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Combining Ability aAnd Genetic Variance Components of Yield and Yield Components in F₁ And F₂ Diallel Crosses of Soybean

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ABSTRACT



Combining ability and genetic components of six soybean parents and their F_1 and F_2 half-diallel crosses were measured in Etay El-Baroud Agriculture Research Station during 2017, 2018 and 2019. mean square due to genotypes; parents, crosses and parent vs. crosses were significant for all studied traits in both generations, except parent vs. crosses for protein and oil contents in F_1 and both number of seeds/pod and 100-seed weight in F_2 . Mean squares due to general and specific combining ability were significant for all studied traits in F_1 and F_2 , except SCA for number of seeds/pod in F_2 . The ratios of GCA/SCA were higher than the unit for all studied traits in both F_1 and F_2 generations. Mean squares due to additive (a) and dominance (b) components were significant for all studied traits in both F_1 and F_2 mean squares due to additive (a) and dominance (b) components were significant for all studied traits in both F_1 and F_2 . The two parents Dr101 and Giza111 and the three crosses Giza111 x Giza83, Dr101 x Giza83 and Dr101 x Giza111 gave the highest seed yield/plant. Dr101 expressed negative \hat{g}_i effect for maturity period and positive \hat{g}_i effect for most yield traits in both generations. The cross combinations of Giza111 and Dr101 with Giza83 had the significant positive \hat{S}_{ij} effect for seed yield/plant in both F_1 and F_2 . The additive genetic variance (D), dominance genetic variations (H1) and (H2) were highly significant for all traits in both F_1 and F_2 hybrids except additive type for number of seeds/pod in F_1 . Pedigree method consider an excellent method to select superior lines in the early segregated.

Keywords: Combining ability, Genetic variation, Seed yield, Soybean.

INTRODUCTION

Soybean [Glycine max (L.) Merrill] is one of the most important summer leguminous crops in the world, as it is a great source for food oils, as the oil content in dry seeds is 16-20%. It is also an important source of protein that reached 36:40% in dry seeds (Soybean meal. 2019), which makes it participate in many industries such as the production of poultry and animal feed and some human foods like baby milk and soy sauce. The area of sovbeans cultivated in the world was estimated at about 120.50 million hectare in 2019, while its area in Egypt did not exceed 14000 hectare in the same year (FAOSTAT, 2019). Due to the importance of soybeans, it has won a lot of interest from plant breeders in the world with the aim of increasing the yield of seeds and raising their quality characteristics. The estimation of the components of genetic variation is one of the most important elements of the success of improving the characteristics of soybeans through breeding programs, as knowledge of genetic variance provides a lot of information about the relationship between parents and offspring and determining the appropriate selection method in isolated generations, which saves time and effort of the breeder during his pursuit of his goals (Cruz et al., 2012). To reach these goals, several genetic designs are available, highlighting the diallel crosses. Diallel method is considered a good method as it allows plant breeders to obtain a lot of

genetic information related to the parents and their offspring through which it is possible to allows inferring about heterosis (Gardner & Eberhart, 1966), estimate the general and specific combining ability (Griffing, 1956) and determined the genetic control of traits (Hayman, 1954a, b). According to Cruz *et al.*, (2012), this last analysis provides information about the genetic control, genetic values of parents and the limits of selection of traits under study.

The present study aimed to determine the genetic control of the seed yield and its components as well seed content of protein and oil traits in a half diallel with six soybean parents, with the main objective of obtaining statistical genetic inferences which helps soybean breeder to the implementation of soybean breeding programs in the future.

MATERIALS AND METHODS

The present study was conducted at Etay EL-Baroud Agriculture Research Station, EL-Behaira, Egypt during three summer agriculture season of 2017, 2018 and 2019.

Six parental varieties and/or lines of soybean (*Glycine max* (L.) Merrill) 2n=40 namely; (D89-8940, Hardin, Giza 83, Gza 111, Dr 101 and Line105 were used in the present study. The names, country of origin, maturity group and pedigree of the parental genotypes of soybean used in the present study are shown in table 1.

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No.	Name	Country of origin	Maturity group	Pedigree			
1	D89-8940	United States	V	Introduced from USA			
2	Hardin	United States	Ι	Introduced from USA			
3	Giza 83	Egypt	Ι	Selected from MBB.133			
4	Gza 111	Egypt	IV	Crawford x Celest			
5	Dr 101	Egypt	V	Selected from Elgin			
6	Line 105	Egypt	1V	Giza 35 x Lamar			

Table 1. The names, country of origin, maturity groupand pedigree of the six soybean parentalgenotypes used in the present study.

Methods:

In 2017 season, the six parental genotypes were used in a half-diallel cross mating design. During this season, all the possible cross combinations (without reciprocals) among all parental genotypes (fifteen crosses) were made by hand. In 2018 season, all F1 hybrid seeds of the fifteen crosses were sown. The F1 plants were selfpollinated to obtain the F2's seeds. In this season also, another cycle of half-diallel mating was made between the six parents to obtain the seeds of F₁ hybrids seeds again. In 2019 season, all the diallel mating progenies (6 parents, 15 F1 seeds and 15 F2 seeds) were evaluated in an experiment designed in a Randomized Complete Block Design (RCBD) with three replications. The plot size was one ridge for F₁ and, four ridges for parents and F₂. Each ridge was three meters long and 70 cm apart. Seeds were planting on one side of the ridge at 20 cm hill spacing with one seed per hill. The wet planting method called (Herati) was used and all the other agricultural practices were followed as recommended. Data for the all traits studied were recorded on 10 and 60 individual guarded plants, chosen at random from each plot for F_1 and F_2 , respectively. The studied traits were; maturity period (day), plant height (cm) number of pods /plant, number of seeds/pod, number of seeds/plant, 100-seed weight (g), seed weight /plant (g), seed content of protein% and seed content of oil %.

Seed content of protein (%) was calculated by determined total nitrogen using the modified Micro-Kjeldahl method (AOAC, 1988). Then the total protein was calculated by multiplying the values of total nitrogen by 6.25. While, seed content of oil (%) was extracted the oil quantity (g) in 100-gram of dry seeds (%) in the laboratory using Sokselt apparatus.

Statistical and genetically analysis

The ordinary analysis of variance of all genotypes, parents, crosses and parents vs crosses was made in one way ANOVA for RCBD according to Gomez and Gomez (1984). Heterosis for each trait computed as parents *vs*. hybrids sum of squares. Heterosis was also determined according to Paschal and Wilcox (1975) for individual crosses as the percentage deviation of F_1 means performance from the better parent means (BP). General and specific combining ability estimates were obtained by employing Griffing's (1956) diallel cross analysis designated as a method-2, model-1 (fixed model). DIAL Win 98 software revised 22 September 2002 were used to estimate several genetic variance components and some genetic ratios in addition to Wr/Vr graph based on diallel cross analysis according to Hayman (1954a and b) as follows. Heritability in both broad and narrow senses were calculated according to Mather and Jinks (1971).

RESULTS AND DISCUSSIONS

Griffing approach.

Analysis of variance:

The ordinary analysis of variance and analysis of variance of combining ability of both F_1 and F_2 diallel crosses are presented in Table 2. The obtained data indicated that mean square due to genotypes; parents and crosses were highly significant for all studied traits in both F1 and F2 as a clear indicator of the wide diversity between all parents in their pedigree and country of origin. Similar results were obtained before by Iqbal et al., (2003) who found highly significant differences between parents and their hybrids were shown by analysis of variance, for all growth, seed yield and seed quality traits. Also, these significant confirmed that all genotypes (parents and crosses) will differ in their performances in both F1 and F2 for all studied traits. Mean square due to parent vs. crosses were highly significant for all studied traits in both F₁ and F₂ except for seed content of protein and oil% in F₁ as well as number of seeds/pod and 100-seed weight in F₂. The significant of parent vs crosses may a clear evidence for the presence of hybrid vigor in both F_1 and F_2 crosses (the progeny will superior their parents). Mean squares due to both general and specific combining ability were highly significant for all studied traits in both F1 and F2, except SCA for number of seeds/pod in F2, indicated that both additive and non-additive genetic effects involving these traits. The ratios of GCA/SCA were higher than the unit for all studied traits in both F_1 and F_2 indicated that the additive genetic variation is the major part in the total genetic variation that involving these traits. In this concern, Agrawal et al., (2005) found that yield attributing characters in soybean might be governed by additive gene effects, whereas the non-additive and complex of additive and non-additive gene effects played an important role in the expression of yield attributing characters. Similarly, Shiv, et al., (2011) found that in soybean general combining ability and specific combining ability mean square were significant for seed yield and its related traits.

