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Evaluation, Classification and Identification of Some Peanut Genotypes Based on New Morphological Characteristics and Multiple Agronomical Traits

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Abstract

This study was carried out during 2021 and 2022 seasons at Shandaweel Research Station, Sohag Governorate, Agriculture Research Center, Egypt to evaluate 16 promising peanut lines comparing to commercial Giza 6 and Ismailia 2 as two check varieties, based on the seed morphological and yield agronomical characteristics; and assess the genetic behavior. The results of this investigation have revealed a large genetic diversity in the peanut collection and growing under Egyptian conditions. Simple correlation revealed that most genotypes with morphological narrow seed embryo shape gave red seed testa color. Also, number and weight of pods and seeds per plant recorded the highest broad sense heritability estimates coupled with highest genetic advance (GA %). Then, selection for highest peanut pods/seeds number or weight would be accompanied by high yielding ability. GT biplot graphs were aligned with those obtained by correlation and cluster analysis pointing to closely related of Line 389, Line 22, and Line 91 genotypes. It also helped to understand that even if the genotypes are geographically distant, some of them have agro-morphological and genetic parameters traits that are close to each other. Then, biplot graph was considered as successful and effective technique beside/instead of these analyses to select the promising genotypes with high yield to be employed in the development of future peanut breeding programs in Egypt.

Keywords: Cluster analysis, GT-biplot, Seed morphological, Classification, Yield.

I. Introduction

Peanut (*Arachis hypogaea* L.) is considered to be one of the most important crops that thrive in newly reclaimed sandy soils as a source of edible oil and a leguminous crop of high nutritive value **[1]**. It is also considered a useful source of fat (34 - 54%) and very important in crop rotation systems as it helps in biological nitrogen fixation **[2,3]**.

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Evaluation and identification of the collection based on agronomic, morphological characteristics and biochemical traits are the starting point of any breeding program **[4, 5, 6]**. New populations can be introduced among different regions and improved promising breeding lines **[7]**. Besides, the evaluation of genetic resources is a key towards efficiency in utilization of these resources through the discovery of new genes as well as for their maintenance. Seed legumes provide large amounts of high-quality proteins that contain relatively more of the essential amino acids not supplied by cereals in which the content of tryptophan and lysine are relatively small **[8]**. Identification of superior genotypes with the desired characteristics plays a critical role in plant breeding programs, especially in selecting criteria useful for producing improved new varieties. **[4, 5, 6, 9, 10, 11, 12]** investigated the genetic diversity of barley, flax, faba bean, peanut and lupine genotypes using several methods, such as molecular markers, morphological traits, yield and its components, which result's indicated that the variation existed within the genotypes for most of the characters and could be investigated using these different techniques. The morphological traits are mostly influenced by environmental conditions **[13]**, morphological descriptors remain important for assessing genetic diversity, as they are the basis for varietal selection at the farm level **[14, 15]**. Understanding the genetic control of the most discriminating among the studied traits for peanut crop would bring significant contribution to the genetic improvement of this important crop **[6]**.

Multivariate analyses have been used to describe variation pattern in population genotypes. These statistical methods can easily select important traits to explore the relationships between traits, Also, dataset can be extract statistically by grouping similar vectors into classes using (hierarchical) analysis **[16].** Knowledge of genetic parameters is a basic step to identify the traits liable to genetic improvement through selection of promising genotypes based on various features (importantly pod yield) that is the main aim in breeding programs. Relationships among yield and yield-traits also play an important role **[16, 17]**. Genotype x trait (GT) biplot permits the visualization of the real correlation among traits and understanding of relationships that facilitate the identification of traits that can be used in indirect selection for a grain yield **[18, 19, 20]**. In addition, GT biplot gives information on the usefulness of cultivars for production as well as information that helps detect less important (redundant) traits. **[21]** used GT biplot graph to visualize the relationships among genotypes and traits.

This study was conducted at Shandaweel Agricultural Research in Sohag Governorate, Upper Egypt, to evaluate agro-morphological performance traits of peanut genotypes under the region's unique arid climate conditions. The objective of this investigation was to: (i) evaluate the agro-morphological performance traits of 18 groundnut genotypes grown under the Egyptian environmental conditions, (ii) classify the genotypes by various multivariate techniques into different groups and (iii) investigate genetic parameters and determine promising genotypes that could be used in improvement program.

II. Materials and Methods

1-Field experiment and plant materials:

This field experiment was carried out at Shandaweel Agriculture Research Station (high Egypt), Sohag Governorate. The geographical coordinates of the study locality were (24° 54' 0" North, 32° 94' 0" East), for two consecutive seasons: 2021 and 2022. The soil properties with the climatic distribution were presented in **Table (1a & b),** respectively.

Table (1a): Soil chemical and physical properties of Shandaweel experimental site in 2021 and 2022 seasons.

Soil properties before sowing (0-30 cm depth)										
Season	Texture grade	pH	EC dS m^{-1}	Soil Cations meq L^{-1}				Soil Anions Meq L^{-1}		
				Ca^{++}	Mg^{++}	Na^{+}	K^{+}	SO_4^{--}	Cl^{-}	HCO_3^{-}
2021	Sandy loam	7.82	0.277	0.51	0.91	1.15	0.44	1.43	0.60	0.68
2022		7.70	0.280	0.64	1.22	1.35	0.56	1.20	0.90	0.75

Table (1b): Monthly mean of air temperature (C^0) and relative humidity (RH %) in seasons 2021 and 2022 at Shandaweel.

Month	Temperature				RH%	
	2021		2022			
	Max.	Min.	Max.	Min.	2021	2022
Apr.	32.03	15.13	34.10	16.73	38.53	31.80
May.	37.74	21.42	34.52	19.10	33.03	29.50
Jun.	36.83	22.80	37.20	22.20	32.80	31.90
Jull.	38.90	25.13	37.45	23.10	31.60	34.00
Aug.	39.26	24.84	37.55	23.84	31.70	38.20
Sept.	35.17	21.93	36.40	22.03	43.20	40.10
Oct.	32.35	17.58	30.00	18.07	46.90	51.80

** Max = maximum temperature, ** Min = minimum temperature.*

Sixteen promising peanut lines with two commercial Ismailia-2 and Giza-6 check varieties (eighteen genotypes) were provided by Oil Crops Research Department, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Egypt, and kindly examined and evaluated by Oil Crops Research Department, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC) and Laboratory of Seed Technology Research Department, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Egypt, were shown in **Table (2) and Figure (1)** with their morphological characteristics.

Table (2): Genotypes of groundnut used in this study and their origin.

