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Diallel Analysis of Seed Yield, its Components and Oil Content in peanut

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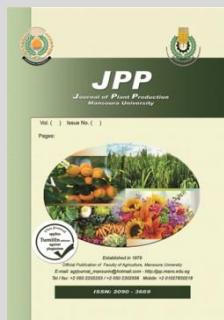


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ABSTRACT

A half diallel set including diverse five parental peanut genotypes was evaluated at Ismailia Agricultural Research Station, ARC, Ismailia Governorate, Egypt using randomized complete block design with three replications to estimate mean performance, combining ability, heterosis and nature of gene action. Highly significant genotypes and its components of parents, crosses and parents vs. crosses mean squares were detected for all studied traits. Highly significance of general and specific combining ability was observed for all studied traits. Additive gene action governed in plant height, number of pods/plant, number of seeds/plant, 100-pod weight and shelling %. Ismailia 2, Line 360 and Giza 6 seemed to be the best combiners for pod yield /feddan and most of its components. The best cross combinations were detected in F₁ crosses, P₂ × P₃ for seed weight /plant and P₃ × P₅ and P₄ × P₅ for pod yield / feddan. Significant or highly significant values and high values of the dominance component (H₁) were also observed for the most studied traits. P₅ carried the most dominant genes responsible for the expression of seed weight/plant and pod yield / feddan, while, P₄ for seed weight / plant and P₁ and P₂ for pod yield / feddan possessed high concentration of recessive genes. It could be concluded that, Ismailia2, Line 360 and Giza6 could be used as donors parents to improve yield and its components of peanut in the breeding program, also, the crosses P₂ × P₃, P₃ × P₅ and P₄ × P₅ with high SCA may be exploited for the development of hybrids as they had high per se performance.

Keywords: *Arachis hypogaea* L., Heterosis, Combining ability, Gene action, graphical analysis



INTRODUCTION

Peanut (*Arachis hypogaea* L.) is an important annual edible oilseed crop cultivated as a food group over the world. Its seed is a rich source of energy because of its high oil content. Groundnut (*Arachis hypogaea* L.) is one of the most important summer oil in the world. Groundnut seeds contain high oil (45%), 26-28 % protein, 20% carbohydrates and 5 % fiber (Fageria *et al.*, 1997). It also is rich in minerals (calcium, magnesium, and iron) and vitamins (E, B1, B2, and Niacin) (Patil *et al.*, 2017). Its straw and cake are important sources of animal feed. In addition, groundnut has the ability to fix atmospheric nitrogen benefitting the following crop. As a cash crop, it is considerably traded locally, regionally, and globally, significantly contributing to rural families' cash income and national economy in Africa. The big gap in oil production in Egypt is due to the lack of areas cultivated with oil crops specially canola, sunflower, and recently cotton. To fill this yield gap, the decrease in the area of these oil crops must be compensated via increasing the cultivated area of the peanut crop and improving its varieties to be suitable for biotic and abiotic stress conditions in Egypt. In Egypt, cultivated area was 142.642 per feddan in average yield 1.393 ton per feddan and total yield 198763 ton. (Anonymous, 2019)

Recently, breeding and crop management have increased the yield of peanut from 849 kg / ha in 1961 to 1655 kg / ha in 2014 (Haile *et al.*, 2019). High pod yield, early maturity, high shelling percentage, high oil, resistance to biotic and abiotic stresses they are the priority traits in peanut breeding in Egypt. Traditional breeding such as

introduction, selection, mutation, and hybridization i.e. pedigree, backcross, and single-seed descent, etc. have been used to develop improved varieties.

The basic requirements of the breeders to improve the traits are knowledge of the genetic composition and the nature of genes action controlling in these traits. Prediction of genetic diversity and combining ability of parents before crossing reduces the number of crosses and progenies to be screened which reduces cost and time (Kumer, 1999). The information on the combining ability of parents and the nature of gene action of yield and its components would help in understanding the inheritance of traits, selection of suitable parents for hybridization and identification of promising early generation crosses so as to design an appropriate and efficient breeding strategy for further genetic improvement of Peanut genotypes (Reddy *et al.*, 2017). Consequently, half diallel mating design was considered as a power tool for obtaining precise information on genes responsible for expression of traits. In this respect, diallel analysis (Haymen 1954, Dabholkar 1992 and Murtaza *et al.*, 2005) helps to identify parents with additive and non-additive effects for specific traits that may be used in breeding. Sprague and Tatum (1942) introduced the concept of general and specific. General combining ability is associated with genes which are additive in effects while specific is attributed primarily deviations from the additive scheme caused by dominance and epistasis (Rojas and Sprague, 1952).

Therefore, the objectives of this study were to estimate the relative importance of additive and non-additive gene action controlling the inheritance of yield and

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its attributes in a 5 × 5 half diallel mating design in peanut, identification of good general combiners to be used as donor parents for the improvement of these traits and identification of specific cross combinations with good combining ability for the improvement of studied traits.

MATERIALS AND METHODS

Five genotypes were obtained from Oil Crops Research Department, Field Crops Research Institute, Agricultural Research Center (ARC), which were selected based on its genetic diversity, to produce ten crosses using half diallel mating design. The crossed genotypes included (Line 190, Line 240, Ismailia 2, Line 360, and Giza 6). Description of five peanut genotypes used in half diallel mating design presented in Table (1). Hand emasculation and pollen transfer were done in 2018 season. The 10 F₁ crosses and their five parents were planted in May 2019, at the El-Ismailia Research Station, Agricultural Research Center. These 15 entries were replicated 3 times in a randomized complete block design (RCBD). Seeds were hand planted in plots, plot size was one 3-meter long row with 60 x 15 cm inter- and intra-row spacing. Agronomic practices includes application of gypsum 1 ton per feddan at the time of soil preparation, pest control, fertilization treatments, and irrigation were done according to peanut recommended practice.

