

## COMBINING ABILITY AND GENE ACTION FOR AGRONOMIC TRAITS IN PEANUT (*Arachis hypogaea* L) UNDER NEW SANDY SOIL CONDITION

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**Key Words:** *Peanut, Combining ability, Gene action, Additive, Dominance, Heritability, yield and yield components*

### ABSTRACT

Ten crosses of peanut resulted from half diallel and five peanut were employed to estimate combining ability. General and specific combining ability, were highly significant for most studied traits. Additive and non additive were the prevailed type in the genetics of the studied traits.

Three crosses i.e,  $P_1 \times P_2$ ,  $P_1 \times P_4$  and  $P_4 \times P_5$  had positive and significant specific combining ability (SCA) for most of yield and yield components. Additive genetic variance (D) and dominance genetic one ( $H_1$  and  $H_2$ ) were highly significant for most of yield and yield components. Average degree of dominance was more than unity and heritability in narrow sense was high for pod weight/pl., 100-pod weight and 100-seed weight (59%, 61%, 83%) respectively.

### INTRODUCTION

Peanut or groundnut is an important oilseed crop in the world. In the recent years, improved cultivars are extensively used in hybridization because they possess many favorable genes which may complement each other in hybrid combination. The ultimate aim of peanut breeding programs is to increase yielding capacity. The first step in improving and breeding any crop depends on genetic variability so, the breeder make efforts for evaluation the parental genotypes.

Combining ability analysis is one of the powerful tools to compare the performance of different lines in different hybrid combinations and aid in selecting desirable parents and crosses for exploitation of heterosis (Rashid *et al.*, 2007; Salgotra *et al.*, 2009). Combining ability is defined as the ability of parents or cultivars to combine amongst each other during the process of hybridization so that favorable genes/characters are transmitted to their progenies. Since *per se* performance of parent may

not reveal its combining ability, so the information on nature of gene action and their expression in terms of combining ability is necessary.

Several investigators studied combining ability and gene action for yield and its components in peanut. **Naazar et al., 1995** and **Naazar et al., 2001** found that estimates of general combining ability were significant for 100-pod weight, pod length and shelling percentage in F<sub>1</sub> cross. Meanwhile, estimates for specific combining ability were significant for 100-seed weight in F<sub>2</sub> generation. **Sanun et al. (2005)** reported that estimates of both general and specific combining ability were significant for number of pods, pods kg<sup>-1</sup> and 100-seed weight, whereas estimates of GCA were greater than SCA estimates. **Abd El-Aal, 2008** and **Abd El-Aal et al., 2013** found that pod and seed traits were largely controlled by additive gene action, while pod number/ plant and pod weight/plant were controlled by non-additive genetic effect. Both genetic effects were equally important for shelling percentage. **Alam et al. (2013)** and reported that the analysis of combining ability suggested that both additive and non-additive gene actions were involved in genetic system. The number of pods/ plant, plant height, 100-pod weight and pod yield/ plot were preponderant by additive gene action. Meanwhile, primary branches/ plant and 100-seed weight were preponderant by non-additive gene action. **Vaithiyalingan (2016)** observed that additive gene action was predominant for all studied traits, except harvest index and single plant yield.

The objective of this research were to estimate some genetic parameters in order to evaluate the ability of some peanut genotypes for the choice of best parents and their crosses at early stages in the program under new sandy soil condition

## MATERIALS AND METHODS

Five parental peanut genotypes (*Arachis hypogaea* L.) varied in their genetic makeup were crossed in diallel fashion, excluding reciprocal to obtain 10 F<sub>1</sub> crosses at Ismailia Agriculture Research Station, during summer growing season 2015 and 2016. Five peanut genotypes were used in this study viz; line 193(P<sub>1</sub>), line 256(P<sub>2</sub>), line 309A (P<sub>3</sub>), line 410(P<sub>4</sub>) and Giza6 (P<sub>5</sub>). These parents were randomly chosen, representing a wide range of variability in most traits (Table 1).

In summer growing season 2016, all possible crosses excluding reciprocals, were made by hand between the five parents. Crossing

technique had been made according to (Norden and Rodriguez, 1971; Patel 1971).

**Table (1): Parents used and their origin**

Genotype	Name	Origin
P <sub>1</sub>	193	India
P <sub>2</sub>	256	China
P <sub>3</sub>	309	India
P <sub>4</sub>	410	ICRISAT
P <sub>5</sub>	Giza 6	Local variety

In summer season 2017, the obtained 10 F<sub>1</sub> crosses together with the five parental peanut genotypes were sown in a randomized complete block design with three replications in Ismailia experimental station, Agriculture Research Center. Experimental plot consisted of five rows, the row length 3meters, distance between rows 60cm and plant to plant spacing were 20cm. All normal recommended agriculture practices for peanut production were done at the suitable time each location.