Code No.	Genotype	Origin	Code No.	Genotype	Origin
G1	**Line 91**	USA	G10	Line 203	India
G2	**Line 105**	Egypt*	G11	Line 89	USA
G3	**Line 39**	Egypt*	G12	Line 179	Icrisat
G4	**Line 115**	Mallawi	G13	Line 182	India
G5	**Line 180**	India	G14	Line 45	USA
G6	**Line 240**	India	G15	Line 117	Mallawi
G7	**Line 327**	China	G16	Line 22	USA
G8	**Line 409**	China	G17	Giza-6	Egypt*
G9	**Line 389**	India	G18	Ismailian-2	Egypt*

Giza-6 and Ismailia-2: commercial varieties in Egypt.

**FCRI: Field Crop Research Institute (Oil Crops Researc*h), Agricultural Research Center, Egypt.

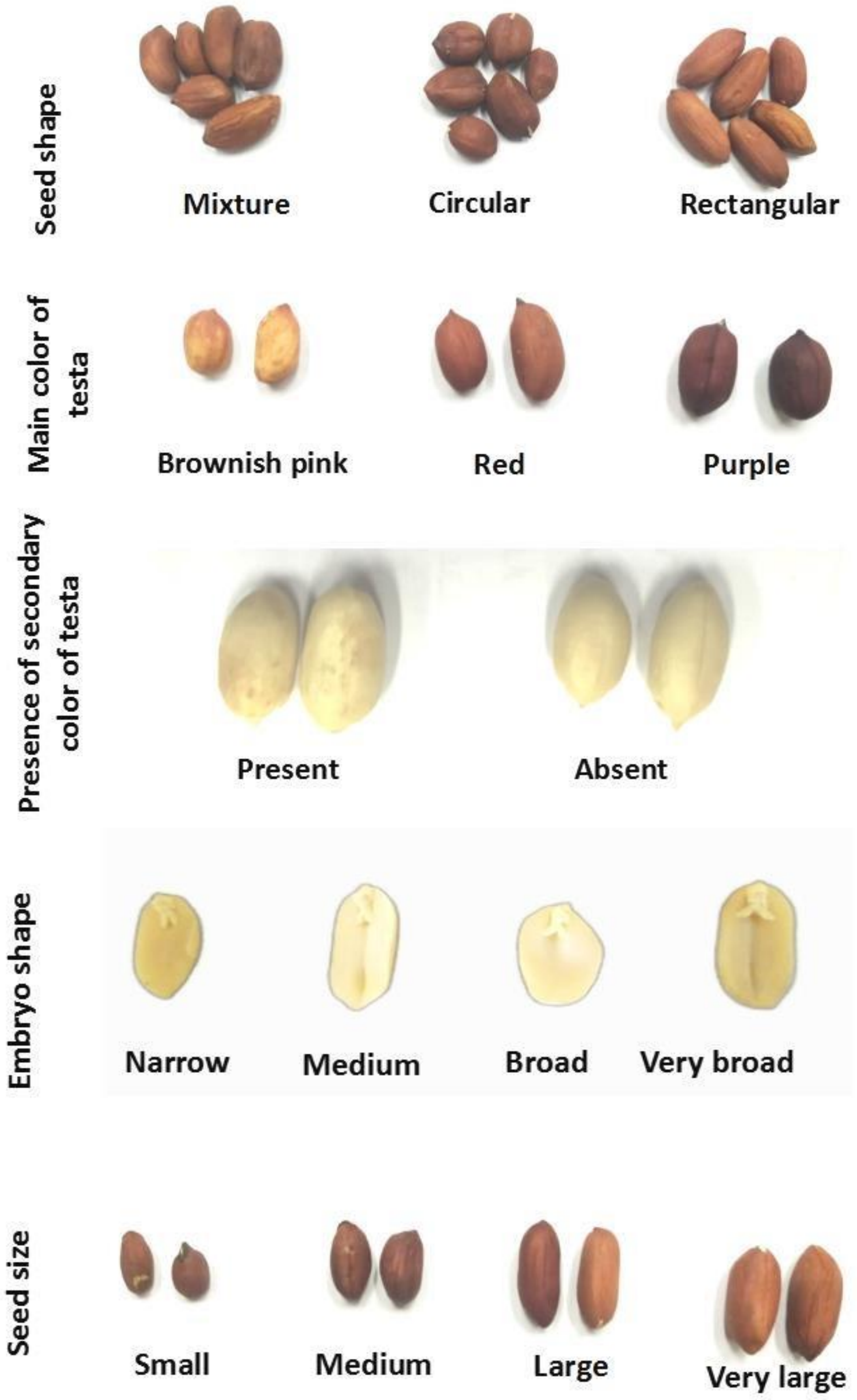


Figure (1): Seed peanut morphological traits showing variability.

In each season, tested eighteen peanut genotypes were sown on the 4th week of April in the field experiments of the both seasons (2021 and 2022) under randomized complete block design (RCBD) with three replications. Plot area was 9.6 m^2 consisted of 4 rows, 4 m long and 60 cm apart. Hills spacing within rows was 10 cm with one plant left per hill after thinning and the other cultural practices were carried out as recommendation packages. Looking to elements lack in the soil **(Table 1a)**; NPK were added at 45/60/24 kg/feddan. P was added during soil preparation meanwhile; N and K were splitted in 3 equal amounts added at sowing, 30 and 45 days after sowing. All recommended cultural practices for groundnut were applied.

2- Morphophological characteristics :

The identification of the studied morphological characteristics were conducted using UPOV(The International Union for the Protection of New Varieties of Plant) version 2014 peanut descriptor on seed morphology as presence of secondary color of testa, addition to new traits were discovered in these genotypes such as seed shape, main color of testa, embryo shape and seed size **(Figure 1)**. The decimal code for the growth stage of legume according to **[22]** was also used to standardize the growing stages of varieties during the morphological description and identification.

3- Agronomic quantitative traits :

Data was recorded for guarded plants to: plant height cm (PH), number of branches/plant (Bra), pod weight/plant g (PWP), number of pods/plant (Podno), number of seed/plant (Sno), seed weight/plant g (SWP) and shelling percentage % (Shl%). Besides, estimate of the seed oil content (Oil %) which is extracted by Soxhlet extraction method according to **[23]**. The two guarded inner rows were combined to determine the pods yield/plot kg and transformed to ardab/feddan (pod Y) [Ardab =75 kg and feddan = 4200 m^2].