Eleven traits were recorded such as plant height(cm), number of branches/plant, number of pods/plant, pods weight (g) per plant, number of seeds/plant, seed weight (g) per plant, 100-pod weight (g), 100-seed weight (g), shelling %, pod yield per feddan (ard) and seed oil content (%oil%) was determined using Soxhelt extraction technique using di-ethyl ether as organic solvent (AOAC 1990).

Table 1. Names and origin of five peanut genotypes used.

Parent	Name	Origin
P1	Line 190	Local
P2	Line 240	Indian
P3	Ismailia 2	Egyptian
P4	Line 360	Icrisat
P5	Giza 6	Egyptian

Table 2. Mean squares of genotypes and its components for all studied traits during summer season of 2019

S.O.V	df	Plant height	Number of branches/plant	Number of pods/plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
Reps	2	6.31	0.45	11.65	3.33	7.37	10.34
Genotypes	14	150.47**	4.24**	231.24**	1051.33**	1033.91**	918.01**
Parents (P)	4	201.90**	7.13**	395.10**	1263.24**	1376.26**	1059.88**
Crosses (C)	9	120.00**	3.27**	149.10**	1028.73**	872.73**	954.61**
P V C	1	219.02**	1.32**	315.10**	407.04**	1115.14**	21.12**
Error	28	3.55	0.15	6.73	12.18	4.62	2.65

Table 2. Continued

S.O.V	df	100-pod weight	100-seed weight	Shelling %	Pod yield per fed	Seed oil content
Reps	2	40.190	24.79	11.12	17.16**	7.02
Genotypes	14	5741.185**	598.39**	206.09**	87.44**	35.02**
Parents (P)	4	875.051**	601.48**	112.83**	31.63**	15.90**
Crosses (C)	9	5029.528**	141.26**	239.95**	55.00**	41.70**
P V C	1	31610.632**	4700.22**	274.44**	602.69**	51.38**
Error	28	123.796	19.37	13.60	0.40	2.45

Statistical analysis

The analysis of variance was done for all studied traits as described by Gomez and Gomez (1984). Heterosis was determined for individual crosses as the percentage deviation of F₁ means performance from either mid parents or better parents values. The analysis of general and specific combining ability was done according to method 2 model 1 of Griffing (1956). The combining ability ratio was calculated according to Baker (1978) as follow: $2MS_{gca} / (2MS_{gca} + MS_{sca})$. Hayman analysis of variance (ANOVA) was computed according to Hayman (1954a) following Jones (1965) modification. A graphical analysis (Hayman 1954 a, and Jinks 1954) was performed to determine the frequency of dominant and recessive alleles in the parental peanut genotypes evaluated. Genetic components along with related genetic parameters were estimated according to Hayman (1954b).

RESULTS AND DISCUSSION

Analysis of variance:

The ordinary analysis of variance for set of 5 parental peanut using half diallel mating design are presented in Table (2). Data revealed that peanut genotypes and their components (parents and their F₁ crosses) were highly significant for all studied traits, indicating presence of sufficient magnitude of genetic variability among these populations, hence that allows to improve these traits. Similar results were reported by Johne *et al.*, (2012) and Muibai *et al.*, (2020), where they reported genetic variation between genotypes either parents or crosses and their interaction. The variations due to parents vs. crosses or non-allelic interaction were considerable significant for all studied traits, indicating existence of sufficient amount of heterosis among crosses. Values of mean deviation of F₁'s from the mid-parents (b₁) (Jones, 1965) as in Table (3) were highly significant for all studied traits. The significant or highly significant of b₂ values were observed by all traits, indicating irregularity of gene distribution for these traits. b₃ was highly significant for studied traits indicating the existence of inconsistent allelic and non-allelic interaction or dominance effects specific to individual crosses for all traits (Kearsey 1965 and Mather and Jinks 1971).

Table 3. Jones analysis for all studied traits during summer season 2019

S.O.V	df	Plant height	Number of branches per plant	Number of pods per plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
a	4	56.28**	1.28**	96.73**	368.68**	431.86**	294.79**
b1	1	73.01**	0.44**	105.03**	135.68**	371.71**	7.04**
b2	4	41.18**	1.58**	82.56**	404.80**	113.17**	151.41**
b3	5	47.87**	1.58**	51.39**	335.32**	454.62**	498.45**
b	10	47.71**	1.46**	69.22**	343.15**	309.75**	310.49**
Error	28	1.18	0.05	2.24	4.06	1.54	0.88

Where; *P<0.05, **P<0.01, a=additive effects, b=total non-additive (dominance) effects, b1=mean deviation of F1's from their mid-parents, b2=test if there is equal or unequal distribution among parents and b3=detect existence of unique dominance of each F1, i.e., presence of considerable amount of heterotic effect specific to some crosses

Table 3. Continued

S.O.V	df	100-pod weight	100-seed weight	Shelling %	Pod yield per fed	Seed oil content
a	4	1943.24**	87.98**	95.98**	20.70**	5.51**
b1	1	10536.88**	1566.74**	91.48**	200.90**	17.13**
b2	4	1565.79**	138.18**	26.01*	12.20**	0.81
b3	5	443.85**	64.23**	76.46**	15.11**	24.21**
b	10	1901.93**	244.06**	57.79**	32.53**	14.14**
Error	28	41.27	6.46	4.53	0.13	0.82

Where; *P<0.05, **P<0.01, a=additive effects, b=total non-additive (dominance) effects, b1=mean deviation of F1's from their mid-parents, b2=test if there is equal or unequal distribution among parents and b3=detect existence of unique dominance of each F1, i.e., presence of considerable amount of heterotic effect specific to some crosses

Per se performance

As shown in Table (4), the parent P5 had the lowest value (32.20 cm) for plant height. The highest values are desirable for yield and yield attributes. In this regard, the highest value for number of branches per plant (6.27 branch) and number of pods per plant (45.33 pod), pods weight (g) per plant (85.17 g), number of seeds per plant (83.60 seed)

and 100-pod weight (g) (208.33 g) were obtained by P2 (Table 4). The highest value of seed weight per plant (g), 100- seed weight (g) (101.73 g) and pod yield per faddan (22.5 ard.) were achieved by P4. The parent P1 had the highest proportion of shelling (86.50 %) and P5 possessed the highest proportion of seed oil content (49.00 %).