Data were recorded on ten guarded plants from each plot in each replicate for parents and their F<sub>1</sub>'s. The studied characters were:

- 1- Number of pods/plant
- 2- Pod weight/plant(g)
- 3- Number of seeds/plant
- 4- Seed weight/plant (g)
- 5- 100-pod weight (g)
- 6- 100-seed weight (g)
- 7- Shelling percentage (%)

#### **Statistical analysis**

The combining ability analysis was carried out according to Model I and Method II of (Griffing, 1956). The fixed effect model (Model I) was considered to be more appropriate in the present investigation since the study was restricted to the parents and direct crosses only. The components of genetic variance were estimated using diallel biometrical approach outlined by (Hayman, 1954 a and b).

## **RESULTS AND DISCUSSION**

#### **Analysis of variance:**

Table (2) showed that variance due to genotypes for yield and yield components were highly significant in all traits, emphasizing on the existence of a fair amount of genetic variability valid for estimating general and specific combining ability. Mean square due to general (GCA) and specific (SCA) combining ability were highly significant for

all studied characters. These results showed that both additive and non-additive gene action controlled all yield and yield components traits. These results are confirmed by (Ali *et al.*, 2001; El-Sawy 2006).

The ratio of  $\delta^2\text{GCA}/\delta^2\text{SCA}$  mean square were more than unity for pod weight/pl., 100-pod weight, no. of seed/plant, seed weight/ plant and shelling percentage indicating the major role of additive gene action in the inheritance of these characters and it could be improved through phenotypic selection breeding method such traits are also reported by (Shabana *et al.*, 1992; Ruraswamy *et al.*, 2001; El-Sawy, 2006; Abd-El-Aal *et al.*, 2013).

**Table (2): Mean squares of five peanut parents and their crosses for 10 traits.**

S.O.V	No. of pods/pl.	Pod weight/pl.	100-pod weight	No. of seeds/pl.	Seed weight/pl.	100-seed weight	Shelling %
Genotypes	66.8**	249.6**	2718**	634.9**	49.6**	735.8**	246.9**
G.C.A	38.3**	189.8**	309.8**	468.9**	60.6**	81.38**	168.8**
S.C.A	46.6**	45.1**	95.6**	125.8**	29.2**	98.2**	61.5**
$\delta^2\text{gca}/\delta^2\text{sca}$	0.82	4.20	3.24	3.72	2.07	0.82	2.74

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

#### General combining ability effects:

Result of general combining ability effects and mean performance for five parental genotypes of peanut for yield and yield components are shown in Table (3). The result of peanut genotype P<sub>1</sub> and P<sub>5</sub> gave positive and significant GCA for pod weight/pl., 100-pod weight and 100-seed weight, indicating that these parents could be involved in breeding program to improve these characters. Genotype P<sub>2</sub> and P<sub>4</sub> gave positive and significant GCA for number of pod/pl., number of seed/pl. and shelling percentage. These parents are good combiner for these traits and could be included in breeding program to improve these traits. Similar results were observed by Sanun *et al.*, (2005); El-Baz *et al.*, (2006); Yadav *et al.*, (2006); Vishnuvardhan *et al.*, 2011; Abd-El-Aal *et al.*, (2013); John and Reddy, (2015).

**Table (3): Estimates of general combining ability (gi) effects and mean performance of five peanut parents for the studied traits.**

S.O.V	No. of pods/pl.	Pod weight/pl. (g)	100-pod weight (g)	No. of seeds/pl.	Seed weight/pl. (g)	100-seed weight (g)	Shelling %
P <sub>1</sub>	5.0**	2.5**	6.8**	-3.2**	-1.08*	7.7**	-5.3**
Mean	33.3	52.9	167.1	52.3	25.0	78.3	47.3
P <sub>2</sub>	1.04*	-5.1**	-17.4**	5.7**	-1.29*	-11.9**	4.9**
Mean	36.7	40.6	124.0	90.6	33.7	56.1	82.8
P <sub>3</sub>	0.96*	3.8**	-28.1**	10.5**	-2.7**	-13.4**	5.14**
Mean	38.8	48.3	101.3	90.3	32.7	50.8	81.8
P <sub>4</sub>	3.3**	2.8**	0.57	2.1**	2.33**	5.5**	1.18*
Mean	39.2	52.3	147.7	68.3	35.7	79.2	73.7
P <sub>5</sub>	-1.23*	3.3**	13.7**	-3.9**	2.17**	2.44**	0.05
Mean	28.9	54.8	177.1	54.3	36.7	68.8	70.3
S.E	0.6	0.76	0.83	0.46	0.48	0.56	1.06