4- The statistical techniques :

Statistical analysis was conducted on quantitative characters for each season and pooled combined analysis was performed after the homogeneity of variances for the two seasons was checked by use of **[24]** test. Genotypes means' across seasons were estimated for all traits. Least significant difference test was used to detect the significant differences among genotype means. Variance components of combined analyses across seasons were estimated according to **[25]**. Estimates of phenotypic (PCV %) and genotypic (GCV %) coefficients of variation, heritability in broad sense ($h_b{}^2$%) and the genetic advance percent (GA %) were calculated for each trait by using variance components method **[26]**.

Person's simple correlation coefficients between seed yield traits and Spearman correlation between qualitative characters were computed according to **[25]**. Cluster analysis was used to gather variables into groups, or clusters that were more similar to each other than within other clusters based on measure of similarity level s and Euclidean distance **[27, 28]**. Twin span (two way indicator species analysis) was used to classify variables producing an order two way table of their occurrence. Cluster analysis using a measure of similarity levels was performed to draw a dendrogram with the procedures of PAST software program**[29]** and was performed using Minitab 21software. GGE Biplot Model: GGT (genotype main effect plus genotype-by-traits interaction) is an application of the GGE biplot to study the genotype by trait data. The GGT graph used to study the genotype by recording the traits data **[18]**. The standardized values of the trait means was used to generate GGT biplot procedure. This biplot was performed with the procedures of the GenStat software package.

III. Results and Discussion

1. Morphological seed qualitative characteristics

The results in **Table (3) and Figures (1&2)** indicated that the seed shape, main color of testa, presence of secondary color of testa, embryo shape and seed size had variation among genotypes under study.

Seed shape was varied among all genotypes such as circular for 3 Lines (Line 389, Line 45 and Line 22), rectangular for 7 Lines (Line 39, Line 115, Line 180, Line 203, Line 179, Line 182 and check Giza-6) and for 8 Lines mixture (Line 91, Line 105, Line 240, Line 327, Line 409, Line 89, Line 117 and check Ismailian-2). Frequency distribution of seed shape was 17 %, 39 % and 44 % from total tested genotypes for circular, rectangular and mixture, respectively.

Meanwhile, main color of testa for all peanut genotypes had testa color ranged from brownish pink for genotypes of (Line 327, Line 179 and Giza-6); purple color for check Ismailian-2 only; red for genotypes of (Line 105, Line 39, Line 115, Line 180, Line 89, Line 182, Line 45 and Line 117); to mixture for (Line 91, Line 240, Line 409, Line 389, Line 203, and Line 22). Frequency distribution of main color testa was 6 %, 17 %, 33 % and 44 % from total tested genotypes for purple, brownish pink, mixture and red, respectively.

Presence of secondary color of testa was present in all genotypes except (Line 180 and Line 240) which were absent. Frequency distribution of secondary testa color was 11 % and 89 % from total tested genotypes for present and absent, respectively.

On the other hand, embryo shape recorded as narrow with genotypes (Line 39, Line 180, Line 203, Line 89, Line 182 and check Ismailian-2); medium with genotypes (Line 91, Line 105 and Line 115; broad with Line 240, Line 327, Line 409, Line 179, Line 45 and Line 117) and very broad with genotypes (Line 389, Line 22 and check Giza-6). Frequency distribution of embryo shape was 17 %, 17 %, 33 % and 33 % from total tested genotypes for medium, very broad, narrow and broad, respectively. These results agree with those obtained by **[4, 5, 6]**, they showed that the seed characters in different crops with different genotypes had high differentiation in many seed characteristics and these characters are very helpful in plant breeding program due to variation.

Table (3): Morphological characteristics of 18 seed peanut genotypes under evaluation.

Code	Genotypes	Seed shape	Main color of testa	Presence of secondary color of testa	Embryo shape	Seed size
G_1	**Line 91**	Mixture	Mixture	Present	Medium	Medium
G_2	**Line 105**	Mixture	Red	Present	Medium	Medium
G_3	**Line 39**	Rectangular	Red	Present	Narrow	Large
G_4	**Line 115**	Rectangular	Red	Present	Medium	Large
G_5	**Line 180**	Rectangular	Red	Absent	Narrow	Large
G_6	**Line 240**	Mixture	Mixture	Absent	Broad	Medium
G_7	**Line 327**	Mixture	Brownish pink	Present	Broad	Medium
G_8	**Line 409**	Mixture	Mixture	Present	Broad	Small
G_9	**Line 389**	Circular	Mixture	Present	Very broad	Medium
G_{10}	**Line 203**	Rectangular	Mixture	Present	Narrow	Very large
G_{11}	**Line 89**	Mixture	Red	Present	Narrow	Large
G_{12}	**Line 179**	Rectangular	Brownish pink	Present	Broad	Very large
G_{13}	**Line 182**	Rectangular	Red	Present	Narrow	Large
G_{14}	**Line 45**	Circular	Red	Present	Broad	Large
G_{15}	**Line 117**	Mixture	Red	Present	Broad	Large
G_{16}	**Line 22**	Circular	Mixture	Present	Very broad	Small
G_{17}	**Giza-6**	Rectangular	Brownish pink	Present	Very broad	Very large
G_{18}	**Ismailian-2**	Mixture	Purple	Present	Narrow	Very large

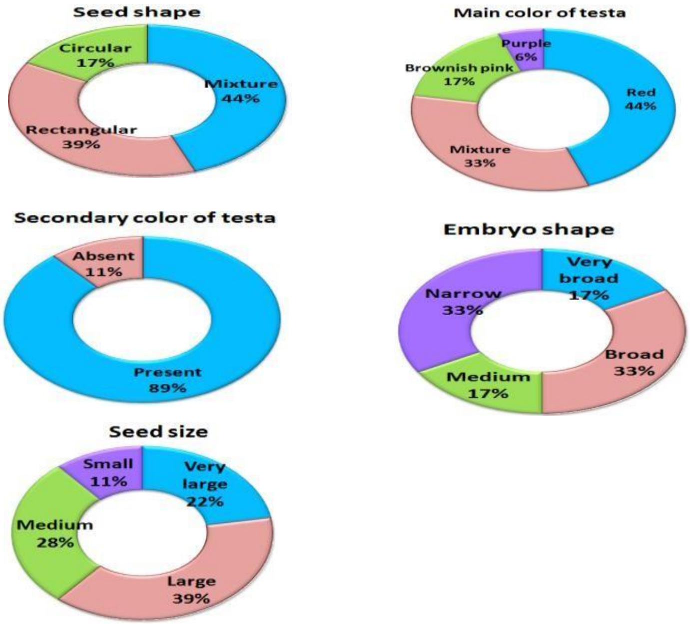


Figure (2): Frequency distribution of morphological qualitative traits for the studied seed peanut genotypes.

