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Generation Mean Analysis for Seed Yield and its Components of some Quantitative Characters on Soybean Crosses

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ABSTRACT

The present study was carried out at Sakha farm, Sakha Agricultural Research Station (SARS), Kafr El-Sheikh, Egypt, during the three summer seasons of 2017, 2018 and 2019. Four crosses of soybean, each with six populations (P1, P2, F1, Bc1, Bc2 and F2) were tested for yield and some growth attributes. The results showed that: Over dominance was observed for flowering date in crosses I and II, for maturity date and plant height in cross II and seed yield per plant in all crosses, while partial dominance was observed for the remaining crosses for most traits. Significant negative heterosis were detected for flowering date for mid-parent in the first cross, significant positive heterotic effects were detected for other traits. The additive effect (a) was highly significant in positive or negative direction in all crosses for all traits, except in the four crosses for number of seeds per pod and 100 seed weight, crosses I and II for flowering date. Additive x additive types of gene action were found to be significant for most traits of all crosses, also additive x dominance and dominance x dominance types of gene effects were found to be significant for most traits. High narrow sense heritability values were obtained for plant height and number of seeds per pod in the first cross. While, the lowest estimates was resulted for number of seeds per pod in the second cross, number of branches per plant in the first cross and seed yield per plant in the fourth cross.

Keywords: Soybean, gene effect, heritability and genetic advance.

INTRODUCTION

Soybean (*Glycin max* (L.) Merrill 2n=40) is one of the most important legume crops for oil and protein production. Soybean it is an important source of protein and oil, its seeds contain about 14 to 24% or more oil and about 45 to 48% protein (Brim and Burton, 1979). It is widely used in Egypt for human and poultry consumption. Moreover in Egypt, the quantity of oil seeds produced, including main oil crops, i.e., cotton, sesame, flax seeds and peanut, is far from being sufficient for excessive demand. Therefore, Egyptian plant breeders have intensified their efforts to increase soybean yield and yield components to meet the increasing demand for oil and protein production (Talwar *et al.*, 1986)

Information about the types and magnitude of genetic variation and the relative importance of additive and non-additive gene action would assist soybean breeders in carrying out the most suitable breeding programs for soybean improvement. Accordingly, the Plant breeder usually has in mind an ideal plant that combines maximum number of desirable characteristics. One of the aims of virtually every breeding project is to increase the yield. Early maturity is another important character since it free land quickly, often allowing an additional planting of the same crop or other crop in the same year. The plant breeder is interested in the determination of gene effects to establish the most advantageous breeding programs for the improvement of the desired characters Talwar and Sharma (1986). especially for soybean because it is an important source of protein and oil , its seeds contain about 14 to 24% or more oil and about 45 to 48% protein (Brim and Burton, 1979) . It is widely used in Egypt for human and poultry consumption. Moreover in

Egypt, the quantity of oil seeds produced, including main oil crops; i.e., cotton, sesame , flax seeds and peanut, is far from being sufficient for excessive demand. Therefore, Egyptian plant breeders have intensified their efforts to increase soybean yield and yield components to meet the increasing demand for oil and protein production. The present investigation was designated to estimate the gene action, heritability, heterosis and predicated genetic gain for some agronomic characters in four soybean crosses.

MATERIALS AND METHODS

The present study was carried out at Sakha farm, Sakha Agricultural Research Station (SARS), Kafr El-Sheikh, Egypt, during the three summer seasons of 2017, 2018 and 2019. Four soybean genotypes of wide divergent origin were used as parental material; namely, Giza 111 , Quinitz, L86-K-96 and Toano. The genotypes Quinitz and L86-K-96 belong to the maturity group III; i.e; it requires 110 days from sowing to the maturity, while the genotypes Giza 111 and Toano belong to the maturity group IV,V it requires 120 ,130 days to maturity respectively .Four crosses; namely, cross I (Giza 111 x Toano), cross II (Giza 111 x Quinitz), cross III (L86-K96 x Quinitz) and cross IV (Quinitz x Toano) were made in 2017. In the second season parents and F₁'s of each cross were planted. F₁ plants in each cross were self-pollinated and back crossed to both parents to obtain the F₂s and the back crossed seeds. Crosses between the parental varieties were repeated to obtain F₁ hybrid seeds.

In the third season (2019), the six populations; namely (P₁, P₂, F₁, BC₁, BC₂ and F₂) of each cross were arranged in (RCBD) with three replications. Each consisted of two rows

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for non-segregating generations; i.e; P₁, P₂ and F₁, four rows of back crosses whereas the F₂ population was presented by eight rows. Each row was 4 m. long, 60 cm width and 20 cm between hills. One seed was planted per hill at one side of the ridge. Before flowering, 20, 40 and 80 plants were kept with caution for non-segregating generation, back cross and F₂ and were tagged in each one of the three plots. A total tagged plants for each cross was 60 P₁, 60 P₂, 60 F₁, 120 BC₁, 120 BC₂ and 240 F₂ plants. nine agronomic characters related to seed yield were chosen for this study these characters were; flowering date, maturity date, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 100 seed weight and seed yield per plant.

