



## Genetic variation, correlation coefficient and pathway analysis for yield and its components in peanut (*Arachis hypogaea* L.)

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### Abstract

In 2018 and 2019 summer seasons form field experiments were carried out at Shandaweel Agric. Res. Station using 15 peanut genotypes to study the genetic parameters like variability, heritability and genetic advance as the percent, in order to develop new varieties. Results showed significant differences for the studied traits in the two seasons and the combined. Lines 11 recorded the highest value for pods weight/plant, 100-pod weight, seeds weight/plant, 100-seed weight and pod yield (ard/fed.) in two seasons and their combined. Phenotypic coefficient of variance (PCV) was more than genotypic coefficient of variance (GCV) showed larger influence of environment for all characters with slight differences in few cases. Heritability estimates along with expected genetic advance as percentage of mean was high for number of pods/plant, number of seeds/plant, seeds weight/plant and shelling percentage%, predicting the importance of additive gene action and ample scope for importance in these traits through selection. Correlations study revealed that pod yield (adr/fed) had highly significantly positive correlation with number of pod/ plant, pods weight/plant, 100-pod weight/plant, number of seeds/ plant, seeds weight/plant and 100-seed weight. Path coefficient analysis indicated that pods weight/plant, 100-pod weight and number of seeds/plant had the highest direct effect on pod yield (ard/fed.). Through these studied results and selecting the yield of peanut pods by these traits would be effective, two types of promising lines (No. 6 and 11), can be development varieties with good cultivation in Upper Egypt governorates.

**Keywords:** Correlation coefficient; Path coefficient analysis; Peanut; phenotypic and genotypic variance.

### 1. Introduction

Food The cultivated peanut (*Arachis hypogaea* L.) is an all tetraploid ( $2n = 40$ ), it is widely grown in more than 144 countries of the world. Peanut is important oil seed crop and also used for different purposes like seed consume directly raw, as roasted and boiled or processed into confections Its seed are source of high-quality edible oil (44-56%), protein (22-30%) on a dry seed basis, the shell used as fuel and animal feed, cattle litter, filler in feed and fertilizer industry; Haulm used as animal fodder or in manuring; roots being legume add the nitrogen (100-152 kg ha<sup>-1</sup>N) and organic matter to soil (Nigam, 2014).

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Peanut is considered one of the most important crops in Egypt due to the profits, its short growing season and it is also considered one of the most important oil crops that are well cultivated in light yellow sandy lands. The crop occupies the second place after cotton in terms of the cultivated area among the group of oil seeds crops, with an average cultivated area of about 147,62 thousand feddan during the period (2005-2019) (Walaa, 2022).

This study was conducted with the aim of estimating the performance of some peanut genotypes, variance, Correlation coefficient and path analysis among yield and its components of these genotypes to obtain some information could be useful for breeding program. Whereas, use the existing variance among them and aid in the selection of a superior genotype through Yield

and related features of the correlation response which in turn can support persistence and Future Peanut Breeding Programs.

## 2. Materials and Methods

The materials for the present study comprised of 15 peanut genotypes. They had grown in an experiment in a randomized complete block design with three replications at Shandaweel Agriculture Research station (ARC), during of 1<sup>st</sup> May 2018 and 2019 summer seasons. The

experiment comprised fourteen peanut diverse lines and a commercial variety Giza 6. The pedigree of these genotypes is shown in Table (1). Each experimental unit comprised 4 rows of 4 meter length keeping row-to row and plant-to-plant spacing at 60 and 10 cm, respectively. Data were recorded from each plot for Plant height (cm), number of branches, number of pods/plant, pods weight/plant (g), 100-pod weight, No. of seeds/plant. Seeds weight/plant, 100-seed weight (g), shelling percentage and pod yield (ard/ fed) = 75 kg.