Table 2. Analysis of variance of ordinary and combining ability data associated with F1 and F2 soybean diallel cross.

SOV	DE	Maturity period (day)		Plant he	Plant height (cm)		pods/plant	Number of se	eds/pod
5. U .V	Dr	F1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	F ₂	\mathbf{F}_1	\mathbf{F}_2
Genotypes	20	279.27**	289.11**	1362.27**	1908.06**	2505.52**	2197.87**	0.09**	0.05**
Parents	5	893.56**	893.56**	1568.46**	1568.46**	1450.77**	1450.77**	0.04**	0.05*
Crosses	14	75.47**	86.69**	1107.74**	2150.18**	2268.43**	2559.36**	0.09**	0.05**
P V Cross	1	60.98**	100.80**	3894.87**	216.40**	11098.42**	872.50**	0.21**	0.03
Error	40	2.35	1.45	25.51	21.92	18.64	10.75	0.01	0.01
GCA	5	309.34**	241.13**	1125.18**	1772.37**	1481.38**	1579.73**	0.05**	0.03**
S CA	15	21.01**	48.12**	230.40**	257.24**	619.77**	450.25**	0.02**	0.01**
Error	40	0.78	0.48	8.50	7.31	6.21	3.58	0.001	0.001
GCA/SCA	-	14.72	5.01	4.88	6.89	2.39	3.51	2.50	3.00

DF	Number of seeds/plant		100-seed weight (g)		Seed yield/plant (g)		Seed content of protein %		Seed content of oil %	
-	\mathbf{F}_1	\mathbf{F}_2	F1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2
20	13435.19**	9847.56**	10.21**	9.82**	423.06**	318.28**	52.12**	43.72**	13.29**	11.59**
5	8722.30**	8270.55**	9.66**	9.66**	235.08**	222.07**	41.04**	25.82**	18.18**	18.18**
14	10602.33**	10721.13**	11.09**	10.57**	396.46**	365.14**	59.35**	52.35**	12.36**	9.47**
1	76659.61**	5502.54**	0.57**	0.004	1735.20**	143.36**	6.19	12.46*	1.74	8.27**
40	206.06	199.27	0.07	0.10	3.63	4.45	2.86	2.79	0.52	0.51
5	8403.02**	7706.24**	10.26**	10.29**	321.42**	272.78**	47.71**	30.85**	7.22**	6.19**
15	3170.19**	1807.94**	1.12**	0.93**	80.89**	50.53**	7.26**	9.15**	3.50**	3.09**
40	68.69	66.42	0.02	0.03	1.21	1.48	0.95	0.93	0.17	0.17
	2.65	4.26	9.16	11.06	3.97	5.40	6.57	3.37	2.06	2.00
	DF 20 5 14 1 40 5 15 40	Number of F1 20 13435.19** 5 8722.30** 14 10602.33** 1 76659.61** 40 206.06 5 8403.02** 15 3170.19** 40 68.69 2.65 2.65	Number of seeds/plant F1 F2 20 13435.19** 9847.56** 5 8722.30** 8270.55** 14 10602.33** 10721.13** 1 76659.61** 5502.54** 40 206.06 199.27 5 8403.02** 7706.24** 15 3170.19** 1807.94** 40 68.69 66.42 2.65 4.26	Number of seeds/plant 100-seed F1 F2 F1 20 13435.19** 9847.56** 10.21** 5 8722.30** 8270.55** 9.66** 14 10602.33** 10721.13** 11.09** 1 76659.61** 5502.54** 0.57** 40 206.06 199.27 0.07 5 8403.02** 7706.24** 10.26** 15 3170.19** 1807.94** 1.12** 40 68.69 66.42 0.02 2.65 4.26 9.16 1.16	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$

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* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Mean performances.

Mean performances of all studied traits for the six parental genotypes and their F1 and F2 diallel crosses are shown in Table 3. For maturity period the two parents Hardin and Giza 83 showed the lowest maturity periods (69.33 and 73.00 days) while, D89-8940 expressed the highest maturity period with averages of 117.33 days. Also, the six cross combinations Giza 83 x Hardin, Giza 111 x Hardin, Dr 101x Hardin, Line 105 x D89-8940, Line 105 x Giza 111 and Line 105 x Dr 101 had the lowest desirable maturity periods in both F₁ and F₂. Respect to plant height the two parents Dr 101 and Giza 111 were the tallest among all tested parents. Moreover the two crosses Giza 111 x Hardin and Giza 111 x Giza 83 were the tallest among all crosses in both F1 and F2. Respect to number of pods/plant the parental genotypes Dr 101, Giza 111 and D89-8940 gave the highest pods number/plant (122.31, 115.33 and 107.67). While, the three crosses Hardin x D89-8940, Giza 111 x Giza 83 and Dr 101 x Giza 83 had the highest number of pods/plant in both F1 and F2. For number of seeds/pod, the parental genotype Dr101 had the highest number of seeds/pod. In the same way the five crosses Giza 83 x Hardin, Giza 111 x Hardin, Dr 101 x Hardin, Dr 101 x Giza 111 and Line 105 x Dr 101 had the highest number of seeds/pod in both F₁ and F₂. Regard to number of seeds/plant, the two parental genotypes Giza 21 and Dr101 had the highest number of seeds/pod. In the same way the five crosses Hardin x D89-8940, Dr 101 x Hardin, Giza 111 x Giza 83, Dr 101 x Giza 83 and , Dr 101 x Giza 111 had the highest number of seeds/plant in both F₁ and F₂. The two parents Giza 83 and Giza 111 had the highest 100-seed weight (16.45 and 14.73 g) while the two crosses Giza 111 x Giza 83 and Dr101 x Giza 83 showed the highest 100-seed weight in both F1 and F2 among all crosses. For seed yield/plant the results revealed that the parental genotypes Dr101 gave the highest seed yield/plant (41.98 g) followed by Giza 111 (36.23 g) while the three crosses Giza 111 x Giza 83, Dr 101 x Giza 83 and Dr 101 x Giza 111 had the highest seed yield /plant among all crosses in both F1 and F2. The two parents Giza 83 and Giza 111showed the highest seed content of protein (45.00 and 41.87 %). In the same line, the six crosses Giza 83 x D89-8940, Giza 111 x D89-8940, Giza 83 x Hardin, Giza 111 x Hardin, Giza 111 x Giza 83 and Dr 101 x Giza 111 gave the highest seed content of protein in both F1 and F2. Regard to oil percentage, the results revealed that, both Hardin and Line 105 among all parents showed the highest seed content of oil with averages of 20.66 and 20.95% while, the three crosses Hardin x D89-8940, Line 105 x D89-8940 and Dr 101 x Giza 111 had the highest seed content of oil in both F1 and F2 among all tested crosses. The results are in agree with those reported by EL-Garhy et al., (2008), Perez et al., (2009) and Waly (2015), which found highly significant differences in mean performances of growth, seed yield and oil percentage on different genotypes of soybean.

