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Line×Tester Analysis for Yield and Quality Traits under Salinity Stress in Cotton (*Gossypium barbadense* L.)

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THE ISSUE OF salinity tolerance in crops has received a great amount of attention recently in Egypt, especially under the climate change phenomenon. The main objective of this experiment was to study the gene action that controls yield and quality traits of Egyptian cotton under normal and saline soil. Nine lines were crossed to three testers in a line × tester mating design. The 27 crosses and their parents were evaluated under normal and saline soil conditions in the seasons of 2018 and 2019 using a randomized complete block design with three replicates. Both additive (σ^2_A) and dominance (σ^2_D) variances were higher under normal soil than under salinity stress conditions for all the analyzed characteristics. Under normal soil, the ratio σ^2_A/σ^2_D was less than unity for seed cotton yield/plant (SCY/p), number of bolls (NB/p), number of seeds (NS/b), boll weight (BW), lint yield (LY/p), and lint%. σ^2_D was not significant for seed index (SI), lint index (LI), days to the first flower (DFF), plant height (PH), and upper half-mean length (UHML). Under normal soil and based on the mean performance the cross (*Giza90 × Aus×Giza85*) × *Giza95* was the best one for SCY/p, LY/p, NB/p, BW, SI and NS/b, and *Ashmouni × Giza90 × Aus×Giza83* for lint%, *Dandara× Giza90 × Aus×Giza83* for LI, *Ashmouni × Giza90 × Aus×Giza83* for DFF, *Giza85×Giza95* for UHML. *Giza95*, *Giza90* and *Giza90 × Aus×Giza83* were the best combiners in all the analyzed traits. These crosses can be used to develop new lines for the two environments.

Keywords: Line × tester analysis, Gene action, *G. barbadense,* Saline soil.

Introduction

Salt stress is one of the most common abiotic stresses. It is a serious threat to agriculture by limiting crop productivity worldwide (Shehzad et al., 2019; Sayed et al., 2021), especially in the arid climate regions. Moreover, about one-fifth of the world's total irrigated land is reported to be affected by salinity, and Egypt is one of the countries most severely affected (Sanower, 2019). Salinity problems in Egypt are mainly caused by poor irrigation management), shallow groundwater, seawater intrusion, drainage water, recycled water, fertilizers, pesticides, unsustainable and bad farming practices and climate changes (Long et al., 2013; Ziemann et al., 2013; Shrivastava & Kumar, 2015; Mohamed, 2016; Hassani et al., 2021; Saradadevi et al., 2021).

Cotton (*Gossypium* spp) is one of the most important natural fiber crops in general and has several uses, the most important of which are as food oil and biofuel (Sharif et al., 2019). The Egyptian cotton (*Gossypium barbadense* L.) of long and extra-long staple have a good reputation worldwide for their good processing fiber properties (Mahdy et al., 2018). Cotton is

placed in the moderately salt-tolerant group of plant species with a salinity threshold level 7.7dS m^{-1} (Ashraf, 2002). The growth and seed yield of cotton being severely reduced at high salinity levels and different salts affect the cotton growth to a variable extent (Ashraf, 2002; Farooq et al., 2020).

In the last decades, many plant breeders, physiologists and geneticists have paid attention to the importance of improving cultivated crops for salt tolerance. Where the evaluation of local varieties and available genetic resources of a crop for salt stress tolerance is a must to produce highly tolerant varieties to reduce yield and quality losses (Ashraf et al., 2006). In addition, studying the inheritance of traits associated with salinity tolerance leads to a deeper understanding of the mechanisms of tolerance, since, salt tolerance is considered a quantitative-complex trait controlled by multiple genes (Roy et al., 2011). Besides that, little is known about the function of these genes and the extent to which they interact with other genes that would influence the salinity tolerance mechanisms (Shannon, 1997; Saradadevi et al., 2021).

To initiate a breeding program for salt stress tolerance in cotton, potential knowledge of the genetic information such as gene action, heritability, combining ability and heterotic effects associated with yield, its yield components, and tolerance traits is critical. Since this information provides necessary information about the selection strategy and is useful in directing toward the best use of promising parents and hybrids in breeding programs in cotton (Ullah et al., 2019; Unay et al., 2019; Sahar et al., 2021; Abdel-Aty et al., 2022). Sunny et al. (2022) revealed that the success of crop variety development is based on the selection of convenient parents, environmental effects, and gene expression of the targeted traits. Furthermore, Unay et al. (2019) reviewed that parents and crosses must be selected based on the combining ability (divides into, general combining ability (GCA) for parents and specific combining ability (SCA) for crosses) and gene action, which are associated with the effectiveness of phenotypic performance. The effects of GCA and SCA are linked to additive and non-additive gene actions, respectively (Falconer, 1989). The analysis of line × tester is one of the most important genetic-statistical

methods which provide significant information about both GCA and SCA effects (Kempthorne, 1957; Usharani et al., 2016). This approach has been applied in both self and cross-pollinated plants to detect the most appropriate parents' genotypes and crosses in relation to investigated characteristics (Kempthorne, 1957).

The main objective of this article was to study the GCA and SCA effects for yield, yield attributes, and quality traits under normal and saline soils conditions using the line × tester approach. The identification of the best genotypes with desirable GCA and SCA effects, can help cotton breeders in developing new salt-tolerant varieties.

Materials and Methods

Plant materials and experimental site

The present investigation was conducted at Al-Ghoraizat village (Saline soil with an average of EC= 13.5 mm/cm), Maragha city (Latitude: 26° 41' N, Longitude: 31° 35'E), Sohag governorate (saline soil) and Izbat Al-Hama, Tema city, Sohag governorate (normal soil) (Latitude: 26°54'N, Longitude 31° 25'E) during the two summer seasons of 2018 and 2019. The characterizations of the genotypes used as well as the physical and chemical properties of the soils in both seasons are given in Tables 1 and 2, respectively.

Line by tester mating design

In season 2018 and under normal soil conditions, nine genotypes as lines and three genotypes as testers were crossed in a Line × Tester mating design in current study (Table 1). The three tester cotton genotypes were selected for their performance and high yielding ability under salinity condition (Mahdy et al., 2021).

Experimental design and set-up

In season 2019, the 27 crosses, the nine lines and the three testers were sown on March 28th and 29th under salinity and normal soil, respectively. A randomized complete blocks design with three replications was used. The plot size was two rows, 4m long, 60cm apart and 40cm between hills within a row. After full emergence, seedlings were thinned to one plant per hill. All the routine agricultural practices and plant protection were adopted in all the plots uniformly throughout the growing season.

