86.67
P1 x P4	82.94	32.56	2.84	39.64	29.61	9.49	6.26	32.67	4.30	10.33	86.43
P1 x P5	55.98	22.09	2.61	39.40	21.38	8.83	5.77	30.90	4.27	9.60	84.40
P2 x P3	59.45	24.37	2.61	40.96	23.30	8.55	5.94	30.27	4.10	10.50	84.43
P2 x P4	58.34	23.72	2.64	40.57	22.41	8.86	6.02	32.73	4.30	10.33	87.73
P2 x P5	75.04	28.84	2.71	37.86	27.82	8.99	5.64	31.63	4.40	9.50	85.47
P3 x P4	48.42	18.85	2.90	40.07	16.86	9.27	6.42	32.07	4.07	10.17	85.47
P3 x P5	56.08	22.00	2.97	39.41	18.88	9.45	6.21	32.27	4.47	9.83	88.23
P4 x P5	86.45	35.18	2.82	40.61	31.23	8.95	6.13	32.60	3.97	10.03	86.23
Grand Mean	69.58	27.79	2.79	40.07	25.12	9.15	6.08	32.16	4.05	10.01	86.12
Double-Cross Hybrids											
(P1 x P2) x (P3 x P4)	67.40	27.70	2.79	41.31	24.25	9.26	6.61	31.90	4.37	10.37	85.67
(P1 x P2) x (P3 x P5)	87.32	33.52	2.97	38.88	29.52	9.55	6.20	34.23	4.13	10.10	89.27
(P1 x P2) x (P4 x P5)	72.99	29.13	3.14	39.98	23.29	9.09	6.07	33.07	4.03	10.50	85.83
(P1 x P3) x (P2 x P4)	45.37	17.67	2.87	38.84	15.83	9.12	5.80	32.87	4.07	10.03	84.37
(P1 x P3) x (P2 x P5)	72.97	28.18	2.86	38.65	25.49	9.67	6.09	33.63	4.20	10.27	87.40
(P1 x P3) x (P4 x P5)	52.97	20.87	2.85	40.15	18.80	9.01	4.79	32.00	4.17	9.93	86.47
(P1 x P4) x (P2 x P3)	80.59	31.25	2.94	38.93	27.52	9.54	6.11	31.60	4.27	10.03	83.30
(P1 x P4) x (P2 x P5)	60.25	23.18	2.99	38.61	20.18	9.74	6.13	32.17	3.67	10.03	82.93
(P1 x P4) x (P3 x P5)	60.93	23.43	2.99	38.49	20.33	9.68	6.14	33.57	4.37	10.27	86.10
(P1 x P5) x (P2 x P3)	64.60	26.16	2.87	40.52	23.07	9.08	6.20	31.93	4.33	10.17	86.90
(P1 x P5) x (P2 x P4)	65.79	26.01	2.89	39.32	23.15	9.37	6.09	31.83	4.30	10.17	85.87
(P1 x P5) x (P3 x P4)	69.21	27.04	2.96	39.08	23.42	9.47	6.09	34.63	4.17	9.93	87.60
(P2 x P3) x (P4 x P5)	47.79	19.04	2.92	39.75	16.37	9.39	6.20	33.40	4.57	10.33	87.10
(P2 x P4) x (P3 x P5)	54.22	22.25	2.88	41.13	18.86	9.54	6.79	32.80	4.27	10.27	84.27
(P2 x P5) x (P3 x P4)	83.73	33.02	2.75	39.78	30.53	8.83	5.48	31.93	4.20	10.03	85.50
Grand Mean	65.74	25.90	2.91	39.56	22.71	9.36	6.05	32.77	4.21	10.16	85.90
L.S.D. 0.05	13.23	5.07	0.26	N.S.	5.36	0.23	N.S.	2.36	N.S.	N.S.	N.S.
L.S.D. 0.01	17.59	6.74	N.S.	N.S.	7.13	0.30	N.S.	3.14	N.S.	N.S.	N.S.

Table 2: Heterosis deviation relative to the mid-parents (M.P.) estimates of 10 F1 hybrids for studied traits in cotton.

Genotypes	Traits										
	S.C.Y./P(g)	L.C.Y/P (g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
P1 x P2	30.88**	31.59**	-6.17	0.58	38.68**	5.75	9.62	5.97	-5.42	-2.76	2.00
P1 x P3	17.63	19.50	-1.51	3.35	19.20	3.86	16.85*	13.28**	-4.68	-0.15	2.93*
P1 x P4	23.96*	24.46*	-5.18	1.26	31.57*	5.86	-9.12	4.71	-30.70**	3.30	1.62
P1 x P5	-10.80	-10.26	-11.53**	0.51	0.07	0.46	1.32	-3.18	3.77	-6.98	-0.39
P2 x P3	-16.55	-15.44	-10.15*	0.89	-5.17	-4.63	-4.04	-1.83	-4.65	4.32	-0.61
P2 x P4	-20.16*	-18.15	-9.74*	2.48	-10.61	1.43	4.60	1.38	-0.46	2.48	2.25
P2 x P5	8.87	5.12	-5.90	-4.50	16.26	5.02	-3.75	-4.15	3.53	-8.65	-0.01
P3 x P4	-24.77*	-25.17*	2.84	1.99	-26.50	4.27	10.59	2.95	-1.93	2.57	-0.06
P3 x P5	-6.87	-6.96	7.03	0.17	-13.39	8.43*	5.08	1.27	9.56*	-3.96	3.56*
P4 x P5	39.32**	47.78**	0.89	5.93	40.04**	5.48	11.96	-2.15	-3.17	-2.15	0.21
L.S.D. 0.05	14.27	5.50	0.25	3.23	6.12	0.62	0.99	2.17	0.36	0.79	2.40
L.S.D. 0.01	19.21	7.41	0.34	4.35	8.24	0.83	1.34	2.92	0.48	1.07	3.24

Table 3: Heterosis deviation relative to the better-parents (B.P.) estimates of 10 F1 hybrids for studied traits in cotton.