	Maturity	Maturity period		height	Number	of pods/	Nu	mber	Number	of seeds/
Genotype	(dag	ys)	(cı	n)	pla	nt	of see	ds /pod	pla	ant
	F 1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	F1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2
D89-8940	117	.33	88.	92	107.	67	2	.01	216	5.26
Hardin	69.	33	70.	46	89.0	00	2	.13	189	9.00
Giza 83	73.	00	91.	22	70.6	57	2	.17	153	3.00
Giza 111	80.	00	107	.82	115.	33	2	.13	245	5.93
Dr 101	81.	00	129	.00	122.	31	2	.37	289	0.11
Line 105	88.	67	69.	10	73.0)7	2	.09	152	2.63
Hardin x D89-8940	89.00	86.00	103.13	87.96	177.98	143.67	2.10	2.03	373.66	291.97
Giza 83 x D89-8940	85.33	89.67	119.77	105.28	122.25	112.33	2.17	2.10	265.04	235.67
Giza 111 x D89-8940	88.00	89.00	123.70	110.21	139.76	126.00	2.07	2.03	288.55	256.67
Dr 101 x D89-8940	87.33	92.33	115.67	89.47	133.77	109.33	2.23	2.17	298.80	236.63
Line 105 x D89-8940	93.00	74.33	73.24	60.48	110.62	89.33	1.95	1.93	215.41	173.20
Giza 83 x Hardin	74.00	74.33	127.26	93.77	114.33	80.00	2.40	2.30	274.67	184.00
Giza 111 x Hardin	78.00	80.00	132.91	116.73	133.33	110.00	2.40	2.30	320.20	253.07
Dr 101 x Hardin	79.33	79.33	111.95	115.74	141.00	123.00	2.50	2.37	352.80	291.23
Line 105 x Hardin	85.00	86.00	74.86	58.65	82.00	61.00	2.27	2.17	185.83	132.00
Giza 111 x Giza 83	80.33	80.00	130.69	133.63	147.33	135.42	2.27	2.10	333.40	284.73
Dr 101 x Giza 83	80.33	81.33	127.59	129.15	161.00	145.67	2.07	2.03	332.50	296.20
Line 105 x Giza 83	80.00	80.00	105.13	94.91	100.00	86.81	2.37	2.33	236.67	202.27
Dr 101 x Giza 111	80.67	80.00	119.32	132.72	140.27	132.67	2.53	2.30	355.41	277.40
Line 105 x Giza 111	80.00	79.33	95.50	61.01	95.43	59.33	2.37	2.23	226.08	132.53
Line 105 x Dr 101	80.33	79.33	91.66	63.13	86.73	66.00	2.47	2.27	214.06	149.57
LSD 5%	2.11	1.65	6.94	6.44	5.94	4.51	0.14	0.16	19.74	19.41
LSD 1%	3.03	2.38	9.99	9.26	8.54	6.49	0.20	0.24	28.40	27.93

Table 3. Mean performances for all studied traits of the six parents and their F1 and F2 diallel crosses.

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Table 3. Cont.

Constring	100-seed	weight (g)	Seed yield	Seed yield /plant (g)		of protein %	Seed content of oil %		
Genotype	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	F2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	
D89-8940	13	.67	29.	56	40.	11	17	.49	
Hardin	11	.37	21.49		33.98		20.60		
Giza 83	16.45		25.17		45.	00	16.22		
Giza 111	14	14.73		23	41.	87	15	.95	
Dr 101	14	.52	41.	98	40.	68	15	.25	
Line 105	12.47		19.	02	38.	22	20	.95	
Hardin x D89-8940	10.70	11.40	39.93	33.27	31.04	32.57	21.80	19.90	
Giza 83 x D89-8940	15.33	15.13	40.61	35.68	43.17	42.50	15.43	15.23	
Giza 111 x D89-8940	15.33	15.17	44.23	38.94	43.65	43.14	15.69	15.52	
Dr 101 x D89-8940	13.70	12.91	40.90	30.49	37.83	35.82	16.27	15.33	
Line 105 x D89-8940	11.83	11.39	25.48	19.74	34.68	33.52	21.44	20.64	
Giza 83 x Hardin	15.00	15.21	41.21	28.01	41.04	41.29	15.42	15.64	
Giza 111 x Hardin	15.97	15.24	51.12	38.56	43.32	41.37	15.37	14.95	
Dr 101 x Hardin	13.80	13.23	48.66	38.54	38.44	36.79	16.27	15.60	
Line 105 x Hardin	12.23	12.34	22.73	16.31	34.20	34.22	17.31	17.46	
Giza 111 x Giza 83	17.27	17.05	57.58	48.55	47.38	39.01	17.76	17.53	
Dr 101 x Giza 83	16.80	16.27	55.85	48.21	39.99	44.07	16.51	15.99	
Line 105 x Giza 83	13.13	13.43	31.08	27.17	38.88	39.53	16.47	16.84	
Dr 101 x Giza 111	14.99	15.39	53.26	42.70	43.51	43.93	18.61	19.11	
Line 105 x Giza 111	12.83	12.21	29.00	16.19	36.61	34.78	18.54	17.64	
Line 105 x Dr 101	12.27	11.57	26.25	17.30	35.50	33.33	17.73	16.72	
LSD 5%	0.36	0.44	2.62	2.90	2.33	2.30	0.99	0.98	
LSD 1%	0.52	0.63	3.77	4.17	3.35	3.30	1.43	1.41	

Heterosis relative to better parent.

Heterosis relative to better parent of 15 F_1 and F_2 crosses is presented in Table 4. For maturity period the results revealed that among all tested crosses the three crosses Dr 101 x Giza 111, Line 105 x Giza 111 and Line 105 x Dr 101 expressed lowest desirable heterotic effect relative to better parent in both F1 and F2 but these values were not significant. In the same way the cross Line 105 x D89-8940 showed the lowest significant negative desirable heterosis for maturity period in F2 only. Seven crosses in F1 and three crosses in F₂ showed significant positive heterotic effect for plant height. Only the three crosses Giza 83 x D89-8940, Giza 111 x Hardin and Giza 111 x Giza 83 expressed significant positive heterosis for plant height in both generations. Eleven crosses in F1 and five crosses in F2 had significant positive heterotic effect relative to better parent for number of pods/plant. The highest desirable positive significant heterosis in this trait were obtained by the four crosses Hardin x D89-8940, Giza 111 x D89-8940, Giza 111 x Giza 83, Dr 101 x Giza 83 and Line 105 x Giza 83 in both F_1 and F_2 . Only the five crosses Giza 83 x Hardin, Giza 111 x Hardin, Line 105 x Giza 83, Dr 101 x Giza 111 and Line 105 x Giza 111 in F₁ showed positive significant desirable heterotic effect relative to better parent for number of seeds/pod. On the other side, there is no any crosses expressed positive and significant heterotic effect for this trait in F₂. For number of seeds/plant, ten crosses in F1 and three crosses in F2 expressed significant positive heterotic effect relative to better parent. The highest positive desirable heterosis for seed yield/plant was showed in the two crosses Hardin x D89-8940 and Line 105 x Giza 83 in both F1 and F2. Only the cross Giza 111 x Giza 83 in F_1 and the cross Dr 101 x Giza 83 in F_2 had significant positive heterosis for seed content of protein among all tested genotypes. The two crosses Giza 111 x Giza 83 and Dr 101 x Giza 111 in both generation and the cross Hardin x D89-8940 in F₁ expressed significant positive heterotic effect for oil percentage among all tested crosses.

The significant negative heterotic effect for maturity and the positive effect in seed yield and seed content of protein and oil for hybrids over their better parents were reported by many authors before such as, Mansour (2002), Mansour et al (2002 a&b) and El-Shaboury et al. (2006), also EL-Garhy et al. (2008), Fayiz (2009) and Perez et al. (2009) found highly significant positive heterotic effect relative to better parent in soybean for plant height, pods number/plant and seed yield/plant.