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

**Specific combining ability effects:**

SCA effect is an index to determine the usefulness of a particular cross combination in the exploitation of heterosis. Since yield is a complex trait having low heritability, *per se*, selection for it is generally ambiguous and leads to unpredictable results. Indirect selection by making use of simple inherited traits have been advocated and used for the improvement of yield since time immemorial (Borojevic, 1990). While selecting the best specific combination for yield, it would be important to give due weight age to yield related traits. Grafius, 1959) had already suggested that there is no separate gene for yield, but yield is an end product of multiplicative interaction among various yield components which were validated by different workers in different crops (Bagheri and Babaeian, 2010; Rani and Satyanarayana, 2014).

Results given in Table (4) showed the estimates of SCA for the studied characters in ten crosses. These results indicated that the crosses (P<sub>1</sub>xP<sub>2</sub>, P<sub>1</sub>xP<sub>4</sub> and P<sub>4</sub>xP<sub>5</sub>) showed significant specific combining ability effects for number of pod/pl., number of seed/pl., 100-seed weight and shelling percentage. Moreover, the cross P<sub>2</sub>xP<sub>3</sub> exhibited positive and highly significant SCA effects for all studied traits except 100-seed weight and shelling percentage. These crosses could account for the highest average performance of the respective traits. In such hybrids, desirable transgressive segregates would be expected in the subsequent genotypes.

**Table (4): Estimates of specific combining ability for ten peanut crosses.**

Genotype	No. of pods/pl.	Pod weight/pl.	100-pod weight	No. of seeds/pl.	Seed weight/pl.	100-seed weight	Shelling %
P <sub>1</sub> xP <sub>2</sub>	4.2**	1.1	-8.5**	4.9**	5.9**	-7.9**	10.9**
P <sub>1</sub> xP <sub>3</sub>	-4.5**	-6.9**	-15.0**	-3.2**	0.6	-1.2*	13.0**
P <sub>1</sub> xP <sub>4</sub>	4.9**	11.8**	17.0**	11.9**	9.6**	6.4**	3.0
P <sub>1</sub> xP <sub>5</sub>	-2.8**	-7.0**	6.8**	-8.4**	-7.2**	7.9**	-2.7
P <sub>2</sub> xP <sub>3</sub>	3.3**	3.1**	4.9**	7.9**	4.0**	-7.2**	0.89
P <sub>2</sub> xP <sub>4</sub>	-3.7**	1.2	10.9**	-1.5*	-0.1	-7.8**	-1.7
P <sub>2</sub> xP <sub>5</sub>	-3.62**	-0.98	-9.8**	-21.0**	-7.0**	-7.3**	-14.0**
P <sub>3</sub> xP <sub>4</sub>	-1.9*	2.3*	-6.2**	5.2**	1.3	-6.1**	3.7**
P <sub>3</sub> xP <sub>5</sub>	5.2**	-8.0**	6.9**	-11.0**	-5.4**	9.1**	-0.4
P <sub>4</sub> xP <sub>5</sub>	-1.9*	3.5**	4.6**	16.9**	7.8**	9.7**	-0.6
S.E.(si-j)	1.64	2.1	2.3	1.1	1.3	1.5	2.90

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

### Estimation of genetic component and heritability:

Statistical analysis (Hayman, 1954a and b) are given in Table (5) and indicated that both additive (D) and dominance (H1 and H2) genetic variance were significant for the all studied traits and indicating the importance of additive and dominance gene effects in controlling these characters. The dominance genetic variance was higher in the magnitude as compare to additive one, resulting in (H1/D) 0.5 exceeding than more unity for all traits except 100-pod weight. In this respect over dominance gene effects reported for agronomic traits by Shabana *et al.*, (1992); Ayub-Khan *et al.*, (2000); El-Baz *et al.*, (2006); Abd-El-Aal, (2008); Abd-El-Aal *et al.*, (2013); Alam *et al.*, (2013); John and Reddy, (2015); Vaithiyalingan, (2016).