Data recorded

The studied traits were recorded based on 10 guarded plants as follow: seed cotton yield/plant (SCY/P, g), lint yield/plant (LY/p, g), Lint%, number of bolls/plant (NB/p), boll weight (BW, g) (estimated from the weight of 25 sound bolls taken randomly from each plot before the first pick), seed index (SI, g), lint index (LI, g), number of seeds /bolls (NS/b) (estimated as boll weight (100- lint %) / seed index), plant height (PH, cm), days to first flower (DFF) (was measured as the days from sowing to the appearance of the first flower on five plants in each plot), fiber fineness, was expressed as Micronaire reading (Mic), fiber length, the UHM length was measured by H.V.I. and fiber strength as Pressley Index (strength) was measured by the H.V.I instrument manufactured by USTER Technologies, Inc. (a testing machine capable of measuring many cotton fiber properties including length, uniformity, Micronaire/fineness, strength, color, etc...)..

Statistical analysis

The Line × Tester analysis was performed as outlined by Kempthorne (1957) and described by Singh & Chaudhary (1979).

TABLE 1. Names, pedigree, and the main characteristics ofthe lines (L) and testers (T) used in this study

	Genotypes	Pedigree	Characteristics
Lines			
L1	Giza 80	G. 66´G. 73	Long-staple variety. It is high in yield and lint percentage (obsolete).
L2	Giza 83	G.67×G.72	The long-staple variety for upper Egypt. it is characterized by high lint percentage and yield.
L3	Giza 85	G.67 × C.B. 58	A long-staple variety, characterized by high yield and earliness variety (obsolete).
L4	(Giza 90 × Aus) × G.85	(Giza90×Aus) ×G.85	A long-staple variety, characterized by high yield and earliness.
L5	Ashmouni	G1	Long-stable variety (obsolete).
L6	Dandara	Selected from Giza-3	Long-stable variety(obsolete).
L7	(G.91×G.90×G.80)	(G.91×G.90×G.80)	Promising line in the 12 generation.
L8	(Giza90×Aus) × (G.83×G.80× Dandara)	(Giza90×Aus) × (G.83×G.80×Dandara)	Promising line in the 14 generation.
L9	(Giza90×Aus) × (G.83×G.72×Dandara)	(Giza90×Aus) × (G.83×G.72×Dandara)	Promising line in the 13 generation.
Testers			
T1	Giza 95	[(G.83 × (G.75 × 5844)) × G.80]	A new long- staple cotton variety, characterized by high yielding ability, high lint percentage, early maturity, and heat tolerance (cultivated).
T2	Giza 90	G.83× Dandara	Long- staple variety for upper Egypt, high yield, and lint percentage (cultivated).
T3	(Giza 90×Aus) × G.85)	G.90 × Australian	Characterized by high yielding and earliness (obsolete).

TABLE 2. Physical and chemical properties of the upper 60 cm of the experimental normal and saline soils in 2018,2019 and 2020 seasons

	Normal soil		Saline soil	
	Seasons		Seasons	
	2018	2019	2018	2019
Physical analysis				
Sand %	19%	21%	19	18
Silty%	48%	51%	23	22
Clay%	33%	28%	58	60
Soil texture	Silty clay loam			
Chemical analysis				
S. P.	67	66	57	56
PH(1:1)	7.66	7.6	8.6	8.5
O.M	1.68	1.7	1.11	1.2
CaCo3%	3.88	3.9	-	-
EC (mm/cm)	1.65	1.63	13	13.5
SO4 meq/L	2	3	38.6	37.8
Clmeq/L	4	4	55.2	54.6
HCO_3 meq/L	10	9.5	52.4	52.2
Ca^{+2} meq/L	8	7.5	12.6	12.4
Mg^{+2}meq/L	6	6.18	59	59.6
Na+ meq/L	2.09	2.25	57	66.2
Total N%	1.6	1.8	1.2	1.4
Total P (ppm)	5.192	5.537	4.192	4.38
Total K (ppm)	223	231	211	205

The physical analysis indicates that the soil texture was silty clay loam. Furthermore, the results explained that the soil was under a medium saline soil class; however, the soil wasn't alkaline according to Na+, Ca+2, and Mg+2 concentrations, where the sodium adsorption ratio was 11.03. In addition, the changes in EC values were insignificant during the three seasons. Likewise, OM content was in the same range through the three seasons. In the same manner, N, P, K contents in the soil were the same during the three seasons. On the other hand, soils containing high concentrations of soluble salts will interfere with the normal growth and development of crops where plants are grown in this soil often seem drought stressed even when adequate water is available because the osmotic potential of the soil prevents the roots from taking in water. As well as the availability of the nutrients N, P, and K affected by soil salinity.

Results and Discussions

Analysis of variance (ANOVA)

The ANOVA revealed significant differences among tested genotypes for all traits under normal soil conditions except for Micronaire reading (Mic) and Pressley index (PI) indicating the presence of variability among crosses and their parents (Table 3). However, under saline soil the genotypes mean squares was significant only for four out of 13 traits; seed cotton yield/plant (SCY/p), number of bolls/plant (NB /p), lint yield/plant (LY/p), and lint index (LI). Under normal soil the technological properties were

least affected by environments. Mahrous (2018) and Abdel-Aty et al. (2022) found significant (P ≤ 0.05 to P ≤ 0.01) variation among all genotypes, parents, their crosses, and parent vs crosses for seed cotton yield/plant, lint yield/plant, lint percentage, number of bolls/plant, seed index, lint index, fiber fineness, fiber strength, fiber length in 2.5% span length and uniformity ratio of Egyptian cotton at good environment. Meanwhile, Farooq et al. (2020) found significant and non-significant differences among yield and its attributes under normal and salinity conditions in upland cotton (*Gossypium hirsutum*) in Pakistan.

