Estimates of heterosis and combining ability in okra under different environments

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ABSTRACT

Ten okra genotypes (*Abelmoschus esculentus L.*) were crossed using half diallel mating design to produce 45 F_1 hybrids. The combining ability and the nature of gene action were determined for economic traits under combined data of tow sowing dates. Genotypic mean squares of were highly significant for all studied traits. Moreover, mean squares due to genotype×environment interaction (G×E) were highly significant for these traits except pod weight, suggesting a differential response of the genotypes from environment to another. The results indicated that the majority of crosses were significantly earlier, taller and higher yielding than their mid parents. Furthermore, there are some crosses showed desirable heterotic values over their better parent for the majority of traits. The results indicated that the magnitudes of the non-additive genetic variance (σ^2D) were higher than those of additive ones (σ^2A) for the majority of studied traits indicating the importance role of non-additive gene action in the inheritance of these traits. However, the magnitudes of $\sigma^2D\times E$ interaction were more than $\sigma^2A\times E$ for all studied traits. The largest value of broad sense heritability (98.80%) was recorded for pod weight, while the lowest value (36.22%) was observed for pod length. The estimates of narrow sense heritability ranged from 18.21% to 45.69% for numbers of days to flowering and plant height, respectively. These findings confirmed the predominance of non-additive genetic variance over additive one in the inheritance of these traits. Therefore, the promising crosses which showed desirable specific combining ability (SCA) effects and gave also high estimates of useful heterosis could be utilized for okra hybrids.

INTRODUCTION

Okra (*Abelmoschus esculentus* (L) Moench.) belonging to the family Malvaceae is the one of the most economically important vegetable crops in Egypt. It is cultivated for its fruits and seeds. The fruit can be cooked in variety ways. Its roots and stems are used for cleaning the cane juice. Crude fibre in mature fruits and stems are used in paper industry. In addition. okra is considered as an important source of vitamins, calcium, potassium and other mineral matters which are often lacking the diet of developing countries. Its seeds contained between 15% and 26% protein and over 14%

edible oil content. Great efforts have been made to improve yield production and quality proprieties in okra under different environmental condition **(El-Gendy and El-Diasty, 2004, El-Gendy and El-Sherbeny, 2005 and Hamada *et al.* 2015).** Heterosis breeding is an important genetic tool that can facilitate yield enhancement and helps enrich many other desirable quantitative and qualitative traits in crops. Combining ability analysis provides a guideline for the assessment of relative breeding potential of the parents or identify best combiners in crops which could be utilized either to exploit heterosis in F_1 or the accumulation of fixable genes to evolve a variety (**Srivastava *et al.* 2008, Pal and Sabesan 2009, Obiadalla-Ali *et al.* 2013, Kumar *et al.* 2013, Nagesh *et al*. 2014, Kumar and Reddy 2016, Pawar *et al*. 2016 and Sabesan *et al.* 2016**).Information on the general (GCA) and specific (SCA) combining abilities will be helpful in the analysis and interpretation of the genetic basis of important traits. GCA and SCA provide a guideline for the nature of gene action involved in the expression of economic traits under different environments (**Ramesh and Singh 1999, El-Gendy and El-Sherbeny 2005, El-Sherbeny *et al* 2005, Mehta *et al.* 2007, Murgan *et al.* 2010, Solankey and Singh 2010, El-Gendy *et al*. 2012 and Hamada *et al.* 2015)**. Improvement of okra yield could be achieved by nature gene action and magnitude of heritability variation. The role of additive as well as non-additive gene effects in controlling yield and other components reported in okra by **Singh *et al*., 2009, Reddy *et al*., 2011 and Paul *et al*. 2017.** Therefore, the present investigation was undertaken to study the amounts of heterosis and the genetic parameters under tow planting dates for choosing suitable breeding program to improve economic traits in okra.

MATERIALS AND METHODS

The present study was carried out at the Experimental Research Farm of Faculty of Agriculture, Sohag University during the three successive seasons of 2014, 2015 and 2016. Ten different genotypes of okra (*Abelmoschus esculentus* (L) Moench.) representing a wide range of diversity were chosen as parents in this investigation. These genotypes were named: Blondy (P_1), Red Okra (P_2), White velevet (P_3), Clemson spineless (P_4), Lee (P_5), Emerald (P_6), Escandrany (P_7), Annie Oakley (P_8), Dwarf long pod green (P_9) and Balady (P_{10}).In the summer season of 2014, all parental genotypes were planted and the self pollination were made for additional seeds from each one.In the summer season of 2015, the ten genotypes were crossed according to half diallel mating design to produce 45 F_1 hybrids. In addition, all parental genotypes were self pollinated to obtain more seeds from each one.In the summer season of 2016, seeds of ten parents and their 45 F_1 hybrids were sown in two planting dates. The first date was March, 15 (favorable date), while the second date was April, 15 (late date). At each date, the ten parents and their 45 F_1 hybrids were grown in a randomized complete blocks design (RCBD) with three replicates. Each replicate contained 55 plots. Each plot consisted of one row with 3.5 m. long and 70 cm. apart between rows. Plants were spaced by 30 cm. within row. All recommended cultural practices for okra production were applied in the two planting dates. Averages of the monthly degrees of temperature (minimum and maximum) were recorded in the growing season 2016 at Sohag Faculty of Agriculture farm.Data were recorded on 10 plants chosen at random from each plot for the following traits: Number of days to 50% flowering (FD); plant height (PH cm.); number of branches per plant (No. B/P); number of pods per plant (No. P/P); pods diameter (PD, cm), pods length (PL, cm), pods weight (PW, gm), early yield per plant (EY/P, gm.), estimated as the yield of the first five picking for each genotypes and total yield per plant (TY/P, gm.). Analyses of variance were carried out according to **Steel and Torrie (1980)**. The combined analysis over the two environments was calculated to partition the mean squares of genotypes and the interaction of genotypes with environments into sources of variations due to GCA, SCA, GCA×E, SCA×E. The genetic components could be obtained from the estimates variance of GCA (σ^2g), SCA (σ^2s), GCA×E (σ^2g×E), SCA×E (σ^2s×E) according to **Matzinger and Kempthorne (1956)** as described by **Singh and Chaudhary (1985).**