**Table 1.** Pedigree of peanut genotypes studied.

No.	Lines	Introduction	Pedigree	Origin
1	Lines 45	Int.341	NC-17	USA
2	Lines 50	Int.455	ICGV87176	India
3	Lines 53	Int. 197	Blauco × alaufredirn 1	Mani
4	Lines 68	Int. 503	X 14-4-B-19-B	India
5	Lines 103	Int. 320	Florigiant	USA
6	Lines 119	Int. 368	IGGM 419	Malawi
7	Lines 121	Int. 371	ICGMS 480	Malawi
8	Lines 126	Int. 376	ICGMS 7	Malawi
9	Lines 132	Int. 382	ICGMS 42	Malawi
10	Lines 145	Int. 398	(Kadiri71 × Chico) F14 B1	ICRISAT
11	Lines 149	Int. 402	(Dh3-20 × Ah330) F9 B1	ICRISAT
12	Lines 150	Int. 405	(Ah65 × Robut33-1) F13 B1	ICRISAT
13	Lines 159	Int. 412	(Florigiant X Ah330 ) F9B1	ICRISAT
14	Lines 171	Int. 424	(Robut33-1 X NC (AC316)F7B1	ICRISAT
15	Giza 6	Local	Local Variety	EGYPT

The analysis of variance for each season was computed separately according to Mather and Jinks (1982). The findings of 2018 and 2019 did not significantly differ based on the homogeneity test; hence the combined analysis of the two seasons was carried out, Bartlett's test by Snedecor and Cochran (1989). Genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV), broad sense heritability and correlation coefficients were calculated by formula given by Singh and Chaudhary (1985). Genetic advance as per cent of means were estimated by using the procedure given by Brim *et al.* (1959). Path coefficient

analysis were conducted as suggested by Dewey and Lu (1959) to measure direct and indirect influence of traits on pod yield/ fed.

## 3. Results and discussion

### 3.1. Analysis of variance

The mean square variance in Table (2) indicated that there is significant variation among peanut all traits, ales these genotypes showed different response in the two seasons for all traits, except plant height because the year × genotypes interactive effect was significant.

**Table 2.** Mean squares for combined analysis of variance for different studied traits.

S.O. V. d.f	Year	Error a	Genotypes	Year × Genotypes	Error b
	1	4	14	14	56
Plant height	568.7**	1.701	13.36*	6.230	6.395
No. of branches	11.59	2.522	2.152**	2.936**	0.645
No. of pods/plant	30.26*	2.559	25.87**	8.952**	2.153
Pods weight/plant	35.68	29.82	143.7**	67.12**	12.78
100-pod weight	660.9	403.5	1840.6**	521.5**	149.9
No. of seeds/plant	155.7**	9.197	100.4**	35.65**	9.675
Seeds weight/plant	30.40	23.89	206.3**	25.82**	6.559
100-seed weight	214.8	135.4	200.2**	73.27*	38.45
Shelling percentage%	22.41	107.7	267.2**	40.44**	17.08
Pod yield (ard/fed.)	3.803	3.179	15.35**	7.157**	1.366

\* and \*\* Significant at 5% and 1% level of probabilities, respectively

### 3.2. Mean performance

Table (3) shows the mean performance of the fifteen peanut genotypes. The results showed significant differences among genotypes for the studied traits in the two seasons and the combined. It could be noted that Lines 2, 3, 8, 13 and 14 recorded the highest plant height (cm), while Line 9 had the highest number of branches

compared to the check genotype Giza 6 in 2018, 2019 seasons and their combined. All genotypes under study gave higher number of pods/plant, pods weight/ plant, number of seeds/plant, seeds weight/plant, 100-seed weight, Shelling percentage (%) and pod yield (ard/fed.) compared to the check genotype Giza 6 in two seasons and their combined.