Table 4. Mean performance of yield and yield attributes for five parental peanut and its F1 crosses during summer season 2019.

Genotype	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pods weight per plant(g)	Number of seeds Per plant	Seed weight per plant(g)
P1	45.80	2.70	29.33	56.87	51.77	39.07
P2	47.47	6.27	45.33	85.17	83.60	61.57
P3	45.00	2.93	21.67	43.47	40.90	39.77
P4	54.93	2.80	42.33	70.43	79.43	80.83
P5	32.20	2.87	20.67	33.93	38.20	38.83
LSD 5%	1.00	0.20	1.37	1.85	1.14	0.86
LSD 1%	1.34	0.28	1.85	2.49	1.53	1.16
P1 × P2	32.60	3.00	28.33	54.80	53.90	58.93
P1 × P3	37.70	4.93	21.20	53.67	30.67	38.93
P1 × P4	47.53	4.93	36.00	74.87	68.93	77.83
P1 × P5	32.60	2.47	22.67	33.10	33.63	38.03
P2 × P3	42.33	5.40	18.00	49.60	75.03	78.97
P2 × P4	44.33	3.20	17.00	54.17	31.07	36.33
P2 × P5	49.60	3.27	33.33	85.47	59.60	65.80
P3 × P4	33.20	2.80	25.00	77.63	30.27	30.83
P3 × P5	38.97	4.43	24.67	66.83	40.40	45.00
P4 × P5	45.13	4.33	36.33	93.40	58.70	64.00
LSD 5%	1.41	0.29	1.94	2.61	1.61	1.22
LSD 1%	1.90	0.39	2.62	3.52	2.17	1.64

Table 4. Continued

Genotype	100-pod weight(g)	100-seed weight(g)	Shelling %	Pod yield Per fed (ard)	Seed oil content (%)
P1	193.90	75.67	86.50	14.53	46.00
P2	208.33	73.67	72.13	16.20	45.67
P3	162.70	97.53	77.93	19.33	47.00
P4	178.10	101.73	72.70	22.50	42.67
P5	186.53	101.63	82.00	20.63	49.00
LSD 5%	5.88	2.33	1.95	0.33	0.83
LSD 1%	7.94	3.14	2.63	0.45	1.12
P1 × P2	253.60	109.33	74.47	23.00	52.67
P1 × P3	218.00	127.00	80.87	26.40	46.00
P1 × P4	161.23	113.00	64.87	25.30	46.33
P1 × P5	258.67	113.00	77.00	28.97	48.33
P2 × P3	309.87	105.20	56.71	30.90	50.67
P2 × P4	257.37	117.27	67.53	19.67	49.00
P2 × P5	281.50	110.40	68.43	22.27	42.00
P3 × P4	217.47	101.80	81.63	24.03	44.00
P3 × P5	245.37	111.33	86.50	32.00	53.33
P4 × P5	218.30	108.93	72.13	31.50	51.00
LSD 5%	8.32	3.29	2.76	0.47	1.17
LSD 1%	11.23	4.44	3.72	0.64	1.58

Significant differences as shown in Table (4) were found among the resulting crosses for all studied traits for plant height, P1 × P2 (32.60 cm) was the shortest cross while, P2 × P5 was the tallest one, P2 × P3 has the greatest number (5.40 branch) of branches per plant, P4 × P5 for number of pods per plant (36.33 pods) and pods weight per plant (93.40 g), P2 × P3 for number of seed (75.03 seed), seed weight per plant (78.97 g) and 100-pod weight (307.87 g), P1 × P2 for 100-seed weight (127.00 g), P3 × P5 for shelling % (86.50 %), P3 × P5 for pod yield per feddan (32 ard.) and seed oil content (53.33 %).

Combining ability

Variations of general (GCA) and specific (SCA) combining abilities were highly significant for all traits as shown in Table (3 and 5). According to (Jones 1965) the item (a) which refers to primary tests of the significance of

additive gene action and item (b) as indicator to the existence of non-additive effects were highly significant for all traits, indicating that both additive and non-additive gene action governed in the gene expression of these traits, but the preponderance was in favor of additive gene action in genetic control of plant height, number of pods per plant, pods weight per plant, number of seeds per plant, 100-pod weight and shelling %, but the remaining traits were governed by dominance gene action. The estimates of backer ratio and (a/b) ratio of Jones method, revealed the feasibility of selection in early segregating generations for plant height, number of pods per plant, number of seeds per plant, 100-pod weight and shelling %. Overall these findings are in accordance with results reported by Reddy *et al.*, (2017) and Waghmode *et al.*, (2017).

Table 5. Combining ability mean squares for all studied traits during summer season 2019.

S.O.V	d.f	Plant height	Number of branches per plant	Number of pods per plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
GCA	4	56.28**	1.28**	96.73**	368.68**	431.86**	294.79**
SCA	10	47.71**	1.46**	69.22**	343.15**	309.75**	310.49**
Error	28	1.18	0.05	2.24	4.06	1.54	0.88
baker ratio		0.70	0.64	0.74	0.68	0.74	0.66

Table 5. Continued

S.O.V	d.f	100-pod weight	100-seed weight	Shelling %	Pod yield per fed ⁻¹ (ard)	Seed oil content (%)
GCA	4	1943.24**	87.98**	95.98**	20.70**	5.51**
SCA	10	1901.93**	244.06**	57.79**	32.53**	14.14**
Error	28	41.27	6.46	4.53	0.13	0.82
baker ratio		0.67	0.42	0.77	0.56	0.44

General combining ability effects (GCA)