RESULTS AND DISCUSSION

Analysis of genotypic variation

Analysis of variance on the basis of combined data for all studies traits are presented in Table 1. The results showed that the mean squares of environment were found to be highly significant for all studied traits. Genotypic mean squares were highly significant for all studied traits, indicating the presence of a large variation among them. Moreover, mean squares due to genotype × environment interaction (G×E) were highly significant for these traits except for pod weight, suggesting a differential response of the genotypes from environment to another. Similar results were obtained by **El-Sherbeny et al 2005, Hussain *et al.* 2006, Oyetunde and Ariyo 2015 and Patil et al., 2016.**

Table 1: Analysis of variances and mean squares on the basis of combined data for all studied traits.

S.V	D.F	Mean squares								
		FD	PH	No. B/P	No. P/P	PD	PL	PW	EY/P	TY/P
Heat	1	118.80**	21569.57**	63.33**	272.18**	5.18**	59.52**	12.06**	2285.47**	18006.77**
Rep.	---	---	---	---	---	---	---	---	---	---
Rep./H	4	3.56	31.72	0.139	3.37**	0.01	0.2	0.06	33.59*	28.32
G.	54	58.93**	2239.10**	3.17**	57.16**	0.25**	2.54**	5.18**	287.80**	3169.34**
G x H	54	4.96**	114.35**	0.41**	1.83**	0.03**	0.95**	0.07	74.02**	103.00**
Error	216	2.54	15.58	0.09	1.00	0.01	0.09	0.06	11.14	13.43

*, ** Significant at 5% and 1% levels of probability, respectively

Estimates of heterosis

1- Heterosis over mid-parents (M.P %)

Estimates of heterosis above mid parents for each cross combination across the tow planting dates for all studied traits are presented in Table 2. The results showed that the best desirable of significant negative heterotic values over mid parents for days to 50% flowering were -12.39, -12.64 and -11.56% obtained from the crosses ($P_6 \times P_9$), ($P_6 \times P_{10}$) and ($P_8 \times P_9$), respectively. Out of 45 crosses, 14, 24, 27, 30, 44, 35 and 38 exhibited showed positive significant heterotic values over mid parents for plant height, number of branches per plant, number of pods per plant, pod diameter, pod length, pod weight and early yield per plant, respectively. Regarding total yield per plant, the cross combinations ($P_6 \times P_7$), ($P_6 \times P_8$), ($P_6 \times P_9$), and ($P_8 \times P_9$) gave the highest yielding with the desirable heterotic values of 71.97%, 56.60%, 73.53% and 65.03%, respectively.

Table 2: Estimates of heterosis (%) over mid-parents of each cross on the basis of combined data for all studied traits.