TABLE 3. The analysis of variance of the line by tester under normal (N) and saline soils (S) environments

`S.O.V.	d.f	SCY/P		LY/P		Lint%		NB/P	
		N	S	N	S	N	S	N	S
Replicates	2	110.37	7.99	10.98	1.12	0.20	0.01	5.07	1.49
Genotypes	38	631.36**	66.29**	107.22**	8.26**	1.61**	0.20	53.14**	10.88**
Parents(P)	11	960.45**	49.87*	171.23**	6.83**	2.48**	0.21	105.68**	4.82
Crosses(C)	26	513.76**	71.52**	84.23**	8.40**	0.77**	0.05	31.31**	13.28**
P vs C	1	69.07	110.82*	0.88	20.29**	13.91**	3.80**	42.68*	15.12*
Lines(L); GCA	8	983.57*	189.97**	181.95**	22.19**	1.49*	0.07	67.35**	34.46**
Testers(T); GCA	2	286.02*	24.66	46.59*	2.82	0.42	0.05	12.50	3.39
L×T (SCA)	16	307.32**	18.15	40.08**	2.20	0.44**	0.04	15.64*	3.93
Residual	76	71.24	20.58	10.24	2.49	0.18	0.16	7.83	3.57

S.O.V.	d.f	BW		SI		LI		NS/B	
		N	S	N	S	N	S	N	S
Replicates	2	0.03	0.007	0.01	0.08	0.003	0.02	0.77	0.60
Genotypes	38	0.07**	0.023	0.22**	0.09	0.20**	0.06*	2.63**	1.28
Parents(P)	11	0.05*	0.048*	0.46**	0.11*	0.29**	0.065*	2.81**	2.46*
Crosses(C)	26	0.08**	0.014	0.07*	0.09	0.03	0.05	2.16**	0.83
P vs C	1	0.02	0.006	1.40**	0.01	3.47**	0.21*	13.13**	0.01*
Lines (L); GCA	8	0.16**	0.013	0.16**	0.14	0.08*	0.07*	3.39*	1.31
Testers (T); GCA	2	0.06	0.009	0.05	0.05	0.006	0.02	2.97*	1.08
L×T (SCA)	16	0.05*	0.014	0.02	0.07	0.02	0.04	1.44*	0.56
Residual	76	0.02	0.022	0.04	0.06	0.03	0.03	0.87	1.15

S.O.V.	d.f	DFF		PH		Mic		UHM Length	
		N	S	N	S	N	S	N	S
Replicates	2	4.01	8.53	8.77	39.10*	0.05	0.06	0.13	0.03
Genotypes	38	45.31**	2.38	43.13**	11.44	0.03	0.02	0.31**	0.04
Parents(P)	11	20.08**	2.41	47.42**	16.51*	0.02	0.03	0.60**	0.08
Crosses(C)	26	3.04	1.21	33.12**	5.25	0.03	0.02	0.16*	0.02
P vs C	1	504.91**	32.50**	256.29**	116.43**	0.02	0.09	0.72**	0.32*
Lines (L); GCA	8	7.18**	1.77	68.24*	8.27	0.09**	0.03**	0.42**	0.03
Testers (T); GCA	2	0.79	0.64	2.08	0.75	0.00	0.01	0.18*	0.01
L×T (SCA)	16	1.26	1.00	19.44	4.30	0.01	0.01	0.03	0.01
Residual	76	2.81	4.36	11.64	9.17	0.02	0.04	0.08	0.05

S.O.V.	d.f	Strength (PI)	
		N	S
Replicates	2	0.23**	0.06
Genotypes	38	0.05	0.04
Parents(P)	11	0.11**	0.07
Crosses(C)	26	0.04	0.02
P vs C	1	0.02	0.41**
Lines (L); GCA	8	0.069	0.02
Testers (T); GCA	2	0.024	0.02
L×T (SCA)	16	0.025	0.02
Residual	76	0.04	0.05

*, **; significant at 0.05 and 0.01 levels of probability, respectively,SCY/P is seed cotton yield/plant; LY/P is lint yield/plant; BW is boll weight; NB/P is number of bolls/plant; SI is seed index; NS/B is number of seeds/boll; LI is lint index; DFF is days to the 1stflower; PH is plant height; Mic isMicronaire reading;UHMLisupper-half mean length and PI is Pressley index.

The analysis of combining ability was performed only on the traits showed significant differences among genotypes. The significant differences among lines and/or testers reflect the presence of general combining ability, in other words the additive as well as the additive-by-additive gene effects in the inheritance of all traits except for LI under normal environment. While, under saline soil lines and/or testers mean squares was significant for six traits; SCY/P, NB/P, LY/P, LI, and Micronaire reading (MIC). The significant mean squares of L×T for SCY/P, LY/P, Lint%, NB/P, BW, and NS/B under the good environment indicated the presence of non-additive (dominance and epistasis) gene actions in the inheritance of these traits. The significant (P≤ 0.01) mean squares of parent's vs crosses depicted the heterotic effects. Our results are consistent with the results of Mahrous (2018), Ullah et al. (2019), Unay et al. (2019), and Farooq et al. (2020).

The significance of additive and non-additive genetic influences in the inheritance of different traits

The total genetic variance was divided into GCA and SCA effects and translated into additive and non-additive (dominance) variance as outlined by Singh & Chaudhary (1985). The additive variance (σ^2_A) and the dominance variance (σ^2_D) were higher under normal soil than under salinity stress conditions for all the analyzed traits (Table 4). Under normal soil, the ratio σ^2_A/σ^2_D was less than unity for SCY/P, NB/P, BW, NS/B, LY/P, and lint%, indicating that the predominant role of dominant gene effects than additive effects in the inheritance of these investigated traits. Therefore, the performance of hybrids cannot be predicted from the effects of the parents' GCA (Baker, 1978). Otherwise, σ^2_D was not significant for, LI, days to first flower (DFF), PH, and UHML depicting the predominant role of the additive and additive by additive variance in the inheritance of these traits. Furthermore, the nature of the gene action was completely different in saline soils, as the three traits could be analyzed, SCY/P, LY/P, and LI showed the predominant of the additive and additive × additive variances and absence of dominance. The results of the normal soil are in line with those described by Basal et al. (2011), Javaid et al. (2014), Kannan & Saravanan (2016), Rehman et al. (2017) and Zafar et al. (2020).

The general and specific combining ability effects

The lines mean of SCY/p (81.9g), males mean (113.36g) with hybrid mean of 91.12g indicating absence of heterosis under normal soil (Tables 5 and 6). The same trend was observed under saline soil. The GCA effects for SCY/p were significant positive (P≤ 0.05 or P≤ 0.01) for genotypes L1, L2, and L3 and negative for genotypes L5, L6 and T2. Meanwhile, T1 and T3 showed positive insignificant GCA effects. However, T2 gave negative significant GCA effects. Only three crosses; (L4×T1), (L5×T3) and (L7×T1) showed positive significant SCA. None of the parents of these crosses had positive significant GCA effects indicating the presence of non-additive effects. Based on the mean performance of the crosses T1(*Giza95*) followed by T3 (*Giza90 × Aus×Giza83*) could be considered the best combiners for SCY/P. Furthermore, non-significant SCA effects was found under saline soil, but the mean of SCY/p indicated that T2 (*Giza 90*), L2 (*Giza83*), L3(*Giza85*), T1(*Giza95*) were the best combiners. Baker (1978) indicated that if non-additive effects are present, the performance of the hybrids cannot be predicted.