Traits											
Genotypes	S.C.Y./P(g)	L.C.Y/P (g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
P1 x P2	20.79*	20.21**	-8.25	-0.51	25.36	3.13	6.68	2.38	-2.38	-3.52	1.10
P1 x P3	13.21	15.20	-6.98	2.98	16.89	3.02	12.82	13.09**	-3.87	-0.99	2.36
P1 x P4	22.66	20.73	-9.84*	-0.92	26.32	2.37	-12.56	0.21	-30.46**	2.58	0.07
P1 x P5	-17.21	-18.09	-17.14**	-1.52	-0.88	-4.75	-0.69	-9.20**	5.96	-9.18*	-1.55
P2 x P3	-25.64*	-25.27*	-13.29**	0.15	-12.73	-6.25	-4.81	-5.32	-0.73	2.64	-0.94
P2 x P4	-27.03*	-27.26**	-12.29*	-0.81	-16.07	0.57	-1.95	0.40	3.12	0.98	1.57
P2 x P5	-6.14	-11.56	-9.97*	-7.43	4.19	2.04	-8.14	-7.05	9.18	-10.12*	-0.30
P3 x P4	-26.86*	-25.64*	2.11	-0.57	-28.07	1.64	2.88	-1.63	-1.45	2.42	-1.04
P3 x P5	-10.32	-12.11	6.07	-2.21	-15.86	3.62	-0.48	-5.17	10.92*	-7.00	2.92
P4 x P5	30.59*	38.78**	-0.70	5.78	33.23*	3.35	9.86	-4.20	-1.49	-5.11	-0.16
L.S.D. 0.05	16.47	6.35	0.29	3.73	7.07	0.71	1.15	2.51	0.41	0.92	2.78
L.S.D. 0.01	22.18	8.55	0.39	5.02	9.52	0.96	1.54	3.37	0.55	1.23	3.74

Table 4: Direction of heterosis as comparisons between each of single crosses (M.F1) vs. mid-parents (M.P) and single crosses (M.F1) vs. better-parent (B.P) for studied traits obtained from the data in diallel cross.

Traits											
Comparisons	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
M.P.	66.84	26.44	2.91	39.57	23.06	8.83	5.828	31.62	4.2	10.14	85.14
B.P.	79.95	32.61	3.15	40.90	26.7	9.27	6.24	34.03	4.03	10.57	86.37
M.F1	69.58	27.78	2.79	40.07	25.11	9.15	6.08	32.15	4.05	10.01	86.12
H (F1, M.P) %	4.10	5.08	-4.05**	1.25	8.92	3.58*	4.32	1.70	-3.45	-1.25	1.15
L.S.D. 0.05	6.38	2.46	0.11	1.44	2.74	0.28	0.44	0.97	0.16	0.36	1.08
L.S.D. 0.01	8.59	3.31	0.15	1.94	3.69	0.37	0.60	1.31	0.21	0.48	1.45
H (F1, B.P) %	-12.97	-14.79*	-11.37**	-2.02	-5.92	-1.29	-2.56	-5.50*	0.62	-5.27	-0.29
L.S.D. 0.05	12.22	4.71	0.22	2.76	5.24	0.53	0.85	1.86	0.30	0.68	2.06
L.S.D. 0.01	16.45	6.34	0.29	3.72	7.06	0.71	1.15	2.50	0.41	0.92	2.77

highly significant positive for seed and lint cotton yield traits, respectively. The cross P₄ x P₅ manifested significant for seed cotton yield/plant and number of bolls/plant traits and highly significant for lint cotton yield/plant. The two crosses P₁ x P₃ and P₁ x P₄ revealed highly significant positive and negative heterosis versus better-parent for 2.5% span length and fiber fineness traits, respectively. While, other studied traits had significant negative or insignificant (positive and negative) heterosis versus better-parent. The significant negative heterosis suggested the importance of additive genetic components [16].

Heterosis over the mid and Better-Parents: The values of heterosis over the mid-parent (mean of the five parents) and better-parents (from five parents) for studied traits are presented in Table 4. The results elicited that, the mean of the F₁ hybrids (M.F₁) were higher than of over the mid-parents (M.P.) for most studied traits. Therefore, there was significant positive and desirable heterosis for most studied traits. On the other hand, the mean of the 10 F₁ hybrids were lower than the better-parent for most

studied traits. These results indicated that, the heterosis over the better-parent were elucidated insignificant and significant or highly significant negative for studied traits. When single crosses are used as parents the genetic distance existing between two parents of each single cross and the genetic distance between the pair of single crosses influences the magnitude of heterosis revealed in double cross [17]. This indicates the importance of low x average, average x average, low x high and high x high parent combinations in the development of crosses exhibiting high level of hybrid vigour for yield and yield related traits. Thus it can be concluded that the parents possessing only high values need not necessarily produce high yielding hybrids as indicated by the present study [9].