Crosses	FD	PH	No. B/P	No. P/P	PD	PL	PW	EY/P	TY/P
P_1 X P_2	-6.05**	-4.03	17.75**	18.61**	2.74**	12.80**	3.06**	63.15**	29.44**
P_1 X P_3	-6.34**	-9.34**	-8.77**	0.21	1.99**	20.52**	13.64**	54.10**	9.91**
P_1 X P_4	-2.90**	-4.77	-6.45**	6.63**	-1.22**	19.37**	12.85**	30.40**	14.21**
P_1 X P_5	-2.97**	-15.11**	2.54**	1.20*	5.66**	33.06**	18.50**	17.00**	18.86**
P_1 X P_6	-3.47**	-18.18**	-15.73**	-7.90**	1.69**	1.29**	20.49**	19.10**	8.56**
P_1 X P_7	-8.09**	4.55	0.33	17.79**	8.22**	20.14**	18.88**	107.28**	36.16**
P_1 X P_8	-7.56**	-1.60	10.94**	34.19**	-0.61**	8.83**	15.92**	114.36**	54.36**
P_1 X P_9	-10.91**	-16.52**	-12.84**	0.74	8.08**	30.11**	21.25**	29.05**	20.50**
P_1 X P_{10}	-10.88**	-19.48**	15.77**	26.24**	2.59**	22.28**	17.47**	118.03**	51.65**
P_2 X P_3	-4.65**	24.18**	-14.82**	-1.85**	7.46**	1.45**	8.62**	1.30	4.15
P_2 X P_4	-3.32**	9.00**	-12.50**	-6.45**	15.38**	13.41**	16.68**	12.53**	7.15**
P_2 X P_5	-0.91	-6.20*	31.32**	-8.24**	17.88**	14.09**	1.87**	-17.92**	-3.65
P_2 X P_6	-3.89**	10.61**	-20.73**	21.24**	6.09**	19.51**	19.03**	49.94**	38.89**
P_2 X P_7	-2.99**	4.68	-11.74**	1.49**	-0.89**	17.91**	8.03**	2.96	3.19
P_2 X P_8	-2.05**	23.94**	6.94**	1.73**	9.03**	13.54**	21.03**	19.65**	18.81**
P_2 X P_9	-2.13**	4.36	-11.06**	-12.05**	10.20**	12.43**	27.14**	-9.57**	10.44**
P_2 X P_{10}	-3.91**	-3.24	25.49**	-4.85**	8.11**	23.52**	22.47**	64.29**	25.41**
P_3 X P_4	-2.30**	-12.52**	-19.69**	4.77**	-4.04**	12.06**	9.25**	53.30**	5.74*
P_3 X P_5	0.90	-14.99**	-10.98**	-9.93**	-3.05**	17.65**	-12.10**	-1.03	-14.78**
P_3 X P_6	-6.95**	-6.94*	-14.43**	-11.47**	-2.37**	7.51**	-10.13**	3.46	-17.03**
P_3 X P_7	-9.12**	1.50	-1.76**	12.08**	-9.09**	20.67**	-1.95**	76.20**	5.32*
P_3 X P_8	-8.08**	-4.09	-15.31**	-0.43	-6.23**	15.49**	-15.98**	-2.11	-15.28**
P_3 X P_9	-8.53**	-5.61*	-8.85**	9.26**	-15.42**	15.98**	-14.73**	32.01**	-4.24
P_3 X P_{10}	-8.80**	-14.16**	19.06**	-1.24**	-8.16**	-0.20	-6.59**	60.74**	-7.07**
P_4 X P_5	-1.51*	-10.93**	-7.53**	18.86**	8.28**	5.80**	14.67**	30.31**	20.80**
P_4 X P_6	-3.53**	-10.34**	-11.41**	41.54**	11.75**	27.36**	11.27**	37.33**	47.82**
P_4 X P_7	-4.08**	7.10*	3.20**	0.71	8.31**	2.09**	6.83**	38.94**	-3.27
P_4 X P_8	-6.63**	-20.12**	-28.33**	29.21**	-1.73**	13.56**	10.25**	104.78**	40.88**
P_4 X P_9	-3.21**	-15.96**	-14.96**	14.17**	-1.32**	10.58**	1.87**	30.55**	16.17**
P_4 X P_{10}	-3.02**	-0.03	18.05**	6.31**	1.48**	17.09**	2.51**	22.45**	6.94**

Table 2: Cont.

P_5 X P_6	-0.47	-11.80**	5.36**	14.55**	14.75**	19.22**	4.72**	51.10**	20.76**
P_5 X P_7	-6.46**	9.26**	25.48**	3.17**	2.48**	18.55**	-11.30**	8.97**	-7.98**
P_5 X P_8	-6.47**	-14.40**	2.70**	32.43**	7.14**	16.36**	-0.56*	93.14**	28.31**
P_5 X P_9	-7.27**	-2.73	-8.49**	14.05**	1.90**	19.28**	9.18**	39.68**	21.56**
P_5 X P_{10}	-4.21**	-6.26*	51.57**	10.42**	5.56**	2.62**	-1.16**	34.92**	16.49**
P_6 X P_7	-11.30**	31.24**	37.93**	62.47**	11.76**	25.19**	8.04**	107.54**	71.97**
P_6 X P_8	-8.18**	12.00**	15.13**	48.85**	32.91**	9.23**	9.04**	80.06**	56.60**
P_6 X P_9	-12.39**	3.72	55.14**	64.50**	22.54**	27.52**	4.35**	58.13**	73.53**
P_6 X P_{10}	-12.64**	3.59	58.17**	58.05**	4.02**	33.65**	-8.45**	53.63**	53.60**
P_7 X P_8	-6.43**	49.01**	22.15**	34.31**	6.20**	8.27**	19.50**	47.78**	41.48**
P_7 X P_9	-10.11**	16.36**	10.69**	34.26**	-3.96**	23.19**	10.43**	52.48**	44.55**
P_7 X P_{10}	-10.35**	11.12**	6.78**	30.38**	-4.41**	15.77**	4.12**	56.05**	31.14**
P_8 X P_9	-11.56**	11.23**	22.73**	58.92**	11.41**	9.05**	2.66**	76.15**	65.03**
P_8 X P_{10}	-10.72**	14.50**	68.96**	48.90**	2.97**	9.88**	4.45**	123.26**	44.06**
P_9 X P_{10}	-11.34**	9.37**	96.09**	48.12**	2.06**	19.92**	7.87**	30.06**	41.85**
SEd	0.69	2.83	0.16	0.48	0.03	0.13	0.19	1.78	2.50
LSD 5%	1.36	5.61	0.32	0.95	0.05	0.25	0.37	3.52	5.12
LSD 1%	1.8	7.43	0.42	1.26	0.07	0.33	0.49	4.67	6.75