Fable 4. Heterosis relative to better parent for all the studied traits of F_1 and F_2 crosses.												
	Maturit	Maturity period		height	Numbe	r of pods	Number	of seeds	Number of seeds			
Cross	(da	(day)		(cm)		/plant		od	/plant			
	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2		
Hardin x D89-8940	28.37**	24.04**	15.98**	-1.08	65.29**	33.44**	-1.22	-4.39	72.78**	35.01**		
Giza 83 x D89-8940	16.89**	22.83**	31.30**	15.41**	13.55**	4.33	0.00	-3.08	22.56**	8.97		
Giza 111 x D89-8940	10.00**	11.25**	14.73**	2.22	21.18**	9.25**	-3.13	0.00	17.33**	9.34		
Dr 101 x D89-8940	7.81**	13.99**	-10.33**	-30.64**	9.37**	-10.61 **	-5.63	-8.45 *	3.35	-18.15 **		
Line 105 x D89-8940	4.88**	-16.17	-17.63**	-31.98**	2.75	-17.03 **	-6.71	-7.35	-0.39	-19.91 **		
Giza 83 x Hardin	6.74**	7.21**	39.51**	2.80	28.46**	-10.11 **	10.77**	6.15	45.33**	-2.65		
Giza 111 x Hardin	12.51**	15.39**	23.26**	8.26*	15.61**	-4.62	12.50**	8.15	30.20**	7.81		
Dr 101 x Hardin	14.42**	14.42**	-13.21**	-10.27**	15.28**	0.57	5.63	0.00	22.03**	0.74		
Line 105 x Hardin	22.60**	24.04**	6.25	-16.76**	-7.87	-31.46 **	6.58	1.88	-1.68	-30.16 **		
Giza 111 x Giza 83	10.04**	9.5**	21.21**	23.93**	27.75**	17.63**	4.62	-3.08	35.57**	21.30**		
Dr 101 x Giza 83	10.04**	11.41**	-1.09	0.12	31.64**	19.10**	-12.68 **	-14.08 **	15.01**	2.45		
Line 105 x Giza 83	9.59**	9.5**	15.25**	4.05	36.86**	18.61**	9.23*	7.69	54.68**	32.20**		
Dr 101 x Giza 111	0.84	0.00	-7.50*	2.88	14.68**	-1.34	7.04*	-2.82	22.93**	-4.05		
Line 105 x Giza 111	0.00	-0.84	-11.43**	-43.42**	-17.25 **	-48.55 **	10.94**	7.03	-8.07	-43.54 **		
Line 105 x Dr 101	-0.83	-2.06	-28.95**	-51.06**	-29.09 **	-46.04 **	4.23	-4.23	-25.96 **	-48.27 **		

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Cross	100-seed weight (g)		Seed yield/	plant (g)	Seed content	of protein %	Seed content of oil %		
Closs	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	
Hardin x D89-8940	-21.71 **	-16.61 **	35.07**	12.55*	-22.62**	-18.81**	5.79*	-3.39	
Giza 83 x D89-8940	-6.79 **	-8.02 **	37.38**	20.69**	-4.07	2.66	-11.77**	-12.92**	
Giza 111 x D89-8940	4.07**	2.96	22.08**	12.55*	4.24	3.04	-10.28**	-11.22**	
Dr 101 x D89-8940	-5.67 **	-11.11 **	-2.57	-27.38 **	-6.99*	-11.95**	-6.96*	-12.33**	
Line 105 x D89-8940	-13.41 **	-16.68 **	-13.81 *	-33.22 **	-13.55**	-16.43**	2.32	-1.48	
Giza 83 x Hardin	-8.81 **	-7.52 **	63.72**	11.27	-8.81**	-0.25	-25.14**	-24.09**	
Giza 111 x Hardin	8.37**	3.46	41.10**	11.47*	3.47	-1.20	-25.41**	-27.43**	
Dr 101 x Hardin	-5.00 **	-8.93 **	15.90**	-8.20	-5.50	-9.56**	-21.02**	-24.28**	
Line 105 x Hardin	-1.87	-0.99	5.77	-24.12 **	-10.53**	-10.47**	-17.39**	-16.65**	
Giza 111 x Giza 83	4.96**	3.63*	58.94**	40.32**	5.30*	-6.83*	9.48**	8.08*	
Dr 101 x Giza 83	2.13	-1.07	33.03**	14.82**	-11.13**	6.46*	1.78	-1.44	
Line 105 x Giza 83	-20.16 **	-18.34 **	23.45**	7.92	-13.60**	-4.51	-21.40**	-19.60**	
Dr 101 x Giza 111	1.74	4.48*	26.86**	1.71	3.91	4.92	16.70**	19.82**	
Line 105 x Giza 111	-12.90 **	-17.10 **	-19.96 **	-53.19 **	-12.57**	-16.94**	-11.50**	-15.78**	
Line 105 x Dr 101	-15.54 **	-20.34 **	-37.47 **	-58.79 **	-12.73**	-18.06**	-15.37**	-20.20**	

* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Combining ability.

General combining ability effects ($\mathbf{\hat{g}}_i$).

The results of general combining ability effects are which presented in Table 5 revealed that the parental genotypes Dr 101 expressed negative significant gi effect for maturity period in addition to highly positive significant gi effect for plant height, number of pods/plant, number of seed/pod, number of seed/plant, 100-seed weight and seed yield/plant in both F_1 and F_2 . In the same way, Giza cv. showed highly positive significant desirable \hat{g}_i effect for plant height, number of pods/plant, number of seeds / plant, 100-seed weight, seed yield/plant and seed content of protein% in addition to the same cultivar showed significant negative desirable gi effect for maturity period in both F1 and F2. So, both Dr101 and Giza 111 seemed to be excellent combiners for earliness, seed yield, protein and oil%. The results also indicated that Giza 83 had significant desirable \hat{g}_i effects for maturity period, plant height, 100-seed weight, seed yield/plant and seed content of protein in both F_1 and F_2 generations. Moreover, Hardin cv seemed to be excellent combiner for oil percentage and maturity period while, Line 105 consider excellent combiner for oil percentage in both F_1 and F_2 .

In this study a significant differ in general combining ability of all parental genotypes were detected in the same way Shiv, *et al.*, (2011) found highly significant differ between soybean parents and crosses for general combining ability and specific combining ability effects in growth and yield traits. The previous results were in the same way with those by El-Shaboury *et al.*, (2006), Chen *et al.*, (2008), Perez *et al.*, (2009) and Waly (2015) which they found highly positive significant general combining ability for branches number/plant, pods and seeds number/plant and seed yield/plant and negative one for flowering and maturity date in soybean. In the same way Nassar, (2013) reported that GCA effect were significant positive for pod and seed yield/plant and negative for some crosses in flowering and maturity.

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Table 5.	Estimates	of gca	effects	(ĝi) for individual	parent for all the studied trait	s.

Dononta	Maturity per	Maturity period (day)		Plant height (cm)		No. of pods/plant		No. of seeds/pod		No. of seeds/plant	
rarents	F1	F ₂	F1	F ₂	\mathbf{F}_1	\mathbf{F}_2	F1	F ₂	\mathbf{F}_1	F ₂	
D89-8940	11.75**	10.72**	-2.87**	-4.82**	9.80**	10.05**	-0.14**	-0.11**	4.29	10.34**	
Hardin	-4.92**	-4.44**	-5.66**	-7.00**	0.67	-2.49**	0.03	0.03	5.69*	-1.71	
Giza 83	-4.67**	-3.61**	7.07**	8.67**	-4.38**	-1.74**	-0.01	0.01	-11.42**	-4.39	
Giza 111	-2.04**	-1.49**	10.18**	12.52**	8.19**	8.35**	0.03	-0.01	21.98**	16.24**	
Dr 101	-1.67**	-0.74**	10.99**	14.80**	10.76**	11.71**	0.11**	0.09**	36.51**	35.66**	
Line 105	1.54**	-0.44	-19.71**	-24.17**	-25.04**	-25.89**	-0.01	-0.01	-57.05**	-56.14**	
LSD gi 5%	0.58	0.45	1.90	1.76	1.63	1.23	0.04	0.05	5.41	5.32	
LSD gi 1%	0.77	0.61	2.55	2.36	2.18	1.65	0.05	0.06	7.23	7.11	
LSD gi-gj 5%	1.58	1.24	5.22	4.84	4.47	3.39	0.10	0.12	14.85	14.60	
LSD gi-gj 1%	2.12	1.66	6.99	6.48	5.97	4.54	0.14	0.17	19.87	19.54	

* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Table 5. Cont.