Statistical analysis

Statistical analysis was used to calculate the means and variances for the six generations. Population means and variances were used to estimate the type of gene action for each character.

A one-tail F-ratio was calculated to test the significance of the F₂ variance from environmental variance, as follows:

$$F = \frac{F_2 \text{ variance}}{\text{Environmental variance}}$$

If the F-ratio was significant, Mather's procedure was used to calculate the components of genetic variance.

Heterosis and inbreeding depression were determined according to Mather and Jinks (1971). The two estimates of epistatic deviation (E₁) and (E₂) were calculated as the deviation of segregating populations; i.e., F₂ and (BC₁ and BC₂) from their non segregating populations (F₁ and mid-parents).

$$E_1 = F_2 - \frac{1}{2} F_1 - \frac{1}{4} P_1 - \frac{1}{4} P_2$$

$$E_2 = BC_1 + BC_2 - F_1 - \frac{1}{2} P_1 - \frac{1}{2} P_2$$

E₁ being the epistatic deviation of F₂ and E₂ the epistatic deviation of BC₁ + BC₂ (Mather and Jinks, 1971). The relative of potence ratio (P) was used to determine the degree of dominance and its direction according to (Mather and Jinks, 1971) as follows:

$$\text{Potence ratio} = \frac{(F_1 - M.P)}{\frac{1}{2}(P_2 - P_1)}$$

Where, p₁ the mean of low parent and p₂ the mean of the high parent.

The six population means in each cross were used to estimate the six parameters for gene effects using the relationships. Given by Gamble (1962); namely, a, d, aa, ad and dd. Where a= additive effect, d= dominance effect, aa= additive x additive types of epistasis, ad= additive x dominance types of epistasis and dd= dominance x dominance types of epistasis.

Mather (1949) derived the expected genetic variance of VBC₁, VBC₂ and VF₂ interms of additive (1/2D) and dominance (1/4H) genetic variance as follows:

$$\frac{1}{2} D = 2VF_2 - (VBC_1 + VBC_2)$$

$$\frac{1}{4} H = VBC_1 + VBC_2 - VF_2 - VE$$

The variance of each of the genetic variance components was estimated as linear function of the variance of the mean squares. The variance of a mean square was calculated as a given by (Anderson and Bancroft (1952). The standard error of the estimate is the squar root of variance.

Heritability estimates were calculated in the F₂ generation as follows:

$$H^2 \text{ (broad sense)} = \frac{(\frac{1}{2} D + \frac{1}{4} H)}{(\frac{1}{2} D + \frac{1}{4} H + E)}$$

$$h^2 \text{ (narrow sense)} = \frac{\frac{1}{2} D}{(\frac{1}{2} D + \frac{1}{4} H + E)}$$

$$E = VP_1 + VP_2 + VF_1 / 3$$

Expected and predicated values of genetic advance (GS and GS %) were calculated according to Johanson *et al* (1955)

Genetic advance as percent of the F₂ mean (GS %) was calculated as given by Miller *et al*, (1958).

$$GS = K \times h^2 \times \sigma_{ph} \quad GS \% = (GS / F) \times 100$$

Where;

K=selection differential (K = 2.06 when selection intensity 5%),
phenotypic standard deviation of F₂.

RESULTS AND DISCUSSION

Generation means:

Table 1 shows that the difference between each two parents were found to be significant in all studied traits in the four crosses. The F₁'s were intermediate between there parental genotypes for the time required for flowering and maturity, while F₂'s later than their F₁'s in all crosses. While, back crosses were closer to back cross parent. Consequently, the genetic parameters needed in this concern were calculated.

The parent Toano was the shortest plant height (about 52 cm.), the parent Quintiz was the earliness variety for flowering and maturity (about 32 and 110 days) and the L86-K96 line was the highest for number of branches per plant (4.93).

Table 1. Average and standard error values of the parents, F₁, F₂ and back crosses for studied characters in the four soybean crosses.