*, ** Significant at 5% and 1% levels of probability, respectively

2- Heterosis over better parents (B.P %)

Heterosis estimates of all cross combinations over better parent on the basis of combined data for studied traits are given in Table 3. The cross combinations (P_1×P_2), (P_1×P_6), (P_6×P_7) and (P_6×P_{10}) were the best for earliness with negative heterotic values of were -4.72%, -3.80%,-3.77% and -3.15%, respectively. The results indicated that, 8, 19, 14, and17 out of 45 crosses exhibited desirable heterotic values over better parent for number of branches per plant, number of pods per plant, pod length, and early yield per plant, respectively. As for total yield per plant, 12 out of 45 crosses recorded significant positive heterosis with the highest estimates of 41.94% and 32.72% for the excellent crosses (P_6×P_7) and (P_6×P_{10}), respectively.

These results indicated that the majority of crosses were significantly earlier, taller and higher yielding than their mid parents. Furthermore, there are some crosses showed desirable heterotic values over their better parent for the majority of traits. These finding reflect high degree of genetic diversity among the parental genotype and support the important role of non-additive gene action controlling these studied traits. Similar results were obtained by **Kumar *et al.*, 2013, Reddy *et al.* 2013, Obiadalla-Ali *et al.* 2013, Bhatt *et al.* 2014, Gajera and Vaddoria 2014, Bhatt *et al.*2016, Kumar and Reddy, 2016 and Pawar *et al.* 2016.**

Table 3: Estimates of heterosis (%) over better-parent of each cross on the basis of combined data for all studied traits.