The negative effect of GCA effects is desirable for plant height, hence P1, P3, and P5 were desirable, as they had negative and highly significant GCA effects. On the other hand, the positive effect of GCA is desirable for yield and yield attributes (Table 6). In this concern, improvement of number of branches per plant achieved by P2 (0.70**), number of pods per plant by P2 (2.66**) and P4 (4.32**), pods weight per plant by P2 (5.86**) and P4 (9.65**),

number of seeds per plant by P2 (10.91**) and P4 (5.34**), seed weight per plant by P2 (6.47**) and P4 (7.54**), 100-pod weight by P2 (25.52**) and P5 (5.22**), 100-seed weight by P3 (1.91*), P4 (2.50**) and P5 (2.85**), shelling % by P1 (3.09**), P3 (1.86*), and P5 (2.79**), pod yield per feddan by P3 (1.30**), P4 (0.37**), P5 (1.87**) and seed oil content by P5 (1.03**). Similar findings were recorded by Johne *et al.*, (2012) and Muibai *et al.*, (2020)

Table 6. General combining ability effects of five peanut parents for all studied traits during summer season 2019

Parents	Plant height	Number of branches per plant	Number of pods per plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
P1	-1.39**	-0.26**	-0.27	-6.17**	-2.82**	-3.72**
P2	1.72**	0.70**	2.66**	5.86**	10.91**	6.47**
P3	-1.37**	0.13	-5.22**	-5.53**	-7.47**	-6.38**
P4	4.04**	-0.24**	4.32**	9.65**	5.34**	7.54**
P5	-3.01**	-0.33**	-1.49**	-3.81**	-5.96**	-3.91**
LSD gi 5%	0.75	0.15	1.04	1.40	0.86	0.65
LSD gi 1%	1.02	0.21	1.40	1.88	1.16	0.88
LSD gi-gj 5%	1.95	0.40	2.68	3.60	2.22	1.68
LSD gi-gj 1%	2.62	0.54	3.61	4.86	2.99	2.27

Table 6. Continued

Parents	100-pod weight	100-seed weight	Shelling %	Pod yield per fed	Seed oil content
P1	-8.72**	-1.90*	3.09**	-1.45**	-0.02
P2	25.52**	-5.35**	-5.31**	-2.09**	0.03
P3	-3.47	1.91*	1.86*	1.30**	0.36
P4	-18.54**	2.50**	-2.43**	0.37**	-1.40**
P5	5.22*	2.85**	2.79**	1.87**	1.03**
LSD gi 5%	4.45	1.76	1.47	0.25	0.63
LSD gi 1%	6.00	2.37	1.99	0.34	0.84
LSD gi-gj 5%	11.49	4.54	3.81	0.66	1.62
LSD gi-gj 1%	15.49	6.13	5.14	0.89	2.18

Specific combining ability effects (SCA)

The desirable interactive of gene between the created combination can be observed in the crosses P3 × P4 and P1

× P2 for plant height, as they had negative effect on plant height (Table 7). The cross combinations P1 × P3 and P1 × P4 for number of branches per plant, P1 × P4, P2 × P5, P3

× P5 and P4 × P5 for number of pods, six crosses out of ten F₁ ones for pods weight per plant, five crosses out of ten F₁ ones for number of seeds, six crosses out of ten F₁ ones for seed weight per plant, nine crosses out of ten F₁ ones for 100-pod weight, eight crosses out of ten F₁ ones for 100-seed

weight, five crosses out of ten F₁ ones for shelling %, seven crosses out of ten F₁ ones for pod yield per feddan and six crosses out of ten F₁ ones for seed oil content, as they had positive effect on improvement of these traits.

Table 7. Specific combining ability effects of five peanuts parents for all studied traits during summer season of 2019.

Crosses	Plant height	Number of branches per plant	Number of pods per plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
P1 × P2	-9.69**	-1.19**	-2.18*	-7.11**	-5.92**	3.20**
P1 × P3	-1.50	1.31**	-1.43	3.14*	-10.78**	-3.96**
P1 × P4	2.92**	1.67**	3.82**	9.16**	14.68**	21.03**
P1 × P5	-4.96**	-0.70**	-3.70**	-19.14**	-9.32**	-7.32**
P2 × P3	0.02	0.82**	-7.56**	-12.96**	19.85**	25.89**
P2 × P4	-3.39**	-1.01**	-18.10**	-23.57**	-36.92**	-30.66**
P2 × P5	8.93**	-0.86**	4.04**	21.20**	2.91**	10.26**
P3 × P4	-11.44**	-0.85**	-2.23*	11.28**	-19.35**	-23.31**
P3 × P5	1.38	0.88**	3.25**	13.95**	2.09*	2.31**
P4 × P5	2.14**	1.14**	5.37**	25.33**	7.58**	7.39**
LSD Sij 5%	1.54	0.32	2.12	2.85	1.75	1.33
LSD Sij 1%	2.07	0.43	2.86	3.84	2.37	1.79
LSD sij-sik 5%	2.92	0.60	4.02	5.41	3.33	2.52
LSD sij-sik 1%	3.94	0.81	5.42	7.29	4.49	3.40
LSD sij-skl 5%	2.66	0.55	3.67	4.93	3.04	2.30
LSD sij-skl 1%	3.59	0.74	4.95	6.66	4.10	3.10

Table 7. Continued

Crosses	100-pod weight	100-seed weight	Shelling %	Pod yield per fed ⁻¹	Seed oil content
P1 × P2	13.41**	12.09**	1.92	2.73**	5.08**
P1 × P3	6.80	22.49**	1.16	2.73**	-1.92**
P1 × P4	-34.89**	7.91**	-10.56**	2.56**	0.17
P1 × P5	38.78**	7.56**	-3.64*	4.73**	-0.25
P2 × P3	64.42**	4.14*	-14.60**	7.88**	2.70**
P2 × P4	27.00**	15.62**	0.51	-2.43**	2.79**
P2 × P5	27.37**	8.40**	-3.81*	-1.33**	-6.63**
P3 × P4	16.08**	-7.11**	7.44**	-1.46**	-2.54**
P3 × P5	20.22**	2.07	7.09**	5.01**	4.37**
P4 × P5	8.23	-0.91	-2.99	5.44**	3.79**
LSD Sij 5%	9.08	3.59	3.01	0.52	1.28
LSD Sij 1%	12.25	4.85	4.06	0.70	1.72
LSD sij-sik 5%	17.23	6.82	5.71	0.98	2.42
LSD sij-sik 1%	23.24	9.19	7.70	1.33	3.27
LSD sij-skl 5%	15.73	6.22	5.21	0.90	2.21
LSD sij-skl 1%	21.22	8.39	7.03	1.21	2.99

Heterosis

Mid-parent (heterosis, M.P) and better parent (heterobeltiosis, B.P) were estimated for all studied traits to

verify the presence of dominance and over dominance types of gene action in the expression of studied traits (Table 8).