Double-Cross Hybrids:

Heterosis Versus Mid-(4P.) And Better-parents (4P.): The heterosis versus mid-parents (M.P) and better-parent (B.P) estimated of 15 double-cross hybrids for studied traits are shown in Tables 5 and 6, respectively. Three double-cross hybrids registered highly significant

Table 5: Heterosis deviation relative to the mid-parents (M.P) compared to the means of double-cross hybrids for studied traits in cotton.

Traits											
Genotypes	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB./P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
(P1xP2)x(P3xP4)	-2.42	0.76	-5.42	3.61*	3.03	3.29	12.22	2.85	3.01	3.36	0.79
(P1xP2)x(P3xP5)	30.33**	25.50**	1.45	-2.56	28.53**	7.58*	4.33	9.10**	-1.84	-0.91	5.22**
(P1xP2)x(P4xP5)	7.47	8.70	6.89*	1.48	0.31	3.74	6.03	3.02	-4.45	2.94	0.66
(P1xP3)x(P2xP4)	-34.32**	-35.72**	-2.71	-2.59	-32.75**	1.73	-1.53	5.97*	-4.07	-0.02	-0.74
(P1xP3)x(P2xP5)	8.91	5.47	-2.31	-3.13	10.98*	8.93**	2.48	7.19*	-0.18	0.76	3.02
(P1xP3)x(P4xP5)	-16.66**	-16.19**	-1.21	2.31	-15.13**	1.92	-16.70	1.48	0.91	-1.85	1.58
(P1xP4)x(P2xP3)	16.67**	13.68**	-0.34	-2.36	16.92**	6.41*	3.74	1.88	0.65	-0.02	-2.00
(P1xP4)x(P2xP5)	-11.29*	-13.50**	1.79	-1.99	-13.08*	11.16**	7.07	0.22	-12.98**	-1.67	-2.74
(P1xP4)x(P3x P5)	-4.14	-5.91	3.64	-1.92	-8.23	9.50**	6.78	6.46*	5.75	1.51	1.15
(P1xP5)x(P2 xP3)	-3.58	-2.09	-1.96	1.55	0.45	2.28	4.33	1.77	2.91	-0.22	2.43
(P1xP5)x(P2xP4)	-3.13	-2.94	-1.62	-0.19	-0.29	6.93*	6.38	-0.84	1.96	-0.29	0.71
(P1xP5)x(P3xP4)	8.88	8.58	2.60	-0.42	5.72	7.13*	5.91	9.82**	0.91	-1.85	2.91
(P2xP3)x(P4xP5)	-28.29**	-27.64**	2.46	0.72	-30.15**	7.62*	6.30	4.13	8.81*	1.70	1.87
(P2xP4)x(P3xP5)	-18.64**	-15.44**	1.05	4.21*	-19.52**	9.34**	16.42	2.26	1.67	1.11	-1.44
(P2xP5)x(P3xP4)	25.64**	25.49**	-3.51	0.79	30.28**	1.20	-6.04	-0.45	0.00	-1.26	0.00
L.S.D. 0.05	6.57	2.59	0.18	1.36	2.40	0.52	1.07	1.77	0.32	0.65	3.02
L.S.D. 0.01	8.78	3.46	0.25	1.82	3.21	0.70	1.43	2.37	0.43	0.87	4.04

Table 6: Heterosis deviation relative to the better-parent (B.P) compared to the means of double-cross hybrids for studied traits in cotton.

Traits											
Genotypes	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
(P1xP2)x(P3xP4)	-15.70**	-15.06**	-11.43**	1.00	-9.18	-0.11	5.93	-2.15	5.81	1.37	-0.81
(P1xP2)x(P3xP5)	9.22	2.79	-5.71	-4.94*	10.56	3.02	-0.64	0.59	2.48	-4.45	4.13
(P1xP2)x(P4xP5)	-8.71	-10.67*	-0.32	-2.25	-12.77*	-1.94	-1.14	-2.82	0.00	-0.66	-0.63
(P1xP3)x(P2xP4)	-43.25**	-45.81**	-8.89*	-5.04*	-40.71**	-1.62	-7.05	0.83	-1.45	-1.96	-2.32
(P1xP3)x(P2xP5)	-8.73	-13.58**	-9.21*	-5.50*	-4.53	4.31	-2.40	-1.18	4.22	-2.84	2.55
(P1xP3)x(P4xP5)	-21.67**	-22.62**	-9.52*	-0.37	-19.80**	-2.80	-23.24*	-5.97	3.47	-6.05	0.12
(P1xP4)x(P2xP3)	0.80	-4.17	-6.67	-4.82*	3.07	2.91	-2.08	-3.07	3.39	-1.96	-3.55
(P1xP4)x(P2xP5)	-24.64**	-28.92**	-5.08	-5.60**	-24.42**	5.07	-0.16	-5.47	-8.93	-5.11	-3.98
(P1xP4)x(P3x P5)	-9.89	-13.13**	-5.08	-4.49*	-13.27*	4.42	-1.60	-1.35	8.44	-2.84	-0.31
(P1xP5)x(P2 xP3)	-19.20**	-19.78**	-8.89*	-0.93	-13.60*	-2.05	-0.64	-6.17	7.44	-3.78	1.36
(P1xP5)x(P2xP4)	-17.71**	-20.24**	-8.25*	-3.86	-13.30*	1.08	-0.81	-6.46	6.70	-3.78	-0.58
(P1xP5)x(P3xP4)	2.35	0.26	-6.03	-3.03	-0.09	2.16	-2.40	1.76	3.47	-6.05	1.42
(P2xP3)x(P4xP5)	-40.23**	-41.61**	-2.99	-2.81	-38.69**	2.96	-0.64	-1.85	13.40**	-2.27	0.85
(P2xP4)x(P3xP5)	-32.18**	-31.77**	-4.32	0.56	-29.36**	8.29*	8.81	-3.61	5.96	-2.84	-2.43
(P2xP5)x(P3xP4)	4.73	1.26	-8.64*	-2.74	14.34*	0.23	-12.18	-6.17	4.22	-5.11	-1.01
L.S.D. 0.05	8.31	3.28	0.23	1.72	3.04	0.66	1.35	2.24	0.40	0.82	3.82
L.S.D. 0.01	11.11	4.38	0.31	2.30	4.06	0.88	1.80	3.00	0.54	1.10	5.11