Character	Generation	Cross I	Cross II	Cross III	Cross IV
(1) flowering date	P1	37.45±0.22	38.34±0.20	45.05±0.25	34.02±0.75
	P2	50.73±0.21	32.23±0.20	33.73±0.22	48.00±1.17
	F1	43.12±0.20	36.23±0.21	48.03±0.26	41.50±1.49
	Bc1	40.11±0.21	40±0.20	44.00±0.23	36.15±2.51
	Bc2	44.14±0.20	38.00±0.21	52.00±0.27	44.00±2.31
	F2	48.16±0.22	42.00±0.22	50.44±0.26	42.65±3.16
(2) maturity date	P1	129.44±0.19	125.40±0.32	122.77±0.28	110.01±2.06
	P2	131.7±0.21	109.90±0.36	111.70±0.31	132.00±1.85
	F1	130.11±0.28	118.35±0.40	126.47±0.33	124.63±1.68
	Bc1	130.35±0.21	122.33±0.36	125.00±0.33	1115.35±3.54
	Bc2	133.54±0.28	118.00±0.40	131.00±0.33	1126.00±3.77
	F2	138.11±0.19	130.00±0.32	130.39±0.28	1118.35±4.50
(3) plant height (cm)	P1	115.62±0.33	117.25±0.61	65.00±0.35	71.35±1.79
	P2	52.77±0.21	68.11±0.66	52.44±0.40	56.22±2.05
	F1	122.22±0.34	98.35±0.73	89.64±0.41	91.13±2.52
	Bc1	120.00±0.21	118.35±0.67	71.86±0.40	80.28±3.74
	Bc2	95.21±0.34	85±0.72	69.55±0.41	71.10±3.87
	F2	125±0.28	112±0.61	61.00±0.35	72.32±4.72
(4) No. of branches / plant	P1	3.88±0.14	3.91±0.14	4.93±0.14	4.17±1.58
	P2	4.74±0.09	4.07±0.17	4.08±0.12	4.77±1.39
	F1	4.20±0.16	4.48±0.15	5.91±0.16	6.00±1.26
	Bc1	3.77±0.09	4.00±0.17	4.45±0.12	4.50±2.31
	Bc2	3.87±0.16	4.20±0.15	4.22±0.15	4.22±2.54
	F2	3.44±0.14	4.30±0.14	4.72±0.14	4.08±2.88
(5) No. of pods / plant	P1	115.01±1.00	118.34±1.02	118.13±1.23	114.36±6.52
	P2	134.80±0.85	113.5±1.09	122.80±1.19	133.00±4.63
	F1	126.12±1.92	168.50±1.43	191.55±1.30	187.57±7.43
	Bc1	120.11±0.85	110.35±1.19	155.11±1.22	155.00±8.68
	Bc2	128.12±0.46	100.00±1.42	162.00±1.19	141.00±9.39
	F2	118.24±1.00	105.24±1.02	142.55±1.30	128.92±9.85
cross I	(Giza 111 x Toano)	cross II	(Giza 111 x Quintz)		
cross III	(L86-K96 x Quintiz)	cross IV	(Quintiz x Toano)		

Table 1. Cont.

Character	Generation	Cross I	Cross II	Cross III	Cross IV
(6)No. of seeds / plant	P1	293.25±2.58	302.95±1.71	266.63±2.16	255.02±11.23
	P2	265.56±2.24	253.17±1.58	268.70±2.05	262.01±12.87
	F1	321.30±3.22	440.16±1.89	427.49±2.35	435.16±14.49
	Bc1	300.00±2.24	268.25±1.58	328.60±2.06	341.00±18.25
	Bc2	257.28±3.22	247.00±1.89	324.00±2.36	284.82±17.35
	F2	274.94±2.58	241.50±1.71	304.37±2.16	29.65±18.99
(7)No. of seeds / pod	P1	2.55±0.03	2.56±0.07	2.22±0.06	2.23±0.19
	P2	1.97±0.03	2.23±0.07	2.11±0.07	1.97±0.14
	F1	2.55±0.04	2.62±0.07	2.23±0.08	2.32±0.35
	Bc1	2.50±0.03	2.44±0.06	2.12±0.07	2.20±0.40
	Bc2	2.01±0.04	2.47±0.66	2.00±0.08	2.02±0.39
	F2	2.33±0.03	2.30±0.07	2.14±0.06	2.27±0.50
(8)100-seed weight (gm)	P1	16.43±0.05	16.43±0.10	11.14±0.12	14.07±0.39
	P2	17.47±0.07	14.07±0.11	14.47±0.11	17.47±0.49
	F1	17.80±0.17	15.35±0.10	16.20±0.15	15.17±0.66
	Bc1	17.22±0.07	16.00±0.10	14.28±0.10	14.03±1.46
	Bc2	15.98±0.17	15.00±0.09	15.20±0.15	14.22±1.31
	F2	17.00±0.05	15.00±0.10	15.05±0.12	12.65±1.72
(9) Seed yield per plant (gm)	P1	48.18±0.38	49.77±0.69	28.97±0.28	35.88±1.57
	P2	38.43±0.39	35.62±0.86	36.43±0.28	37.91±1.91
	F1	57.19±1.23	67.56±0.96	69.25±0.34	66.01±32.31
	Bc1	51.66±0.39	42.94±0.86	46.92±0.28	47.84±2.62
	Bc2	41.66±0.1.23	39.22±0.95	49.92±0.34	40.50±2.69
	F2	46.74±0.38	37.43±0.67	49.95±0.27	36.76±2.83
cross I (Giza 111 x Toano)		cross II (Giza 111 x Quintz)			
cross III (L86-K96 x Quinitz)		cross IV (Quinitz x Toan)			

Scaling test:

The results obtained in the present investigation for individual scaling test are presented in Table (2). All nine quantitative characters for four crosses contributed significantly in individual scaling tests, indicating the presence of epistasis. The results of gene effects are presented in Table (3) are discussed as below. Individual scaling test i.e. A, B, C and D of Mather (1949) were used to detect presence of epistasis by using the data of various generations in all four crosses. The results of this study can help in devising proper breeding strategies as per trait desired. A and B testes provides evidence the presence of all types non- allelic gene interactions. The significant of C scale suggests (dd)type of epistasis. The significant D scales reveal (aa) gene interactions, significant of C and D scales indicates (aa) and (dd) type of gene interactions . The test of adequacy of scales is important because in most cases the estimation of additive and dominance components of the variance are made assuming absence of gene interaction. These result were in agreement with those reported by Raut (2002), Adsul *et al.* (2016) and Thakare *et al.* (2017).

