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Genetic Analysis of Yield and Fiber Traits in Cotton (*Gossypium barbadense* L.) under Normal Irrigation and Drought Stress Conditions

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DROUGHT stress is a serious abiotic stress affecting crop production in Egypt. The aim of this article was to study the gene action controlled seed cotton yield (SCY/P) and fiber properties under normal irrigation and water deficit conditions. Ten cotton genotypes (*G. barbadence* L.) were crossed as lines to three as testers. The parents and hybrids were evaluated in a randomized complete block design with three replications under normal and water deficit at the Agriculture Research Center, Sohag Governorate, Egypt. The two hybrids [G95 × (G90 × Aust.)] and [Aust. × (G90 × Aust.)] were the best hybrids for most studied traits and should be considered in breeding program for drought stress and normal irrigation, and the parents G.95, (G95 × Aust.) and Aust. depicted their good combining ability. Mean reduction % of the parents varied greatly from 2.99 for lint % to 31.79 for SCY/P, while it varied for the hybrids from 5.11 for fiber strength to 33.93 for SCY/P. The additive (σ^2A) and the dominance variance (σ^2D) were larger under normal irrigation than under water stress conditions for most traits. The ratio σ^2A/σ^2D was less than unity for all traits indicating that the role of dominance was more important than additive effects in the inheritance of these traits. The contribution of lines was larger than that of testers and lines x testers interaction in most traits at both environments indicating the importance of selection of lines for hybridization, and selection should be delayed to later generations.

Keywords: Additive and dominance variances, Drought stress, *G. barbadense*, Line X tester analysis.

Introduction

Drought is one of the serious abiotic stresses affects 45% of crop production worldwide (Abdelraheem et al., 2019). Egypt suffers from water scarcity required for agriculture. Moreover, it has become necessary to grow cotton in newly reclaimed desert areas. The drought stress significantly affects many agronomic traits and seed cotton yield (Zhang et al., 2012). In *G.barbadence* drought stress reduced seed cotton yield by 31.44 to 42% (Mohamed et al., 2009; Veesar et al., 2018; Mahdy et al., 2021). The best way to resist drought is to develop new varieties that can better withstand water deficit. The first step for a successful breeding program

is to evaluate the available germplasm to select appropriate tolerant parents for drought. The different methods of diallel analyses are good tools to detect appropriate parents and superior crosses in terms of the investigated traits (Akiscan & Gencer, 2014; Waqar et al., 2015). The line x tester design can be used to estimate general and specific combining abilities in both self and cross-pollinated plants (Kempthorne, 1957). Under drought stress both additive and dominance components were significant for all traits (Soomro et al., 2012a), and the average degree of dominance for lint index, lint%, staple length and fiber strength were greater than a unity, displaying over dominance type of gene action (Mohamed et al., 2009; Soomro et al., 2015; Prakash et al.,

2018). In contrary, Vasconcelos et al.(2018) found that the additive effects were found for seed yield, lint percentage, days to blooming and boll weight, whereas, dominance effect was found only for plant height. The generation mean analysis under drought stress indicated that the additive, dominance and their interaction controlled the agronomic traits, fiber traits (fiber fineness, length and strength) and physiological traits (relative water content and excised leaf water loss) (Ahmad et al., 2009). Hence, selection for drought tolerance could be delayed to later generations. In line-tester analysis the higher contribution in total variance was for lines for earliness and proline contents, and drought tolerance was found to have a strong association with early maturity (Mahmood et al., 2021).

Under a non-stressed environment both additive and non-additive controlled five traits (Panhwar et al., 2008). Significant differences were detected among the estimates of combining abilities. The additive gene effects were predominant for the evaluated traits (De Aguiar et al., 2007; Samreen et al., 2008; Mohamed et al., 2009). Otherwise, dominance effects (H1 and H2) mainly contributed for number of bolls per plant, and partial dominance was involved for plant height, number of sympodial branches, boll weight, and yield of seed cotton, lint percentage, staple length and fiber strength (Raza et al., 2013). In line-tester analysis, the additive variance was significant for fiber length, fiber fineness and fiber elongation, and non-additive gene effects for seed cotton yield, lint yield, lint%, fiber strength and fiber uniformity (Karademir et al., 2009; Shaukat et al., 2013; Memon, 2017; Mahrous, 2018; Makhdoom et al., 2019). Likewise, the ratio δ^2GCA/δ^2SCA depicted the predominance of non-additive types of gene action for plant height, seed cotton yield and its components and fiber length and fiber strength (Karademir et al., 2009; Khokhar et al., 2018; Munir et al., 2018; Patil et al., 2018; Unay et al., 2019). The variances due to SCA were more than GCA variances for various fiber quality parameters which indicates the preponderance of non-additive nature of gene action (Ali & Awan, 2009; Shaukat et al., 2013; Simon et al., 2013). The discrepancy and differences between the results of the researchers could be due to the divergence among the parents in the diallel analysis and the nature of the trait studied in terms of the number of genes is what determines whether the genes act in additive or

non-additive, and many studies indicate that the non-additive gene action is more apparent under drought stress. The objectives of this work were to determine a) the genetic variability of parental lines, testers and their F_1- hybrids for seed cotton yield, yield components and fiber traits under drought stress and normal irrigation, b) the best hybrids and parents tolerant to drought stress, based on GCA and SCA estimates which could be used as a source material for further improvement in Egyptian cottons, c) the additive and dominance components for various traits.

Materials and Methods

The experiments of the present study were carried out at Shandaweel Research Station, Sohag Governorate, Agricultural Research Center (A.R.C), Egypt, (Longitude: 31.125 N, Latitude: 27.25 E, Elevation: 45m/148 Feet); during the two-summer seasons of 2018 and 2019. Ten genotypes were crossed as lines with three as testers in a line-tester method to give 30 F_1-hybrids.

Soil samples
Disturbed and undisturbed soil samples were collected from plots of each irrigation level at vertical depths of 0-15, 15-30, 30-45 and 45-60cm before and after irrigation. Measurement of the soil moisture content was carried out using the difference in the soil moisture content in each layer before and after irrigation using the gravimetric method. The sum of the soil moisture deficits of the four layers were added in the next irrigation to reach the field capacity.

Soil physical chemical properties
The soil physical and chemical properties were measured as the following: (1) Particle size distribution according to Gee & Bauder (1986). (2) Field capacity was determined according to Cassel & Nielsen (1986). (3) Available water was calculated from the values of field capacity and wilting point. (4) Bulk density was determined according to Blake & Hartge (1986). The soil moisture content of the experimental field i.e., field capacity, wilting point and available soil moisture were determined and were 30.69 %, 12.63%, and18.06 %, respectively. The soil was clay loamy in texture with bulk density 1.22g/cm³ and pH 7.9. Soil samples were taken from each 15cm depth up to 60cm from the ground surface. The amount of water consumed during each irrigation period was obtained from the difference

between soil moisture content before the following irrigation and that of the preceding one according to the following formula as described by Israelsen & Hansen (1962). Soil moisture constants and soil physical and chemical properties were measured and recorded in Tables 1 and 2 as follows:

Actual water consumptive use 'WCU' (Actual evapotranspiration)

Water consumptive use (actual evapotranspiration) was computed as the difference in soil moisture in the soil samples taken before and after irrigations. It was affected by the amounts and intervals of irrigation. It calculated according to the equation of Israelsen & Hansen (1962) as follows:

$$CU = D \times Bd \times \left(\frac{Q_2 - Q_1}{100}\right)$$

where: CU= Actual water consumptives use in (mm), D= Irrigation soil depth, Bd= Soil bulk density (g cm^{-3}), Q1= Soil moisture percent before next irrigation, Q2= Soil moisture percent after irrigation by 48h, CU (m^3 fed^{-1})= CU (mm) x 4.2.