Seed size had highly different in all genotypes, such as small type (Line 409 and Line 22), medium (Line 91, Line 105, Line 240, Line 327 and Line 389), large (Line 39, Line 115, Line 180, Line 89, Line 182, Line 45 and Line 117) and very large (Line 203, Line 179, check Giza-6 and check Ismailian-2). Frequency distribution of seed size was 11 %, 22 %, 28 % and 39 % from total tested genotypes for small, very large, medium and large, respectively.

2. Agronomic quantitative traits

Results of **[30]** confirmed the homogeneity of variances for the agronomic traits which allowed following the combined analysis. Accordingly, mean square and performance of eighteen peanut genotypes for yield and its related traits over the two seasons 2021 and 2022 was presented in **Tables (4 & 5).**

2.1. Analysis of variance

Combined analysis of variance exhibited that seasons were significant for plant height, number of seed/plant, pod weight/plant, pod yield ard/fed and shelling %, indicating that these traits performance of the measured peanut genotypes was significantly affected by environment.

Pods yield (ard/fed) performance pointed to differences of climatic conditions from year to year at the same location **(Figure 3)**. Similar results were obtained by **[16, 17].** Meanwhile, insignificant effects of seasons on the performance of some important traits such as number of branches/plant, number of pods/plant, seeds weight/plant and oil % due to the evaluation for two seasons under the same location had narrower environmental fluctuation.

Table (4): Mean square ANOVA for yield and agronomic traits for tested peanut genotypes.

S. O. V	D. F	Plant height	Branches	Pod Yield (ard/ fed)	Pod weight /plant (g)	No. of pod plant	No. of seed / plant	Seed weight /plant (g)	Shelling %	Oil %
Year	1	92.41**	0.85	15.99**	637.76*	12.01	85.58*	0.43	1045.67**	0.18
Residual	4	3.54	0.57	0.16	40.13	3.45	8.58	1.27	37.67	0.13
Genotype	17	80.18**	1.38**	21.01**	135.10**	217.66**	857.31**	165.34**	340.45**	13.08**
Y * G	17	9.86**	0.19	2.76**	43.82**	2.05	10.31	30.73**	88.68**	1.37**
Residual	68	4.07	0.14	0.28	9.58	2.62	7.59	4.97	25.35	0.03

*Ns, * and ** mean not significant and significant at p-value of 0.05, and 0.001, respectively.*

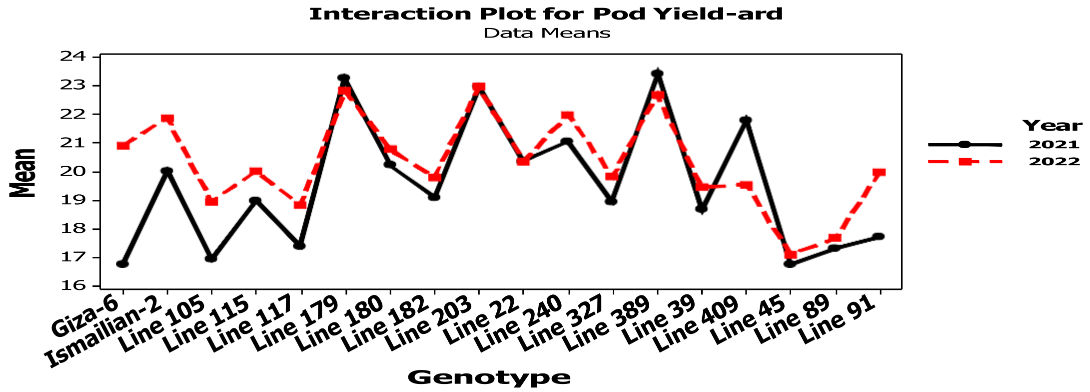


Figure (3): Year main effect on the pod yield (ard/fed) performance of studied peanut genotypes.

Concerning on genotypes, results cleared that the observed genotypes had significant variation for all measured traits, pointing to presence of considerable amount of genetic differences between the tested groundnut materials. Similar observes were reported by **[16, 17, 31]** that confirmed presence of differences in growth traits and yield productivity.

Regarding interaction, results showed that genotypes x year's interaction were significant for all studied traits except for number of branches/plant, number of pods/plant and number of seeds/plant. This suggested the presence of sufficient variability observed for plant height, pods weight/plant, seed weight/plant, seed yield ard/fed, shelling % and oil content %. These results were in agreed with those obtained by many authors **[16, 17, 30, 32]**.

2.2. Mean performance

Results of mean comparison **Table (5)** shows the mean performance of the eighteen peanut genotypes. revealed that genotypes of G13 Line 182, G18 Ismailian-2 and G6 Line 240 possessed the tallest plants (48.45, 47.83 and 46.25 cm) whereas; G2 Line 105; G7 Line 327 and

G11 Line 89 exhibited the shortest plants (37.03, 37.50 and 37.90 cm). For number of branches per plant, genotypes of G8 Line 409 and G12 Line 179 showed the profuse plants (9.14 and 9.08 branch) whereas the genotype G14 Line 45 possessed the lowest branched plants (7.68 branch). The highest number of pods/plant and number of seeds/plant (33.45 and 31.35 pod – 62.70 and 57.60 seed) were recorded for genotypes of G9 Line 389 and G6 Line 240, respectively, whereas the lowest values (13.74 and 13.88 pod – 22.93 and 22.02 seed) was scored for G12 Line 179 and G14 Line 45 genotypes, respectively.

However, genotypes of G6 Line 240 and G9 Line 389 possessed the highest pod weight/plant (62.75 and 62.11 g) whereas; G14 Line 45 and G11 Line 89 genotypes exhibited the lowest pod weight/plant (44.51and 46.79 g). The highest seeds weight/plant genotypes were G9 Line 389, G_{15} Line 117 and G_{16} Line 22 recording (45.83, 40.47 and 40.45 g), respectively.

On the other hand, G_{15} Line 117 and G_{16} Line 22 gave the highest values of shelling percentage that were scored (78.13 and 77.44 %, respectively), however; G_4 Line 115 revealed the lowest value (52.41%). Genotypes G_{17} Giza-6 and G_{13} Line 182 established the highest values of oil content % which presented (53.20 and 51.88 %, respectively), but G9 Line 389 revealed the lowest content (47.44 %). Concerning to pods yield ard/fed, G9 Line 389, G12 Line 179 and G10 Line 203 genotypes possessed the highest values (23.07, 23.05 and 22.97 g, respectively) whereas; G14 Line 45 gave the lowest values (16.93 g).