The values of A, B, C and D should significantly differ than zero within the limits of their standard error. However , the results table (3) indicated that, the values of scaling test were significantly differ than zero for all studied traits in all crosses, which mean the presence of non- allelic gene interaction and the six parameters model must be done in all cases.

Type of gene action using generation means:

The estimated values of the six parameters describing the nature of gene action are presented in Table (3), the estimated mean effect (m) which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci was highly significant. The additive effect (a) was highly significant in positive or

negative direction in all crosses for all traits, except in the four crosses for number of seeds per pod and 100seed weight, crosses I and II for flowering date. Dominance gene effects (d) were highly significant for seed yield and its major components in the four crosses except number of seeds per pod for crosses (II and IV) and 100-seed weight for crosses (II and IV) which exhibited insignificant value. Thus would suggest that dominance gene effects have a significant contribution to the inheritance of these traits in these crosses.

Table 2. Estimation of individual scaling test for detecting non-allelic interactions for yield contributing traits in soybean.

character	Cross	Scaling tests			
		a	b	c	d
(1) flowering date	I	-0.35**	-5.57**	18.22**	12.07**
	II	5.66	7.77	25.43	6
	III	-5.06	5.24	9.94	4.88
	IV	-3.5	-1.50**	5.60**	5.3
(2) maturity date	I	1.15**	5.27**	31.08**	12.33**
	II	-5.40**	13.10**	47.70**	20
	III	0.76**	3.83*	14.15**	4.78**
	IV	-4.63**	-4.63**	-17.86**	-4.30**
(3) plant height (cm)	I	65.01**	-47.42**	87.17**	34.79**
	II	69.55**	-45.60**	65.95**	21.00**
	III	1.60**	-32.63**	-9.63**	10.70**
	IV	13.43**	-20.48**	-20.25**	-6.60**
(4) No. of branches / plant	I	-0.54	-0.51	-2.59	-0.77
	II	-0.38	-0.54	-0.12	0.4
	III	-1.94	-1.56	-1.98	0.76
	IV	-1.47	-1.63	-4.22**	-0.56
(5)No. of pods / plant	I	-0.91*	-4.68**	-29.09**	-11.75**
	II	-66.34**	-91.53**	-147.87**	5.00**
	III	1.17**	-2.50**	-66.41**	-32.54**
	IV	8.07**	-38.57**	-106.82**	-38.16**
(6)No. of seeds / plant	I	-14.55**	-72.30**	-101.65**	-7.40**
	II	-206.31**	-199.33**	-470.44**	-32.40**
	III	-30.32**	-45.05**	-163.08**	-43.86**
	IV	-8.19**	-127.53**	-216.76**	-40.52**
(7)No. of seeds / pod	I	0.48	-1.08	-0.3	0.15
	II	0.03	-0.24	-0.83	-0.31
	III	0.04	-0.45	-0.09	0.16
	IV	0.11	-0.51	0.24	0.32
(8)100-seed weight (gm)	I	2.17	-2.27	1.50**	0.8
	II	2.58	-0.02	0.8	-0.88
	III	-2.11	3.06	2.19	0.62
	IV	-1.58	-0.8	-8.64	-3.13
(9) Seed yield per plant (gm)	I	7.70**	-23.15**	-14.03**	0.71**
	II	-17.30**	-38.89**	-70.80**	-7.30**
	III	-13.83	0.28	-22.67**	-4.56
	IV	-8.24*	-20.89**	-58.80**	-14.83

*and **significant at 0.05 and 0.01 levels of probability, respectively.

cross I (Giza 111 x Toano) cross II (Giza 111 x Quintz)
cross III (L86-K96 x Quinitz) cross IV (Quinitz x Toano)