To obtain the actual water consumptive use CU, the soil moisture percentage was determined gravimetrically on dry basis just before irrigation. Soil samples for moisture determination were taken from each 15cm depth up to 60cm from the soil surface by a regular auger. The samples were weighted and then oven dried. The amount of water consumed in each irrigation interval was obtained from the difference between soil content before the following irrigation and field capacity.

First season (2018)

The thirteen genotypes shown in Table 3 were sown in plots in three sowing dates, 7 days in between for crossing. Ten genotypes were crossed to three testers as shown in Table 3 using line × tester method to give 30 F$_1$ - hybrids.

Second season (2019)

The 30 hybrids and their parents (13 parents) were sown under water stress and normal irrigation conditions in a randomized complete blocks design of three replications. Each plot consisted of two rows, four-meter-long, 0.6m apart and 40cm between hills within a row. After full emergence, seedlings were thinned to one plant per hill. The normal irrigation experiment was irrigated as required, while the water stressed experiment was irrigated just before the wilting point throughout the growing season. The soil moisture percentage was determined gravimetrically on dry basis just before irrigation.

TABLE 1. Soil profile and physical analysis of the experimental site at Shandaweel Agricultural Research Station

depth (cm)	Particle distribution, %				Texture	Hydraulic conductivity, cm/h	Bulk density, gm/cm^3	Soil water content, %		
	Course sand	Fine sand	Silt	Clay				Saturation	Field capacity	Permanent wilting point
(1-15)	7.80	16.20	38.20	37.80	clay loam	2.90	1.34	56	27.60	15.50
(15-30)	6.90	15.50	39.50	38.10	clay loam	2.90	1.36	50	28	14.1
(30-45)	10.00	35.50	45.20	9.30	sandy loam	11.50	1.56	27.1	12.2	7.2
(45-60)	15.50	33.90	42.10	8.50	sandy loam	10.70	1.57	29.3	15.1	6.4

TABLE 2. Concentration of soil available macro-and micro elements, electrical conductivity (EC), pH, and calcium carbonate in the site at Shandaweel Agricultural Research Station

Season	Concentration, mg/100g soil							EC, Ds/m (1:5)	pH	N%	CaCO$_3$%
	HCO^{-3}	Cl$^-$	SO4$^=$	Ca^{++}	Mg^{++}	Na$^+$	K$^+$				
2018	0.30	0.88	1.02	0.52	0.26	1.26	0.16	0.263	7.3	0.20	1.26
2019	0.26	0.79	1	0.50	0.24	1.17	0.14	0.246	7.8	0.17	1.41

Actual water consumptive use 'WCU' (Actual evapotranspiration)

TABLE 3. Name of lines and testers were used in this study

Genotype	Used as	Genotype	Used as
Giza 95	Tester	Krashinki	Line
Dandara	Tester	Giza 90×Australian	Line
Australian	Tester	(A)- [(Giza 91 ˣ Giza 90) ˣ Giza 80]	Line
Giza 80	Line	(B)- [(Giza 90 ˣ Australian) × Giza 85]	Line
Giza 83	Line	(C)- [(Giza 90 ˣ Australian) ˣ {(Giza 83×Giza 72) ˣ Dandara}]	Line
Giza 85	Line	(D)- [(Giza 90 ˣ Australian) ˣ {(Giza 83×Giza 75) ˣ 5584}]	Line
Ashmouni	Line	-	

At flowering, days to first flower (DFF) was recorded for five plants/row. Before picking, 10 open sound bolls were picked from each plot to measure boll weight (BW, g). Bolls/plant (NB/P) was counted for ten guarded plants in each plot. Seed cotton yield (SCY/P, g) was determined for each plot. After ginning, lint% was calculated. The technological properties were determined for a mixed sample from each replicate. The Micronaire reading (MR), fiber strength as Pressley index (PI) and Upper half mean length (UHM, mm) were measured by the H.V.I instrument (a testing machine capable of measuring many cotton fiber properties including length, uniformity, Micronaire/fineness, strength, color, etc..)

Statistical analysis

The analysis of variance and significance tests were performed on plot mean basis as outlined by Steel et al. (1997). The line-tester analysis was performed as outlined by Singh & Chaudhary (1985). The data were analyzed using MS Excel 2016.

Results and Discussion

Line tester analysis

Mean squares was significant (P≤ 0.01) for genotypes of all the investigated traits under both environments, indicating the presence of variability among hybrids and their parents, hence the analysis for combining ability was possible (Table 4). The total genetic variability was partitioned to general and specific combining abilities and translated to the additive and dominance variances. Furthermore, mean squares of the parents, crosses, parents vs crosses, lines, testers, and lines ˣ testers for all the studied traits under both environments was significant (P≤ 0.01) except for testers for lint% under drought stress indicating that both additive and non-additive effects of genes controlled the characters. The significant (P≤ 0.01)

mean squares of parent's vs crosses reflects the high level of heterozygosity, in other words non-additive gene actions in the inheritance of these traits, in consequence heterosis. But the heterotic effects were not calculated, because of the hybrid vigor in cotton does not exploited commercially worldwide till now. These results are in line with those noted by Mahrous (2018) and Ullah et al. (2019).

Means of the parents for all traits under both environments are shown in Table 5. Giza 95 gave the best performance for SCY/P, lint%, and BW under both environments. Lint yield/plant behaved as SCY/P in all the analysis and was omitted from the tables. None of the parents was superior in all traits. The best performance in the other traits was distributed among the parents. The drought stress caused great reduction in all traits for all parents.

Mean SCY/P of the lines was 91.44g and the males mean was 96.52g with hybrid mean of 103.44g indicating the presence of non-additive effects and heterosis under normal irrigation. The same trend was observed under drought stress, and for lint%, BW, DFF, Micronaire reading, fiber length and strength under both environments.

The high positive GCA effects are preferable for all traits except DFF and Micronaire reading in which the negative GCA is desirable. The line 'G90 ˣ Aus' showed the highest GCA effects (P≤0.01) for SY/P, lint%, and fiber length (UHM) under both environments and BW under the normal environment (Table 5). This line could be considered the good combiner for these traits. The line A-genotype was the good combiner for NB/P for both environments. The good combiner for DFF was the line Karashiniki, and the lines C– and A-genotypes for Micronaire reading, line D for fiber strength (PI) under both environments. The line 'G.90 ˣ Aust.' showed the best performance of

SCY/P was 110.90 and 73.80g/plant, and for lint% was 38.87 and 37.93% at normal and stressed environments, respectively, and 36.18 for NB/P at stressed environment and 2.87g for BW under normal environment. Concern the tester lines, G.95 was the best combiner for NB/P, Aust. for SCY/P, BW and DFF under both environments. There was no line or tester depicted to be the good combiner for all traits.