**Table 3.** Mean performance for some characters of 15 peanut genotypes in 2018 and 2019 seasons and their combined.

Genotypes	Plant height(cm)			No. of branches			No. of pods/ plant			Pods weight/plant		
	2018	2019	Com.	2018	2019	Com.	2018	2019	Com.	2018	2019	Com.
1	39.33	32.74	36.04	9.267	8.167	8.717	20.10	18.25	19.18	57.58	55.02	56.30
2	41.27	36.44	38.86	8.767	8.033	8.400	22.37	18.59	20.48	56.53	56.07	56.30
3	38.70	37.74	38.22	10.47	7.500	8.984	21.66	21.05	21.36	59.13	66.28	62.71
4	34.57	32.13	33.35	9.433	9.200	9.317	22.52	17.59	20.06	60.95	55.08	58.02
5	37.20	34.74	35.97	10.60	8.300	9.450	24.64	20.92	22.78	64.43	55.69	60.06
6	38.43	33.57	36.00	10.71	10.11	10.41	24.67	25.85	25.26	60.86	69.74	65.30
7	37.37	29.80	33.59	8.100	9.833	8.967	19.93	19.70	19.82	57.00	61.74	59.37
8	41.70	37.75	39.73	10.43	8.967	9.700	21.98	16.51	19.25	61.68	50.46	56.07
9	38.10	34.73	36.42	9.567	7.867	8.717	18.77	20.62	19.70	49.94	58.75	54.35
10	39.73	32.37	36.05	10.63	8.767	9.700	23.70	23.83	23.77	65.27	71.10	68.19
11	38.77	33.50	36.14	8.433	8.867	8.650	21.81	24.36	23.09	65.32	72.18	68.75
12	39.53	33.63	36.58	9.600	10.10	9.850	21.12	19.93	20.53	58.42	66.19	62.31
13	40.83	33.53	37.18	10.70	8.767	9.734	23.15	23.01	23.08	64.91	61.93	63.42
14	39.47	34.43	36.95	9.600	9.200	9.400	19.70	17.86	18.78	57.13	53.94	55.54
15	38.73	34.43	36.58	9.333	11.10	10.23	17.97	18.17	18.07	51.68	55.36	53.52
L.S.D <sub>0.05</sub>	3.87	4.54	2.92	1.64	0.95	0.93	2.79	2.06	1.70	6.05	5.87	4.13

**Table 3.** Cont.

Genotypes	100-pod weight (g)			No. of seeds/plant			Seedsweight/plant (g)		
	2018	2019	Com.	2018	2019	Com.	2018	2019	Com.
1	200.5	206.9	203.7	40.21	36.53	38.37	31.28	36.03	33.66
2	173.9	200.6	187.3	44.75	37.23	40.99	36.99	34.20	35.60
3	213.2	228.9	221.1	43.48	39.10	41.29	34.74	35.30	35.02
4	198.6	201.4	200.0	45.46	35.01	40.24	38.06	32.77	35.42
5	220.6	210.7	215.7	41.76	48.87	45.32	43.05	42.59	42.82
6	174.9	183.8	179.4	48.49	51.75	50.12	37.67	42.48	40.08
7	223.9	215.5	219.7	40.16	39.41	39.79	29.14	36.00	32.57
8	213.9	189.0	201.5	44.28	33.00	38.64	33.95	29.21	31.58
9	166.6	172.1	169.4	38.18	41.24	39.71	26.02	27.51	26.77
10	224.3	223.6	224.0	43.96	48.73	46.35	40.62	42.22	41.42
11	225.1	230.9	228.0	47.47	47.55	47.51	44.34	48.84	46.59
12	195.6	222.4	209.0	42.20	39.84	41.02	32.70	36.61	34.66
13	202.9	186.9	194.9	45.81	46.12	45.97	35.23	32.84	34.04
14	181.2	192.4	186.8	39.48	35.72	37.60	27.49	24.64	26.07
15	189.5	217.5	203.5	36.19	36.34	36.27	24.18	31.64	27.91
L.S.D <sub>0.05</sub>	7.45	27.9	14.2	5.69	4.64	3.59	3.67	4.79	2.97