Crosses	FD	PH	No of B/P	No of P/P	PD	PL	PW	EY/P	TY/P
P_1 X P_2	-4.72**	-50.49**	-19.30**	10.67**	-35.29**	-19.62**	-44.92**	36.84**	-19.09**
P_1 X P_3	0.00	-50.38**	-24.33**	-7.94**	-22.84**	-12.56**	-17.66**	17.45**	-9.58**
P_1 X P_4	0.00	-56.47**	-31.16**	-12.19**	-30.19**	-8.26**	-31.70**	1.93	-28.00**
P_1 X P_5	-2.21	-57.68**	-22.26**	-8.76**	-27.60**	10.84**	-25.86**	-2.54	-16.20**
P_1 X P_6	-3.80**	-61.32**	-28.49**	-10.48**	-35.30**	-18.94**	-30.53**	17.71**	-23.52**
P_1 X P_7	0.00	-47.03**	-9.50**	8.90**	-17.68**	-8.61**	-23.04**	36.12**	4.34
P_1 X P_8	-1.89	-56.00**	-15.73**	22.35**	-30.17**	-15.20**	-26.32**	59.67**	9.35**
P_1 X P_9	-2.51	-58.49**	-33.54**	-17.65**	-16.38**	-9.64**	-13.92**	9.16**	-18.42**
P_1 X P_{10}	-0.94	-42.35**	-7.42**	13.02**	-14.66**	-4.13**	-9.94**	50.02**	22.08**
P_2 X P_3	3.15*	-21.64**	-39.47**	-10.92**	-22.38**	-21.69**	-21.17**	-36.78**	-16.43**
P_2 X P_4	0.94	-41.03**	-46.00**	-24.00**	-22.41**	-7.57**	-29.24**	-27.58**	-34.62**
P_2 X P_5	1.26	-45.38**	-16.02**	-18.29**	-23.28**	0.34	-36.14**	-42.96**	-34.00**
P_2 X P_6	-2.83	-38.44**	-42.15**	16.51**	-36.21**	1.20**	-31.24**	27.49**	-4.97
P_2 X P_7	6.92**	-38.20**	-30.86**	-7.30**	-28.02**	-4.82**	-30.00**	-46.60**	-23.02**
P_2 X P_8	5.34**	-34.15**	-31.45**	-8.39**	-27.16**	-6.20**	-22.94**	-27.40**	-18.25**
P_2 X P_9	8.49**	-39.40**	-42.73**	-29.08**	-18.54**	-16.7**	-9.59**	-36.00**	-27.48**
P_2 X P_{10}	8.17**	-22.65**	-14.55**	-15.87**	-13.79**	2.58**	-5.96**	-9.64**	-1.59
P_3 X P_4	7.23**	-49.88**	-38.90**	-16.38**	-23.28**	-7.23**	-12.98**	-13.06**	-14.59**
P_3 X P_5	8.49**	-47.81**	-30.27**	-21.08**	-24.57**	5.00**	-28.19**	-38.80**	-24.77**
P_3 X P_6	-0.94	-45.27**	-25.22**	-16.19**	-28.90**	-7.57**	-30.99**	-20.00**	-26.83**
P_3 X P_7	5.04**	-36.90**	-8.90**	0.76	-22.41**	-1.03**	-17.78**	-22.10**	-0.62
P_3 X P_8	3.77**	-46.00**	-33.54**	-11.75**	-25.43**	-3.10**	-30.54**	-48.09**	-24.96**
P_3 X P_9	6.28**	-42.17**	-28.19**	-13.46**	-26.72**	-12.56**	-23.16**	-16.66**	-18.19**
P_3 X P_{10}	7.55**	-28.65**	-1.78**	-14.10**	-15.09**	-15.83**	-10.53**	-23.90**	-8.72**
P_4 X P_5	2.21	-53.34**	-36.20**	-7.17**	-21.15**	-1.03**	-20.00**	-16.90**	-16.58**
P_4 X P_6	-0.94	-55.40**	-30.87**	20.51**	-24.13**	14.97**	-27.84**	8.94**	1.92
P_4 X P_7	7.23**	-43.03**	-14.00**	-19.05**	-12.95**	-11.88**	-23.16**	-35.86**	-27.32**
P_4 X P_8	1.90	-62.24**	-50.46**	2.23*	-26.72**	0.17	-21.99**	12.58**	-2.30
P_4 X P_9	8.81**	-56.20**	-41.00**	-20.44**	-19.40**	-11.90**	-20.35**	-15.04**	-23.09**
P_4 X P_{10}	10.70**	-25.90**	-13.65**	-17.65**	-11.21**	3.79**	-14.04**	-39.63**	-15.52**
P_5 X P_6	0.00	-52.43**	-15.43**	6.48**	-24.57**	15.32**	-29.94**	27.62**	-7.68*
P_5 X P_7	2.51	-37.40**	7.42**	-9.02**	-19.83**	10.00**	-34.40**	-44.10**	-23.96**
P_5 X P_8	0.00	-56.00**	-26.71**	15.11**	-22.41**	10.15**	-27.60**	16.09**	-1.39
P_5 X P_9	2.21	-45.16**	-34.42**	-11.62**	-18.97**	2.75**	-12.40**	-1.93	-10.40**
P_5 X P_{10}	7.23**	-26.70**	14.25**	-5.84**	-9.91**	-2.41**	-15.09**	-26.57**	0.77
P_6 X P_7	-3.77**	-28.15**	30.56**	54.73**	-18.10**	12.05**	-25.38**	38.71**	41.94**
P_6 X P_8	-2.83*	-45.30**	-7.42**	39.87**	-10.34**	-0.17	-25.96**	36.21**	20.15**
P_6 X P_9	-4.40**	-44.18**	25.22**	39.05**	-8.62**	5.68**	-21.40**	35.60**	27.73**
P_6 X P_{10}	-3.15*	-21.60**	33.54**	45.90**	-16.38**	22.73**	-25.90**	7.50**	32.72**
P_7 X P_8	7.55**	-22.16**	4.80**	19.81**	-15.09**	-5.34**	-10.41**	-37.22**	17.33**
P_7 X P_9	6.28**	-33.44**	-4.75**	7.11**	-16.38**	-2.75**	-9.01**	-19.82**	15.32**
P_7 X P_{10}	7.55**	-12.14**	-4.15**	14.16**	-11.21**	1.72**	-8.30**	-42.57**	21.41**
P_8 X P_9	2.21	-42.95**	-11.87**	24.80**	-9.48**	-11.88**	-16.59**	8.15**	22.12**
P_8 X P_{10}	4.72**	-16.24**	27.60**	28.44**	-10.34**	-1.38**	-9.24**	1.84	25.06**
P_9 X P_{10}	6.92**	-14.56**	48.70**	13.90**	-3.88**	-2.58**	1.75**	-27.53**	18.67**
SE(d)	1.30	3.22	0.24	0.85	0.07	0.25	0.20	2.72	3.00
LSD 5%	2.62	6.49	0.49	1.71	0.14	0.50	0.40	5.49	5.91
LSD 1%	3.50	8.68	0.65	2.28	0.19	0.67	0.54	7.33	7.79

*, ** Significant at 5% and 1% levels of probability, respectively

Combining ability effects

1- General combining ability effects (g_i)

Estimates of general combining ability effects (g_i) of each parent for all studied traits are presented in Table 4. The results indicated that the parental genotypes Red okra (P_2) and Emraled (P_6) exhibited negative and highly significant general combining ability effects toward earliness. Whereas, Blondy (P_1) and Balady (P_{10}) were the poorest general combiners for this trait. The results revealed that, 4, 3, 5, 4, 5, 4 and 4 out of 10 parental genotypes were considered to be good general combiners for plant height, number of branches per plant, number of pods per plant, pod diameter, pod length, pod weight and early yield per plant, respectively. For total yield per plant, parents Escandrany (P_7), Annie Oakley (P_8), Dwarf LPG (P_9) and Balady (P_{10}) possessed positive and significant general combining ability effects, the other six parents were considered to be poor general combiners. Consequently, these promising parents which possessed general combining ability effects, could be utilized in okra breeding program to improve studied traits.