The ratio of dominance to recessive alleles (KD /KR) in the parents which was >1 for number of pods/plant, number of seeds/plant, seed weight and shelling percentage; indicated the preponderance of dominance alleles for these traits, Heritability estimates in broad sense (Hb) were high and ranged from 0.73 (number of pods/plant) to 0.99 (100-pod weight) for all the studied traits. Heritability values in narrow sense (Hn) found to be high (>50 %) for pod weight/pl.(0.59), 100-pod weight(0.61) and 100-seed weight (0.83). Thus phenotypic selections were effective in improving these traits. Whereas, (Hn) values was moderate for number of pods/plant (0.32), number of seeds/plant (0.45), seed weight/plant (0.27) and shelling percentage (0.43), thus selection on phenotypic base was ineffective.

**Table (5): Estimates of genetic components and their derived parameters for the studied traits.**

Genetic parameter	No. of pods/pl.	Pod weight/pl.	100-pod weight	No. of seeds/pl.	Seed weight/pl.	100-seed weight	Shelling %
D±S.E	37.2**	25.8	102.8**	337.9**	19.6	189.3**	167.1**
F±S.E	18.6**	-49.6	-363.8	222.9	21.3	-213.1	187.9
H <sub>1</sub> ±S.E	52.3**	175.1**	334.7**	571.3**	141.6**	288.6**	255.3**
H <sub>2</sub> ±S.E	52.1**	151.3**	276.7**	479.3**	105.4**	201.5**	167.4**
h <sup>2</sup>	1.87	3.78	43.0	18.78	-0.17	-2.74	1.31
E±S.E	3.63**	2.35	6.45	2.05	2.53	3.03	12.88
(H1/D) <sup>0.5</sup>	1.4	2.15	0.72	1.38	2.82	1.26	1.35
H <sub>2</sub> /4H <sub>1</sub>	0.22	0.20	0.21	0.20	0.20	0.17	0.18
KD/KR	1.65	0.58	0.58	1.60	1.59	0.38	2.49
Hb	0.73	0.95	0.98	0.97	0.93	0.93	0.87
Hn	0.32	0.59	0.61	0.45	0.27	0.83	0.34

## CONCLUSION

Generally, it could be concluded from results of the diallel analysis of this study, the dominance gene effects were the predominant components and accounted for the major part in the total variation for yield and its components.

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### القدرة علي التآلف والفعل الجيني لبعض الصفات المحصولية في الفول السوداني تحت ظروف الاراضي الرملية الجديدة

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يهدف هذا البحث الي دراسة القدرة علي الائتلاف وتحديد الفعل الجيني لبعض الصفات المحصولية في الفول السوداني. تم التهجين بين خمسة أباء متباينة في صفاتها المورفولوجية والمحصولية هي سلالة 193، سلالة 256، سلالة 309 سلالة 410 الصنف التجاري جيزه 6 باستخدام نظام الهجن الدائرية ما عدا الهجن العكسية في الموسم الزراعي الصيفي 2016، تم تقييم الخمسة أباء والعشر هجن الناتجة منها في الموسم الصيفي بمحطة البحوث الزراعية بالاسماعيلية لدراسة الصفات المحصولية التالية: عدد القرون/النبات ، وزن القرون/النبات ، وزن ال100- قرن، عدد البذور/النبات، وزن البذور/النبات، وزن ال100- بذرة، نسبة التصافي لجميع التراكيب الوراثية تحت الدراسة.

أظهر تحليل التباين للقدرة العامة والقدرة الخاصة علي التآلف معنوية لكل الصفات تحت الدراسة مشيرة الي أهميه كلا من الفعل الجيني المضيف وغير المضيف في وراثه جميع الصفات تحت الدراسة موضحا أهميه استخدام هذه الهجن في برامج التربية.

أظهرت دراسة القدرة الخاصة علي التآلف تأثيرات موجبه ومعنوية لثلاثة هجن وهي (الأب الأول×الأب الثاني و الأب الأول×الأب الرابع و الأب الرابع×الأب الخامس) لمعظم الصفات تحت الدراسة .

أظهرت الدراسة ان الفعل الجيني السياتي له الدور الأكبر في وراثه معظم الصفات تحت الدراسة بالمقارنه بالفعل الجيني المضيف حيث كانت درجات السيادة أكبر من الوحدة لجميع الصفات تحت الدراسة ما عدا صفة وزن ال100- قرن. كانت درجة التوريث بمعناها الضيق عاليه لصفات وزن القرون/النبات، ووزن ال100- قرن ووزن ال100- بذرة بقيم (59%- 61%- 83%) علي التوالي.