Table 7: Heterosis deviation relative to the mid-parents (F1 and P) compared to the means of double-cross hybrids for studied traits in cotton.

Traits											
Genotypes	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
(P1xP2)x(P3xP4)	-7.03	-4.57	-3.63	2.30	-3.64	-1.65	1.93	-1.54	6.98	3.49	-0.17
(P1xP2)x(P3xP5)	14.41	9.54	1.37	-2.92	12.78	0.47	-2.82	5.32	-3.62	2.54	2.37
(P1xP2)x(P4xP5)	-20.24**	-21.67**	9.98*	-1.65	-28.01**	-1.78	-4.26	1.24	-0.12	5.53	-0.43
(P1xP3)x(P2xP4)	-32.73**	-35.50**	3.05	-5.35	-34.91**	-0.92	-11.18	-1.04	-1.57	-1.18	-3.25
(P1xP3)x(P2xP5)	-3.73	-5.93	1.42	-2.60	-5.68	4.31	-3.94	2.95	0.36	5.50	1.55
(P1xP3)x(P4xP5)	-35.01**	-37.00**	-0.87	-2.20	-34.56**	-2.59	-27.26**	-3.47	5.04	-0.70	0.02
(P1xP4)x(P2xP3)	13.20	9.78	7.79	-3.40	4.03	5.76	10.89	0.41	22.00**	-3.70	-2.49
(P1xP4)x(P2xP5)	-23.72**	-24.50**	7.85	-0.36	-29.72**	5.41	14.37	0.06	0.55	1.16	-3.51
(P1xP4)x(P3x P5)	-12.34	-14.11	2.93	-2.62	-16.15	2.22	8.77	3.39	18.59**	1.88	-1.41
(P1xP5)x(P2 xP3)	11.93	12.61	9.96*	0.85	3.27	4.49	5.89	4.40	3.46	1.19	2.94
(P1xP5)x(P2xP4)	15.10	13.56	10.10*	-1.66	5.73	5.94	3.31	0.05	0.35	2.06	-0.23
(P1xP5)x(P3xP4)	32.59**	32.10**	7.44	-1.65	22.49	4.64	-0.08	9.99**	0.00	0.46	3.14
(P2xP3)x(P4xP5)	-34.49**	-36.05**	7.55	-2.54	-39.96**	7.31	2.73	6.25	13.26**	0.63	2.07
(P2xP4)x(P3xP5)	-5.23	-2.67	2.67	2.85	-8.65	4.21	11.04	0.92	-2.62	1.88	-4.22**
(P2xP5)x(P3xP4)	35.64**	38.48**	-1.96	2.09	36.66**	-3.29	-9.12	0.25	-0.83	1.98	0.04
L.S.D. 0.05	12.31	4.72	0.25	2.60	4.92	0.67	1.26	2.11	0.35	0.79	3.27
L.S.D. 0.01	16.41	6.30	0.33	3.47	6.56	0.89	1.68	2.82	0.46	1.06	4.35

Table 8: Heterosis deviation relative to the better-parent (F1 or P) compared to the means of double-cross hybrids for studied traits in cotton.