The SCA effects was positive and significant for the hybrids of two parents or at least one parent has positive GCA effect in most cases under normal irrigation and drought stress, indicating that additive and non-additive effects of genes control this trait. On top of that, some hybrids had an SCA effects in reverse their direction in their respective parents. For example, the hybrid [Aust. × (G.90 × Aust)] exhibited negative SCA effects (P≤0.01) for SCY/P under both environments in reverse of the significant (P≤0.01) GCA effects of its parents, also the hybrid [G.95 × C (-3.203)] under normal environment for NB/P, [Dandara × G.83] and [Dandara × G.85] under stress, [G95 × C] under both environments for lint%, [G95 × (G90 × Aust.)] under the two environments for

DFF, all these hybrids and others in all traits, their SCA effects were in the reverse directions of their respective parents. These findings confirmed the preponderance of the non-additive effects in the inheritance of these traits. Abdel-Monaem et al. (2018) indicated that the variance due to general combining ability (GCA) was lower than specific combining ability (SCA) for all the studied characters indicating that all traits controlled by non-additive gene action. Mahrous (2018) noted that the non-additive of genetic variance was larger than additive genetic variance in all yield traits, and the additive genetic variance was higher than the dominance variance for all fiber quality traits. Sultan et al. (2018) illustrated that the variance due to general combining ability was lower than that of specific combining ability and the ratio of s^2 GCA / s^2 SCA was less than unity for all the studied traits indicating preponderance of non–additive gene action (dominance and epistasis). Ullah et al. (2019) found that the variance due to specific combining ability was greater as compared to the general combining ability variance for all the traits indicating the dominant role of non-additive genes under normal and drought condition.

TABLE 4. Mean squares of line tester analysis under normal irrigation (N) and drought stressed (S) environments

S.O.V.	d.f.	SCY/P		NB/P		Lint%		BW	
		N	S	N	S	N	S	N	S
Reps	2	13.85	1.64	1.64	8.41**	1.16	1.58	0.04	0.002
Genotypes	42	980.43**	39.06**	39.06**	60.09**	8.43**	9.20**	0.32**	0.27**
Parents(P)	12	784.65**	42.90**	42.90**	66.96**	8.53**	11.58**	0.14**	0.13**
Crosses(C)	29	985.24**	37.05**	37.05**	54.30**	7.11**	5.60**	0.24**	0.21**
P vs C	1	3190.14**	51.18**	51.18**	145.39**	45.55**	85.00**	4.93**	3.56**
Lines(L)	9	1451.03**	44.23**	44.23**	66.45**	12.44**	10.09**	0.39**	0.33**
Testers(T)	2	19991.40**	69.37**	69.37**	128.14**	14.09**	0.51	0.60**	0.43**
L×T	18	940.56**	29.86**	29.86**	40.02**	3.67**	3.93**	0.12**	0.13**
Error	84	17.80	1.90	1.90	3.92	0.44	0.54	0.006	0.005

S.O.V.	d.f.	DFF		Mic.		Length (UHM)		Strength (PI)	
		N	S	N	S	N	S	N	S
Reps	2	2.11	1.49	0.02	0.02	1.01	0.11	0.02	0.02
Genotypes	42	64.56**	48.42**	0.50**	0.26**	20.87**	19.49**	1.70**	1.33**
Parents(P)	12	61.63**	24.52**	0.59**	0.34**	25.59**	13.01**	1.41**	0.89**
Crosses(C)	29	64.17**	57.17**	0.48**	0.20**	15.08**	18.24**	1.87**	1.53**
P vs C	1	110.89**	81.42**	0.11**	0.98**	132.01**	133.42**	0.003	0.86**
Lines(L)	9	64.74**	43.97**	0.69**	0.23**	18.32**	18.97**	3.43**	2.36*
Testers(T)	2	549.87**	506.34**	2.73**	1.02**	89.89**	112.98**	9.02**	9.24**
L×T	18	9.92**	13.86**	0.12**	0.10**	5.15**	7.34**	0.30**	0.26**
Error	84	0.72	1.67	0.009	0.005	0.41	0.28	0.007	0.007

*, **; Significant at 0.05 and 0.01 levels of probability; respectively. SCY/P: Seed cotton yield, g; NB/P: Numbers of bolls /plant; BW: Boll weight, g; DFF: Days to first flowers; Mic: Micronaire reading; length, (UHM, mm), strength (Pressley index).

TABLE 5. Means, estimates of general combining ability effects for males and female lines, and specific combining ability effects of the hybrids for the studied traits under normal irrigation (N) and drought stress (S) conditions

Genotypes	SCY/P, g				NB/P			
	Means (N)	GCA (N)	Means (S)	GCA (S)	Means (N)	GCA (N)	Means (S)	GCA (S)
Female (Lines)								
G.80	97.70	-11.988**	69.80	-10.172**	38.06	-2.856**	35.66	-3.681**
G.83	105.60	-15.743**	71.40	-13.906**	38.65	-1.947**	32.03	-3.045**
G.85	95.10	5.257**	62.87	6.517**	34.17	-0.030	30.47	0.782
G.90 × Aust.	110.90	19.112**	73.80	16.717**	38.69	2.137**	36.18	3.153**
Ashmouni	81.77	-9.354**	51.70	-7.283**	33.18	-1.636**	24.25	-1.118
Krashinki	86.03	1.946	48.80	-0.061	33.95	-0.099	26.97	-0.014
A - genotype	101.80	14.290**	72.40	14.150**	39.26	3.13**	30.19	3.512**
B - genotype	90.63	8.723**	64.27	6.217**	35.84	2.555**	28.32	2.653**
C - genotype	67.50	4.368**	50.15	2.783*	27.73	1.361**	25.49	1.109
D - genotype	77.40	-16.610**	55.20	-14.961**	30.65	-2.617**	26.72	-3.350**
Famale Mean	91.44		62.04		35.02	-	30.13	-
S.E.(GCA)L	-	1.4059	-	1.2557	-	0.4595	-	0.6605
S.E.(gi-gi)	-	1.9883	-	1.7759	-	0.6499	-	0.9342
Male testers								
G.95	126.63	3.990**	85.33	4.026**	39.18	1.390**	34.14	1.874**
Aust.	74.90	5.383**	53.40	4.246**	30.78	0.234	27.35	0.343
Dandara	88.03	-9.373**	60.50	-8.271**	32.82	-1.624**	27.55	-2.217**
Male mean	96.52	-	66.41	-	34.26	-	29.68	-
S.E.(GCA)T	-	0.7700	-	0.6878	-	0.2517	-	0.3618
S.E.(gi-gi)	-	1.0890	-	0.9727	-	0.3559	-	0.5116
Crosses								
G.95 × G.80	103.57	8.121**	71.83	8.886**	32.70	0.697	27.12	1.216
G.95 × G.83	96.70	5.010*	64.77	5.552*	33.35	0.437	25.56	-0.979
G.95 × G.85	112.03	-0.657	80.07	0.430	34.30	-0.536	29.65	-0.714
G95 × (G.90×Aust.)	134.47	7.921**	93.90	4.063	38.05	1.053	33.16	0.424
G.95 × Ashmouni	89.67	-8.412**	59.00	-6.837**	32.03	-1.194	27.23	-1.235
G.95 × Karashinki	93.53	-15.846**	60.03	-13.026**	31.55	-3.213**	26.51	-3.063**
G.95 × A	125.03	3.310	90.47	3.197	37.15	-0.847	33.33	0.234
G.95 × B	118.30	2.143	79.93	0.597	38.18	0.764	33.81	1.574**
G.95 × C	91.30	-20.501**	57.17	-18.737**	33.02	-3.203**	26.80	-3.893**
G.95×D	109.73	18.910**	74.03	15.874**	38.29	6.042**	32.67	6.436**
Aust. × G.80	94.67	-2.172	61.93	-1.234	32.27	1.425	25.45	1.071
Aust. × G.83	80.67	-12.417**	47.63	-11.801**	29.86	-1.897*	22.72	-2.293*
Aust. × G.85	106.77	-7.317**	73.20	-6.657**	31.43	-2.242**	26.79	-2.052
Aust. × (G.90 × Aust.)	117.80	-10.139**	81.10	-8.957**	32.72	-3.120**	28.14	-3.073**
Aust. × Ashmouni	121.30	21.828**	86.97	20.910**	36.41	4.338**	32.82	5.880**
Aust. × Karashinki	129.77	18.994**	88.83	15.557**	36.38	2.776**	31.19	3.148**
Aust. × A	104.50	-18.617**	71.87	-15.623**	34.81	-2.026*	28.74	-2.826*
Aust. × B	122.80	5.250*	84.37	4.810*	37.21	0.952	31.44	0.733
Aust. × C	126.60	13.406**	87.70	11.577**	36.87	1.805*	30.96	1.795
Aust. × D	83.40	-8.817**	49.80	-8.579**	29.08	-2.010*	22.32	-2.383*
Dandara×G.80	76.13	-5.949*	43.00	-7.651**	26.87	-2.121**	19.53	-2.287*
Dandara×G.83	85.73	7.407**	53.17	6.249**	31.36	1.460	25.72	3.272**
Dandara×G.85	107.30	7.973**	73.57	6.227**	34.60	2.778**	29.04	2.766*
Dandara×(G.90×Aust.)	115.40	2.218	82.43	4.897*	36.05	2.066*	31.30	2.649*
Dandara × Ashmouni	71.30	-13.416**	39.47	-14.073**	27.07	-3.143**	19.73	-4.645**
Dandara × Karashinki	92.87	-3.149	58.23	-2.529	32.19	0.437	25.40	-0.085
Dandara × A	123.67	15.307**	87.40	12.427**	37.85	2.873**	31.60	2.592*
Dandara × B	95.40	-7.393**	61.63	-5.407*	32.69	-1.715*	25.84	-2.307*
Dandara × C	105.53	7.096**	70.77	7.160**	34.61	1.398	28.70	2.098
Dandara × D	67.37	-10.093**	38.57	-7.296**	25.20	-4.032**	18.09	-4.053**
Hybrid mean	103.44		69.09	-	33.47	-	27.71	-
S.E.SCA	-	2.4352	-	2.1750	-	0.7960	-	1.1441
S.E.(sij-skl)	-	3.4439	-	3.0760	-	1.1257	-	1.6181
LSD 0.05	6.82	-	6.09	-	2.23	-	3.20	-
LSD 0.01	9.02	-	8.05	-	2.95	-	4.23	-