Table 8. Heterosis of mid (MD) and better (BP) parents of ten peanut F₁ crosses for all studied traits during summer season 2019

Crosses	Plant height		Number of branches per plant		Number of pods per plant		Pods weight per plant		Number of seeds per plant		Seed weight per plant	
	MD	BP	MD	BP	MD	BP	MD	BP	MD	BP	MD	BP
P1 × P2	-30.09**	-28.82**	-33.09**	-52.13**	-24.11**	-37.50**	-22.84**	-3.63	-20.36**	4.12*	17.12**	50.85**
P1 × P3	-16.96**	-16.22**	75.15**	68.18**	-16.86**	-27.73**	6.98**	23.47**	-33.81**	-25.02**	-1.23	-0.34
P1 × P4	-5.63**	3.78*	79.39**	76.19**	0.47	-14.96**	17.62**	31.65**	5.08**	33.16**	29.83**	99.23**
P1 × P5	-16.41**	1.24	-11.38**	-13.95**	-9.33**	-22.73**	-27.09**	-2.46	-25.23**	-11.95**	-2.35	-2.06
P2 × P3	-8.44**	-5.93**	17.39**	-13.83**	-46.27**	-60.29**	-22.88**	14.11**	20.54**	83.46**	55.86**	98.58**
P2 × P4	-13.41**	-6.60**	-29.41**	-48.94**	-61.22**	-62.50**	-30.38**	-23.10**	-61.89**	-60.89**	-48.97**	-40.99**
P2 × P5	24.52**	54.04**	-28.47**	-47.87**	1.01	-26.47**	43.52**	151.87**	-2.13	56.02**	31.08**	69.44**
P3 × P4	-33.56**	-26.22**	-2.33**	-4.55**	-21.88**	-40.94**	36.32**	78.60**	-49.70**	-26.00**	-48.87**	-22.46**
P3 × P5	0.95	21.01**	52.87**	51.14**	16.54**	13.85**	72.70**	96.95**	2.15	5.76**	14.50**	15.88**
P4 × P5	3.60*	40.17**	52.94**	51.16**	15.34**	-14.17**	78.98**	175.25**	-0.20	53.66**	6.96**	64.81**
LSD 5%	2.73	3.15	0.56	0.65	3.76	4.34	5.06	5.84	3.11	3.59	2.36	2.72
LSD 1%	3.68	4.25	0.76	0.87	5.07	5.85	6.82	7.88	4.20	4.85	3.18	3.67

Table 8. Continued

Crosses	100-pod weight		100-seed weight		Shelling %		Pod yield per fed		Seed oil content	
	MD	BP	MD	BP	MD	BP	MD	BP	MD	BP
P1 × P2	26.10**	21.73*	46.43**	44.49**	-6.11*	-13.91**	49.67**	58.26**	14.91**	14.49**
P1 × P3	22.27**	12.43	46.65**	30.21**	-1.64	-6.51*	55.91**	81.65**	-1.08	-2.13
P1 × P4	-13.32	-16.85	27.40**	11.07**	-18.51**	-25.01**	36.63**	74.08**	4.51**	0.72
P1 × P5	35.99**	33.40**	27.47**	11.18**	-8.60**	-10.98**	64.74**	99.31**	1.75	-1.36
P2 × P3	67.03**	48.74**	22.90**	7.86*	-24.42**	-27.23**	73.92**	90.74**	9.35**	7.80**
P2 × P4	33.20**	23.54*	33.71**	15.27**	-6.74*	-7.11*	1.64**	21.40**	10.94**	7.30**
P2 × P5	42.58**	35.12**	25.96**	8.63*	-11.20**	-16.54**	20.90**	37.45**	-11.27**	-14.29**
P3 × P4	27.62**	22.10*	2.17	0.07	8.39**	4.75	14.90**	24.31**	-1.86	-6.38**
P3 × P5	40.52**	31.54**	11.80**	9.54*	8.17**	5.49	60.13**	65.52**	11.11**	8.84**
P4 × P5	19.74*	17.03	7.13*	7.08	-6.74*	-12.03**	46.06**	52.67**	11.27**	4.08**
LSD 5%	16.12	18.61	6.38	7.36	5.34	6.17	0.92	1.06	2.27	2.62
LSD 1%	21.74	25.10	8.60	9.93	7.21	8.32	1.24	1.43	3.06	3.53

The negative heterosis for plant height was observed in seven crosses for mid-parents (MP) and five crosses for better-parents (BP) out of ten F₁ crosses. The considerable positive effect of heterosis was obtained by five crosses for MP and four crosses out of ten F₁ crosses for BP for number of branches per plant. The number of pods per plant can be improved by two crosses for MP and one cross out of ten F₁ crosses for BP. The promising cross combination for pods weight per plant was six crosses for MP and seven crosses out of created combinations for BP. The improvement of number of seeds per plant can be achieved by three crosses for MP and six for BP out of created combinations. Seed weight per plant can be improved by six crosses for MP and BP out of created combinations. The highest heterosis of MP and BP was detected in nine crosses for 100-pod weight. The all cross combinations relative to MP and BP were promising for improvement of 100-seed weight, two crosses of created combinations for MP and BP in terms of shelling %, ten crosses in MP and ten in BP out of created combinations for pod yield per feddan and seven crosses in MP and six crosses in BP out of created combinations for seed oil content. The results obtained were similar to the findings of John *et al.*, (2012).