Table (5): Combined mean values of seed yield and its attributes as affected by 18 genotypes combinations at Shandaweel Agri. Res. Sta. across the two seasons.

Code	Genotype	PH	Bra	Pods No. /plant	Seeds No. /plant	Pods weight /plant	Seeds weight /plant	Pods Yield-ard	Shelling %	Oil %
G_1	**Line 91**	43.9	8.1	23.51	42.76	52.08	36.14	18.85	70.13	50.23
G_2	**Line 105**	37.03	8.38	16.51	29.37	52.25	30.01	17.94	58	48.35
G_3	**Line 39**	40.33	8.67	18.27	29.57	52.61	31.37	19.07	60.26	49.91
G_4	**Line 115**	42.07	8.43	16.75	31.23	57.9	30.26	19.5	52.41	50.67
G_5	**Line 180**	42.73	7.87	18.22	32.42	56.43	31.88	20.52	56.55	48.41
G_6	**Line 240**	46.25	8.38	31.35	57.6	62.75	39.51	21.53	62.99	48.77
G_7	**Line 327**	37.5	8.36	18.15	31.92	53.88	29.27	19.39	54.45	50.26
G_8	**Line 409**	41.03	9.14	22.55	40.7	49.53	30.63	20.67	61.84	51.18
G_9	**Line 389**	38.43	7.75	33.45	62.7	62.11	45.83	23.07	74.15	47.44
G_{10}	**Line 203**	38.37	8.49	16.47	29.2	56.76	35.34	22.97	63.46	48.48
G_{11}	**Line 89**	37.9	8.93	15.59	26.95	46.79	26.47	17.48	56.75	49.2
G_{12}	**Line 179**	38.33	9.08	13.74	22.93	48.36	28.93	23.05	60.22	48.32
G_{13}	**Line 182**	48.45	7.75	15.27	26.3	52.81	32.71	19.45	62.36	51.88
G_{14}	**Line 45**	41.37	7.68	13.88	22.02	44.51	27.64	16.93	62.25	48.85
G_{15}	**Line 117**	46.72	8.35	18.86	33.4	51.83	40.47	18.12	78.13	49.52
G_{16}	**Line 22**	40.07	8.83	28.13	51.63	52.37	40.45	20.37	77.44	49.21
G_{17}	**Giza-6**	41.43	7.87	14.27	24.62	52.26	36.38	18.83	70.03	53.2
G_{18}	**Ismailian-2**	47.83	8.97	14.44	25.18	56	35.88	20.96	64.35	51.19
	Mean	41.65	8.39	19.41	34.47	53.40	33.84	19.93	63.65	49.73
LSD$_{0.05}$										
Year (Y)		1.01	Ns	Ns	1.56	3.39	Ns	0.22	3.28	Ns
Genotype(G)		2.32	0.43	1.87	3.17	3.57	2.57	0.61	5.80	0.21
Y*G		3.27	Ns	Ns	Ns	5.50	3.56	0.85	8.31	0.32

Plant height, cm (PH); Number of branches/plant, (Bra); Number of pods/plant (Podno); Number of seeds/plant (Sno); Pods weight/plant, g (PWP); Seeds weight/plant, g (SWP); Pods yield, ard/fed (PodY); Shelling percentage (Shl %) and Seeds oil content (Oil %).

From the obvious results, it could be concluded that Ismailia 2 followed by G6 Line 240, G9 Line 389 and G10 Line 203 showed high pods weight/plant, seeds weight /plant and seeds yield (ard/fed) coupled with the lowest oil content (%). These results reflect that the selection prospects within these genotypes to improve the performance through breeding program. The obtained results are in agreement with those observed by **[16, 17, 31, 32]**.

3. Relationship studies

3.1. Phenotypic correlation

Knowledge of the relationship between measured traits is useful for the identification of selection traits to be used for yield improvement. Simple phenotypic correlation coefficients for all comparisons among the morphological seed and agronomic yield traits in the tested genotypes were interconnected as presented in **Figure (4 a, b).**

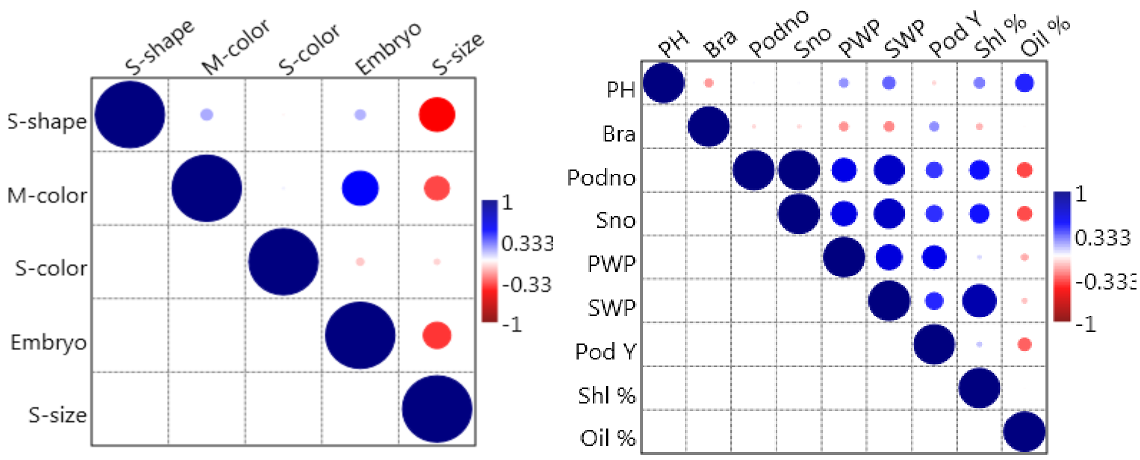
3.1.1. Morphological seed qualitative characteristics

Spearman phenotypic correlation analysis was proceeded to determine the more correlated morphological seed traits as shown in **(Figure 4a)**. This graph illustrated strong positive correlation between main colors of seed testa with seed embryo shape; whereas, most genotypes with narrow seed embryo shape (Line 39, Line 180, Line 89, Line 182) gave red seed testa color. In addition, brownish pink testa color appeared in genotypes with broad and very broad embryo shape (Line 327, Line 179 and Giza-6). However, strong negative associations were clear between seed size with each of seed shape, main color of seed testa and embryo shape, indicating that all large seed size type (Line 39, Line 115, Line 180, Line 89, Line 182, Line 45 and Line 117) genotypes had only red main color of seed testa; meanwhile, all genotypes coupled rectangular seed shape with narrow embryo shape types (Line 39, Line 180, Line 203, Line 182) were recorded in large and very large seed size type. These traits may be useful when were interconnected with yield traits as morphological markers.