Genotypes	Traits										
	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
(P1xP2)x(P3xP4)	-30.21**	-29.34**	-3.79	1.52	-27.55**	-3.14	0.92	-2.54	7.37	5.07	-0.58
(P1xP2)x(P3xP5)	-9.58	-14.49*	0.00	-4.45	-11.80	-0.10	-5.34	4.58	0.73	2.33	1.18
(P1xP2)x(P4xP5)	-24.42**	-25.69**	8.65	-1.74	-30.42**	-4.92	-7.33	1.04	1.51	6.38	-0.46
(P1xP3)x(P2xP4)	-40.73**	-43.13**	-2.05	-6.41	-39.65**	-4.50	-17.61	-2.46	2.52	0.60	-3.83
(P1xP3)x(P2xP5)	-4.68	-9.30	-2.39	-6.87	-8.38	1.26	-13.49	-0.21	5.79	3.01	0.84
(P1xP3)x(P4xP5)	-38.73**	-40.68**	-2.73	-3.25	-39.80**	-5.65	-31.96**	-5.04	5.04	-1.00	-0.23
(P1xP4)x(P2xP3)	-2.83	-4.02	3.52	-4.96	-7.06	0.53	2.86	-3.28	47.24**	-2.90	-3.62
(P1xP4)x(P2xP5)	-27.36**	-28.81**	5.28	-2.60	-31.85**	2.63	8.69	-1.53	26.55**	-2.90	-4.05
(P1xP4)x(P3x P5)	-26.54**	-28.04**	0.67	-2.90	-31.34**	2.00	-1.13	2.75	50.69**	-0.58	-2.41
(P1xP5)x(P2xP3)	8.66	7.35	8.71	-1.07	-0.99	2.83	4.38	3.33	5.61	-3.14	2.93
(P1xP5)x(P2xP4)	12.77	9.65	9.47	-3.08	3.30	5.76	1.16	-2.75	0.70	-1.55	-2.12
(P1xP5)x(P3xP4)	23.63**	22.41**	2.07	-2.47	9.54	2.16	-5.14	7.98*	2.46	3.44	2.49
(P2xP3)x(P4xP5)	-44.72**	-45.88**	3.55	-2.95	-47.58**	4.92	1.14	2.45	15.11**	2.99	1.01
(P2xP4)x(P3xP5)	-7.06	-6.20	-3.03	1.38	-15.84	0.95	9.34	0.21	-0.70	-0.58	-4.49**
(P2xP5)x(P3xP4)	11.58	14.49	-5.17	-0.72	9.74	-4.75	-14.64	-0.44	3.19	5.58	0.04
L.S.D. 0.05	14.21	5.46	0.28	3.00	5.69	0.77	1.46	2.44	0.40	0.91	3.77
L.S.D. 0.01	18.95	7.27	0.38	4.01	7.58	1.03	1.94	3.25	0.54	1.22	5.03

Table 9: Direction of heterosis over the mid-parents (M.P), mid-F1's hybrids (M.F1), better-parent (B.P), better-F1 hybrids (B.F1) and mean parents and single-cross {M.(P, F1)} hybrids compared to the means of double-cross hybrids (DCH) for yield, yield components and fiber quality traits in cotton.

Comparisons	Traits										
	S.C.Y./P(g)	L.C.Y/P(g)	B.W.(g)	L. %	No. ofB. / P	S.I.(g)	L.I.(g)	2.5 % S.L.	F.F.	F.S.	U.F.%
M.P.	66.84	26.44	2.91	39.57	23.06	8.834	5.828	31.62	4.2	10.14	85.14
B.P.	79.95	32.61	3.15	40.90	26.70	9.27	6.24	34.03	4.03	10.23	86.37
M.F1	69.58	27.78	2.792	40.07	25.11	9.15	6.08	32.157	4.05	10.01	86.12
B.F1	96.57	39.20	2.97	41.50	33.47	9.56	7.04	33.7	2.9	9.87	87.73
M. (P, F1)	68.21	27.12	2.851	39.82	24.09	8.992	5.954	31.88	4.12	10.07	85.63
M.DCH	65.74	25.89	2.91	39.56	22.70	9.356	6.05	32.77	4.20	10.16	85.90
H (DCH, M.P)%	-1.64	-2.07	0.05	-0.04	-1.54	5.91**	3.85	3.64**	0.19	0.22	0.89
L.S.D. 0.05	3.03	1.20	0.09	0.63	1.11	0.24	0.49	0.82	0.15	0.30	1.40
L.S.D. 0.01	4.06	1.60	0.11	0.84	1.48	0.32	0.66	1.09	0.20	0.40	1.87
H (DCH, B.P)%	-17.77**	-20.59**	-7.58**	-3.27*	-14.95**	0.93	-3.00	-3.70	4.42	-0.66	-0.54
L.S.D. 0.05	6.07	2.39	0.17	1.26	2.22	0.48	0.99	1.64	0.30	0.60	2.79
L.S.D. 0.01	8.11	3.20	0.23	1.68	2.97	0.64	1.32	2.19	0.39	0.80	3.73
H (DCH, M.F1)%	-5.52	-6.81*	4.27**	-1.27	-9.60**	2.25	-0.45	1.91	3.77**	1.49	2.45**
L.S.D. 0.05	4.10	1.57	0.08	0.87	1.64	0.22	0.42	0.70	0.12	0.26	1.09
L.S.D. 0.01	5.47	2.10	0.11	1.16	2.19	0.30	0.56	0.94	0.15	0.35	1.45
H (DCH, B.F1)%	-31.92**	-33.94**	-1.98	-4.67	-32.16**	-2.13	-14.02	-2.76	45.10**	2.96	0.57
L.S.D. 0.05	10.38	3.98	0.21	2.19	4.15	0.56	1.07	1.78	0.29	0.67	2.75
L.S.D. 0.01	13.84	5.31	0.28	2.92	5.54	0.75	1.42	2.38	0.39	0.89	3.67
H {DCH, M(P,F1)}%	-3.62*	-4.49**	2.12**	-0.66	-5.74**	4.05**	1.66	2.77**	1.95**	0.85	0.32
L.S.D. 0.05	1.87	0.72	0.04	0.40	0.76	0.10	0.19	0.33	0.06	0.12	0.50
L.S.D. 0.01	2.49	0.95	0.05	0.53	1.01	0.13	0.25	0.44	0.08	0.17	0.66