Graphical analysis:

Graphical analysis of the parent- offspring covariance (Wr) and array variance (Vr) and their related statistics was performed to obtain a clear picture about the inheritance for all studied traits (Table 9 and Figures 1 -11).

Additive-dominance model of inheritance was observed as regression coefficient (b) of (Wr/Vr) insignificant departed from unity for all studied traits, except for number of seeds per plant, this explains the existence of an interaction between alleles in the inheritance of these traits. Graphical analysis showed the presence of partial dominance in the inheritance of number of pods per plant, number of seeds per plant, seed weight per plant and seed oil content where the regression line intercepted the positive side of the Wr axis, while it passed below the point of origin for the rest of traits indicating presence of over-dominance in the inheritance of these ones.

The contradiction between both types of analysis might be a logical result of the presence of complementary type of non-allelic interaction which inflated the ratios of (H₁/D)^{1/2} and distorted the (Vr, Wr) graphs (Hayman 1954b and Mather and Jinks 1971). The array points of parental

genotypes were widely scattered for all traits, indicating presence of genetic diversity among the tested parents.

The following parental genotypes, P3 for plant height, P5 and P4 for number of branches per plant, P3 for number of pods, P1, P3 and P4 for pods weight per plant, P5 for number of seeds per plant, P5 and P2 for seed weight per plant, P5 and P2 for 100-pod weight, P5 and P4 for 100-seed weight, P4, P2 and P5 for shelling %, P4 for pod yield per feddan and P1 for seed oil content seemed to possess the most dominant genes responsible for the expression of these traits which being closer to the origin of regression graph. In the contrary, the parental following genotypes, P4 and P5 for plant height, P2 for branches number per plant, and number of pods per plant, P5 for pods weight per plant, P4 for number of seeds per plant, and seed weight per plant, P3 for 100-pod weight, P1 and P2 for 100-seed weight, P3 for shelling %, P1 and P2 for pod yield per feddan and P2 and P5 for seed oil content contained the recessive genes for these traits which might be due to be farthest ones from the origin of regression graph.