Domente	100-seed	Weight (g)	Seed yield	l /plant (g)	Seed content	of protein %	Seed conte	ent of oil %
Farents	\mathbf{F}_1	F ₂	\mathbf{F}_1	F ₂	\mathbf{F}_1	F ₂	F1	F ₂
D89-8940	-0.49**	-0.47**	-1.27**	0.01	-0.72*	-0.37	0.40**	0.18
Hardin	-0.96**	-0.86**	-1.73**	-2.44**	-2.55**	-2.06**	0.63**	0.57**
Giza 83	1.54**	1.62**	2.03**	2.60**	3.01**	2.31**	-1.04**	-0.82**
Giza 111	0.97**	0.94**	5.90**	4.62**	2.73**	1.91**	-0.56**	-0.44**
Dr 101	0.31**	0.17**	6.06**	5.51**	0.03	0.57	-0.81**	-0.87**
Line 105	-1.36**	-1.40**	-10.99**	-10.30**	-2.51**	-2.36**	1.38**	1.38**
LSD gi 5%	0.10	0.12	0.72	0.79	0.64	0.63	0.27	0.27
LSD gi 1%	0.13	0.16	0.96	1.06	0.85	0.84	0.36	0.36
LSD gi-gj 5%	0.27	0.33	1.97	2.18	1.75	1.73	0.75	0.74
LSD gi-gj 1%	0.37	0.44	2.64	2.92	2.34	2.31	1.00	0.99

Specific combining ability effects (\hat{S}_{ij}) .

Estimates specific combining ability effects of fifteen F_1 and F_2 crosses are presented in Table 6. For maturity period the results indicated that six and six crosses in F₁ and F₂ generations, respectively expressed significant negative desirable \hat{S}_{ii} effect. Among these crosses the four crosses Giza 111 x D89-8940, Line 105 x D89-8940, Line 105 x Giza 111 and Line 105 x Dr 101 showed negative significant \hat{S}_{ij} effect in both generations. For plant height, eight crosses in F1 and nine crosses in F2 had significant positive \hat{S}_{ij} effect. The highest significant positive \hat{S}_{ij} effect for this trait was obtained by the two crosses Giza 111 x Hardin and Line 105 x Giza 83 in both generations. The three crosses Hardin x D89-8940, Giza 111 x Giza 83 and Dr 101 x Giza 83 showed the highest significant desirable \hat{S}_{ij} effect for number of pods/plant in both F_1 and F_2 among ten crosses in F₁ and seven crosses in F₂ showed the same positive significant Sij effect. Regard to number of seeds/pod seven crosses in F1 and two crosses in F2 expressed positive significant Si effects among these crosses only the two cross combinations Giza 111 x Hardin and Line 105 x Giza 83 showed positive significant \hat{S}_{ij} effect for this trait in both generations. For number of seeds/pod the two crosses Hardin x D89-8940 and Giza 111 x Giza 83 had the highest significant positive \hat{S}_{ij} effect in both F1 and F2 generation among eight crosses in F1 and six crosses in F_2 showed also positive significant \hat{S}_{ij} effect for this trait. For 100-ssed weight eight crosses in F₁ and seven crosses in F_2 expressed positive significant \hat{S}_{ij} effect. The highest significant positive \hat{S}_{ij} effect for 100-seed weight were obtained by the two crosses Giza 111 x D89-8940 and Giza 111 x Hardin in both F_1 and F_2 generations. For seed yield/plant ten crosses in F_1 and eight crosses in F_2 expressed positive significant \hat{S}_{ij} effect. The highest significant positive \hat{S}_{ij} effect for seed yield/plant were obtained by the two crosses Giza 111 x Giza 83 and Dr 101 x Giza 83 in both F_1 and F_2 generations. Four crosses in F_1 and six crosses in F_2 showed significant positive \hat{S}_{ij} effect for seed content of protein and only the two crosses Giza 111 x D89-8940 and Giza 111 x Hardin had positive significant \hat{S}_{ij} effect for this trait in both generations. For oil percentage only the four crosses, Hardin x D89-8940, Line 105 x D89-8940, Giza 111 x Giza 83 and Dr 101 x Giza 111 showed positive and significant \hat{S}_{ij} effects for this trait in both generations.

In this study a significant differ in spcific combining ability of all parental genotypes were detected in the same way Shiv, *et al.*, (2011) found highly significant differ between soybean parents and crosses for general combining ability and specific combining ability effects in growth and yield traits. The previous results were in the same way with those by El-Shaboury *et al.*, (2006), Perez *et al.*, (2009) and Waly (2015) which they found highly positive significant specific combining ability for branches number/plant, pods and seeds number/plant and seed yield/plant and negative one for flowering and maturity date in soybean. In the same way Nassar, (2013) reported that SCA effect were significant positive for pod and seed yield/plant and negative for some crosses in flowering and maturity.

Table 6. Estimate	s of sca effects	(Ŝii)) of individual	crosses for a	all t	he studied	trait in	both F	1 and F2
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	Mat	,, irity	Pla	ant	No. of	pods	No.	of	No	. of
Cross	Period	(day)	heigh	t (cm)	/pla	int	seeds	/pod	seeds	/plant
	F 1	F2	F1	F ₂	F ₁	F ₂	F1	F ₂	F1	F ₂
Hardin x D89-8940	-1.17	-3.17**	6.48**	4.10*	50.17**	33.88**	-0.03	-0.06	100.87**	62.78**
Giza 83 x D89-8940	-5.08**	-0.33	10.38**	5.74**	-0.50	1.79	0.08	0.04	9.36	9.15
Giza 111 x D89-8940	-5.04**	-3.13**	11.20**	6.83**	4.44*	5.38**	-0.06	-0.01	-0.53	9.53
Dr 101 x D89-8940	-6.08**	-0.54	2.37	-16.20**	-4.12*	-14.66**	0.03	0.02	-4.81	-29.93**
Line 105 x D89-8940	-3.63**	-18.83**	-9.37**	-6.21**	8.54**	2.94*	-0.14**	-0.12*	5.36	-1.56
Giza 83 x Hardin	0.25	-0.50	20.66**	-3.58	0.72	-18.00**	0.14**	0.10	17.59**	-30.47**
Giza 111 x Hardin	1.63*	3.04**	23.20**	15.53**	7.15**	1.92	0.10*	0.12*	29.72**	17.97**
Dr 101 x Hardin	2.58**	1.62**	1.44	12.26**	12.24**	11.55**	0.12**	0.08	47.79**	36.72**
Line 105 x Hardin	5.04**	8.33**	-4.95*	-5.86**	-10.95**	-12.85**	0.01	-0.03	-25.62**	-30.71**
Giza 111 x Giza 83	3.71**	2.21**	8.25**	16.75**	26.20**	26.83**	0.01	-0.06	60.04**	52.32**
Dr 101 x Giza 83	3.33**	2.79**	4.35*	9.99**	37.29**	33.47**	-0.27**	-0.23**	44.60**	44.36**
Line 105 x Giza 83	-0.21	1.17*	12.58**	14.73**	12.10**	12.07**	0.15**	0.17**	42.33**	42.23**
Dr 101 x Giza 111	1.04	-0.67	-7.04**	9.72**	3.99*	-1.62	0.16**	0.06	34.10**	4.93
Line 105 x Giza 111	-2.83**	-1.63**	-0.15	-23.02**	-5.04**	-25.35**	0.11*	0.09	-1.67	-48.13**
Line 105 x Dr 101	-2.87**	-2.38**	-4.80*	-23.18**	-16.31**	-22.05**	0.13**	0.02	-28.22**	-50.52**
LSD Sij 5%	1.31	1.03	4.31	4.00	3.69	2.80	0.09	0.10	12.26	12.06
LSD Sij 1%	1.75	1.37	5.77	5.35	4.93	3.75	0.11	0.14	16.41	16.13
LSD sij-sik 5%	2.36	1.86	7.80	7.23	6.66	5.06	0.15	0.18	22.16	21.79
LSD sij-sik 1%	3.16	2.48	10.43	9.67	8.92	6.77	0.21	0.25	29.65	29.16
LSD sij-skl 5%	2.19	1.72	7.22	6.69	6.17	4.69	0.14	0.17	20.51	20.17
LSD sij-skl 1%	2.93	2.30	9.66	8.95	8.26	6.27	0.19	0.23	27.45	27.00