positive heterosis relative to mid-parents for seed and lint cotton yields. One double-cross hybrid for boll weight and uniformity ratio traits and two, four, nine and five double-cross hybrids for lint percentage, number of bolls/plant, seed index and 2.5% span length traits, respectively, revealed significant and highly significant positive heterosis versus mid-parents. As for, highly

significant negative heterosis was observed for one double-cross hybrids relative to mid-parents of fiber fineness trait. In respect to, lint index and fiber strength traits exhibited insignificant heterosis relative to mid-parents. On the other hand, only one double-crosse hybrid evidenced significant heterosis versus better-parent for number of bolls/plant and seed index

traits. Other studied traits had shown insignificant heterosis versus better-parent (undesirable). From the previous results can conclude that, the double-cross hybrids ($P_1 \times P_2$) \times ($P_3 \times P_5$) for seed cotton yield/plant, lint cotton yield/plant and uniformity ratio traits, the cross ($P_1 \times P_2$) \times ($P_3 \times P_4$) for lint percentage and fiber strength traits, the cross ($P_2 \times P_5$) \times ($P_3 \times P_4$) for number of bolls/plant, the cross ($P_2 \times P_4$) \times ($P_3 \times P_5$) for seed index and lint index traits, ($P_1 \times P_5$) \times ($P_3 \times P_4$) for 2.5% span length and the cross ($P_1 \times P_4$) \times ($P_2 \times P_5$) for fiber fineness exhibited the best heterosis versus better-parent. These hybrids are considered the promising crossed to be used in breeding programs for produce hybrid cotton and improvement for these traits.

Heterosis Versus Mid-f₁ Hybrids and Better-f₁ Hybrids:

The values of heterosis relatively to the mid-F₁ hybrids and better-F₁ hybrids for studied traits are presented in Tables 7 and 8, respectively. Highly significant positive heterosis was observed of two double-cross hybrids over mid-F₁ for seed and lint cotton yields/plant. Significant positive heterosis relative to mid-F₁ hybrids of three double-cross hybrids for boll weight was found. In case of number of bolls/plant and 2.5% span length traits, highly significant positive heterosis had noticed for one double-cross hybrids relative to mid-F₁ hybrids. However, insignificant and undesirable heterosis relative to mid-F₁ manifested for lint percentage, seed index, lint index, fiber fineness, fiber strength and uniformity ratio traits. Concerning, heterosis versus better-F₁ hybrids, one double-cross hybrid was denoted for seed cotton yield/plant, lint cotton yield/ plant and 2.5% span length traits. Generally, more double-cross hybrids showed useful heterosis versus better-F₁ hybrids for most studied traits, such as the cross ($P_1 \times P_5$) \times ($P_3 \times P_4$) for seed cotton yield/plant, lint cotton yield/plant and 2.5% span length traits, the cross ($P_1 \times P_5$) \times ($P_2 \times P_4$) for boll weight and seed index traits, the cross ($P_1 \times P_2$) \times ($P_3 \times P_4$) for lint percentage trait, the cross ($P_2 \times P_5$) \times ($P_3 \times P_4$) for number of bolls/plant traits, the ($P_2 \times P_4$) \times ($P_3 \times P_5$) for lint index and fiber fineness traits, the cross ($P_1 \times P_2$) \times ($P_4 \times P_5$) for fiber strength trait and the cross ($P_1 \times P_5$) \times ($P_2 \times P_3$) for uniformity ratio trait. These hybrids are considered the promising crosses to be used in breeding programs for produce hybrid cotton and improvement for these traits. Kumar [9] mentioned that the potential double cross was heterotic over single crosses confirming the diversity existing between single cross parents. This diversity is crucial for creating variability for combining ability to combine with opposite F₁ to be used as tester at a later stage (F₄ stage).

Heterosis Over the Mid-parents (M.P), Mid-F₁ Hybrids (M.F₁), Better-parent (B.P), Better-F₁ Hybrids (B.F₁) and Mid-parents and F₁ Hybrids [M.(P.F₁):