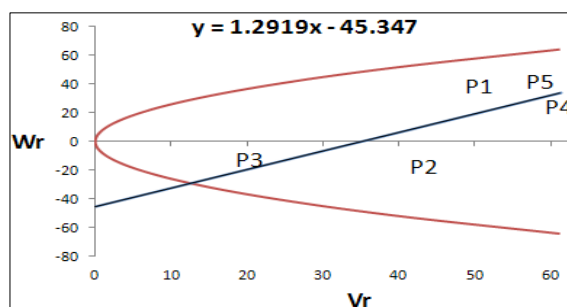


Fig. 1. Wr/Vr graphs for plant height during summer season 2019

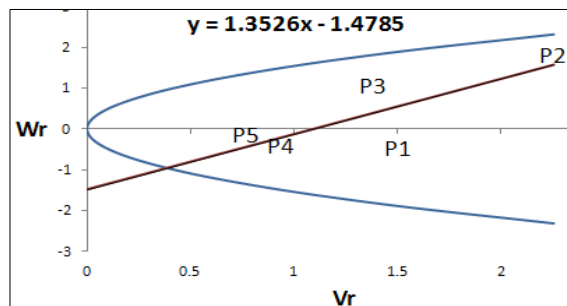


Fig. 2. Wr/Vr graphs for number of branches per plant during summer season 2019

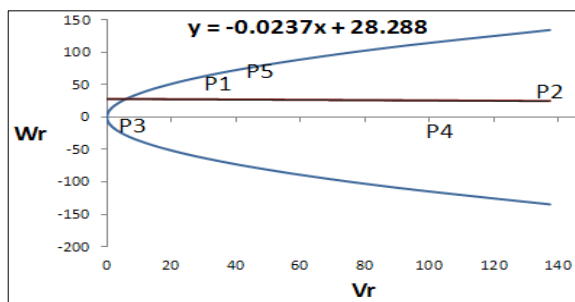


Fig. 3. Wr/Vr graphs for number of pods per plant during summer season 2019

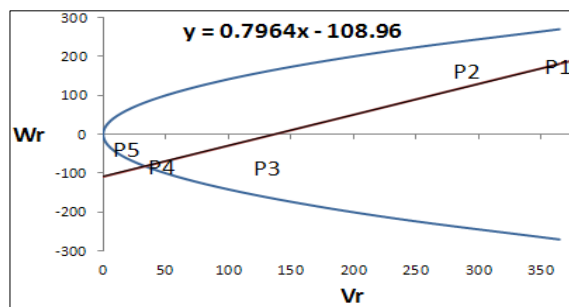


Fig. 8. Wr/Vr graphs for 100-seed weight during summer season 2019

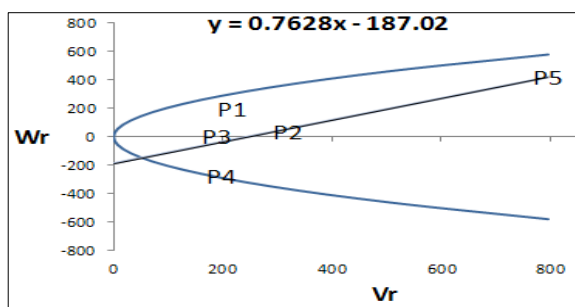


Fig. 4. Wr/Vr graphs for pods weight(g) per plant during summer season 2019

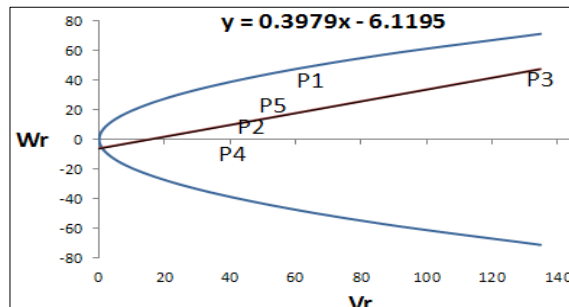


Fig. 9. Wr/Vr graphs for Shelling % during summer season 2019

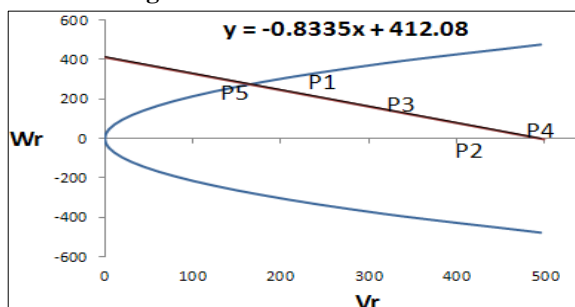


Fig. 5. Wr/Vr graphs for number of seeds per plant during summer season 2019

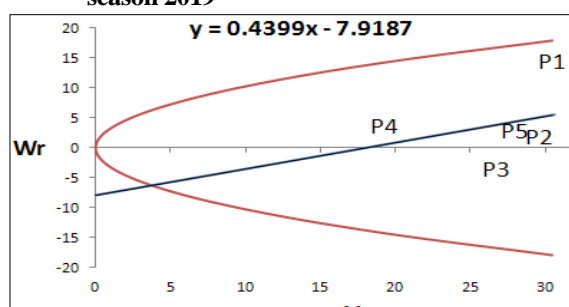


Fig. 10. Wr/Vr graphs for Pod yield per feddan during summer season 2019

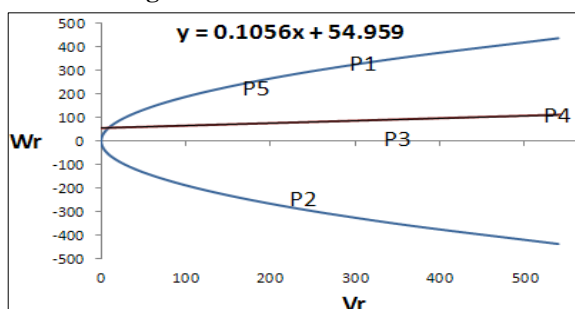


Fig. 6. Wr/Vr graphs for seed weight per plant during summer season 2019

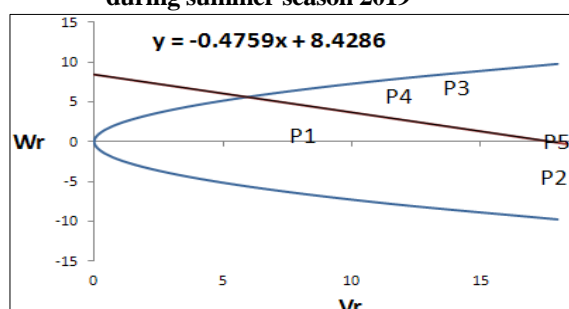


Fig. 11. Wr/Vr graphs for seed oil content during summer season 2019

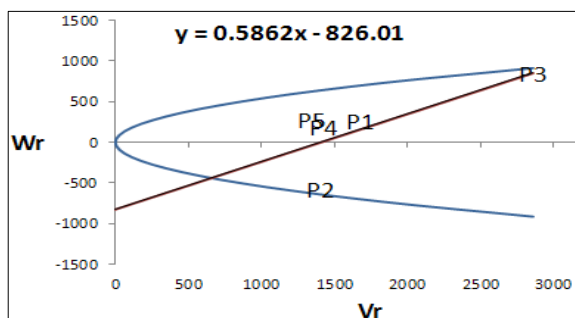


Fig. 7. Wr/Vr graphs for 100-pod weight during summer season 2019

Genetic components and related genetic parameters

The genetic components were estimated by the hayman's diallel analysis as in Table (9). The data showed that the components of additive (D) and dominance (H1 & H2) effects were positive and significant or highly significant for most traits, referring that the importance of both additive and non-additive components in the inheritance of such traits. Results showed that the presence of over-dominance for the studied traits due to higher significant or highly significant of the magnitude of dominance (H1 & H2) than additive components (D) for all traits, also, the results have shown clearly that frequency of

gene distribution in the parents was unequal this was evidenced by the results presented in Table (9) which showed that values of H1 were greater than H2 and that was also supported by the ratio of H2 / 4H1 (<0.25) which showed asymmetrical gene distribution at the loci in the parents showing dominance for all the traits.

The positive value of F and high value of KD/KR for all traits indicated that the presence of a higher number of dominant than recessives genes. Most of the dominant genes had positive influences because the overall dominance effects of heterogeneous loci (h^2) were positive. For the environmental variance estimates (E) were not significant for all the studied traits, indicating that all the traits were not

highly affected by the environmental factors. (H_1/D)^{1/2} ratio was calculated to measure the average degree of dominance overall loci (Table 9), which was found to be greater than unity for all traits, and this indicates the role of over dominance gene effects in the inheritance of these traits. The h_2/H_2 values (Table 9) were less than two for all studied traits that governed by one to two genes. Broad sense heritability, for all traits was very high and ranged from 0.94 to 1.00. While, narrow-sense heritability was found to be low to medium for all studied traits, indicating that selection should be delayed to late segregating generations. Similar results were founded by Arif and Akash (2019).

Table 9. Estimation of genetic components for all studied traits during summer season 2019.