3.1.2. Agronomic quantitative traits

Pearson' phenotypic correlation coefficients among 9 agronomic yield traits, relationships were illustrated in **(Figure 4b).** This graph showed strong positive correlation between PH with oil% and seeds weight/plant. Pods yield had a positive correlation with all traits except the oil% and PH. Pods yield exhibited high correlation coefficient values with each of weight of pods/plant, number of pods/plant, number of seeds/plant and weight of seeds/plant. The maximum correlation coefficient value was detected between number of pods/plant and each of number of seeds/plant and weight of seeds/plant. In the same context, weight of seeds/plant exhibited high correlation coefficient values with each of shelling % and number of seeds/plant. Meanwhile, strong negative correlation was detected between oil% and each of number of seeds/plant, number of pods/plant and pods yield (ard/fed).

In general, strong correlation suggested that pod yield may be raised through selection for the more number or weight of pods and seeds per plant. Then, results pointed to selection for highest number or weight of pods and seeds per plant in peanut would be accompanied by high yielding ability. These findings were similar with those obtained by **[16, 17, 31, 31, 33, 34, 35]**.



a- *Sperman' correlation of morphological traits.*

S-shape: seed shape, M-color: main color of testa, S-color: absent of secondary color of testa, Embryo: embryo shape and S-size: seed size.

b- *Pearson' correlation of agronomic traits*. *Plant height, cm (PH); number of branches/plant, (Bra); number of pods/plant (Podno); number of seeds/plant (Sno); pods weight/plant, g (PWP); seeds weight/plant, g (SWP); pods yield, ard/fed (PodY); shelling % (Shl%) and seeds oil content (Oil %).*

Figure (4): Simple correlation graphs for all comparisons among the morphological and agronomic traits in the studied genotypes.

3.2. Cluster analysis

Cluster analysis used to establish the relationship between different items. So, it is considered as an effective method to identify a hierarchical classification between the studied genotypes/items. This study used cluster analysis to classify 18 groundnut genotypes with diverse backgrounds base on 9 pod yield and 5 morphological traits **(Tables 6a, b).** Heatmap dendrogram in **Figures (5a, b)** was constructed to analyze the genotypes (row) performance across the tested traits (column), showing that scaling color key ranged from red color (highest value) to blue color (lowest value).

3.2.1 Morphological traits

Results in **Figure (5a)** illustrated the cluster heatmap dendrogram for genotypes and morphological traits. The genotypes were grouped in three different clusters. Row graph showed the similarity between the eighteen genotypes, which were distributed into three main clusters.

The first cluster (clu1) contained 6 genotypes (Line 91, Line 240, Line 327, Line 409, Line 389 and Line 22) and the third cluster (clu3) included 3 genotypes (Giza-6, Line 203 and Line 179); whereas, second cluster (clu2) contained the other 9 genotypes. Meanwhile, column graph cleared the similarity between 5 morphological traits, divided into three main clusters (clu1, clu2 and clu3), containing (embryo shape and main testa), (seed shape and, secondary testa color) and (seed size), respectively. The relationships between the 18 genotypes and the 5 morphological traits presented that genotypes clu1 mostly showed Mixture seed shape and main testa color with Present secondary testa color.

The result of a clustering is presented the similarity between the genotypes showed that (clu1) showed similar characters for almost traits as mixture seed shape and main testa color with present secondary testa color. Clu2 mostly had Red main testa and present secondary testa color with large seed size. Meanwhile, all clu3 genotypes cleared Rectangular seed shape, present secondary testa color and very large seed size.

3.2.2. Agronomical traits

Concerning to pod yield traits, cluster analysis and heatmap based on the different studied 9 yield traits and various 18 groundnut genotypes was obtained. Graphical representation of the genotypes across yield traits was illustrated in heatmap graph, showing the hierarchical clustering calculation. Resulted dendrogram **(Figure 5b)** and **Table (6b)** established the similarity between the 18 genotypes that were distributed into three main clusters (clu1, clu2 and clu3), concluding (12, 3 and 3 genotypes, respectively). The third cluster contained 3 genotypes (Line 240, Line 389 and Line22) and the second comprised 3 genotypes (Line 91, Line 409 and Line 117). Meanwhile, the other 12 genotypes were found in the first cluster.

Table (6a): Summary of cluster analysis showed the tested genotypes and cluster phenotypes of the 18 groundnut using morphological characters.

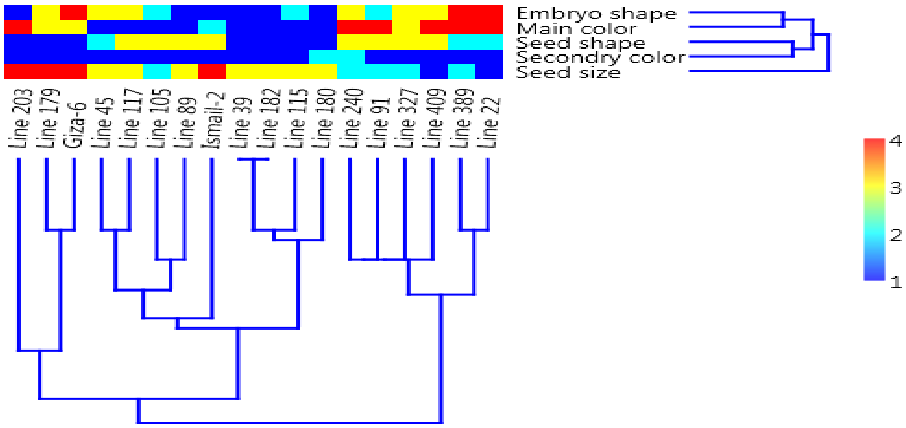
Cluster (No.)	**Included genotypes**	**Cluster phenotype**				
		Seed shape	**Main testa color**	**Secondary testa color**	**Embryo shape**	**Seed size**
Clu1 (6)	Line 91, Line 240, Line 327, Line 409, Line 389 and Line 22	4 Mixture / 2Circular	5 Mixture / 1Brownish pink	5 Present / 1 Absent	3Broad / 2 very broad / 1Medium	4 Medium / 2 small
***Similarity percent from total cluster**		4 Mixture /6 = 66.67%	5 Mixture/ 6 = 83.33%	5 Present /6 = 83.33%	3 Broad /6 = 50.00 %	4 Medium/ 6 = 66.67%
Clu2 (9)	Line 105, Line 45, Line 117, Line 39, Line 182, Line 180, Line 115, Line 89 and Ismailian-2	4Rectangular/ 4 Mixture / 1Circular	8 Red / 1Purple	8 Present / 1 Absent	5 Narrow / 2Medium / 2 Broad	7 Large / 1very large/ 1Medium
***Similarity percent from total cluster**		4Rectangular/9= 44.44%	8 Red /9 = 88.89%	8 Present /9 = 88.89%	5 Narrow /9 = 55.56%	7 Large /9 = 77.78%
Clu3 (3)	Giza-6, Line 203 and Line 179	3 Rectangular	2 Brownish pink / 1 Mixture	3 Present	Very broad /Broad/ Narrow	3 Very Large
***Similarity percent from total cluster**		3Rectangular/3= 100.00%	2 Brownish pink/3= 66.67%	3 Present/3 = 100.00%	Very broad/3 =33.33%	3 Very Large/ 3= 100.00%