Table 4: Estimates of general combining ability effect (gi) for each parent on the basis of combined data for all studied traits.

Genotypes	FD	PH	No of B/P	No of P/P	PD	PL	PW	EY/P	TY/P
P_1	6.36**	-8.20**	-0.65**	-6.70**	-0.29**	-2.63**	-1.81**	-17.58**	-64.92**
P_2	-10.59**	-55.27**	-0.73**	1.07**	-0.58**	-1.38**	-2.01**	27.21**	-17.93**
P_3	1.08**	31.29**	-1.71**	-5.63**	-0.16**	-0.96**	0.32**	-10.60**	-36.32**
P_4	1.69**	-20.09**	-1.42**	-8.13**	-0.28**	-0.38**	-0.45**	-10.49**	-55.61**
P_5	-0.14	-42.55**	-1.46**	-4.80**	-0.08**	1.32**	-0.60**	-7.12**	-40.23**
P_6	-6.92**	-30.96**	-0.21**	1.66**	-0.41**	1.80**	-1.81**	11.98**	-13.60**
P_7	-3.64**	19.46**	2.77**	11.48**	0.34**	1.56**	-0.90**	7.80**	66.18**
P_8	0.97**	4.67**	-0.04**	7.27**	0.03**	0.43**	0.71**	-0.91**	52.06**
P_9	1.97**	-5.48**	0.07**	0.73**	0.50**	-0.75**	2.30**	5.30**	31.38**
P_{10}	9.24**	107.12**	3.38**	3.06**	0.94**	0.99**	4.25**	-5.58**	78.79**
SE(gi)	0.21	0.53	0.04	0.14	0.01	0.04	0.03	0.45	0.49
LSD 5%	0.49	1.20	0.09	0.32	0.03	0.09	0.07	1.02	1.12
LSD 1%	0.70	1.73	0.13	0.46	0.04	0.13	0.11	1.46	1.61

*, ** Significant at 5% and 1% levels of probability, respectively

2- Specific combining ability effects (S_{ij})

Estimates of specific combining ability effects (S_{ij}) of each cross for all studied traits are presented in Table 5. The results showed that, all studied traits exhibited significant SCA effects in most cases either positive or negative significant. The results indicated that the best crosses for days to 50% flowering were ($P_1 \times P_5$), ($P_1 \times P_6$), ($P_7 \times P_8$), ($P_7 \times P_9$) and ($P_7 \times P_{10}$) with desirable SCA effects toward earliness. These crosses were a results of crossing (good × poor) and (poor × poor) general combiners. The highest desirable SCA effects toward tallness were obtained from the crosses ($P_1 \times P_2$), ($P_1 \times P_{10}$) and ($P_8 \times P_{10}$), resulting from crossing (good x poor) and (poor × poor) general combiners. Moreover, 4, 7, 6, 4, 11 and 6 out of 45 crosses were the promising hybrids for increasing number of branches per plant, number of pods per plant, pod diameter, pod length, pod weight, pod length, pod weight and early yield per plant, respectively. Concerning total yield per plant, the crosses ($P_1 \times P_3$), ($P_2 \times P_{10}$), ($P_3 \times P_6$), ($P_5 \times P_6$), ($P_7 \times P_9$), ($P_7 \times P_{10}$), and ($P_9 \times P_{10}$) exhibited desirable SCA effects for high yielding. These hybrids were resulted from (good × good), (good × poor) and (poor × poor) general combiners. Therefore, it is not necessary that parents having high estimates of GCA effects would also give high estimates of SCA effects in their respective crosses. In addition, the promising crosses which showed desirable SCA effects, gave also high estimates of useful heterosis as previously mentioned. These finding indicate that non additive gene action played an important role in the inheritance of these traits.

Table 5: Estimates of Specific combining ability effect (S_{ij}) for each cross on the basis of combined data for all studied traits