Concerning LY/p under normal soil the lines L1(*Giza80*), L2 , and L3 had significant positive GCA effects, while L5 and L6 gave significant negative GCA effects. Four crosses showed significant SCA effects, only one cross (L4×T1) had positive SCA effects, and other three had negative significant SCA. The four crosses shared the male parent T1 (*Giza95*) which had positive significant SCA, the lines of the four crosses showed insignificant GCA, indicating non-additive effects. Therefore, T1(*Giza95*) could be considered the best combiner for LY/P. Under saline soil none of the crosses showed significant SCA. The best combiners for LY/P under saline soil were L2 (*Giza83*) and T2 (*Giza90*). In consequence, T1 (*Giza95*), T2 *Giza90*), and T3 (*Giza90 × Aus×Giza83*) could be considered the best combiners for SCY/P and LY/P under both environments.

For lint % only two crosses had significant SCA effects (L5×T3, L5×T2). However, their parents showed insignificant GCA effects. Based on the performance of the crosses T3 could be considered the best combiner for lint% under normal soil.

TABLE 4. The additive (σ²A) and dominance (σ²D) variances with their standard error (SE) for the studied traits in the two environments

Traits	Genetic comp.	Normal (N)	Salinity (S)
SCY/P	Additive(σ²A) ±SE	8.5196±2.44	2.2025±1.0
	Dominance(σ²D) ± SE	78.6943±4.87	-0.8114±2.62
	σ²A/σ²D	0.1082	††
LY/P	Additive(σ²A) ± SE	1.8222±0.72	0.2558±0.02
	Dominance(σ²D) ± SE	9.9449±1.85	-0.0971±0.91
	σ²A/σ²D	0.1832	††
Lint%	Additive(σ²A) ± SE	0.0132±0.001	†
	Dominance(σ²D) ± SE	0.0875±0.03	†
	σ²A/σ²D	0.1508	†
NB/P	Additive(σ²A) ± SE	0.6466±0.04	0.3858±0.09
	Dominance(σ²D) ± SE	2.6030±1.01	0.1200±1.09
	σ²A/σ²D	0.2484	††
BW	Additive(σ²A) ± SE	0.0014±0.001 0.081 0.081	†
	Dominance(σ²D) ± SE	0.0089±0.001	†
	σ²A/σ²D	0.1573	†
SI	Additive(σ²A) ± SE	0.0018±0.001	†
	Dominance(σ²D) ± SE	-0.0045±0.006	†
	σ²A/σ²D	††	†
LI	Additive(σ²A) ± SE	0.02±0.01	0.0003±0.0001
	Dominance(σ²D) ± SE	-0.0023±0.1061 ns	0.0029±0.1129 ns
	σ²A/σ²D	††	††
NS/B	Additive(σ²A) ± SE	0.0295±0.002	†
	Dominance(σ²D) ± SE	0.1904±0.01	†
	σ²A/σ²D	0.2314	†
DFF	Additive(σ²A) ± SE	0.0737±0.003	†
	Dominance(σ²D) ±SE	-0.5177±0.97 ns	†
	σ²A/σ²D	††	†
PH	Additive(σ²A)±SE	0.5646±0.08	†
	Dominance(σ²D)±SE	2.5995±1.96 ns	†
	σ²A/σ²D	††	†
UHML	Additive(σ²A)±SE	0.0053±0.001	†
	Dominance(σ²D)±SE	-0.0153±0.1684 ns	†
	σ²A/σ²D	††	†

†† = insignificant dominance variance, †=the trait could not be analyzed because of insignificant genotypes,SCY/P is seed cotton yield/plant; LY/P is lint yield/plant; BW is boll weight; NB/P is number of bolls/plant; SI is seed index; NS/B is number of seeds/boll; LI is lint index; DFF is days to the 1stflower; PH is plant height;and UHMLisupper-half mean length.

TABLE 5. Means and estimates of general combining ability (GCA) for lines (female genotypes) and testers (male genotypes) for the studied traits under normal soil (N) and saline soil (S) conditions.

Genotype	SCYp, g Means (N)	GCA (N)	Means (S)	GCA (S)	LY/p, g Means (N)	GCA (N)	Means (S)	GCA (S)	Lint% Means (N)	GCA (N)	Means (S)	GCA (S)	NB/p Means (N)	GCA (N)	Means (S)	GCA (S)	BW, g Means (N)	GCA (N)	Means (S)	GCA (S)
Female (Lines)																				
L1	105.28	18.32**	44.47	10.12**	39.56	7.76**	15.37	3.48**	37.61	0.843	38.64	0.843	23.39	4.866**	4.195**	4.866**	2.73	4.866**		
L2	88.33	10.12**	44.10	4.70**	33.25	4.01**	15.23	1.56**	37.65	0.202	33.69	0.202	22.51	2.486**	2.297**	2.486**	2.63	2.486**		
L3	84.55	7.54*	39.30	-0.90	32.32	3.05**	13.47	-0.34	38.21	0.206	30.65	0.206	19.73	1.833*	-0.432	1.833**	2.77	1.833**		
L4	74.49	-3.45	47.30	-2.34	28.44	-1.12	16.20	-0.76	38.20	0.094	26.29	0.094	23.62	-1.849*	-1.024	-1.849**	2.83	-1.849**		
L5	67.07	-11.64**	40.67	-4.32**	24.77	-7.77**	13.87	-1.46**	36.93	-0.571	25.26	-0.571	20.12	-3.786**	-1.975**	-3.786**	2.67	-3.786**		
L6	73.86	-14.02**	41.33	-3.14*	27.50	-2.97**	14.20	-1.08*	37.24	-0.202	28.87	-0.202	21.21	-2.853**	-0.608	-2.853**	2.57	-2.853**		
L7	80.43	-2.35	44.05	-1.03	30.03	-1.18	15.27	-0.32	37.35	-0.381	30.92	-0.381	22.09	0.051	-0.896	0.051	2.60	0.051		
L8	87.32	0.84	47.47	-0.206	32.43	0.24	16.47	-0.069	37.11	-0.115	35.85	-0.115	23.35	0.120	-0.432	0.120	2.43	0.120		
L9	75.80	-5.35	42.00	-2.871	28.43	-2.01	14.47	-0.991	37.52	-0.076	30.10	-0.076	21.51	-0.868	-1.126	-0.868	2.53	-0.868		
Females' Mean	81.90	0.0012	43.41	0.0014	30.75	0.001	14.95	0.002	37.54	0	31.14	0	21.95	-0.232	-0.0001	-0.232	2.64	-0.232		
S.E.(GCA) L	-	2.81	-	1.51	-	1.06	-	0.526	-	1.067	-	1.067	-	0.932	0.630	0.051	-	0.051		
S.E. (gi-gi)	-	3.97	-	2.13	-	1.50	-	0.744	-	1.509	-	1.509	-	1.319	0.891	0.072	-	0.072		
Male (testers)																				
T1	101.94	1.92	51.61	0.159	38.84	1.50**	18.07	0.075	38.14	0.017	35.11	0.017	23.13	0.783	-0.090	0.783**	2.90	0.783**		
T2	112.14	-3.75*	52.02	0.867	42.86	-0.92	18.13	0.279	38.20	0.117	41.62	0.117	22.28	-0.328	0.391	-0.328**	2.70	-0.328**		
T3	126.00	1.83	46.70	-1.025	50.86	-0.58	16.20	-0.354	40.39	-0.133	44.43	-0.133	21.65	-0.454	-0.301	-0.454**	2.83	-0.454**		
Males' mean	113.36	0	50.11	0.0003	44.18	0	17.47	0	38.91	0.0003	40.38	0.0003	22.35	0.0003	0	0	2.81	0		
S.E.(GCA)T	-	1.62	-	0.87	-	0.61	-	0.303	-	0.616	-	0.616	-	0.538	0.363	0.029	-	0.029		
S.E. (gi-gi)	-	2.29	-	1.23	-	0.87	-	0.429	-	0.871	-	0.871	-	0.761	0.514	0.041	-	0.041		