Table 6.Cont.

	100	Seed	yield	Seed c	ontent	Seed content		
Crosses	weig	ght (g)	/plan	t (g)	of prot	ein %	of oil %	
	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_{1}	\mathbf{F}_2
Hardin x D89-8940	-1.87**	-1.14**	5.72**	4.67**	-5.17**	-3.67**	3.29**	1.99**
Giza 83 x D89-8940	0.26*	0.11	2.65**	2.04*	1.40	1.88*	-1.41**	-1.30**
Giza 111 x D89-8940	0.84^{**}	0.84**	2.39**	3.28**	2.16**	2.93**	-1.63**	-1.38**
Dr 101 x D89-8940	-0.14	-0.66**	-1.09	-6.05**	-0.96	-3.07**	-0.81*	-1.15**
Line 105 x D89-8940	-0.34**	-0.62**	0.53	-0.99	-1.57*	-2.42**	2.17**	1.91**
Giza 83 x Hardin	0.41**	0.59**	3.71**	-3.18**	1.09	2.37**	-1.64**	-1.29**
Giza 111 x Hardin	1.94**	1.31**	9.74**	5.36**	3.66**	2.85**	-2.18**	-2.35**
Dr 101 x Hardin	0.43**	0.05	7.12**	4.45**	1.47*	-0.39	-1.03**	-1.27**
Line 105 x Hardin	0.54**	0.74**	-1.76*	-1.98*	-0.23	-0.03	-2.18**	-1.66**
Giza 111 x Giza 83	0.74**	0.63**	12.45**	10.30**	2.16**	-3.88**	1.88**	1.62**
Dr 101 x Giza 83	0.93**	0.62**	10.56**	9.08**	-2.54**	2.51**	0.88^{**}	0.50
Line 105 x Giza 83	-1.06**	-0.65**	2.82**	3.85**	-1.11	0.91	-1.35**	-0.89**
Dr 101 x Giza 111	-0.30**	0.42**	4.10**	1.55	1.26	2.78**	2.50**	3.25**
Line 105 x Giza 111	-0.79**	-1.19**	-3.12**	-9.15**	-3.10**	-3.44**	0.25	-0.46**
Line 105 x Dr 101	-0.70**	-1.07**	-6.03**	-8.93**	-1.51*	-3.55**	-0.32	-0.96**
LSD Sij 5%	0.23	0.27	1.63	1.80	1.44	1.43	0.62	0.61
LSD Sij 1%	0.30	0.36	2.18	2.41	1.93	1.91	0.83	0.82
LSD sij-sik 5%	0.41	0.49	2.94	3.26	2.61	2.58	1.12	1.11
LSD sij-sik 1%	0.55	0.66	3.94	4.36	3.49	3.45	1.49	1.48
LSD sij-skl 5%	0.38	0.45	2.72	3.01	2.42	2.39	1.03	1.02
LSD sij-skl 1%	0.51	0.61	3.64	4.03	3.23	3.20	1.38	1.37

* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Hayman approach.

Analysis of variance.

The analysis of variance according to Hayman method is presented in Table 7. Results showed that mean squares due to additive (a) and dominance (b) components were highly significant for all studied traits in both F₁ and F₂ generations. The significant of both additive and nonadditive consider a clear evidence that both additive and non-additive gene actions were important in governing the inheritance of these traits. Also, the results showed that additive (a) component were larger than non-additive component in all studied traits and this may be indicated that the additive gene effect had the majority in the inheritance of these traits. This findings are in the same line with the result obtained by, Barelli et al., (2000) who indicated the preponderance of additive gene action in the inheritance of growth, yield and oil percentage of sovbean. Dominance direction (b₁) and SCA (b₃) components were significant for all studied traits in F1and F2 except for number of seeds/pod in F2 and both seed content of protein and oil in F_1 , indicating the presence of directional dominance and specific dominance effects relative to individual crosses while the insignificant b_1 and b_3 for number of seeds/pod in F2 and both seed content of protein in F₁confirmed the absence of directional and oil dominance and specific dominance effects relative to individual crosses. The genes' distribution (b₂) component, were highly significant for all studied traits in both F₁ and F₂ except for number of seeds/pod in F₂, indicating that gene asymmetry will presence of in the expression of the significant traits and absence in the insignificant one. The higher additive mean squares than the dominance mean squares reveal the predominance of additive effects on the control of all traits, although non-additive effects may also be involved these traits (Baker, 1978). Isik, et al., (2003) pointed that additive effects of genes are the main sources of genetic variation exploited by most breeding programs since it is responsible for setting the traits of interest. In this sense, the selection based on the morphological traits, which are useful in soybean breeding programs, can be carried out at initial generations due to the predominance of additive effects in segregation generations. This generates time savings in the evaluation, contributing to greater efficiency of breeding programs.

Table 7. Ana	alysis of variance	according to Hayma	an method for all the s	studied traits in F1 ar	nd F ₂ generations.

SOV		Maturity period (day)		Plant he	ight (cm)	Number of	pods/plant	Number of seeds/pod		
501	D.F	F1	F ₂	\mathbf{F}_1	F ₂	\mathbf{F}_1	F ₂	F1	F ₂	
a	5	309.34**	241.13**	1125.18**	1772.37**	1481.38**	1579.73**	0.05**	0.03**	
b	15	21.01**	48.12**	230.40**	257.24**	619.77**	450.25**	0.02**	0.01*	
b1	1	20.33**	33.60**	1298.29**	72.13**	3699.47**	290.83**	0.07**	0.01	
b_2	5	48.29**	87.41**	340.26**	484.99**	470.27**	559.83**	0.01**	0.01	
b 3	9	5.92**	27.90**	50.70**	151.28**	360.64**	407.09**	0.02**	0.01*	
Error	40	0.78	0.48	8.50	7.31	6.21	3.58	0.0004	0.0003	

* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Table 7. Cont.