Crosses	FD	PH	No. B/P	No. P/P	PD	PL	PW	EY/P	TY/P
P_1 X P_2	-0.19	17.47**	-0.54*	0.46	-0.23**	-0.09	-1.11**	-6.67**	-15.06**
P_1 X P_3	2.56	4.74	0.68**	1.68	0.25**	-0.04	1.55**	-0.69	34.77**
P_1 X P_4	-1.59	-7.83*	-0.03	-0.69	0.05	0.31	-0.29	0.17	-7.36*
P_1 X P_5	-3.47*	9.45**	0.14	0.94	-0.10	0.64*	0.09	1.67	10.34**
P_1 X P_6	-2.94*	-0.70	0.43	1.54	-0.25**	0.14	-0.45*	3.99	2.78
P_1 X P_7	5.91**	-3.76	0.05	-2.41**	0.14*	-0.27	0.54**	-10.10**	-3.76
P_1 X P_8	1.92	-16.71**	-0.21	-1.76*	-0.05	0.24	-0.07	-3.90	-10.96**
P_1 X P_9	5.17**	-0.18	-0.22	-3.09**	0.16*	-0.45	0.81**	-0.84	-15.47**
P_1 X P_{10}	5.91**	33.35**	-0.79**	-2.14*	0.32**	0.15	1.29**	-5.33	1.95
P_2 X P_3	0.35	-6.97*	0.37	0.17	0.15*	0.16	0.82**	2.42	12.03**
P_2 X P_4	0.20	-2.68	0.07	0.13	0.004	0.27	-0.19	-1.16	-4.21
P_2 X P_5	-0.51	1.21	0.38	-0.17	0.01	0.95**	0.35	-3.02	5.49
P_2 X P_6	0.35	-6.81*	-0.15	-2.05*	-0.09	-0.90**	0.25	-3.17	-9.60**
P_2 X P_7	1.53	0.72	-0.25	-1.46	0.13	-0.23	0.66**	2.07	2.32
P_2 X P_8	-0.62	-8.16*	0.24	1.71*	-0.08	-0.33	-0.03	9.62**	11.57**
P_2 X P_9	-1.20	-9.20**	-0.39	-2.95**	0.13	0.28	0.64**	-3.45	-15.01**
P_2 X P_{10}	-1.47	-14.59**	-0.33	1.30	0.06	0.17	0.49*	8.59**	19.44**
P_3 X P_4	-2.22	-2.58	-0.19	-0.06	0.08	0.21	-0.57**	1.57	-7.14*
P_3 X P_5	-1.59	-3.09	0.83**	0.01	0.01	0.25	-1.12**	-2.79	-10.25**
P_3 X P_6	-2.06	3.80	-0.36	3.87**	-0.21**	0.17	-0.39	8.51**	16.26**

P_3 X P_7	2.28	-8.46*	-0.72**	-2.33**	-0.21**	-0.11	-0.51*	-7.34**	-24.32**
P_3 X P_8	0.30	0.96	-0.05	-1.44*	-0.11	0.09	-0.31	-0.79	-15.33**
P_3 X P_9	1.71	-3.87	-0.45	-3.08**	-0.02	-0.23	0.42*	-4.30	-20.72**
P_3 X P_{10}	0.45	-8.41*	-0.33	-1.58	-0.03	0.45	0.25	4.43	-2.97
P_4 X P_5	2.09	6.32	0.29	0.20	0.01	0.37	-0.25	-1.87	5.11
P_4 X P_6	-1.22	7.01*	0.14	-0.65	-0.01	-0.49	-0.18	-2.34	-3.91

Table 5: Cont.

P_4 X P_7	1.13	6.26	-0.06	-0.44	-0.05	-0.04	0.71**	-1.78	6.11*
P_4 X P_8	-0.69	-2.94	-0.18	-1.35	-0.04	0.12	-0.77**	-5.54*	-18.19**
P_4 X P_9	0.40	5.00	-0.03	0.01	-0.19**	-0.14	-0.54**	0.09	-5.28
P_4 X P_{10}	-0.04	-4.06	0.03	-0.67	-0.03	-0.76**	0.05	1.15	-6.30*
P_5 X P_6	-0.76	-1.58	-0.05	4.30**	0.05	0.40	0.13	3.41	25.12**
P_5 X P_7	2.76*	3.17	-0.22	-4.39**	0.12	-1.10**	0.29	-5.77*	-28.26**
P_5 X P_8	-1.23	-20.19**	-0.75**	0.01	-0.13	-0.12	-0.01	7.46**	3.87
P_5 X P_9	2.19	-9.00**	-0.45	-1.92*	-0.07	-0.52*	-0.27	-0.39	-14.73**
P_5 X P_{10}	2.09	5.42	-0.36	-2.07*	0.02	-0.04	-0.21	-3.28	-17.91**
P_6 X P_7	1.95	8.27*	0.19	-4.42**	0.05	0.05	-0.36	-12.42**	-31.07**
P_6 X P_8	-0.54	-14.29**	-0.26	0.43	0.06	0.34	-0.19	3.49	-1.74
P_6 X P_9	0.38	3.52	-0.54*	-2.15*	0.02	0.21	0.71**	-2.17	-6.87*
P_6 X P_{10}	1.95	1.47	0.27	-1.82*	0.13	-0.52*	-0.001	-5.08	-5.95
P_7 X P_8	-2.85*	-11.80**	-0.35	1.88*	0.15*	-0.20	-0.27	9.12**	2.94
P_7 X P_9	-3.94**	-7.71*	0.73**	3.38**	0.08	0.44*	-0.28	7.43**	16.77**
P_7 X P_{10}	-4.37**	-4.01	0.18	3.88**	-0.21**	0.99**	-1.14**	3.75	10.63**
P_8 X P_9	0.58	11.12**	0.41	-0.60	-0.03	0.23	0.38	-3.04	6.13*
P_8 X P_{10}	0.15	13.01**	-0.39	1.60	-0.01	0.05	-0.05	-5.50*	1.23
P_9 X P_{10}	-1.60	9.81**	0.65**	2.77**	-0.11	0.17	-0.53*	3.08	17.06**
SEd	0.09	0.24	0.02	0.06	0.01	0.02	0.02	0.20	0.22
LSD 5%	2.62	6.49	0.49	1.71	0.14	0.50	0.40	5.49	6.04
LSD 1%	3.50	8.68	0.65	2.28	0.19	0.67	0.54	7.33	8.07