Abbreviations: S-shape: seed shape, M-color: main color of testa, S-color: presence of secondary color of testa, Embryo: embryo shape and S-size: seed size.
**Similarity percent from total cluster group = highest performance number/ total cluster number (6).*

The similarity divided 9 yield traits into three main clusters. The 1st cluster concluded 3 traits (pods yield, pods number and branches), only shilling % trait was attended in 2nd cluster, but 3rd one contains other 5 traits (Plant height, Oil %, pods weight/plant, seeds weight/plant, and number of seeds/plant).

Results showed that 3rd cluster which was containing (Line 240, Line 389 and Line22) had the highest values for almost yield traits while had lowest values for oil % trait. Then, 3rd cluster had the best values for most important yield agronomical traits except plant height, number of branches /plant and oil % traits. On the contrary, 2nd cluster that contained (Line 91, Line 409 and Line 117) was distinguished in plant height, number of branches /plant and oil %

traits. Therefore, agronomic yield traits revealed the most correlated each to other, meaning estimate any of the detected traits may be index to the desired objective pod/oil yield.



a- morphological: S-shape: seed shape, **M-color**: main color of testa, **Sec-color:** presence of secondary color of testa, **Embryo**: embryo shape and **S-size**: seed size

b-agronomical: Plant height, (**PH**); number of branches / plant, (**Bra**); number of pods/plant (**Podno**); number of seeds/plant (**Sno**); pods weight/plant, (PWP); seeds weight/plant, (**SWP**); pods yield, ard/fed (**PodY**); shelling percentage (**Shl**%) and seeds oil content (**Oil** %).

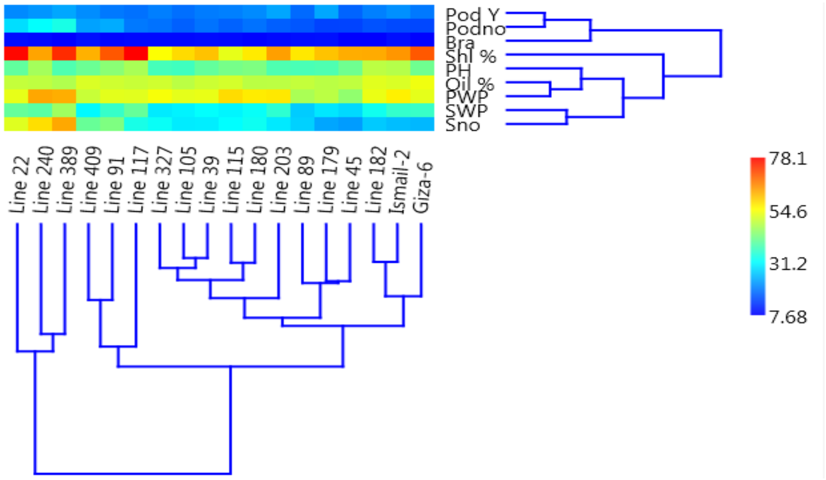


Figure (5): Cluster heatmap dendrogram for 18 groundnut genotypes across (A) 5 morphological traits and (B) 9 pod yield traits.

Table (6b): Summary of cluster analysis showed the tested 18 groundnut genotypes using agronomical traits.

Cluster no.	Included genotypes	Cluster traits average								
		PH	Bra	Podno	Sno	PWP	SWP	PodY	Shl %	Oil %
Clu1 (12)	**Line 105, Line 39, Line 115, Line 180, Line 327, Line 203, Line 182, Ismailian-2, Giza-6, Line 89, Line 179 and Line 45.**	41.11	8.37	15.96	27.64	52.55	31.35	19.67	60.09	49.89
Clu2 (3)	**Line 91, Line 409 and Line 117**	*43.88*	*8.53*	21.64	38.95	51.15	35.75	19.21	70.03	*50.31*
Clu3 (3)	**Line 240, Line 389 and Line22**	41.58	8.32	*30.98*	*57.31*	*59.08*	*41.93*	*21.66*	*71.53*	48.47

Abbreviations: Plant height, cm (PH); number of branches /plant, (Bra); number of pods/plant (Podno); number of seeds/plant (Sno); pods weight/plant, g (PWP); seeds weight/plant, g (SWP); pods yield, ard/fed (PodY); shelling percentage (Shl%) and seeds oil content (Oil %).

3.3. Genetic parameters

Significant differences of groundnut genotypes for all the traits indicated to genetic variability with existing chance to improvement. Separating genetic component estimates (phenotypic, σ^2_{ph}; genotypic σ^2_g and environmental σ^2_e variance) were used to calculate their respective phenotypic (PCV %) and genotypic (GCV %) coefficient of variation with broad sense heritability (h_b^2 **%**). All these genetic parameters, in addition to grand mean, expected genetic advance (GA) and expected genetic advance percent (GA %) were established in **Table (7).**

Results in **Table (7)** cleared that phenotypic variance (σ^2_{ph}) was greater than the genotypic variance (σ^2_g) for all studied traits. Correspondingly, phenotypic coefficient of variability (PCV %) was higher than corresponding genotypic (GCV %) ones, demonstrating the environmental effects on the traits. Traits of number of pods per plant and number of seeds per plant had the highest (PCV %) and (GCV %) values recording, (31.04 and 30.88 %), (34.66 and 34.47 %) and seeds weight /plant (15.10 and 14.00 %), respectively. This indicates the presence of exploitable genetic variability for these traits. Similar results were obtained by **[16].**

Broad sense heritability (h_b^2 %) can be predicted only from the degree of correspondence between phenotypic and genotypic values **(Table 7 and Figure 6).** The importance of heritability may be as predictive role in the genetic studies of quantitative traits and calculate possible genetic advance (GA %) through selection based on phenotypic values. Heritability (h_b^2 %) and expected genetic advance (GA %) estimates can provide information about the expected genetic grain in the following generations. heritability (h_b^2 %) values were generally high for all observed traits that scored estimates from 98.97 % for number of pods / plant to 73.80 % for pods weight /plant. Generally, the number of pods / plant, number of seeds /plant, oil % and seeds yield/fed traits had higher heritable estimates. Then, it can be supposed that phenotypes of most yield traits are mainly determined by their genotypes. High estimates of broad heritability gave only a rough additive gene effect may be successful in phenotypic selection. However, high heritability (h_b^2 %) would be associated with high genetic gain GA% for improving yield traits **[16, 17, 36]**.