*, **; significant at 0.05 and 0.01 levels of probability, respectively, SCY/p is seed cotton yield/plant; LY/p is lint yield/plant; BW is boll weight, and NB/P is number of bolls/plant.

TABLE 5. Cont.

Genotype	SI		LI, g				NS/b		DFF		PH		UHML	
	Means (N)	GCA (N)	Means (N)	GCA (N)	Means (S)	GCA (S)	Means (N)	GCA (N)	Means (N)	GCA (N))	Means (N)	GCA (N)	Means (N)	GCA (N)
Female (Lines)														
L1	10.13	0.152	5.96	0.125	6.52	0.139	16.82	0.503	77.33	-0.642	171.67	4.346**	31.80	0.040
L2	9.00	0.119	6.71	-0.025	6.13	-0.129	18.24	0.453	77.00	-1.086*	169.33	-1.321	31.90	-0.127
L3	9.03	0.052	6.85	0.020	6.07	0.025	18.94	0.428	76.33	1.136	160.00	2.068	32.03	0.240*
L4	9.07	-0.081	6.82	0.077	6.10	-0.027	19.32	0.397	76.67	0.025	162.67	1.012	32.33	-0.249**
L5	8.87	-0.293	6.60	0.041	6.02	0.090	18.97	-1.368**	75.33	1.691**	161.67	-5.210**	32.30	-0.405**
L6	9.30	-0.070	6.38	-0.008	6.00	0.091	17.33	0.249	75.67	-0.198	167.00	-2.043	32.53	0.062
L7	9.60	-0.015	6.21	-0.093	6.03	-0.047	16.97	-0.235	74.00	-0.420	168.00	-0.988	32.30	0.073
L8	9.07	0.107	6.51	-0.099	6.17	-0.108	16.89	0.050	73.00	-0.642	167.67	1.346	32.20	0.206*
L9	9.00	0.030	6.67	-0.041	6.01	-0.034	17.59	-0.476	76.67	0.136	168.00	0.790	32.70	0.162
Females' Mean	9.23	0	6.52	-0.0003	6.11	0	17.89	0.0001	75.77	-0.00002	166.22	0	32.23	0.0002
S.E.(GCA) L	-	0.067	-	0.061	-	0.652	-	0.311	-	0.559	-	1.137	-	0.097
S.E. (gi-gi)	-	0.095	-	0.086	-	0.092	-	0.441	-	0.791	-	1.608	-	0.137
Male (Testers)														
T1	9.40	0.030	6.56	-0.015	6.11	0.018	19.10	0.266	76.33	0.099	164.00	-0.321	31.90	0.080
T2	9.87	0.022	6.27	0.017	6.25	0.019	16.90	-0.372*	68.00	0.099	162.33	0.160	33.17	0.006
T3	9.53	-0.052	7.11	-0.001	6.23	-0.037	17.71	0.106	76.00	-0.198	172.00	0.160	31.47	-0.086
Males' mean	9.6	0	6.64	0.0003	6.19	0	17.90	0	73.44	0	166.11	-0.0003	32.18	0
S.E.(GCA)T	-	0.038	-	0.035	-	0.037	-	0.180	-	0.322	-	0.656	-	0.056
S.E. (gi-gi)	-	0.055	-	0.050	-	0.053	-	0.254	-	0.456	-	0.928	-	0.079

*, **, significant at 0.05 and 0.01 levels of probability, respectively; SI is seed index; LI is lint index; NS/b is number of seeds/boll; DFF is days to the 1st flower; PH is plant height; Mic is Micronaire reading; UHML is upper-half mean length; and PI is Pressley index.

TABLE 6. Means performance and estimates of specific combining ability (SCA) of the best three or four hybrids for the studied traits under normal soil (N) and saline soil (S) conditions

SCY/P, g

Crosses	Mean (N)	SCA (N)	Crosses	Mean (S)	SCA (S)
L4 × T1	109.32	19.413**	L2 × T2	57.4	4.638
L5 × T3	67.37	15.63**	L3 × T1	50.12	3.665
L4 × T3	75.2	-14.61**	L9 × T3	45.93	2.636
L7 × T1	80.77	10.24*			
Mean	91.12	0.73	Mean	47.19	-0.064
S.E.SCA	-	4.87	S.E.SCA	-	2.61
S.E. (sij-skl)	-	6.89	S.E. (sij-skl)	-	3.7
LSD 0.05	7.88	-	LSD 0.05	4.24	-
LSD 0.01	10.41	-	LSD 0.01	5.6	-