TABLE 5. Cont.

Genotypes	Lint%				BW, g			
	Means (N)	GCA (N)	Means (S)	GCA (S)	Means (N)	GCA (N)	Means (S)	GCA (S)
Female (Lines)								
G.80	37.16	0.258	37.29	.-0.561*	2.57	-0.094**	1.97	-0.0039
G.83	37.12	0.279	34.34	-1.089**	2.73	-0.294**	2.23	-0.234**
G.85	38.04	0.021	37.13	0.434	2.78	0.184**	2.07	0.188**
G.90 × Aust.	38.87	1.876**	37.93	1.303**	2.87	0.373**	1.80	0.316**
Ashmouni	36.94	-1.455**	33.82	0.145	2.47	-0.010**	2.13	-0.195**
Krashinki	34.86	-2.405**	34.14	-1.717**	2.53	0.067*	1.80	0.005
A - genotype	38.39	0.367	35.58	0.977**	2.60	0.139**	2.40	0.194**
B - genotype	38.07	-0.110	36.07	0.850**	2.53	0.034	2.27	0.011
C - genotype	35.06	0.751**	36.85	0.830**	2.43	0.011	1.97	0.011
D - genotype	35.13	0.417	37.55	-1.172**	2.53	-0.270**	2.07	-0.256**
Famale Mean	36.96	-	36.07	-	2.61	-	2.07	-
S.E.(GCA)L	-	0.2230	-	0.2450		0.0268		0.0247
S.E.(gi-gi)	-	0.3154	-	0.3465		0.0379		0.03501
Male testers								
G.95	40.64	0.32²*	39.69	0.014	3.23	0.001	2.50	-0.004
Aust.	36.32	-0.787**	34.52	0.123	2.43	0.141**	1.97	0.123**
Dandara	35.95	0.465**	32.90	-0.137	2.68	-0.143**	2.20	-0.119**
Male mean	37.65	-	35.70	-	2.78	-	2.22	-
S.E.(GCA)T		0.1221		0.1342		0.0147		0.0135
S.E.(gi-gi)		0.1727		0.1897		0.0208		0.0191
Crosses								
G.95 × G.80	39.5	0.054	37.60	0.389	3.17	0.187**	2.65	0.226**
G.95 × G.83	38.92	-0.092	37.46	0.785	2.90	0.121*	2.53	0.304**
G.95 × G.85	37.67	-1.086**	38.85	0.647	3.27	0.010	2.70	0.048
G95 × (G.90×Aust.)	41.58	0.965*	38.56	-0.512	3.53	0.087	2.83	0.054
G.95 × Ashmouni	38.30	1.017*	36.27	-1.638**	2.80	-0.124**	2.17	-0.102*
G.95 × Karashinki	36.78	0.446	36.51	0.458	2.97	-0.174**	2.27	-0.202**
G.95 × A	40.40	1.295**	38.64	-0.101	3.37	0.154**	2.72	0.059
G.95 × B	38.04	-0.592	39.36	0.746	3.10	-0.007	2.37	-0.107*
G.95 × C	37.57	-1.917**	37.14	-1.462**	2.77	-0.318**	2.13	-0.341**
G.95×D	39.06	-0.090	37.28	0.687	2.87	0.063	2.27	0.059
Aust. × G.80	39.19	1.299**	37.52	0.207	2.93	-0.186**	2.43	-0.117**
Aust. × G.83	37.00	-0.908*	34.85	-1.937**	2.70	-0.219**	2.10	-0.256**
Aust. × G.85	38.85	1.196**	38.21	-0.100	3.40	0.003	2.73	-0.045
Aust. × (G.90 × Aust.)	38.49	-1.019**	38.30	-0.878*	3.60	0.014	2.88	-0.023
Aust. × Ashmouni	35.54	-0.629	38.75	0.727	3.33	0.270**	2.65	0.255**
Aust. × Karashinki	34.79	-0.437	37.26	1.103*	3.57	0.286**	2.85	0.255**
Aust. × A	36.65	-1.347**	39.28	0.430	3.00	-0.353**	2.50	-0.284**
Aust. × B	37.63	0.017	38.76	0.029	3.30	0.053	2.68	0.083
Aust. × C	39.73	1.352**	39.76	1.048*	3.43	0.209**	2.83	0.233**
Aust. × D	38.43	0.385	36.08	-0.628	2.87	-0.077	2.23	-0.101*
Dandara×G.80	37.79	-1.353**	36.46	-0.596	2.83	-0.002	2.20	-0.109*
Dandara×G.83	40.16	1.000*	37.68	1.152*	2.73	0.098*	2.07	-0.048
Dandara×G.85	38.79	-0.110	37.50	-0.547	3.10	-0.013	2.53	-0.003
Dandara×(G.90×Aust.)	40.81	0.054	40.31	1.390**	3.20	-0.102*	2.63	-0.031
Dandara × Ashmouni	37.04	-0.388	38.67	0.911*	2.63	-0.146**	2.00	-0.153**
Dandara × Karashinki	36.47	-0.009	34.34	-1.561**	2.88	-0.113*	2.30	-0.053
Dandara × A	39.30	0.052	38.26	-0.329	3.27	0.198**	2.77	0.224**
Dandara × B	39.26	0.484	37.69	-0.775	2.92	-0.046	2.38	0.024
Dandara × C	40.20	0.565	38.86	0.414	3.05	0.110*	2.47	0.108*
Dandara × D	39.00	-0.295	36.39	-0.059	2.67	0.014	2.13	0.041
Hybrid mean	38.42	-	37.75	-	3.07	-	2.47	-
S.E.SCA	-	0.3863	-	0.4243	-	0.0465	-	0.0428
S.E.(sij-skl)	-	0.5463		0.6001	-	0.0657	-	0.0606
LSD 0.05	1.07	-	1.19	-	0.13	-	0.11	-
LSD 0.01	1.42	-	1.57	-	0.17	-	0.15	-