The interaction between additive x additive (aa) was also highly significant for all studied traits in the four crosses except number of branches per plant for crosses (I, II and IV) also, number of seeds per pod and (I, II and IV) which exhibit non-significant. The additive x dominance effect (ad) was significant and highly significant for all studied characters in all crosses except Flowering and maturity date, number of seeds per pod and 100-seed weight in crosses (I, II and IV) were non-significant, also number of pod per plant in crosses (I and IV) showed also non-significant. The dominance x dominance effect (dd) was insignificant in crosses (I, II, III and IV) for plant height, number of pods

and seeds per plant and seed yield plant, either non-significant was observed for number of seeds per pod for crosses (I, II and IV) and 100-seed weight for crosses (II and IV). While positive and negative significant, highly or significant were observed for the remaining of the studied characters in those crosses. Generally, significant one or more of the three types of epistatic gene effects were exhibited in all crosses for all the studied traits. Therefore, it could be concluded that, homozygous x homozygous and heterozygous x homozygous non- allelic interaction were more important than the heterozygous x heterozygous interaction in the inheritance of most studied traits. The

epistatic gen effects were important than additive and dominance El-hosary Hosary (1981), Talwar and Sharma *et al.* (1986), Toledo (1996), Bastawisy *et al.* (1997) El-hosary Hosary *et al.* (2002), Rahangdale and Raut (2002), Datt *et al.* (2011), Bhor (2014), Adsul, *et al.* (2016) and Thakare *et al.* (2017). gen effects for most of the traits. These result were in agreement with those reported by El-Hosary (1981), Talwar *et al.* (1986), Toledo (1996), Bastawisy *et al.* (1997) El-Hosary *et al.* (2002), Rahangdale and Raut (2002), Datt *et al.* (2011), Bhor (2014), Adsul, *et al.* (2016) and Thakare *et al.* (2017).

Table 3. Gene action parameters using generation means in the four soybean crosses characters.

character	Cross	Gamble parameters					
		m	a	d	aa	ad	dd
(1) flowering date	I	48.16	-4.03	-25.11**	-24.14**	2.61	30.06**
	II	42	2.00	-11.29**	-12.00**	-1.06	-1.43
	III	50.44**	-8.00**	-9.61**	-9.76**	-5.15**	9.58**
	IV	42.65	-8.00**	-10.10**	-10.60**	-1.00	15.60**
(2) maturity date	I	138.11	-3.19**	-25.12**	-24.66**	-2.06	18.24**
	II	130	4.00**	-40.15	-40.00**	-9.2	32.3
	III	130.39**	-6.00**	-10.32**	-9.56**	-1.54**	4.97**
	IV	118.35	-11.00**	12.23**	8.60**	0.01	0.66**
(3) plant height (cm)	I	125	24.79**	-31.56**	-69.58**	-6.63**	51.99**
	II	112	33.00**	-36.33**	-42.00**	8.43**	18.05**
	III	71.85**	11.00**	9.35**	-21.40**	4.89**	52.43**
	IV	72.34	9.28	40.66**	13.20**	1.61**	-6.15**
(4) No. of branches / plant	I	3.44**	-0.11**	1.77**	1.54	-0.01**	-0.49**
	II	4.30**	-0.20**	-0.52	-0.8	0.08	1.72**
	III	4.72**	0.24**	-0.09**	-1.52**	-0.19**	5.02**
	IV	4.08**	0.28**	2.85**	1.12	0.08	1.98
(5) No. of pods / plant	I	118.24**	-8.01**	24.72**	23.50**	1.88**	-17.91**
	II	105.00**	10.00**	52.07**	-10.00**	7.60**	147.87**
	III	142.23**	-7.00**	130.82**	65.08**	1.84**	-63.75**
	IV	128.92**	14.00**	140.21**	76.32**	23.32**	-45.82**
(6) No. of seeds / plant	I	274.94**	42.72**	56.70**	14.80**	28.87**	72.05**
	II	241.5	21.40**	226.90**	64.80**	-3.49**	340.84**
	III	304.37**	4.60**	252.41**	87.71**	7.36**	-12.34**
	IV	292.65**	56.18**	257.69**	81.05**	59.67**	54.67**
(7) No. of seeds / pod	I	2.33	0.49	-0.01**	-0.3	0.2	0.9
	II	2.3	-0.03	0.85	0.62	-0.2	-0.41
	III	2.14	0.12	-0.19*	-0.32**	-0.01**	0.73**
	IV	2.27	0.18	-0.42	-0.64	0.05	1.04
(8) 100- seed weight (gm)	I	17	1.24	0.75**	-1.6	0.26	1.70**
	II	15.5	0.12	1.86	1.76	-1.06	-4.32
	III	15.05	-0.92	2.16**	-1.24**	0.75**	0.29**
	IV	12.56	-0.19	7.16	6.26	0.01	-3.88
(9) Seed yield per plant (gm)	I	46.74**	10.55**	12.48**	-1.41**	5.67**	16.86**
	II	37.43	3.72**	39.47**	14.61**	-3.36**	41.58**
	III	45.81**	-2.32**	44.67**	9.11**	2.41**	4.44**
	IV	36.76	7.34**	58.78**	29.66**	8.36**	-0.53**

*and **significant at 0.05 and 0.01 levels of probability, respectively.

cross I (Giza 111 x Toano) cross II (Giza 111 x Quintz) cross III (L86-K96 x Quintz) cross IV (Quintiz x Toano)