LY/P, g

Crosses	Means (N)	SCA (N)	Crosses	Mean (S)	SCA (S)
L4 × T1	40.96	6.65**	L2 × T2	20.00	1.677
L7 × T1	29.57	-4.67*	L3 × T1	17.47	1.258
L4 × T3	27.87	-4.34*	L9 × T3	16.07	0.932
L9 × T1	29.7	-3.70*			
Mean	-	1.84	Mean	-	0.911
S.E.SCA	-	2.61	S.E.SCA	-	1.289
S.E. (sij-skl)	-	-	S.E. (sij-skl)	1.47	-
LSD 0.05	3.95	-	LSD 0.05	1.95	-
LSD 0.01	-	1.84	LSD 0.01	-	0.911

Lint%

Crosses	Means (N)	SCA (N)
L5 × T3	35.49	-0.943**
L5 × T2	37.49	0.814**
L8 × T3	37.18	0.292
Mean	37.13	-0.0003
S.E.SCA	-	0.248
S.E. (sij-skl)	-	0.351
LSD 0.05	0.40	-
LSD 0.01	0.53	-

NB/p

Crosses	Means (N)	SCA (N)	Crosses	Means (S)	SCA (S)
L4 × T1	37.68	3.981*	L6 × T1	24.28	2.146*
L6 × T1	36.06	3.372*	L2 × T2	27.34	1.82
L7 × T3	36.39	2.029	L3 × T1	23.54	1.236
Mean	34.76	0.00003	Mean	22.80	0.00003
S.E.SCA	-	1.615	S.E.SCA	-	1.091
S.E. (sij-skl)	-	2.285	S.E. (sij-skl)	-	1.544
LSD 0.05	2.61	-	LSD 0.05	1.77	-
LSD 0.01	3.45	-	LSD 0.01	2.33	-

SI, g

Crosses	Means (N)	SCA (N)
L4 × T1	9.67	0.159
L8 × T3	9.77	0.152
L5 × T2	9.37	0.078
Mean	9.55	0
S.E.SCA	-	0.116
S.E. (sij-skl)	-	0.165
LSD 0.05	0.19	-
LSD 0.01	0.25	-

UHML

Crosses	Means (N)	SCA (N)
L3 × T1	32.57	0.198
L9 × T3	32.3	0.175
L7 × T2	32.23	0.105
Mean	32.05	0
S.E.SCA	-	0.168
S.E. (sij-skl)	-	0.238
LSD 0.05	0.27	-
LSD 0.01	0.36	-

BW, g

Crosses	Means (N)	SCA (N)
L4 × T1	2.9	3.981**
L6 × T1	2.7	3.372**
L4 × T3	2.53	-2.758**
L7 × T2	2.6	-2.430**
Mean	2.61	0.237
S.E.SCA	-	0.089
S.E. (sij-skl)	-	0.125
LSD 0.05	0.14	-
LSD 0.01	0.19	-

*, **, significant at 0.05 and 0.01 levels of probability; respectively;SCY/P is seed cotton yield/plant; LY/P is lint yield/plant; BW is boll weight; NB/P is number of bolls/plant; SI is seed index; NS/B is number of seeds/boll; LI is lint index; DFF is days to 1stflower; PH is plant height; Mic is Micronaire reading; UHML is upper-half mean length;and PI is Pressley index.

TABLE 6. Cont.

Crosses	LI			LI			NS/b			DFF			PH		
	Means (N)	SCA (N)	Crosses	Means (S)	SCA (S)	Crosses	Means (N)	SCA (N)	Crosses	Means (N)	SCA (N)	Crosses	Means (N)	SCA (N)
L5 × T3	6	-0.221*	L1 × T1	6.57	0.184	L4 × T1	18.77	0.931	L6 × T1	66.67	-0.877	L7 × T3	166.67	4.506*
L5 × T2	6.41	0.168	L5 × T2	6.5	0.165	L8 × T3	18.22	0.891	L5 × T3	68.33	-0.802	L7 × T1	157.33	-4.346*
L6 × T3	6.27	0.099	L9 × T1	6.34	0.131	L3 × T1	18.53	0.669	L8 × T3	66	-0.802	L4 × T3	160	-4.160*
Mean	6.18	-0.006	Mean	6.23	0	Mean	17.17	-0.0001	Mean	67.64	0.00003	Mean	162.98	0
S.E.SCA	-	0.106	S.E.SCA	-	0.112	S.E.SCA	-	0.540	S.E.SCA	-	0.968	S.E.SCA	-	1.969
S.E. (sij-skl)	-	0.150	S.E. (sij-skl)	-	0.159	S.E. (sij-skl)	-	0.764	S.E. (sij-skl)	-	1.370	S.E. (sij-skl)	-	2.785
LSD 0.05	0.17	-	LSD 0.05	1.00	-	LSD 0.05	0.87	-	LSD 0.05	1.57	-	LSD 0.05	3.18	-
LSD 0.01	0.23	-	LSD 0.01	1.33	-	LSD 0.01	1.15	-	LSD 0.01	2.07	-	LSD 0.01	4.21	-

*, **; significant at 0.05 and 0.01 levels of probability, respectively;SCY/P is seed cotton yield/plant; LY/P is lint yield/plant; BW is boll weight; NB/P is number of bolls/plant; SI is seed index; NS/B is number of seeds/boll; LI is lint index; DFF is days to 1stflower; PH is plant height; Mic is Micronaire reading; UHML is upper-half mean length; PI is Pressley index.

Under normal soil the lines L1, L2, and L3 had positive and significant GCA effects for NB/p, while the lines L4, L5 and L6 showed significant and negative GCA effects. The GCA effects of the testers were not significant. Only two crosses; L4×T1 (3.981) and L6×T1 (3.372) showed significant positive SCA effects. However, their lines which showed negative GCA effects shared one tester T1 (*Giza95*) which gave positive insignificant GCA. Therefore, the crosses cannot be expected from their parents' GCA. Irrespective of the GCA of the parents, the best three crosses in NB/p under both environments shared T1, T2 or T3 and considered the best combiners.

Under normal soil the best mean performance of BW was 2.90g for the tester T1 (*Giza 95*) and the lowest for the line L8 (Table 4). Lines L1, L2, and L3 gave positive and significant (P≤0.01) GCA, while L4, L5, and L6 had negative significant (P≤0.01) GCA effects. Twenty-five crosses showed significant (P≤0.01) SCA effects (not included). The crosses which gave positive significant SCA effects for BW had one parent, or both showed significant GCA except few cases. The crosses L4×T1 and L6×T1 gave positive significant SCA effects, their parents had negative GCA. These results indicate the existence of both additive and non-additive effects in the inheritance of BW in these materials. The best combiners for BW were T1 followed by T2 and T3.