The data demonstrated that, the comparisons of average overall double-cross hybrids with their all parents and single crosses noticed that the presence of useful heterosis for most studied traits (Table 9). The heterosis over M.P for seed index and 2.5% span length traits, over M.F₁ for boll weight and uniformity ratio traits and over M. (F₁.P) for boll weight, seed index and 2.5% span length traits had recorded highly significant positive and desirable. While, the heterosis over M.P. M.F₁ hybrids, B.P. B.F₁ hybrids and M. (P.F₁) were desirable for some studied traits. These results indicated that, the average of all double-cross hybrids were higher than the mean of mean parents, mean single crosses, better parent, better single crosses and the mean of single crosses and parents. The high level of heterosis obtained in the double-cross hybrids can mainly be attributed to the cumulative action of component traits like boll weight, number of bolls/plant, seed index, 2.5% span length and uniformity ratio in all the five classes i.e. over mid-parent, mid-F₁ hybrids, better-parent, better-F₁ hybrids and the mean of single crosses and parents. Krishna [17] reported that, if the double cross F₁ shows heterosis over mid-parents (average of the parental single crosses) it indicates that the genetic distance between the parental single crosses is considered far more than the genetic distance between the lines involved in the parental single crosses. In contrast to this if the double cross F₁ is not heterotic over mid-parents (average of the parental single crosses) it indicates that the genetic distance between the parental single crosses is considered less than the genetic distance existing between the lines of parental single crosses involved. This suggests that the double cross F₁ should be as heterotic as possible over single cross parents to ensure maximum genetic distance between the parental single crosses. This principle was involved in predicted double cross performance developed by Jenkins [18]; where in average of non parental single cross is given importance to predict the performance of double cross while the parental single cross performance is not considered. Balestre *et al.* [19] stated that, the heterosis was also observed in the intergroup hybrids. This fact may be correlated with the complementation of the loci among these hybrids, that is, of the divergence among them as observed, only one crossing showed positive heterosis with low divergence between the parents. It was, therefore, inferred that the markers were efficient in placing hybrids in different heterotic groups and in most

Table 10: Magnitude of components of genetic variance and heritability from the diallel analysis for studied traits in cotton.

Traits	Components				
	s ² A	s ² D	s ² E	h ² _{bs} %	h ² _{ns} %
S.C.Y./P (gm)	2.76	611.03	32.29	95.00	0.43
L.C.Y/P (gm)	1.55	108.71	4.80	95.83	1.35
B.W. (gm)	0.00	0.06	0.01	85.71	0.00
L. %	0.56	0.00	1.65	25.34	25.34
No. of B. / P	0.00	66.02	5.95	91.73	0.00
S.I. (gm)	0.06	0.24	0.06	83.33	16.67
L.I. (gm)	0.04	0.00	0.16	20.00	20.00
2.5 % S.L.	0.00	3.83	0.75	83.62	0.00
F.F.	0.00	0.05	0.02	71.43	0.00
F.S.	0.00	0.09	0.10	47.37	0.00
U.R. %	0.00	3.19	0.92	77.62	0.00

Table 11: Magnitude of components of genetic variance and heritability from the double-cross hybrids analysis for studied traits in cotton.

Items	s ² A	s ² D	s ² AA	s ² AD	s ² DD	s ² AAA	s ² E	h ² _{bs} %	h ² _{ns} %
S.C.Y./P (g)	0.00	0.00	3348.98	8426.02	0.00	0.00	8.92	99.92	28.42
L.C.Y/P (g)	0.00	0.00	453.57	1179.93	0.00	0.00	1.44	99.91	27.74
B.W. (g)	0.01	0.00	0.31	1.02	0.00	0.00	0.01	99.26	23.70
L. %	0.00	0.00	28.80	77.33	0.00	0.00	0.33	99.69	27.05
No. of B. / P	0.00	0.00	398.96	1000.84	0.00	0.00	0.86	99.94	28.48
S.I. (g)	0.00	0.00	3.27	10.05	0.00	0.00	0.07	99.48	24.42
L.I. (g)	0.00	0.00	9.99	33.87	0.00	0.00	0.28	99.37	22.63
2.5 % S.L.	0.00	0.00	44.94	119.60	0.00	0.00	0.64	99.61	27.21
F.F.	0.01	0.00	1.26	3.69	0.00	0.00	0.02	99.60	25.50
F.S.	0.00	0.00	2.80	9.67	0.00	0.00	0.09	99.28	22.29
U.R. %	9.84	0.00	65.32	242.71	0.00	0.00	2.26	99.29	23.48

Table 12: Correlations between the mean performances and heterosis for studied traits in single and double-cross hybrids.

Traits	Hybrids					
	Single crosses			Double-cross hybrids		
	M.P.	B.P.	M.P.	B.P.	M.F1	B.F1
S.C.Y./P (g)	0.95**	0.91**	0.99**	0.93**	0.74**	0.59*
L.C.Y/P (g)	0.93**	0.88**	0.98**	0.91**	0.74**	0.60*
B.W. (g)	0.85**	0.80**	0.92**	0.83**	0.62*	0.61*
L. %	0.78**	0.82**	0.96**	0.96**	0.74**	0.81**
No. of B. / P	0.97**	0.92**	0.99**	0.96**	0.82**	0.72**
S.I. (g)	0.78**	0.77**	0.95**	0.82**	0.66*	0.63*
L.I. (g)	0.68*	0.65*	0.98**	1.00**	0.81**	0.85**
2.5 % S.L.	0.76*	0.79**	0.91**	0.81**	0.76**	0.78*
F.F.	0.20	0.23	0.98**	0.98**	0.48	0.07
F.S.	0.98**	0.93**	0.93**	0.76**	0.68**	0.41
U.R. %	0.89**	0.89**	0.99**	0.99**	0.88**	0.84**

cases the intergroup double hybrids were superior to the intragroup double cross hybrids. Kumar [9] reported that some hybrids revealed positive heterosis but the extent of heterosis was very low. The double-cross hybrids were exhibited significant and highly significant heterosis values versus M.P, M-F₁, B.P and B-F₁ for most studied traits [20].