Heterosis, inbreeding depression, F₂ deviation and potence ratio

The data presented in Table (4) indicated that heterosis over mid and better parent for all characters were highly positive & negative significant flowering date in the first cross, maturity date in the first, second and third crosses and number of seed per pod in the first cross over mid parents, and also, number of seeds per plant and number of seeds per pod in the fourth and third crosses over better parents. The inbreeding depression was positive and negative highly significant for all traits studied except, flowering date in Cross (III and IV), maturity date in cross (I, III and IV) 100- seed weight in cross II

were non-significant. Significant effects for the both heterosis and inbreeding depression seem logic since the expression of heterosis in F₁'s was followed by considerable reduction in the F₂ performance. Also, reduction in values of non- additive genetic components is expected caused by means of inbreeding depression. In addition, the conflicting estimates of heterosis and inbreeding depression were associated in most traits. Potance ratio were less than unity but not equal zero for most traits concerning yield and its components, indicating partial dominance. The presence of heterosis over better parent with respect to the crosses(I, II, III and IV) for flowering date and seed yield per plant, number of pods and seeds per plant in the

second third crosses, which would indicate that progeny of these crosses could be used in breeding program for high yielding ability. Similar findings were also reported by Talwar and Singh (1983), Malik (1987), Bastawisy *et al.* (1997), Habeeb (1998), Khattab (1998), Rahangdale and Raut (2002), Mansour (2002), Chandel *et al.* (2013), Abirami *et al.* (2014), Bhor (2014) and Adsul *et al.* (2016).

Table 4. F₂ deviation (E₁), Back cross deviation (E₂), heterosis, inbreeding depression percentage and potency ratio for character studied in four crosses of soybean.

Character	Cross	(E ₁)	(E ₂)	Heterosis		Inbreeding depression %	Potence ratio (P)
				M.P.	B.P.		
-1 flowering date	I	3.75**	2.55**	-2.20**	15.14**	-11.69**	0.15
	II	8.24**	10.48**	2.03**	11.70**	-16.67**	0.23
	III	2.49**	0.09	0.31	5.61**	-5.02	-0.05
	IV	1.40**	-2.50**	1.22**	22.06**	-2.77	-0.07
-2 maturity date	I	5.04**	-0.94	-0.35	0.52	-6.15	0.41
	II	18.47**	16.92**	-0.13	12.49**	-10.17**	-0.01
	III	3.54	2.30**	-0.6	3.01**	-3.1	0.17
	IV	-4.47**	-4.63*	3.00**	13.30**	5.04	-0.33
-3 plant height (cm)	I	-11.45**	-15.33**	45.16**	5.71**	-2.27	1.21
	II	31.61**	42.22**	6.12**	-16.12**	-13.88**	0.23
	III	-2.41**	-15.52**	52.21**	37.89**	19.84**	5.03
	IV	-5.06**	-3.53**	43.12**	27.72**	20.62**	3.58
-4 No. of branches / plant	I	-0.95**	-1.23**	5.66**	3.19**	18.10**	-2.37
	II	-0.03**	-0.46*	6.68**	12.30**	14.34**	-2.69
	III	-0.50**	-1.75**	31.78**	20.28**	20.40**	3.33
	IV	-1.06**	-1.55**	40.52**	34.23**	32.00**	8.65
-5 No. of pods / plant	I	-22.14**	-26.33**	0.97	-6.44**	6.25**	-0.12
	II	-9.73**	-19.47**	44.91**	41.96**	37.50**	21.65
	III	-16.60**	-0.66	52.19**	42.21**	25.81**	-7.14
	IV	-26.71**	-15.25*	51.66**	41.03**	31.27**	-6.68
-6 No. of seeds / plant	I	-45.21**	-55.41**	15.00**	9.57**	14.43**	3.03
	II	-24.12**	-15.83	58.30**	45.29**	45.13**	6.51
	III	-40.77**	-37.68**	62.67*	60.98**	28.80**	-59.59
	IV	-54.19**	-67.86**	68.33**	5.03	32.75**	-50.56
-7 No. of seeds / pod	I	0.06	0.01	12.83**	12.94**	19.10**	-2.14
	II	-0.02**	0.29**	9.39**	2.34**	12.21**	-1.36
	III	-0.02*	0.21*	6.44**	0.45	4.04**	-1.08
	IV	0.06	-0.2	3.01	-0.44**	2.16**	-1.69
-8 100- seed weight (gm)	I	-0.76**	0.3	15.21**	9.34**	4.49**	-2.4
	II	0.84**	2.56**	0.66**	6.57**	-0.98	-0.8
	III	0.55**	-0.47**	26.51**	11.96**	7.10**	2.4
	IV	-2.16	-1.19	7.13**	-6.73**	17.21**	4.5
-9 seed yield per plant (gm)	I	-12.35**	-11.27**	32.07**	18.70**	18.27**	-2.85
	II	-1.73**	3.85**	58.24**	35.74**	44.60**	-3.51
	III	-5.67**	-6.78**	105.52**	80.23**	33.85**	7.52
	IV	-14.70**	-14.57**	89.28**	83.12**	44.32**	28.67