*, ** Significant at 5% and 1% levels of probability, respectively

Combining ability analysis of variance

Analysis of variance and mean squares of general and specific combining ability and their interactions with environments for all studied traits are given in Table 6. The results showed that mean squares of general (GCA) and specific (SCA) combining ability were highly significant for all studied traits with ratio of GCA/SCA more than unity. The interaction of GCA × E mean squares were highly significant for all studied traits except number of branches per plant and pod weight. However, the interaction of SCA × E mean squares were highly significant for all studied traits except pod weight. The ratio of GCA × E / SCA × E mean squares were more than one for all studied traits except for numbers of pod per plant.

Generally, the significance of GCA and SCA mean squares support that all types of gene action are involved in the inheritance of these traits. The results also showed that the interactions of GCA × E and SCA × E mean squares were highly significant for most studied traits, revealing that the magnitudes of all types gene action fluctuated from normal date to stress date conditions. In addition, the obtained ratios of GCA × E/ SCA × E which exceeded one for the majority of studied traits reflect that non additive gene action was more stable over the environments than additive ones. Similar results were obtained by (**Pal and Sabesan 2009, Bhatt *et al*. 2014 Oyetunde and Ariyo 2015 and Patil *et al*. 2016)**. In contrast, **El-Sherbeny et al 2005**, found that the magnitudes of additive genetic variance (σ^2A) were larger than those of non-additive ones (σ^2D) for the same studied traits.

Table 6: Combining ability analysis of variance on the basis of combined data for all studied traits.

S.V		Mean squares								
	D.F	FD	PH	No. B/P	No. P/P	PD	PL	PW	EY/P	TY/P
GCA	9	51.34**	3196.39**	4.52**	60.69*	0.33**	3.17*	6.00**	264.51**	4170.60**
SCA	45	13.31**	256.36**	0.36**	10.81**	0.04**	0.38**	0.87**	62.22**	478.04**
GCA × Env.	9	2.48*	52.45**	0.11	1.35**	0.02*	0.69**	0.02	65.28**	36.22**
SCA × Env.	45	1.49**	35.25**	0.14**	0.50*	0.01*	0.24**	0.02	16.55**	25.82**
Error	216	0.85	5.19	0.03	0.33	0.003	0.03	0.02	3.71	4.48
GCA/SCA	---	3.86	12.47	12.56	5.61	8.25	8.34	6.90	4.25	8.72
GCA×E/SCA×E		1.67	1.49	0.79	2.72	2.69	2.85	1.00	3.94	1.40

*, ** Significant at 5% and 1% levels of probability, respectively

Genetic parameters

The estimates of genetic parameters for all studied traits are presented in Table 7. The results indicated that the magnitudes of the non-additive genetic variance (σ^2D) were higher than those of additive ones (σ^2A) for the majority of studied traits indicating the importance role of non-additive gene action in the inheritance of these traits. However, the magnitudes of σ^2D×E interaction were more than σ^2A×E for all studied traits. Therefore, non-additive gene effect was more influenced by heat stress than additive ones. The estimates of broad sense heritability were higher than those of narrow sense for all studied traits. The largest value of broad sense heritability (98.80%) was recorded for pod weight, while the lowest value (36.22%) was observed for pod length. The estimates of narrow sense heritability ranged from 18.21% to 45.69% for numbers of days to flowering and plant height, respectively. These findings ensure the predominance of non additive genetic variance over additive one in the inheritance of these traits. These results are agree with those obtained by **(El-Gendy and El-Sherbeny 2005, Pal and Sabesan 2009, El-Gendy *et al.* 2012, Reddy *et al*. 2012, Solankey *et al*. 2012, Reedy *et al*. 2013, Hamada *et al.* 2015, Verma and Sood 2015 and Paul *et al*. 2017.**

Table7: **Estimates of genetic parameters on the basis of combined data for all studied traits.**

Traits / genetic parameters	FD	PH	No. B/P	No. P/P	PD	PL	PW	EY/P	TY/P
σ^2 A	6.17	487.14	0.70	8.17	0.05	0.39	0.85	25.59	613.69
σ^2 D	23.64	442.22	0.44	20.62	0.06	0.28	1.70	91.33	904.44
σ^2 A x E	0.66	11.46	0.02	0.57	0.01	0.30	0.001	32.49	6.93
σ^2 D x E	2.56	120.23	0.46	0.66	0.02	0.85	0.01	51.36	85.38
Error	0.85	5.19	0.03	0.33	0.003	0.03	0.02	3.71	4.48
h^2_{NS} %	18.21	45.69	42.42	26.92	34.97	21.08	32.94	21.22	38.00
h^2_{BS} %	87.99	87.16	69.09	94.86	76.92	36.22	98.80	96.92	94.01

Generally, the results of this study showed that mean squares of G x E interaction were found to be highly significant for all studied traits. This findings suggested a differential response of the genotypes from environment to another. The amounts of heterosis obtained from this study reflect high

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