Gene Action

Diallel Crosses: The estimates of the different genetic variance components of single crosses for studied traits are presented in Table 10. Both the additive (σ^2A) and dominance (σ^2D) genetic variances were observed for seed cotton yield/plant, lint cotton yield/plant and seed index traits. The σ^2A was negative and estimated to zero

for boll weight, number of bolls/plant and all studied fiber quality traits. While, the σ^2D had negative and equivalent to zero for lint percentage and lint index traits. The σ^2D were greater than the σ^2A for all studied traits except lint percentage and lint index traits were recorded σ^2A were higher than σ^2D . Predominance of additive effects σ^2A in the genetic mechanism lint percentage and lint index advocated that the genes for the traits are fixed and the traits could be improved via selection by exploiting pedigree method right from F_2 generation. On the other hand, higher values of σ^2D over σ^2A suggested the preponderance of dominant genes for other studied traits which revealed that the variation in these parameters was controlled by genes having dominant effects at most of the loci and manipulation of the parents may be useful through exploitation of heterosis for improving these quality attributes. Ali *et al.* [21] stated that additive component was lower in magnitude than dominant component for fiber quality traits.

Double-Cross Hybrids: The estimation of genetic variances of double-cross hybrids for studied traits is presented in Table 11. The additive (σ^2A), dominance (σ^2D), dominance x dominance (σ^2DD) and additive x additive x additive (σ^2AAA) genetic variances were negative for all studied traits except σ^2A for boll weight, fiber fineness and uniformity ratio traits. The genetic variances which showed negative values were made equal to zero. Concerning epistatic variances, additive x additive (σ^2AA) and additive x dominance (σ^2AD) genetic variances displayed positive and larger than the other types of epistatic genetic variances for all studied traits. The σ^2AD had higher than the σ^2AA for all studied traits. The relatively magnitude of epistatic genetic components revealed the predominance of σ^2AA and σ^2AD for all studied traits, hence improvement of these traits would therefore need delayed selection and intermitting the segregants followed by recurrent selection. Thus, quadriallel analysis had clearly elucidated its advantages over diallel analysis by giving additional information on magnitude of types of epistatic components and also on order of parents to be crosses in double-cross hybrids for obtaining superior transgressive segregants. Said [20] and Abd El-Bary [22] reported that, the magnitudes of dominance genetic variances were positive and larger than those of additive genetic variance for most studied traits in double-cross hybrids. Concerning, epistatic variances, additive x additive, additive x dominance and additive x additive x additive were positive and considerable magnitude for most studied traits.

Heritability

Diallel Crosses: The results in Table 10 displayed that, the broad sense heritability estimates (h^2_{bs} %) were high (over 50%) for most studied traits. The h^2_{bs} % values were higher than the heritability in narrow sense (h^2_{ns} %) values for most studied traits, thus suggesting that improvement for these traits can be made through selection. Concurrently, the h^2_{bs} % value was equal the h^2_{ns} % value, this result indicated the additive genetic variance values were negative, which may be considered as zero for lint percentage and lint index traits. The low h^2_{ns} % was observed for all studied traits. The h^2_{ns} % was estimated to zero because of the negative values of additive genetic variances. Murtaza *et al.* [23] mentioned that low to moderate estimates of narrow sense heritability was obtained for seed cotton yield/plant and lint percentage traits. Narrow sense heritability is a reflection of the amount of additive, fixable, heritable variation.

Double-Cross Hybrids: High h^2_{bs} % values (over 99 %) were obtained and higher than their corresponding h^2_{ns} % values for all studied traits (Table 11). Estimates of h^2_{ns} % had low (less than 30 %) for all studied traits. This indicated that, the low values of h^2_{ns} % could be due to relatively them great influence of environmental conditions. These results could be due to the low magnitude of the additive genetic variance and the great amount of environmental effects. Also, these results indicating the minor and major role of additive and dominance genetic variances in genetic expression of these traits, respectively. The estimates values of broad sense heritability were larger than their corresponding of narrow sense heritability for these traits, thus suggesting that improvement for these traits can be made through selection. As yield improvement is the main objective of any breeding program, in this regard the progeny of the double-cross hybrids should be given due importance in order to select high yielding segregants as these crosses showed highest heritability. Said [20] mentioned that high broad sense heritability estimates (over 50%) in double-cross hybrids were obtained for yield, yield components and fiber quality traits and larger than their corresponding heritability values in narrow sense for the most studied traits.

Correlation: Table 12 shows the correlations between the mean performances and heterosis for yield, yield components and fiber quality traits in single and double-cross hybrids. Mean performances had positive and significant or highly significant correlation with heterosis versus mid- and better-parents in single crosses

for all studied traits except fiber fineness trait. All studied traits showed significantly or highly significantly positively correlated with heterosis versus mid-parents (M.P.), better-parent (B.P.), Mid-F₁ hybrids (M.F₁) and better-F₁ hybrids in double-cross hybrids except fiber fineness for heterosis over M.F₁ hybrids and B.F₁ hybrids and fiber strength for heterosis over B. F₁ hybrids. Balestre *et al.* [19] reported that high and significant correlation was observed for yield and heterosis. The high correlation among heterosis and Mean performances observed in this study shows that the heterosis was efficient in the choice of parents or populations [24]. According to Falconer [25], heterosis can be explained by divergence and also by the effect of dominance of the alleles that control the trait in question. Thus, by the theory of quantitative genetics, both parameters would be correlated and in this experiment these parameters were highly correlated.

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