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TABLE 5. Cont.

Genotypes	DFF				Mic			
	Means (N)	GCA (N)	Means (S)	GCA (S)	Means (N)	GCA (N)	Means (S)	GCA (S)
Female (Lines)								
G.80	68.00	-1.956**	59.33	-0.978**	4.63	0.071*	3.65	-0.017
G.83	66.67	-3.067**	56.67	-2.422**	4.40	0.038	3.32	0.105**
G.85	66.00	-0.299	58.00	0.467	4.37	-0.129**	3.47	-0.039
G.90 ⤬ Aust.	67.00	-1.844**	55.33	-1.533**	3.73	-0.129**	3.08	-0.056*
Ashmouni	71.00	3.267**	62.00	2.911**	4.90	0.282**	3.63	0.161**
Krashinki	58.00	-4.289**	52.67	-3.756**	4.67	0.504**	3.93	0.316**
A - genotype	66.33	2.822**	58.67	2.689**	3.67	-0.440**	3.26	-0.278**
B - genotype	68.33	1.044**	56.00	-0.200**	3.80	-0.151**	2.88	-0.023
C - genotype	64.33	1.600**	55.00	2.022**	3.47	-0.251**	3.85	-0.089**
D - genotype	69.67	2.711**	60.00	0.800**	4.20	0.204**	4.06	-0.078**
Famale Mean	66.53	-	57.37	-	4.18	-	3.51	-
S.E.(GCA)	-	0.2842	-	0.4318	-	0.0331	-	0.0242
S.E.(gi-gi)	-	0.4020	-	0.6107	-	0.0469	-	0.0342
Male testers								
G.95	62.00	-0.865**	53.00	-0.522*	3.90	-0.006	3.68	0.015
Aust.	56.00	-3.789**	57.00	-3.822**	4.30	0.304**	3.46	0.177**
Dandara	70.00	4.644**	53.30	4.344**	4.53	-0.299**	3.71	-0.192**
Male mean	59.33	-	54.33	-	4.24	-	3.62	-
S.E.(GCA)	-	0.15571	-	0.2365	-	0.0181	-	0.0132
S.E.(gi-gi)		0.2202		0.3345		0.0257		0.0187
Crosses								
G.95 ⤬ G.80	60.00	-0.811	55.00	-1.922*	4.27	-0.061	3.80	0.074
G.95 ⤬ G.83	58.33	-1.367**	53.67	-1.811*	4..50	0.206**	3.97	0.118**
G.95 ⤬ G.85	62.00	-0.478	57.67	-0.700	4.40	0.272**	3.87	0.163**
G95 ⤬ (G.90×Aust.)	64.33	3.411**	59.33	2.967**	4.10	-0.028	3.63	-0.054
G.95 ⤬ Ashmouni	66.00	-0.033	61.33	0.522	5.57	0.028	3.90	-0.004
G.95 ⤬ Karashinki	58.67	0.189	53.00	-1.144	4.80	0.039	4.00	-0.059
G.95 ⤬ A	63.33	-2.256**	58.33	-2.256**	3.70	-0.117*	3.40	-0.065
G.95 ⤬ B	63.67	-0.144	58.67	0.967	3.87	-0.239**	3.53	-0.187**
G.95 ⤬ C	65.33	0.967	60.67	0.744	4.03	0.028	3.60	-0.054
G.95×D	66.00	0.522	61.33	2.633**	4.33	0.128*	3.73	0.068
Aust. ⤬ G.80	57.00	-0.878	52.62	-0.956	4.73	0.096	4.07	0.179**
Aust. ⤬ G.83	56.67	-0.100	52.33	0.156	4.77	0.162**	4.17	0.157**
Aust. ⤬ G.85	58.00	-1.544**	53.33	-1.733*	4.23	-0.204**	3.70	-0.166**
Aust. ⤬ (G.90 ⤬ Aust.)	56.00	-1.989**	52.00	-1.067	4.37	-0.071	3.80	-0.049
Aust. ⤬ Ashmouni	62.33	-0.767	57.33	-0.178	4.60	-0.249**	3.93	-0.132**
Aust. ⤬ Karashinki	56.33	0.789	52.67	1.822*	4.87	-0.204**	4.13	-0.088*
Aust. ⤬ A	65.00	2.344**	60.00	2.711**	4.30	0.173**	3.72	0.090*
Aust. ⤬ B	61.33	0.456	56.00	1.600*	4.70	0.284**	4.18	0.301**
Aust. ⤬ C	61.00	-0.433	55.33	-1.289	4.20	-0.116*	3.78	-0.032
Aust. × D	64.67	2.122**	54.33	-1.067	4.90	0.129*	3.57	0.260**
Dandara⤬G.80	68.00	1.689**	64.67	2.878**	4.00	-0.034	3.27	-0.253**
Dandara⤬G.83	66.67	1.467**	62.00	1.656*	3.63	-0.368**	3.37	-0.275**
Dandara⤬G.85	70.00	2.022**	65.67	2.433*	3.77	-0.068	3.50	0.003
Dandara⤬(G.90×Aust.)	65.00	-1.422**	59.33	-1.900*	3.93	0.099	3.58	0.103*
Dandara ⤬ Ashmouni	72.33	0.800	65.33	-0.344	4.47	0.221**	3.83	0.136**
Dandara ⤬ Karashinki	63.00	-0.988	58.33	-0.678	4.63	0.166**	4.00	0.147**
Dandara ⤬ A	71.00	-0.089	65.00	-0.456	3.47	-0.057	3.23	-0.025
Dandara ⤬ B	69.00	-0.311	60.00	-2.567**	3.77	-0.046	3.40	-0.114**
Dandara ⤬ C	69.33	-0.533	65.33	0.544	3.80	0.088	3.53	0.086*
Dandara × D	68.33	-2.644**	62.00	-1.567*	4.17	-0.001	3.65	0.192**
Hybrid mean	63.62	-	58.42	-	4.26	-	3.73	-
S.E.SCA	-	0.4924	-	0.7480	-	0.0469	-	0.0419
S.E.(sij-skl)	-	0.6963	-	1.0578	-	0.0813	-	0.0593
LSD 0.05	1.37	-	2.09	-	0.15	-	0.11	-
LSD 0.01	1.81	-	2.76	-	0.20	-	0.15	-

TABLE 5. Cont.