**Table 3.** Cont.

Genotypes	100-seed weight			Shelling percentage%			Pod yield (ard/fed.)		
	2018	2019	Com.	2018	2019	Com.	2018	2019	Com.
1	85.07	87.13	86.10	54.26	65.24	59.75	18.81	17.98	18.40
2	94.24	91.96	93.10	65.85	61.23	63.54	18.47	18.32	18.40
3	89.38	90.01	89.70	58.77	53.39	56.08	19.32	21.65	20.49
4	92.37	93.66	93.02	62.36	59.53	60.95	19.91	17.99	18.95
5	94.20	94.38	94.29	68.82	76.54	72.43	21.05	18.19	19.62
6	93.19	87.17	90.18	62.26	60.91	61.59	19.88	22.78	21.33
7	85.92	91.29	88.61	51.05	58.36	54.71	18.62	20.17	19.40
8	95.89	88.75	92.32	55.02	58.35	56.69	20.15	16.48	18.32
9	84.63	72.44	78.54	50.25	49.68	49.97	16.88	18.08	17.48
10	96.23	88.75	92.49	62.42	58.44	60.43	21.33	23.23	22.28
11	100.3	101.9	101.1	67.98	68.74	68.36	22.27	23.58	22.93
12	92.61	91.83	92.22	55.89	55.62	55.76	19.08	21.62	20.35
13	100.2	90.54	95.41	54.45	53.56	54.01	21.20	20.23	20.72
14	87.77	68.85	78.31	48.36	45.77	47.07	18.66	17.62	18.14
15	84.39	87.26	85.83	48.49	53.83	51.16	16.32	19.19	17.76
L.S.D <sub>0.05</sub>	9.05	11.50	7.16	6.13	7.60	4.78	1.98	1.92	1.35

Show Lines 11 recorded the highest value for pods weight/ plant, 100-pod weight, seeds weight/plant, 100-seed weight and pods yield (ard/fed.) while, Line 6 gave the highest value for number of branches, number of pods/plant, number of seeds/ plant and shelling percentage (%) in two seasons and their combined. Similar results reported by Naguib *et al.* (2011), Abd El-

aal *et al.* (2013), Rehab *et al.* (2013) and Mahesh *et al.* (2018).

### 3.3. Genetic variability

In all studied traits phenotypic coefficient of variance (PCV) was more than genotypic coefficient of variance (GCV) showed larger

influence of environment for the expression of these characters (Table 4). The high and moderate GCV and PCV were observed in plant height, number of branches, number of pods/plant, 100-pod weight, 100-seed weight, number of seeds/plant and pod yield (ard/fed.). The results were in accordance with Zaman *et al.* (2011), John *et al.* (2012), Mukesh *et al.* (2014), Narasimhulu *et al.* (2012), Salih *et al.* (2014),

Yadav *et al.* (2014) and Vasanti *et al.* (2015). Thus, it that good way for yield improvement through phenotypic selection. The low GCV and PCV was observed in pods weight/plant and shelling percentage (%) whereas; similar results reported by Shinde *et al.* (2010), Yadav *et al.* (2014) and Mahesh *et al.* (2018). The low GCV was indicating the large influence of environment for the expression of these traits.

**Table 4.** Genetic parameters for 10 morphological yield and yield attributes of 15peanut genotypes combined over two seasons.

Characters	PCV	GCV	ECV	h <sup>2</sup> b	GAM (at 5 %)
Plant height	8.11	4.19	6.95	26.63	3.80
No. of branches	11.46	7.58	8.59	43.78	8.83
No. of pods/plant	15.10	13.39	6.99	78.59	20.89
Pods weight/plant	12.52	11.01	5.96	77.35	17.04
100-pod weight	13.14	11.68	6.02	78.99	18.26
No. of seeds/plant	15.06	13.11	7.42	75.76	20.09
Seeds weight/plant	24.47	23.35	7.33	91.03	39.21
100-seed weight	10.68	8.16	6.89	58.37	10.98
Shelling Percentage%	12.25	11.71	7.11	83.00	25.19
Pod yield (ard/fed.)	17.52	15.01	5.96	77.33	17.04

\* and \*\* Significant at 5% and 1% level of probabilities, respectively

Heritability in broad sense is the ratio of genetic variance to the phenotypic variance which is heritable. High heritability in broad sense does't always means better response to selection, and is also inclusive of non-additive genetic factors. And therefore, estimation of genetic advanced further narrow down the response of selection. Heritability coupled with genetic advance as percentage of mean gives a very good indication of nature inheritance and effectiveness of selection for a particular trait (Johnson *et al.*, 1955).