*and **significant at 0.05 and 0.01 levels of probability, respectively.

cross I (Giza 111 x Toano) cross II (Giza 111 x Quintz)
cross III (L86-K96 x Quintz) cross IV (Quintz x Toano)

Talwar (1983), Malik (1987), Bastawisy *et al.* (1997), Habeeb, (1998), Khattab (1998), Rahangdale, (2002), Mansour, S.H. (2002), Chandel *et al.* (2013), Abirami, *et al.* (2014) Bhor (2014) and Adsul, *et al.* (2016), F₂ deviation (E₁) and back cross deviation (E₂) for all traits studied were either positive or negative significant or highly significant, however (E₁) for maturity date and 100-seed weight in crosses (III and IV), (E₂) for maturity date and 100-seed weight in crosses (I and IV) also, in both (E₁) and (E₂) for number seeds per plant in crosses (I and IV) were non-significant. Over dominance was observed for flowering date in crosses I and II, for maturity date and plant height in cross II and for seed yield per plant in all

crosses, while partial dominance was observed for the remaining of crosses for most of traits.

These results are in agreement with those reported by El-Hosary (1981), Talwar and Singh (1983), Talwar *et al.* (1986), Malik (1987), Bastawisy *et al.* (1997), Mansour (2002), Rahangdale and Raut (2002), Datt *et al.* (2011) and Adsul *et al.* (2016).

Heritability and genetic advance:

Heritability values are important to the breeder since it quantifies the expected improvement upon selection to achieve genetic improvement through selection, heritability must be reasonably high. In the present investigation the data in table (5) showed high values of heritability in broad sense were obtained. The high broad sense heritability values were obtained for plant height, number of seeds per plant and number of seeds per pod in the first cross being (96.75, 94.59 and 94.98 respectively).

Table 5. Heritability in broad and narrow senses and genetic advance for character studied in four crosses of soybean.

characters	Cross	Heritability		Genetic advance	
		Broad sense	Narrow sense	Δ G	Δ G %
(1) flowering date	I	92.80	75.57	6.67	13.84
	II	57.67	53.00	1.89	4.50
	III	70.50	60.11	3.11	6.17
	IV	86.23	83.40	5.43	12.74
(2) maturity date	I	92.81	86.16	8.26	5.98
	II	64.71	50.24	3.51	2.70
	III	80.18	66.67	5.32	4.08
	IV	83.10	68.11	6.32	5.34
(4) plant height (cm)	I	96.75	92.86	16.37	13.10
	II	58.14	33.10	3.89	3.47
	III	79.38	73.50	7.16	9.96
	IV	79.42	70.07	6.82	9.43
(4) No. of branches / plant	I	63.06	39.75	1.01	29.34
	II	73.95	69.52	2.08	48.26
	III	75.16	60.00	1.89	40.14
	IV	80.58	58.74	3.49	85.55
(5) No. of pods / plant	I	94.59	85.78	55.86	47.24
	II	75.31	59.89	16.64	15.85
	III	74.57	58.24	16.19	11.38
	IV	62.15	44.12	9.31	7.22
(6) No. of seeds / plant	I	94.49	82.02	106.94	38.90
	II	61.56	45.53	14.38	5.95
	III	54.98	52.19	19.23	6.32
	IV	57.96	27.25	11.23	3.84
(7) No. of seeds / pod	I	94.58	93.82	1.38	59.38
	II	37.68	29.13	0.29	12.51
	III	57.14	37.14	0.45	21.15
	IV	80.07	76.00	0.78	34.48
(8) 100- seed weight (gm)	I	90.46	85.04	3.33	19.61
	II	79.91	58.65	1.41	9.11
	III	69.14	65.48	1.68	11.16
	IV	90.51	69.48	2.46	19.57
(9) Seed yield per plant (gm)	I	92.43	82.04	26.09	55.81
	II	89.17	89.00	25.80	68.94
	III	66.78	59.69	3.56	7.76
	IV	52.34	22.78	1.33	3.61
cross I	(Giza 111 x Toano)	cross II	(Giza 111 x Quintz)		
cross III	(L86-K96 x Quintz)	cross IV	(Quintz x Toano)		

Meanwhile, the lowest estimates were resulted for number of seeds per pod in the second cross, number of seeds per plant in the third cross and seed yield per plant in the fourth cross being (37.68, 54.98 and 52.34 respectively). High narrow sense heritability values were obtained for plant height and