Genotypes	Length, (UHM)				Strength (PI)			
	Means (N)	GCA (N)	Means (S)	GCA (S)	Means (N)	GCA (N)	Means (S)	GCA (S)
Female (Lines)								
G.80	32.07	-0.330	29.07	-0.292	10.20	-0.184**	9.40	-0.082**
G.83	30.10	-0.519*	27.87	-0.492**	10.40	-0.307**	9.70	-0.182**
G.85	32.40	-0.052	29.77	0.797**	9.90	-0.151**	9.10	-0.104**
G.90 × Aust.	26.27	2.114**	24.50	2.241**	9.17	0.227**	8.60	0.118**
Ashmouni	28.63	-2.541**	26.63	-2.748**	9.03	-0.718**	8.40	-0.627**
Krashinki	25.03	-1.930**	23.90	-1.848**	8.83	-1.107**	8.63	-0.949**
A - genotype	31.03	1.348**	27.97	0.597**	10.90	0.227**	9.60	0.173**
B - genotype	33.37	0.481*	29.33	1.074**	9.97	0.471**	8.93	0.384**
C - genotype	27.20	1.048**	25.73	0.719**	10.63	0.649**	9.93	0.518**
D - genotype	29.93	0.381	28.20	-0.048	9.73	0.893**	9.03	0.751**
Female Mean	29.60	-	27.30	-	9.88	-	9.13	-
S.E.(GCA)	-	0.2137	-	0.1785	-	0.0296	-	0.0278
S.E.(gi-gi)	-	0.3022	-	0.2524	-	0.0419	-	0.0394
Male testers								
G.95	32.37	1.176**	30.63	1.576**	9.50	0.154**	8.70	0.197**
Aust.	28.40	-1.988**	26.73	-2.168**	9.80	-0.609**	9.73	-0.627**
Dandara	24.60	0.812**	25.43	0.592**	8.70	0.454**	8.30	0.430**
Male mean	28.46	-	27.60	-	9.33	-	8.91	-
S.E.(GCA)	-	0.1170	-	0.0977	-	0.0162	-	0.0152
S.E.(gi-gi)	-	0.1655	-	0.1382	-	0.0229	-	0.0216
Crosses								
G.95 × G.80	31.83	-0.553	30.70	-0.164	9.70	-0.032	9.33	-0.041
G.95 × G.83	31.40	-0.798*	29.87	-0.798*	9.53	-0.077	9.27	-0.008
G.95 × G.85	32.47	-0.198	31.43	-0.520	9.80	0.034	9.40	0.048
G95 × (G.90×Aust.)	35.20	0.369	32.80	-0.598	10.07	-0.077	9.60	0.026
G.95 × Ashmouni	29.77	-0.409	27.90	-0.509	9.33	0.134*	8.90	0.070
G.95 × Karashinki	33.47	2.680**	31.37	2.058**	8.90	0.090	8.60	0.092
G.95 × A	33.87	-0.198	31.73	-0.020	9.97	-0.177**	9.50	-0.130**
G.95 × B	33.07	-0.131	31.87	-0.364	10.30	-0.088	9.77	-0.074
G.95 × C	34.03	0.269	32.63	0.758*	10.60	0.034	10.00	0.026
G.95×D	32.07	-1.031**	31.27	0.158	10.97	0.157**	10.20	-0.008
Aust. × G.80	28.70	-0.523	26.03	-1.088**	8.83	-0.136**	8.50	-0.051
Aust. × G.83	28.00	-1.034**	25.80	-1.121**	8.70	-0.147**	8.23	-0.218**
Aust. × G.85	29.00	-0.501	27.47	-0.743*	8.63	-0.369**	8.13	-0.396**
Aust. × (G.90 × Aust.)	31.77	0.099	29.90	0.246	9.17	-0.213**	8.47	-0.284**
Aust. × Ashmouni	27.57	0.554	25.47	0.801*	8.93	0.498**	8.40	0.393**
Aust. × Karashinki	27.03	-0.590	26.03	0.468	8.50	0.453**	8.10	0.416**
Aust. × A	30.13	-0.768*	26.80	-1.210**	9.37	-0.013	8.70	-0.107*
Aust. × B	30.33	0.299	28.30	-0.188	9.57	-0.058	8.93	-0.084
Aust. × C	30.67	0.066	28.20	0.068	9.87	0.064	9.37	0.216**
Aust. × D	32.33	2.399**	30.13	2.768**	9.97	-0.080	9.50	0.116*
Dandara×G.80	33.10	1.077**	31.13	1.252**	10.20	0.168**	9.70	0.092
Dandara×G.83	33.67	1.832**	31.60	1.919**	10.13	0.223**	9.73	0.226**
Dandara×G.85	33.00	0.699	32.23	1.263**	10.40	0.334**	9.93	0.348**
Dandara×(G.90×Aust.)	34.00	-0.468	32.77	0.352	10.73	0.290**	10.07	0.259**
Dandara × Ashmouni	29.67	-0.146	27.13	-0.292	8.87	-0.632**	8.60	-0.463**
Dandara × Karashinki	28.33	-2.090**	25.80	-2.526**	8.57	-0.543**	8.23	-0.508**
Dandara × A	34.67	0.966*	32.00	1.230**	10.63	0.190**	10.10	0.237**
Dandara × B	32.67	-0.168	31.80	0.552	10.83	0.146**	10.23	0.159**
Dandara × C	33.07	-0.334	30.07	-0.826*	10.77	-0.099	9.97	-0.241**
Dandara × D	31.37	-1.368**	27.20	-2.926**	11.03	-0.077	10.33	-0.108*
Hybrid mean	31.34	-	29.58	-	9.76	-	9.26	-
S.E.SCA	-	0.3702	-	0.3092	-	0.0514	-	0.0483
S.E.(sij-skl)	-	0.5235	-	0.4373	-	0.0727	-	0.0683
LSD 0.5	1.04	-	0.86	-	0.14	-	0.14	-
LSD 0.1	1.37	-	1.13	-	0.18	-	0.18	-

G: Giza, N: Normal irrigation, S: Drought stress, SCY/P: Seed cotton yield, g, NB/P: Numbers of bolls /plant, BW: Boll weight, g, DFF: Days to first flowers, Mic.: Micronaire reading, length, (UHM), strength (Pressley Index).

The hybrids of the best performance were [G95 × (G90 × Aust.)] (134.47 and 93.90g/p) for SCY/P, [Dandara × (G90 × Aust.)] (40.81and 40.31%) for lint%, [Aust. × (G90 × Aust.)](3.6 and 2.88g) for BW, [Aust. × (G90 × Aust.)] (56.00and 52.00) for DFF, [Dandara × G.83] (3.63 and 3.37) for Micronaire reading, [G95 × (G90 × Aust.)] (35.20 and 32.80 mm) for UHM length under normal and stressed environments, respectively, [G95 × D (38.29)] for NB/P under normal and [G95 × B (33.81)] under stress, [G.95 × D] (10.97 PI) under normal and [Dandara × D] (10.33PI) for fiber strength. It could be noticed that except for fiber strength and Micronaire reading the two hybrids [G95 × (G90 × Aust.)] and [Aust. × (G90 × Aust.)] were the best hybrids for most studied traits and should be considered in breeding program for drought stress and normal irrigation and the parents G.95, (G95 × Aust.) and Aust. depicted their good combining ability.