The high heritability and GAM % is a sign of additive gene action and the ensuing high extended genetic gain from selection of superior genotypes. In present study, heritability estimates along with expected genetic advance as percentage of mean was high for number of pods/plant, number of seeds/plant, seeds weight/plants and shelling percentage% (ard/fed.). Pods weight/plant, 100-pod weight and pod yield

had high heritability and moderate GAM%. The moderate heritability and low GAM % was observed in plant height and number of branches. It noted that high heritability do not always indicate high genetic gain and preponderance of non-additive gene action governing the inheritance of these traits so phenotypic selection is not effective. The similar results reported by Kachhadia (2010), Rehab *et al.* (2013), Pathulothu *et al.* (2018) and Mahesh *et al.* (2018).

### 3.4. Correlation coefficient analysis

Yield is a complex quantitative trait governed by large number of genes and is greatly affected by environment. Hence, the selection of superior genotypes based on yield will not give a fruitful result. Association of yield components and yield therefore, assumed special importance as the basis for selecting desired strains. Genetic correlation

between different characters often arises due to its tight linkage or pleiotropy.

Simple correlation coefficients calculated among studied characteristics are shown in Table (5) Significant and positive correlations of pod yield (ard/fed) with number of pods/plant (0.779), pods weight/plant (1.00), 100-pod weight/plant (0.464), number of seeds/plant (0.746), seeds weight/plant (0.792) and 100-seed weight (0.344) were found. There were positive and significant correlations between number of pods/plant with pods weight/plant (0.779), number of seeds/plant (0.980), seeds weight/plant (0.712), 100-seed weight (0.406) and shelling percentage% (0.335). Also, was positively and significantly correlated between pods weight/plant with 100-pod weight (0.464), number of seeds/plant (0.746), seeds weight/plant (0.792) and 100-seed weight (0.344). The characters, seeds weight/plant (0.309) and 100-seed weight (0.223) showed positively and

significantly correlated with 100-pod weight, and seeds weight/plant, 100-seed weight and shelling percentage% with number of seeds/plant, as well, 100-seed weight and shelling percentage% with seeds weight/plant, also, 100-seed weight with shelling percentage%. Other characters like pods weight/plant and shelling percentage (%) had positive correlation but not significant with pods yield (ard/fed.).

The significant correlation indication of there is strong association among various traits and pods yield/ plant. A positive correlation between studied characters is favorable to the plant breeder because it helps in simultaneous improvement of both characters. There were positive and significant correlations between pod yield (ard/fed), numbers of pods/ plant and 100-seed weight Jogloy *et al.* (2011), Narasimhulu *et al.* (2012), Rao *et al.* (2014) and Fatih and Beycioglu (2022).

**Table 5.** Correlation co-efficient between yield and yield attributing characters for 15 peanut genotypes combined over two seasons.

Characters	Plant height	No. of branches	No. of pods/plant	Pods weight/plant	100-pod weight	No. of seeds/plant	Seeds weight/plant	100-seed weight	Shelling percentage %	Pod yield (ard/fed.)
Plant height	---	0.169	0.133	-0.082	-0.054	0.139	-0.141	0.166	-0.120	-0.082
No. of branches		---	0.016	-0.031	-0.036	0.045	-0.154	0.012	-0.199	-0.031
No. of pods/plant			---	0.779**	0.144	0.980**	0.712**	0.406**	0.335**	0.779**
Pod weight/plant				---	0.464**	0.746**	0.792**	0.344**	0.140	1.00**
100-pod weight					----	0.110	0.709**	0.223*	0.057	0.464**
No. of seeds/plant						----	0.711**	0.409**	0.356**	0.746**
Seeds weight/plant							----	0.552**	0.807**	0.692**
100-seed weight								---	0.509**	0.344**
Shelling percentage%									--	0.140
Pod yield (ard/fed.)										--

\* and \*\* Significant at 5% and 1% level of probabilities, respectively

The path coefficient analysis proposed by Dewey and Lu (1959) has identified the effective measure of direct and indirect causes of association and also depicts the relative importance of each factor involved in contributing to the end product that is produced. Since there is a more neglected value at the genetic level, only pathway analysis at the

phenotypic level is discussed below. Estimates of direct and indirect effects of yield attribute characters on pod yield (ard/fed.) using simple correlation are presented in Table (6). It was showed that the number of seeds/plant (0.857) followed by 100-pod weight (0.613) and pods weight/plant (0.093) had highest positive direct

effect on pod yield. The direct effects of these characters on pod yield (ard/fed.) could be considered as cause of such high correlation. While, number of pods/plant had negative direct

effect (-0.289.). Similar results were agreement with Zaman *et al.* (2011), Rao *et al.* (2014) and Mahesh *et al.* (2018).