SOV	Number of seeds/plant		100-seed weight		Seed /pl	yield ant	Seed c of pro	ontent tein %	Seed content of oil %		
	D.F	F ₁	\mathbf{F}_2	F1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	F ₁	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2
a	5	8403.02**	7706.24**	10.26**	10.29**	321.42**	272.78**	47.71**	30.85**	7.22**	6.19**
b	15	3170.19**	1807.94**	1.12**	0.93**	80.89**	50.53**	7.26**	9.15**	3.50**	3.09**
b 1	1	25553.20**	1834.18**	0.19**	0.0004	578.40**	47.79**	2.06	4.15*	0.58	2.76**
b ₂	5	2202.01**	2348.80**	1.62**	1.84**	101.42**	87.15**	11.23**	10.01**	2.18**	1.97**
b 3	9	1221.06**	1504.56**	0.94**	0.53**	14.20**	30.49**	5.63**	9.22**	4.56**	3.74**
Error	40	68.69	66.42	0.02	0.03	1.21	1.48	0.95	0.93	0.17	0.17

Estimates of genetic variance components:

The computed parameters for maturity period, plant height, seed yield and its components as well seed content of both protein and oil are presented in Table 8. From this table it could be clear that the additive genetic component (D) was highly significant for all traits in both F_1 and F_2 hybrids except number of seeds/pod in F₁. It was an evidence for the importance of the additive effect in the inheritance of these traits. With regard to dominance genetic variations (H_1) and (H_2) , the results indicated that the highly significant and/or significant were presented in all studied traits in both F1 and F2 generations. Comparing between the magnitude of additive and dominance components revealed that, the dominance component was more importance than additive components for all traits in both generation except maturity period and this finding could be interest to breeder to use the hybrid vigor in F_1 and F₂ to introduce hybrids with highly seed yield. Values of (H_2) were lower than those of (H_1) indicating the unequal proportions of positive U and negative V alleles at all loci for these traits. in this study additive component was larger than dominance component and both additive and dominance are important in the inheritance in all studied traits these results were in agree with those reported by Bhor et al., (2014) who found that both additive and non-additive gene effects were significantly involved in the expression of number of clusters and yield per plant with duplicate epistasis. Bi-parental mating design should be used to improve these characters. Complementary epistasis observed for days to 50% flowering, maturity plant height, pods per cluster and 100 seed weight suggests that selection can be practiced in segregation generation onwards for improvement of these characters. The significant of additive gene revealed that selection for this trait would be useful to start from the early segregating generation (Shinde, 2010). The significance of additive effect is indicative of the existence of parents who contribute to a greater number of favorable alleles for these traits to be transmitted to offspring (Ramalho et al., 2012). With respect to (F) parameter data showed that the values of (F) parameter was insignificant for all studied traits in F_1 and F_2 except for maturity period in both generations and seed yield/plant and oil percentage in F1. The insignificant values of (F) parameters for these traits may indicate that there is asymmetric gene distribution or the equality in the relative frequencies or dominant and recessive genes in the parent. On the other side, the (F) values were positive significant for maturity period in both generations. This finding indicates that the gene was more frequent in the parental lines and the majority for the dominant genes. Moreover, (F) value was negative significant for seed vield/plant in F₁ and this will refer to that the recessive gene were more frequent in the parental lines and the majority is for the recessive genes. For dominance effects of heterozygous loci (h²) highly significant and positive were presented for plant height, number of pods/plant, number of seeds / pod, number of seeds/plant and seed yield/plant in F1 and this indicate that dominance component over all heterozygous loci is important in the inheritance of these traits. The Significant of dominance effects reveal that there are deviations in the behavior of the hybrids compared to what was expected based on the parent's additive variation (Cruz, and Vencovsky 1989). The environmental variation (E) were not significant for all studied traits in both F1 and F2 indicating the absence of the environmental effect on these traits.

 Table 8. Estimates genetic variance components for all the studied traits of F1 and F2 generations, according to Hayman.

Donom	Maturity Period (day)		Plant he	Plant height (cm)		Number of pods/plant		Number of seeds/ pod_		Number of seeds/plant	
r ai aili.	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	\mathbf{F}_1	\mathbf{F}_2	
<u>л</u>	297.10**	297.39**	512.64**	514.40**	477.61**	479.54**	0.01	0.01*	2833.40**	2691.12**	
D	± 5.79	± 41.93	± 86.84	±120.72	± 179.99	± 106.43	± 0.01	± 0.01	± 834.32	±410.20	
U 1	101.22**	226.35*	901.42**	1214.04**	2261.10 **	2006.71**	0.07**	0.04*	10622.77**	7896.62**	
111	± 14.70	± 106.44	± 220.44	± 306.46	± 456.91	± 270.19	± 0.02	± 0.01	± 2118.00	± 1041.34	
บา	58.80 **	148.97	605.75**	788.55**	1847.06**	1511.79**	0.06**	0.03*	8714.78**	5852.61**	
112	± 13.14	± 95.09	±19693	±273.77	± 408.17	± 241.37	± 0.02	± 0.01	± 1892.06	±930.25	
E	222.10 **	294.04**	160.24	-172.39	-37.26	-40.55	-0.01	0.00	-356.13	16.53	
Г	± 14.15	± 102.43	± 212.14	± 294.92	± 439.71	± 260.02	± 0.02	± 0.01	± 2038.25	± 1002.12	
h2	12.76	21.52	835.83**	42.08	2394.49**	186.25	0.04**	0.00	16521.14**	1152.30	
11	± 8.84	± 64.00	±132.55	± 148.26	± 274.73	± 162.46	± 0.01	± 0.01	± 1273.48	±626.12	
E	0.75	0.46	10.18	8.42	5.98	4.05	0.00	0.01*	74.03	65.73	
Ľ	± 2.19	± 15.85	± 32.82	±45.63	± 68.03	± 40.23	± 0.00	± 0.00	± 315.34	± 155.04	

* and ** referred to significant at both 5 and 1% levels of probability, respectively.

Table 8. Cont.

Domomotors	100- seed	weight (g)	Seed yield	/plant (g)	Seed content	of protein %	Seed content of oil %		
rarameters	\mathbf{F}_1	F ₂	F ₁	F ₂	\mathbf{F}_1	F ₂	F1	F2	
D	3.20**	3.19**	77.09**	72.57**	12.40**	7.37**	5.83**	5.83**	
D	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	± 1.08							
u.	5.11**	4.46**	300.97**	231.69**	30.38**	37.27**	14.28**	12.31**	
	±1.31	±0.51	±75.88	±57.57	±8.05	±6.05	±2.24	±2.74	
U.	3.68**	2.84**	211.66**	155.19**	21.25**	29.20**	12.50**	10.71**	
Π 2	±1.17	±0.45	±67.79	±51.43	±7.19	±5.41	±2.01	±2.45	
Б	-1.49	-1.38	-43.87**	-26.98	-7.79	-4.07	4.41*	4.97	
Г	±1.26	±0.49	±73.02	± 55.40	±7.75	±5.82	±2.16	±2.64	
h2	0.11	-0.02	374.18**	30.17	0.63	2.00	0.25	1.66	
11	±0.79	±0.31	±45.62	±34.61	± 4.48	±3.64	±0.33	±1.65	
E	0.02	0.03	1.27	1.45	1.28	1.24	0.23	0.23	
E	±0.19	± 0.08	±11.30	±8.57	±1.20	±0.90	±0.35	±0.41	

Estimates of genetic ratios:

The results in Table 9 revealed that the average degree of dominance $((H_1/D)^{0.5})$ was less than the unit for maturity period in both generations, indicating the persence of partial dominance in this trait while, H1/D)^{0.5} was larger than the unit in all other traits in both F_1 and F_2 indicating that over dominance was involving these traits. Data in Table 9 showed that the $H_2/4H_1$ ratios were close to 0.25 for pods number/plant, seeds number/pod, seeds number/plant and oil percentage in both F1 and F2 as well as protein percentage in F2. These findings indicating that the alleles have symmetrical distribution between the parents. In contrast, H₂/4H₁were not close to 0.25 for maturity period, 100-seed weight and seed yield/plant in both generations and protein percentage in F1 as clear evidence that non symmetry in the distribution of favorable and unfavorable alleles for the increase of these traits.

For dominant / recessive relationship K_D / K_R indicated that recessive alleles were larger than dominant ones for all studied traits in both F_1 and F_2 generations

except for maturity period and oil percentage in both seasons as well as plant height in F_1 and number of seeds/plant in F_2 . It was noticed through the data presented in Table 10 that the difference between the broad and narrow sense heritability values was small in all traits in both the F_1 and F_2 generations, except for the oil percentage in both generations as a clear evidence of the predominance of the additive genes over the dominant genes in these traits, as well as a great stability in those traits.