The reduction % caused by drought effects

The reduction% of parents and crosses for the studied traits are shown in Table 6. Low reduction% for a genotype means, this is due to tolerant these genotypes to drought stress, and high means susceptible to drought stress. Mean reduction% of the parents varied greatly from 2.99 for lint% to 31.79 for SCY/P, while it varied for the hybrids from 5.11for fiber strength to 33.93 for SCY/P. The most tolerant parent was C-genotype and the most susceptible was Karashinki for SCY/P. Respect lint% the tolerant parent was D-genotype and the susceptible one was Dandara. The tolerance of the parents varied from trait to another. Likewise, none of the hybrids was tolerant for all traits. Hence, the important thing is not the reduction%, but the performance of the parent or the hybrid under optimal and drought conditions. These results agree with those reported by Mohamed et al. (2009), Soomro et al. (2012b), Zhang et al. (2012), Prakash et al. (2018), Vasconcelos et al. (2018), Veesar et al. (2018) and Mahmood et al. (2021).

The role of additive and non-additive gene effects in the inheritance of different traits

The additive variance (σ^2A) was larger under normal irrigation than under water stress conditions for seed cotton yield, lint percentage, boll weight, days to first flower, fiber fineness and fiber strength, however, it was larger under water stress for number of bolls/plants, and fiber length (Table 7). The dominance variance (σ^2D) was larger at normal irrigation than at water stress conditions for seed cotton yield, number of bolls /plants, fiber fineness, fiber length and fiber strength however, it was larger under drought stress for boll weight, and days to first flowers.

The ratio σ^2A/σ^2D was less than unity for all traits indicating that the role of dominance was more important than additive effects in the inheritance of these traits. Therefore, the performance of the hybrids could not be expected from their GCA effects of the parents. Furthermore, σ^2A was not significant in many cases indicating the importance of dominance or non-additive in the inheritance of these traits in these materials. Rehman et al. (2017) noted predominance of non-additive genetic effects in the inheritance of the characters studied. Kannan & Saravanan (2016) found that ratio of variance due to GCA to that of SCA was less than one for all the character under study indicating importance of dominance gene effects in the inheritance of all characters. Javaid et al. (2014) revealed that variance due to specific combining ability was significant for seed cotton yield, number of bolls and boll weight signifying the importance of non-additive gene action. Basal et al. (2011) noted significant GCA and SCA mean squares for all the traits, however, non-additive gene action was predominant.

Contribution of lines, testers, and their interaction to total variance

The sum of squares of the crosses was divided to sum of squares due to lines, testers and their interaction and presented in Table 8. The proportional contribution of lines was larger than that of testers for all traits except for DFF and fiber length at both environments, and for Micronaire reading under drought stress. Furthermore, the contribution of lines was larger than that of lines x testers interaction in all characters except for NB/P at both environments indicating the importance of selection of lines for hybridization. The contribution of line x tester was about 40% for yield and NB/P depicting the importance of non-additive type of gene action. These results are in accordance with those reported by Ullah et al. (2019) and Mahmood et al. (2021).

TABLE 6. Reduction% caused by drought stress for parent and hybrids for all traits

Genotypes	Reduction%							
	SCY/P	NB/P	Lint %	BW	DFF	MIC	UHM	PI
Females								
G.80	28.56	6.30	-0.34	23.38	12.75	21.22	9.36	7.84
G.83	32.39	17.13	7.49	18.29	15.00	24.62	7.42	6.73
G.85	33.89	10.83	2.38	25.75	12.12	20.48	8.13	8.08
G.90 ˣAust.	33.45	6.49	2.43	37.21	17.41	17.41	6.73	6.18
Ashmouni	36.77	26.89	8.44	13.51	12.68	25.85	6.98	7.01
Karashinki	43.28	20.56	2.08	28.95	9.20	15.83	4.53	2.26
A	28.88	23.10	7.31	7.69	11.56	11.06	9.88	11.93
B	29.09	20.97	5.25	10.53	18.05	24.12	12.09	10.37
C	25.70	8.09	-5.10	19.18	14.51	-11.06	5.39	6.58
D	28.68	12.85	-6.89	18.42	13.88	3.31	5.79	7.19
Males								
G.95	32.61	12.85	2.35	-12.11	14.52	5.56	5.36	8.42
Aust.	31.28	16.07	4.04	18.93	23.81	19.51	5.87	0.68
Dandara	28.70	11.16	9.41	17.91	-1.79	18.26	-3.39	4.60
Parental mean	31.79	13.87	2.99	17.51	13.36	15.09	6.47	6.76
Crosses								
G.95 ˣ G.80	30.64	17.07	3.72	16.32	8.33	10.94	3.56	3.78
G.95 ˣ G.83	33.02	23.35	3.75	12.64	8.00	11.85	4.88	2.80
G.95 ˣ G.85	28.53	13.53	-3.12	17.35	6.99	12.12	3.18	4.08
G95 ˣ (G.90×Aust.)	30.17	12.84	7.26	19.81	7.77	11.38	6.82	4.64
G.95 ˣ Ashmouni	34.20	14.98	5.29	22.62	7.07	14.60	6.27	4.64
G.95 ˣ Karashinki	35.82	15.97	0.73	23.60	9.66	16.67	6.27	3.37
G.95 ˣ A	27.65	10.27	4.34	19.31	7.89	8.11	6.30	4.68
G.95 ˣ B	32.43	11.43	-3.49	23.66	7.85	8.62	3.63	5.18
G.95 ˣ C	37.39	18.83	1.16	22.89	7.14	10.74	4.11	5.66
G.95 ˣ D	32.53	14.66	4.56	20.93	7.07	13.85	2.49	6.99
Aust.ˣ G.80	34.58	21.16	4.24	17.05	7.60	14.08	9.29	3.77
Aust. ˣ G.83	40.95	23.92	5.81	22.22	7.65	12.59	7.86	5.36
Aust. ˣ G.85	31.44	14.79	1.63	19.61	8.05	12.60	5.29	5.79
Aust. ˣ (G.90ˣAust.)	31.15	14.02	0.48	19.91	7.14	12.98	5.88	7.64
Aust. ˣ Ashmouni	28.30	9.86	-9.01	20.50	8.02	14.49	7.62	5.97
Aust. ˣ Karashinki	31.54	14.27	-7.12	20.09	6.51	15.07	3.70	4.71
Aust. ˣA	31.23	17.44	-7.19	16.67	7.69	13.57	11.06	7.12
Aust. ˣ B	31.30	15.51	-3.00	18.69	8.70	10.99	6.70	6.62
Aust. ˣ C	30.73	16.03	-0.06	17.48	9.29	9.92	8.04	5.07
Aust. ˣ D	40.29	23.23	6.12	22.09	15.98	27.21	6.80	4.68
Dandara ˣ G.80	43.52	27.33	3.51	22.35	4.90	18.33	5.94	4.90
Dandara ˣ G.83	37.99	17.97	6.18	24.39	7.00	7.34	6.14	3.95
Dandara ˣ G.85	31.44	16.05	3.32	18.28	6.19	7.08	2.32	4.49
Dandara ˣ(G.90 ˣAust.)	28.57	13.18	1.23	17.71	8.72	8.90	3.63	6.21
Dandara ˣ Ashmouni	44.65	27.10	-4.41	24.05	9.68	14.18	8.54	3.01
Dandaraˣ Karashinki	37.29	21.09	5.84	20.23	7.41	13.67	8.94	3.89
Dandara ˣA	29.33	16.52	2.63	15.31	8.45	6.73	7.69	5.02
Dandara ˣB	35.39	20.94	3.98	18.29	13.04	9.73	2.65	5.54
Dandara×C	32.94	17.06	3.32	19.13	5.77	7.02	9.07	7.43
Dandara ˣD	42.75	28.19	6.71	20.20	9.27	12.40	13.28	6.34
Mean	33.93	17.62	1.61	19.78	8.16	12.26	6.27	5.11

G: Giza, Red%= (mean at N-mean at S)/mean at N * 100, SCY/P: seed cotton yield, g , NB/P: numbers of bolls /plant, BW: boll weight, g, DFF: days to first flowers, Mic : Micronaire reading, UHM: length (mm), PI: Pressley index (strength).