**Table 6.** Direct and indirect effects of different characters towards seeds yield /plant at genotypic level in peanut.

Path way association	Direct effect P	Indirect effects PX	R
1- No.of pods/plant			
a). Direct effect ( $P_1Y$ )	-0.289		
b). Indirect effect via			
Indirect effect via. pods weight/plant $r_{12}Py_2$		0.072	
Indirect effect via. 100-pod weight $r_{13}Py_3$		0.088	
Indirect effect via. no. of seeds/plant $r_{14}Py_4$		0.840	
(c). Total effect			0.712**
2- Pods weight/plant			
(a). Direct effect ( $P_2Y$ )	0.093		
(b). Indirect effect via			
Indirect effect via. no. of pods/plant $r_{12}Py_1$		-0.225	
Indirect effect via. 100-pod weight $r_{23}Py_3$		0.284	
Indirect effect via. no. of seeds/plant $r_{14}Py_4$		0.840	
(c). Total effect			0.792**
3- 100-pod weight			
(a). Direct effect ( $P_3Y$ )	0.613		
(b). Indirect effect via			
Indirect effect via. no. of pods/plant $r_{13}Py_1$		-0.042	
Indirect effect via. pods weight/plant $r_{23}Py_2$		0.043	
Indirect effect via. no. of seeds/plant $r_{34}Py_4$		0.094	
(c). Total effect			0.094
4- No. of seeds/plant			
(a). Direct effect ( $P_4Y$ )	0.857		
(b). Indirect effect via			
Indirect effect via. no. of pods/plant $r_{14}Py_1$		-0.283	
Indirect effect via. pods weight/plant $r_{24}Py_2$		0.069	
Indirect effect via. 100-pod weight $r_{34}Py_4$		0.094	
(c). Total effect			0.711**
5- Residual effect		0.296	

Direct Path ( $p$ ); Indirect Path ( $px$ ) and Represent correlations ( $r$ )

The residual effect of the present study was 0.296 indicating that the characters studied contributed 0.704 of the yield. It has been suggested that maximum emphasis should be given to the above characteristics in selecting peanuts of higher yield.

#### 4. Conclusions

From the results, it can be concluded that peanut genotypes tested varied in their yield characters.

Lines 11 recorded the highest yield. Pod yield (ard/fed.) had a strong positive phenotypic correlation and high direct effect with pods weight/plant, 100-pod weight and number of seeds/plant. These traits appear to be the main contributor to the production of the pods, indicating the need for more focus on these components to increase the yield of the peanut pods.

also, phenotypic selection would be more effective for improvement the number of branches, number of pods/plant, Pods weight/plant, 100-pod weight, 100 seed weight, number of seeds/plant, seeds weight/plants, shelling percentage (%) and pod yield (ard/fed.) because above characters had high and moderate GCV, PCV, GAM and heritability. Both at phenotypic and genotypic level number of pod/ plant, pod weight/ plant, 100-pod weight/ plant, number of seeds/ plant, seeds weight/plant and 100-seed weight had significant and positive correlations on pod yield (adr/fed).

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All authors contributed to this research.

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#### Institutional Review Board Statement

All Institutional Review Board Statements are confirmed and approved.

#### Data Availability Statement

Data presented in this study are available at fair request from the respective author.

#### Ethics Approval and Consent to Participate

This work carried out at Oil crops Research Department, Field Crops Research Institute, Agricultural Research Center and followed all the department instructions.

#### Consent for Publication

Not applicable.

#### Conflicts of Interest

The authors declare no conflict of interest.

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