Genetic parameter	Plant height	Number of branches per plant	Number of pods per plant	Pods weight per plant	Number of seeds per plant	Seed weight per plant
E	1.25±6.12	0.06±0.22	2.35±21.39	3.86±55.21	1.60±83.52	1.05±79.23
D	66.06±14.99**	2.32±0.53**	129.35±52.40*	417.21±135.23**	457.15±204.58*	352.24±194.09
F	72.42±37.44	3.18±1.33*	153.71±130.88	532.81±337.81	362.75±511.04	348.36±484.82
H1	190.75±40.48**	6.21±1.43**	283.69±141.50*	1486.56±365.22**	1216.10±552.49*	1292.60±524.15*
H2	156.90±36.72**	4.92±1.30**	215.75±128.34	1148.85±331.25**	1122.00±501.11*	1166.05±475.41*
h^2	55.27±24.79*	0.30±0.88	79.16±86.65	101.73±223.65	284.45±338.32	4.73±320.97
(H_1/D) ^{0.5}	1.70	1.64	1.48	1.89	1.63	1.92
$H_2/4H_1$	0.21	0.20	0.19	0.19	0.23	0.23
K_D/K_R	1.95	2.44	2.34	2.02	1.64	1.70
h^2/H_2	0.35	0.06	0.37	0.09	0.25	0.00
h^2 (n.s)	0.25	0.14	0.28	0.28	0.25	0.18
H^2 (b.s)	0.98	0.96	0.97	0.99	1.00	1.00

Table 9. Continued

Genetic parameter	100-pod weight	100-seed weight	Shelling %	Pod yield per fed)	Seed oil content
E	39.407±137.47	6.58±19.62	4.48±8.75	0.51±2.12	0.92±2.34
D	252.28±336.73	193.91±48.06**	33.13±21.42	10.04±5.20	4.38±5.74
F	-254.05±841.14	285.32±120.05*	-13.90±53.51	4.91±13.00	2.39±14.34
H ₁	6383.02±909.37**	758.19±129.78**	214.22±57.85**	101.04±14.05**	51.72±15.51**
H ₂	5091.41±824.81**	646.07±117.72**	195.06±52.47**	91.09±12.75**	51.59±14.06**
h^2	8067.10±556.87**	1199.05±79.48**	67.39±35.43	153.97±8.61**	12.56±9.49
(H_1/D) ^{0.5}	5.03	1.98	2.54	3.17	3.44
$H_2/4H_1$	0.20	0.21	0.23	0.23	0.25
K_D/K_R	0.82	2.18	0.85	1.17	1.17
h^2/H_2	1.58	1.86	0.35	1.69	0.24
h^2 (n.s)	0.41	0.06	0.38	0.24	0.07
H^2 (b.s)	0.98	0.96	0.95	0.98	0.94

CONCLUSION

Based on the obtained results of this investigation, highly significant genotypes and its components of parents, crosses and parents vs. crosses mean squares and highly significance of general and specific combining ability were observed for all studied traits. The additive gene action governed in plant height, number of pods, number of seeds per plant, 100-pod weight and shelling %, but the remaining traits were governed by dominance gene action. The parent, Ismailia 2, Line360 and Giza 6 seemed to be the best combiners for pod yield per feddan and most of its components. The most desirable specific cross combinations were detected in F₁ crosses, P₂ × P₃ for seed weight per plant and P₃ × P₅ and P₄ × P₅ for pod yield per feddan. The parent P₅ for seed weight per plant and pod yield feddan carried the most dominant genes responsible for the expression of these traits, while, P₄ for seed weight per plant, P₁ and P₂ for pod yield per feddan possessed high concentration of recessive genes.

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التحليل التبادلي للمحصول ومكوناته ونسبة الزيت في الفول السوداني

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أجرى هذا البحث بهدف دراسة المكونات الوراثية لصفة المحصول وبعض الصفات المرتبطة به لمحصول الفول السوداني وقد استخدم لهذا الغرض 5 تراكيب وراثية متباينة من الفول السوداني قيمت بمحطة البحوث الزراعية بالاسماعيلية - محافظة الاسماعيلية - مصر حيث تم عمل هجن تبادلية (دون العكسية) في الموسم الاول 2018 وفي موسم 2019 تم تقييم كل من الاء والهجن الناتجة في تصميم قطاعات كاملة العشوائية في ثلاث مكررات وسجلت النتائج للصفات والتي تم تحليلها بطريقة جريفينج 1956 و هايمين 1954 وطريقة التحليل البياني جينكز 1965 وكانت أهم النتائج المتحصل عليها كالآتي :- سجلت فروق عالية المعنوية بين التراكيب الوراثية (الاء والهجن) والاء X الهجن لكل الصفات تحت الدراسة. - القدرة العامة والخاصة على الإنتلاف كانت عالية المعنوية لكل الصفات تحت الدراسة - كان الفعل الجيني المضيف هو المتحكم في وراثه صفة طول النبات وعدد القرون/النبات وعدد البذور/النبات ووزن ال100 بذرة بينما كان الفعل الجيني السيادة هو المتحكم في وراثه باقي الصفات. -الاء إسماعيلية 2 و سلالة 360 و جيزة 6 كانت أفضل الاء لصفة محصول القرون للقدان ومعظم مكوناته بناء على تقديرات القدرة العامة على الإنتلاف. - حقق الهجين $P2 \times P3$ تفوقا معنويا لصفة وزن البذور للنبات والهجين $P5 \times P4$ لمحصول القرون للقدان حيث كان أفضل الهجن في قوة الهجين على أساس متوسط الأبوين والاب الأفضل. - كانت السيادة الفارقة ذات التأثير الأكبر في معظم الصفات. - أظهر الاب P5 أنه يحمل معظم الجينات السائدة المسنولة عن صفتي وزن البذور للنبات ومحصول القرون للقدان وعلى العكس الاء P4 لصفة وزن البذور للنبات و P1 و P2 لصفة المحصول للقدان كانت تحمل معظم الأليلات المتنحية في إظهار تلك الصفات. توصى الدراسة بإمكانية إستغلال الاء إسماعيلية 2 و سلالة 360 و جيزة 6 في برنامج تربية الفول السوداني لتحسين المحصول ومكوناته وكذا يمكن الإستفادة من الهجن $P2 \times P3$ و $P3 \times P5$ و $P4 \times P5$ ذات القيم العالية للقدرة الخاصة على الإنتلاف حيث إتصفت بمتوسط أداء وقوة هجين عالية.