According to Brogin, *et al.* (2003) the broad heritability values are considered low when they are lower than 0.30, intermediate when they are between 0.30 and 0.60, and high when they are higher than 0.60. These authors also mention that a heritability greater than 30% allows genetic gains through selection in early generations of inbreeding, as in the F_3 or F_4 progenies. It is also shown that the heritability estimate refers to a population trait that is specific to the environment in which the genotypes were evaluated.

Table 9. Estimates genetic ratios for all the studied traits of F_1 and F_2 generations, according to Hayman.

Dation	Maturity pe	Maturity period (day)		Plant height (cm)		pods/plant	Number of seeds/ pod	
Kauos	F1	F ₂	\mathbf{F}_1	F ₂	\mathbf{F}_1	F ₂	\mathbf{F}_1	F ₂
$(H_1/D)^{0.5}$	0.58	0.87	1.33	1.54	2.18	2.05	2.59	1.77
$H_2/4H_1$	0.15	0.16	0.17	0.16	0.20	0.19	0.21	0.21
K _D /K _R	4.56	3.62	1.27	0.80	0.96	0.96	0.65	0.97
h ² (n.s)	0.79	0.52	0.67	0.73	0.50	0.57	0.47	0.41
h^2 (b.s)	0.99	0.99	0.98	0.99	0.99	0.98	0.90	0.77

Table 9. Cont

D. (*	Number of seeds/plant		100-seed weight (g)		Seed yield/plant (g)		Seed content of	Seed content of oil %		
Ratios	F1	F ₂	F1	F ₂	F ₁	F ₂	\mathbf{F}_1	F ₂	F1	F ₂
$(H_1/D)^{0.5}$	1.94	1.71	1.26	1.18	1.98	1.79	1.57	2.25	1.57	1.45
$H_2/4H_1$	0.21	0.19	0.18	0.16	0.18	0.17	0.17	0.20	0.22	0.22
K _D /K _R	0.94	1.00	0.69	0.69	0.75	0.81	0.67	0.78	1.64	1.83
h ² (n.s)	0.53	0.61	0.76	0.81	0.66	0.69	0.69	0.53	0.32	0.30
h ² (b.s)	0.98	0.98	0.99	0.99	0.99	0.99	0.94	0.93	0.95	0.94

Wr/Vr Graphical analysis.

The results in fig 1 confirmed that the Wr/Vr graph showed that the regression line intercepted the Wr-axis under the origin point in both F_1 and F_2 , for number of pods/plant, number of seeds/pod, number of seeds/plant, seed yield/plant and seed content of oil indicating that the inheritance of this trait was governed by over dominance. While, the regression line intercepted the Wr-axis above the origin point for maturity period, plant height, 100-seed weight, and seed content of protein in both F_1 and F_2 generations indicating the presence of partial dominance.

The regression line slopes significantly deviate from the unit for all studied traits in both generations except maturity period in F_1 as an indicator that epistasis was involved in the inheritance of the trait.

Line 105 for plant height, number of pod/plant,

number of seed/plant, 100-seed weight, seed yield/plant and seed content of protein, Dr 101 for maturity period and plant height, D89-8940 for number of pods/plant and G82 for oil percentage were closest to the origin point in both in both F_1 and F_2 as clear evidence that more dominant genes for these traits. On the other side, the farthest from the origin point in both generations was D89-8940 for maturity period, seed content of protein and oil percentage, Hardin for plant height, number of seeds/pod, number of seeds/plant and 100-seed weight and Giza 83 for number of pods/plant and seed yield/plant, seemed to carry most recessive genes for the expression of the previous traits.

The scattered distribution of array points on the regression line were shown for all the studied traits, except maturity period and this often confirmed the presence of genetic variation among parents in this trait.



 $F_1 \ Number \ of \ seed \ / \ plant \\ F_2 \ Number \ of \ seed \ / \ plant \\ F_3 \ L \ Wr \ yr \ graphs \ for \ all \ the \ studied \ traits \ of \ F_1 \ and \ F_2 \ generations.$





Fig. 1. Cont.

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القدرة على التآلف ومكونات التباين الوراثي للمحصول ومكوناته لهجن فول الصويا التبادلية في الجيل الأول والثاني فايز السيد والى و رضاً على إبراهيم . قسم بحوث المحاصيل البقولية- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة-مصر

تم تقدير القدرة على التالف ومكونات النباين الوراثي لسنة أباء من فول الصويا مع هجنهم النصف تبادلية في الجيلين الأول والثاني في المزرعة البحثية لمحطة البحوث الزراعية بإيتاي البارود خلال المواسم 2017 و2019 و2019. كان التباين الراجع إلى التراكيب الوراثية؛ الأباء, الهجن وقوة الهجين كان عالى المعنويةً لجميع الصفات المدروسة في كلا الجيلين باستثناء قوة الهجين لمحتوى البراعي وترادع. لمن سببي الرابع في الجيل الورابية ، وتربي الهجن وتروا الهجين على على المعقوية المجمع الصفات المدروسة في كلا الجيلين باستثناء قوة الهجين لمحتوى البنرو من البروتين والزيت في الجيل الأول بالإضافة إلى عدد البذور/القرن ووزن 100 بذرة في الجيل الثاني. كان التباين الراجع لكل من القدرة العامة والخاصة على التألف معنويا لجميع الصفات في كلا الجيل الأول والإضافة إلى عدد البذور/القرن ووزن 100 بذرة في الجيل الأول بالإضافة إلى عدد البذور/القرن ووزن 100 بذرة في الجيل الثاني. كان التباين الراجع لكل من القدرة العامة على التألف معنويا لجميع الصفات في كلا الجيل الألى باستثناء القدرة العامة والخاصة على التألف أعلى من الوحدة لجميع الصفات المدروسة في كلا الجيلين. كان تباين الإسافة إلى كان التباين الراجع لكل من القدرة العامة والخاصة على التآلف معنويا لجميع من الوحدة لجميع الصفات المدروسة في كلا الجيل الألى كان التباين الراجع لكل من القدرة العامة والخاصة على التآلف معنويا لحمي من الوحدة لجميع الصفات المدروسة في كلا الجيلين. كان تابين الراجع لكل من القدرة العامة والخاصة على التآلف ألم معنويا لحمي من الوحدة لجميع الصفات المدروسة في كلا الجيلين. كان تباين القدرة العامة والخاصة على التآلف أعلى من الوحدة لجميع الصفات المدروسة في كلا الجيلين. كان تابين القدرة العامة والخاصة على التآلف أعلى من الوحدة لجميع الصفات المدروسة في كلا الجيلين. كان تباين الإضافة (أ والسيادة (ب) عالى المعنوبة لجميع الصفات المدروسة في كلا من الجيل الأول والثانى. في كلا الجيلين، أعطت الأباء دى أر 101 وجيزة اً 11 والهجن جيزة111 × جيزة83 ، دى أر 101× جيزة83 ، دى أر 101 × جيزة111 أعلى محصول بذور/نبات. أظهر الصنف دى أر 101 معنوبة سالبة في فترة النضج بالإضافة إلى تأثير معنوي موجب في معظم الصفات المحصولية للقدرة العامة على التآلف في كلا الجيلين. تم الحصول على أعلى تأثير موجب للقدرة الخاصة على التآلف في محصول البذور / نبات من الهجينين جيزة111 × جيزة83 ودي أر 101 × جيزة83 في كلا الجيلين. كانت التباين الإضافي (د) والسيادي (ها و ه) عالى المعنوية في كلا الجيلين ما عدا عدد البذور /قرن في الجيل الأول. تعتبر طريقة سجلات النسب طريقة ممتازة لإنتخاب سلالات مميزة في الأجيال الإنعز البة المبكرة لهذه الدر اسة.