number of seeds per pod in the first cross being (92.86 and 93.83 respectively). Meanwhile, the lowest estimates was resulted for number of seeds per pod in the second cross, number of branches per plant in the first cross and seed yield per plant in the fourth cross being (29.13, 39.75 and 22.75 respectively). The values of heritability in narrow sense which indicate to the proportion of phenotypic variance that results from additive genetic variance, were high in magnitude but were lower than their corresponding broad sense values. The estimates of genetic advance from selection 5% superior plant of the F₂ generation reflected high values for number of seeds per plant, number of seeds per pod and seed yield per plant in the first cross being (106.94, 55.86 and 26.09 respectively). Low values for the traits of all crosses for number of seeds per pod, 1.38, 0.29, 0.45 and 0.78 and for 100-seed weight, 1.41 and 1.68 in the second and third crosses respectively. While the genetic advance as percentage of F₂ mean (G.S/F₂%) ranged from 7.22 to 47.24 for number of pods per plant, from 3.84 to 38.90 for number of seeds per plant, from 12.51 to 59.38 for number of seeds per pod, from 9.11 to 19.61 for 100-seed weight and from 3.61 to 68.94 for seed yield plant of all the four crosses. The genetic advance under selection depends on the amount of genetic variability, the magnitude of masking effect of the environment and intensity of selection that is practiced. In terms of the progress expected, the confounding of non-additive with the additive genetic variance will have an effect in future generations, due to the non-additive variance included in the estimates. Therefore, the expected genetic advance for characters in this study was derived by using heritability in narrow sense. Present findings are in agreement with the findings of by, El-Hosary (1981), Talwar and Singh (1983), Budak (1986), Talwar *et al.* (1986), Malik (1987), Halvankar (1993), Bastawisy *et al.* (1997), Mehetre *et al.* (1998), Mansoure (2002), Rahangdale, (2002), Sayad *et al.* (2005), Shinde (2010), Datt *et al.* (2011) and Adsul *et al.* (2016).

CONCLUSION

Mean values of F₁ from all crosses exceeded than of better parent for most of the yield contributing characters viz., plant height, primary branches per plant, clusters per plant, pods per clusters, pods per plant, 100 seed weight and seed yield per plant. The gene action in four crosses was mostly additive and additive x additive contributed with greater magnitude towards yield and yield contributing characters viz., number of primary branches per plant, number of clusters per plant, number of pods per cluster, 100 seed weight and yield per plant. These characters can be improved by progeny row selection from respective crosses. The high magnitude of dominance effect suggested that selection of high yielding genotypes could be postponed till later generation when the dominant effect would be diminished. Additive x additive types of gene action were found to be significant for most traits of all crosses, also additive x dominance and dominance x dominance types of gene effects were found to be significant for most traits, also additive x dominance and dominance x dominance types of gene effects were found to be significant for most traits. Revealed that, the trait can be improved by selections in F₃ generations onwards. The selection in early generations would not be effective for want of fixable

components of variation. Such gene effects can however, be exploited by intermitting the selected segregates and delaying the selections to the advanced generation.

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تحليل متوسط الاجيال لمحصول البذور ومكوناته لبعض الصفات الكمية في هجن فول الصويا.

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أجريت هذه الدراسة بالمزرعة البحثية بمحطة البحوث الزراعية بسخا مركز البحوث الزراعية- مصر خلال الفترة 2017 وحتى 2019 على أربعة هجن من فول الصويا وشملت الدراسة لكل منها ست عشائر (P1 و P2 و F1 و Bc1 و Bc2 و F2) تم اختبارها للمحصول وبعض صفات النمو. ويمكن تلخيص اهم النتائج كالتالي : لوحظت السيادة الفائقة لتاريخ التزهير في الهجين الأول والثاني ، لتاريخ النضج وارتفاع النبات في الهجين الثاني ولمحصول البذور لكل نبات في جميع الهجن ، في حين لوحظت السيادة الجزئية لبقية الهجن لمعظم الصفات. تم الكشف عن قيم إيجابية عالية المعنوية للتربية الداخلية لجميع الصفات التي تمت دراستها باستثناء تاريخ التزهير في الهجين الثالث والرابع ، وتاريخ النضج في الهجين الأول والثالث والرابع ، كان وزن 100 بذرة في الهجين الثاني غير معنوي. كانت قوة الهجين معنوية وسالبة لتاريخ التزهير لمتوسط الابوين في الهجين الأول، كان تأثير قوة الهجين لباقي الصفات عالية المعنوية و موجبة. كان التأثير الإضافي (a) عالي المعنوية في الاتجاه الموجب أو السالب في جميع الهجن لجميع الصفات ، باستثناء صفة عدد البذور لكل قرن ووزن بذور النبات للأربع هجن وتاريخ التزهير للهجين الأول والثاني. كان الفعل الجيني الإضافي x الإضافي عالي المعنوية لمعظم الصفات في جميع الهجن، كما وجد أن الفعل الجيني الإضافي x السيادة والسيادة x الإضافي عالي المعنوية لمعظم الصفات في جميع الهجن. كانت قيم المكافئ الوراثي بالمعنى الضيق عالية المعنوية لصفات ارتفاع النبات وعدد البذور لكل قرن في الهجين الأول. وفي الوقت نفسه ، تم الحصول على اقل قيم لصفة عدد البذور للقرن في الهجين الثاني ، عدد الفروع لكل نبات في الهجين الأول ومحصول البذور لكل نبات في الهجين الرابع