TABLE 7. Additive (σ²A), dominance (σ²D) variances with their standard error (SE) and σ²A/ σ²D ratio for studied traits under normal irrigation and drought stress

Genetic component	Trait	Normal irrigations (N)	Drought stress (S)	Trait	Normal irrigations (N)	Drought stress (S)
Additive(σ²A)		12.8896 ±2.1759	10.0668 ± 3.1230		2.0287 ± 0.4399	1.6195 ± 0.7289
Dominance(σ²D)	SCY/P	207.5900± 2.4352	163.5331±2.170	DFF	3.0665 ± 0.4924	4.0614 ± 0.7480
σ²A/σ²D		0.0621	0.0616		0.6616	0.3988
Additive(σ²A)		0.1286 ± 0.3451	0.0627 ± 0.5205		0.0132 ± 0.0512	0.0038 ± 0.0601
Dominance(σ²D)	Lint%	1.0768± 0.3863	1.1300 ± 0.4243	Mic	0.0399 ± 0.0469	0.0330 ± 0.0419
σ²A/σ²D		0.1194	0.0555		0.3308	0.1152
Additive(σ²A)		0.2686 ± 0.7112	0.5338 ± 1.1578		0.3714 ± 0.3307	0.4074 ± 0.4679
Dominance(σ²D)	NB/P	9.3220 ± 0.7960	12.0339 ± 1.1441	UHM	1.5803 ± 0.3702	2.3536 ± 0.3092
σ²A/σ²D		0.0288	0.0444		0.2350	0.1731
Additive(σ²A)		0.0085 ± 0.0415	0.0030 ± 0.0600		0.0587 ± 0.0458	0.0475 ± 0.0666
Dominance(σ²D)	BW	0.0397± 0.0465	0.0428 ± 0.0428	PI	0.0993 ± 0.0514	0.0868 ± 0.0483
σ²A/σ²D		0.2141	0.0701		0.5911	0.5472

G: Giza, SCY/P: Seed cotton yield, g, NB/P: Numbers of bolls /plant, BW: Boll weight, g, DFF: Days to first flowers, Mic: Micronaire reading, UHM: Length (mm), PI: Strength (Pressley index).

TABLE 8. Contribution of lines, testers, and their interaction for studied traits in the two environments

Contribution%	Traits	Normal irrigations(N)	Drought stress (S)	Traits	Normal irrigations (N)	Drouht stress (S)
Con. of lines%		45.7062	45.8005		31.3091	23.8687
Con. of testers%		13.9394	13.7185	DFF	59.0899	61.0805
Con. of L×T%	SCY/P	40.3543	40.4809		9.6009	15.0506
Con. of lines%		54.2728	55.8639		44.5219	34.9108
Con. of testers%		13.6542	0.6311	Mic	38.8677	33.9238
Con. of L×T%	Lint%	32.0729	43.5048		16.6103	31.1636
Con. of lines%		37.0536	37.9752		37.7012	32.2867
Con. of testers%		12.9124	16.2736	UHM	41.0987	42.7130
Con. of L×T%	NB/P	50.0339	45.7511		21.200	25.0001
Con. of lines%		50.1370	47.6948		56.7688	47.7665
Con. of testers%	BW	17.4051	13.9473	Strength	33.1184	41.4393
Con. of L×T%		32.4579	38.3573		10.1124	10.7936

Conclusion

from above results, it could be concluded that the reduction% caused drought stress in the parents varied greatly from 2.99 for lint% to 31.79 for SCY/P, while it varied for the hybrids from 5.11for fiber strength to 33.93 for SCY/P. The additive (σ²A) was larger under normal irrigation than under water stress. Likewise, the dominance variance (σ²D) was larger at normal irrigation than at water stress conditions for seed cotton yield, number of bolls /plants, fiber fineness, UHM length and fiber strength. The ratio σ²A/σ²D was less than unity for all studied traits under both environments indicating that the role of dominance was more important than additive effects in the inheritance of these traits especially under stress. The good combiner of parental lines and specific combiners varied from trait to another under both environments. Except for the fiber strength and Micronaire reading, the two hybrids [G95 × (G90 × Aust.)] and [Aust. × (G90 × Aust.)] were the best hybrids for most studied traits and should be considered in breeding program for drought stress and normal irrigation, and the parents G.95, (G95 × Aust.) and Aust. depicted their good combining

ability. The contribution of lines was larger than that of tester and lines x testers interaction in all characters except for NB/P at both environments indicating the importance of selection of lines for hybridization.

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التحليل الوراثي للمحصول وصفات التيلة في القطن (جوسيبيوم باربادنس ل) تحت ظروف الرى والجفاف

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الجفاف من أخطر أنواع الاجهاد تأثيرا على انتاجيه المحاصيل في مصر. يهدف هذا البحث إلى دراسة طبيعة فعل الجين الذي يحكم وراثه محصول الزهر وصفات التيلة تحت ظروف الري العادي وظروف الجفاف. اختير لذلك عشره أمهات وثلاثة تراكيب ككشاف هجنت سويا لتعطى 30 هجين (سلاله-كشاف). وقيمت الإباء والهجن في تصميم القطاعات الكاملة العشوائية من ثلاثة مكررات لكل بيئة في مركز البحوث الزراعية بسوهاج، مصر. وتشير النتائج إلى أن أفضل هجينين في الأداء تحت ظروف البيئتين هما (ج95 x (ج90 xأسترالي))، (أسترالي x (ج90 xأسترالي)) وذلك لمعظم الصفات. كما ان الإباء ج 95، (ج 95x أسترالي) افضل الإباء في القدرة العامة على الائتلاف لمعظم الصفات. ولهذا فان هذين الهجينين وهذين الابين يمكن اخذهما في الاعتبار لاستنباط أصناف سواء تحت الظروف العادية أو ظروف الجفاف. اختلف مقدار النقص في الاباء نتيجة للجفاف من 2.99% في نسبه الشعر إلى 31.79% في محصول الزهر للنبات. بينما اختلفت الهجن في مقدار النقص من 5.11% في متانه الشعر إلى 33.93% في محصول الزهر للنبات. وكان التباين المضيف والتباين السيادي اعلى تحت ظروف الري العادي عنه تحت ظروف الجفاف. وكانت النسبة بين التباين المضيف إلى التباين السيادي اقل من الوحدة لكل الصفات في البيئتين دلاله على ان النبأين غيرالمضيف هو الأكثر اهميه في وراثه كل الصفات. ونظرا لزيادة التباين غير المضيف عن التباين المضيف فيجب تأخير الانتخاب إلى الأجيال المتأخرة. وكانت مساهمه الأمهات من مجموع المربعات الكلى اعلى من الإباء وكذلك اعلى من التفاعل بين الأمهات والاباء مما يدل على اهميه اختيار الأمهات عند التهجين في أي برنامج تربيه.