Concerning SI under the good environment, L1 (*Giza 80*) showed the best performance (10.13g) and L5 (*Ashmouni*) gave the lowest one (8. 87g). The best three crosses in SI, but not significant were L8×T3 followed by L4×T1 and L5×T2. However, their parents showed insignificant GCA.

Results of NS/b under normal soil, only L5 (*Ashmouni*) and T2 had significant negative GCA, and none of the crosses had significant SCA effects. Results of DFF showed that the parents L2 had negative GCA and L5 had positive significant GCA effects. The other males and female parents and crosses gave insignificant GCA and SCA effects. High positive GCA effects are preferred for all traits except for DFF and Micronaire reading where negative GCA and SCA are preferred.

Results of PH, the lines L1 and L5 had significant positive and negative GCA effects, respectively. Three crosses, L4×T3, L7×T1, and

L7×T3 gave significant negative SCA for the first two crosses, and significant positive for the third cross. It could be noticed that positive GCA of female and male gave negative SCA, negative GCA of female with negative GCA of male gave negative SCA, and negative female with positive male gave positive SCA. This confirmed that in the existence of non-additive effects, the performance of the crosses cannot be predicted from the GCA of the parents.

The results of UHML length indicated that lines L3 and L8 gave positive GCA effects, and lines L4 and L5 showed negative GCA effects. None of the crosses gave significant SCA effects.

It could be concluded that in all traits studied under good and bad environments the GCA effects of the tested parents in current study were not indicative to the SCA effects of their crosses and their performance. Therefore, the non-additive effects were predominant in the inheritance of these traits.

Generally, under normal soil and based on the mean performance of the crosses, L4×T1was the best one for SCY/p, NB/p, BW, NS/b, SI and LY/p, and L5×T3 for lint%, L6×T3 for LI, L5×T3 for DFF, L7×T3 for PH, L3×T1 for UHML. Furthermore, T1, T2 and T3 were the best combiners in all the analyzed traits.

Under saline soil the best cross was L2×T3 for SCY/p, and L2×T2 for LY/p. The two crosses have one parent showed significant GCA effects. The best crosses for LI (L1×T1) and NB/p (L6×T1) were negative × negative GCA effects. These results are in line with Coyle & Smith, (1997), Imran et al. (2012), Simon et al. (2013), Abdel-Monaem et al. (2018), Mahrous (2018), Makhdoom et al. (2019), and Ullah et al. (2019).

Patel et al., (2014) found greater values of the ratio GCA/SCA than unity for boll weight, and seed cotton yield/plant which indicated a predominance of additive effects in the inheritance of these characters. Furthermore, the ratio of σ^2_{GCA} / σ^2_{SCA} was less than one for the number of bolls per plant. Unay et al. (2019) estimated non-additive effects for seed cotton yield (SCY/P), fiber length (FL), and fiber strength (FS), they estimated the additive effects for fiber fineness (FF).

Contribution of lines, testers, and their interaction

to total variance

The sum of squares of the crosses was divided into the sum of squares due to lines, testers, and their interaction and presented in Figs. 1 and 2. The relative contribution of the lines was greater than that of the testers for all traits in normal soils, and for SCY/p, NB/p, LY/p and LI in saline soils. Moreover, the contribution of lines was greater than the interaction of lines by testers in all traits under both environments except LI under saline soil, referring to the importance of the selection of lines for crossing. Abdel-Monaem et al., (2018), Mahrous (2018) and Farooq et al. (2020) referred that line × tester analysis in cotton revealed greater contribution of lines than that observed for testers. Moreover, Sultan et al. (2018) found that the contribution of the female lines were greater than of the interaction for earliness, since the mean squares were significant; boll weight, seed index and lint index. In addition, the tester × line contribution was approximately 30% for most traits, reflecting the importance of the non-additive effects. This result is in line with those obtained by Mahrous (2018) who found that the lines × testers interactions were high in the magnitude of the contribution of lines or testers for all yield traits which ranged from 78.80 for the number of bolls/plant to 40.00% for the seeding index.

Conclusion

Salinity adversely affects the growth, yield components, and quality-related traits of cotton. Twenty-seven cotton crosses derived from the hybridization between nine lines and three testers using line × tester approach, were used in current study. These genotypes (38 genotypes) were evaluated under normal and saline soil conditions to determine the combing ability and gene actions govern yield, quality and related traits. Despite of the significant variation which observed among genotypes for most of the studied traits, a few numbers of lines and testers exhibited significant effects under both treatments. In addition, the highly significant mean squares of the parents vs. crosses reflect the high level of heterozygosity, indicating the effects of non-additive gene action in the inheritance of most of the studied traits. This result was confirmed by the values of σ^2_A, σ^2_D and σ^2_A/σ^2_D. The genotypes L1 *(Giza 83)*, L2 *(Giza 80)*, and T2 *(Giza 90)* had significant and positive GCA effects and considered good combiners for yield components of cotton under salinity. The

crosses L4 × T1 *((G.90×Asu) × G85) × G.95)* and L5 ×T2 *(Ashmouni ×G.90)* had desirable SCA effects and considered good crosses. Based on these results herein, these genotypes performed well for most of the yield components under both conditions and they could be used in improving salt tolerance ability in cotton.
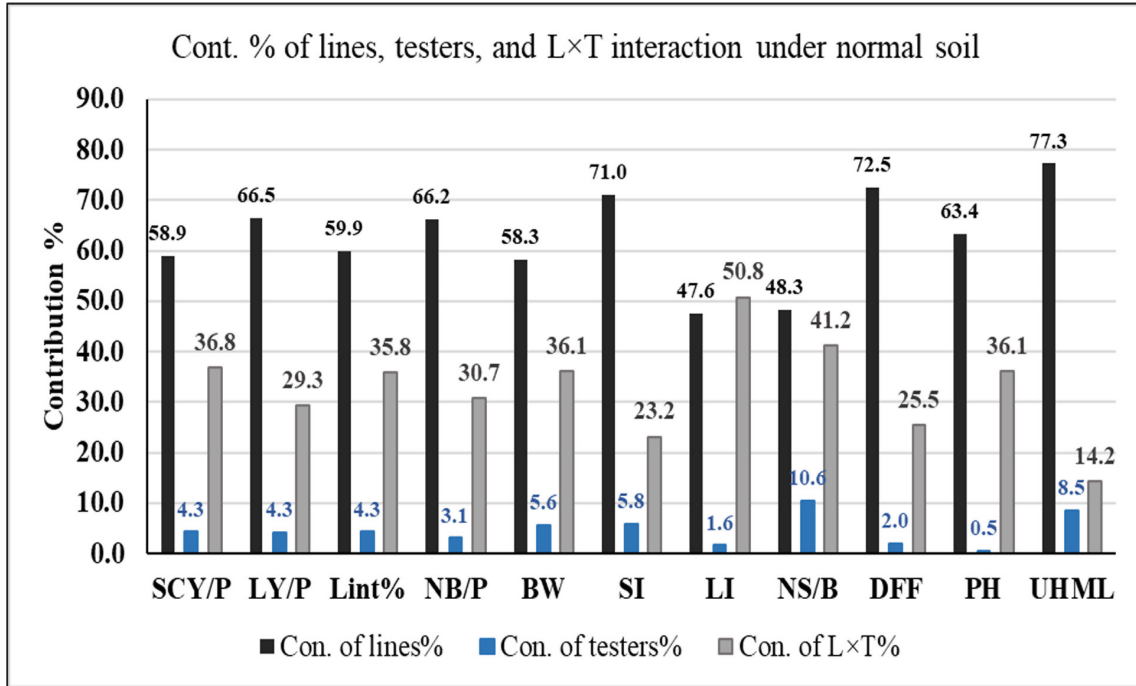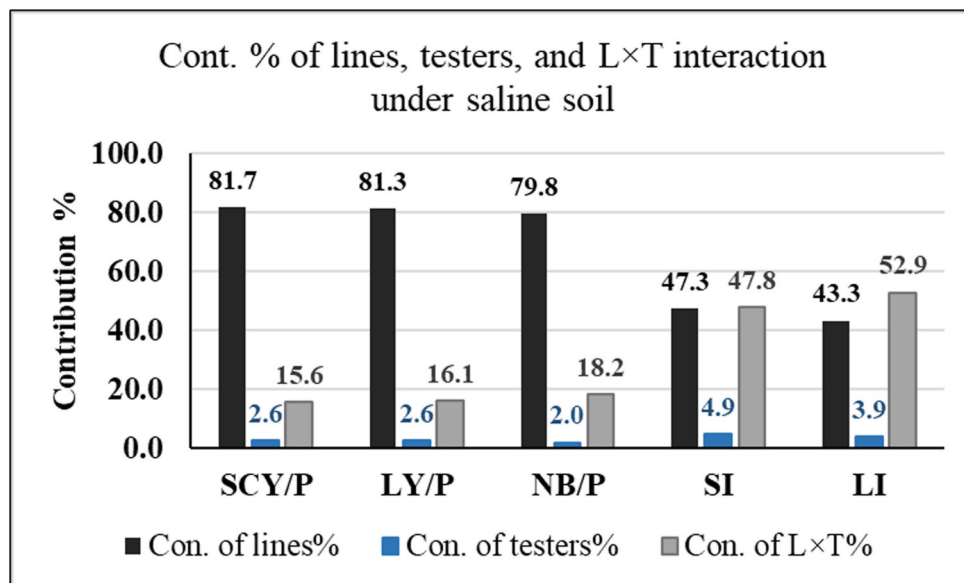

Fig. 1. Contribution percentage of lines; testers; and Line × Tester interaction to the total sum of squares under normal soil conditions. SCY/p is seed cotton yield/plant; LY/p is lint yield/plant; BW is boll weight; NB/p is number of bolls/plant; SI is seed index; NS/b is number of seeds/boll; LI is lint index; DFF is days to 1st flower; PH is plant height;and UHML is upper-half mean length

Fig. 2. Contribution percentage of lines; testers; and Line × Tester interaction to the total sum of squares under saline soil conditions. SCY/p is seed cotton yield/plant; LY/pis lint yield/plant; NB/p is number of bolls/plant; SI is seed index; and LI is lint index

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تحليل السلالة في الكشاف لصفات المحصول والجودة تحت الإجهاد الملحي في القطن (جوسيبيوم باربادنس)

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مؤخراً، حازَ موضوع تحمل الملحية على قدراً هائلاً من الاهتمام في مصر، خاصة في ظل ظاهرة تغير المناخ. يهدف هذاالبحث إلى دراسة الفعل الجيني المتحكم في صفات المحصول والجودة في القطن المصري تحت ظروف التربة العادية والمالحة.لتحقيق هذا الهدف تم تهجين 9 سلالات بثلاث كشافات بنظام تزاوج السلالة × الكشاف، الـ 27 هجيناً وآبائها قيمت تحت ظروف تربة عادية وملحية باستخدام تصميم القطاعات كاملة العشوائية فيثلاث مكررات.كان التباين المضيف والتباين السيادي كبيران تحت الظروف العادية عن الظروف الملحية لكل الصفات المدروسة. تحت الظروف العادية، كانت نسبة التباين الإضافي إلى السيادي أقل من الوحدة لمحصول القطن الزهر، محصول الشعر، نسبة الشعر، عدد اللوز للنبات، وزن اللوزة، وعدد البذور في اللوزة. في حين كان التباين السيادي غير معنوي لمعامل البذور، معامل الشعر، عدد الأيام حتى تفتح أول زهرة، إرتفاع النبات وطول الشعرة. بينما تحت الظروف الملحية، كان التباين الإضافي والتباين الإصافي × الإصافي أكثر تأثيراً من الفعل السيادي. بصفة عامة، تحت الظروف العادية وبناءاً على متوسط الأداء، كان الهجين (Giza90 × Giza95) × (Aus×Giza85) أفضل الهجن لصفات محصول القطن الزهر، محصول الشعر، عدد اللوز على النبات، وزن اللوزة، وعدد البذور باللوزة. بينما الهجين Aus×Giza83 × Giza90 ×Ashmouni كان أفضلللنسبة الشعر، والهجين Aus×Giza83 × Giza90 ×Dandaraلمعامل الشعر، والهجين Ashmouni× Giza90 × Aus×Giza83 لصفة عدد الأيام حتى تفتح أول زهرة، والهجين Giza85×Giza95 لطول الشعرة. إضافة لذلك، كانت التراكيب الوراثية جيزة 95، جيزة 90، جيزة 90 × أسترالي × جيزة 83 أفضل التراكيب الوراثية التآلفية لكل الصفات المحللة. هذه الهجن يمكن أن تستخدم لتطوير سلالات جديدة لكلا البيئتين.