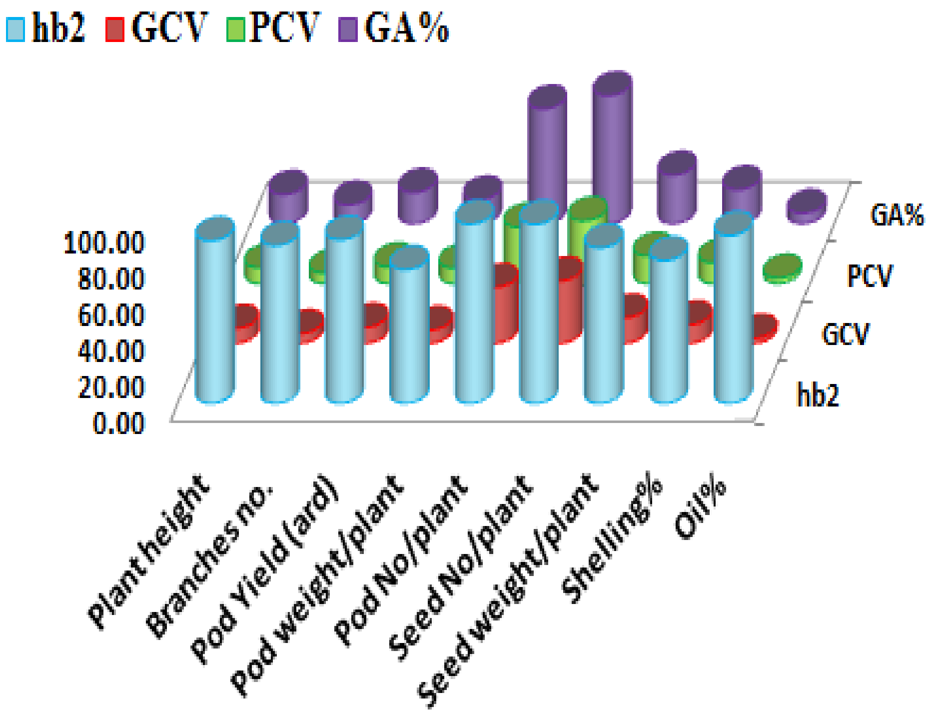
Table (7): Phenotypic variance components and genetic parameters for 9 agronomic studied yield traits in 18 groundnut genotypes.

Traits	σ^2_g	σ^2_e	σ^2_{ph}	h_b^2 %	GCV %	PCV %	GA	GA %
PH	11.72	4.07	13.04	89.86	8.21	8.66	6.69	16.03
Bra	0.20	0.14	0.23	87.15	5.30	5.68	0.86	10.20
Pod Yield (ard/fed)	3.04	0.28	3.36	90.43	8.75	9.20	3.42	17.14
Pod weight /plant	15.21	9.58	20.61	73.80	7.30	8.50	6.90	12.93
Pod No/plant	35.93	2.62	36.31	98.97	30.88	31.04	12.29	63.29
Seed No/plant	141.17	7.59	142.73	98.90	34.47	34.66	24.34	70.61
seed weight /plant	22.44	4.97	26.13	85.88	14.00	15.10	9.04	26.72
Shelling%	41.96	25.35	53.22	78.84	10.18	11.46	11.85	18.62
Oil%	1.95	0.03	2.11	92.69	2.81	2.92	2.77	5.57

σ^2_{ph}: Phenotypic variance, σ^2_g: Genotypic variance, σ^2_e: Environmental variance, h_b^2 %: Broad sense heritability, PCV %: Phenotypic coefficient of variation and GCV% = Genotypic coefficient of variation, GA: genetic advance and GA %: expected genetic advance percent.

Regarding (GA %) in **Table (7)** and **Figure (6)**, results illustrated that higher estimate of expected genetic advance percent (GA %) were observed for number of seeds per plant (70.61 %), number of pods per plant (63.29 %) and seeds weight per plant (26.72 %). High GA % estimates indicated that selection based on these traits may be successful in groundnut improvement **[16, 17, 36]**.

From previous results in **Figure (6)**, it is clear that traits of number of seeds per plant, number of pods per plant and seeds weight per plant had high genotypic coefficient of variability (GCV) coupled with high broad heritability (h_b^2 %) and high genetic advance percent (GA %). therefore, it can be concluded that all these traits were controlled by additive type of gene action as reported by other workers. Similar results were also obtained by **[16, 17, 36, 37]** who reported that high genotypic variability coupled with high heritability and genetic advance for most quantitative yield traits.



h_b^2 %: Broad sense heritability, PCV %: Phenotypic coefficient of variation and GCV%: genotypic coefficient of variation and GA %: expected genetic advance percent.

Figure (6): Genetic parameters for 9 agronomic studied yield traits in 18 groundnut genotypes.

3.4. Genotype by trait (GT) biplot

Genotype by trait (GT) biplot was obtained as application of GGE-biplot method **[18, 19]** to identify particularly good genotypes in desired aim for selection, therefore can be nominee in groundnut breeding program **[38]**. The polygon view and comparison of a genotype by trait (GT) biplot graph is the best way to visualize the interaction patterns between genotypes and traits explaining a sufficient amount of the total variation.

3.4.1 Morphological traits

The GT biplot graph **(Figures 7a, b)** presented the relationship among the tested groundnut genotypes and morphological traits. This graph illustrated the classification of the genotypes by multiple traits that may be used as phenotypic markers traits in distinguishing these genotypes.

The GT biplot **(Figure 7a)** of the performance of the groundnut seed traits explained 75.68 % of the total variation of seed performance. The first two principal components (PC1 and

PC2) explained 54.41% and 21.26%, respectively. The first two PC's proportion reflected more than 60 % of the total variation, confirming the goodness of fit for GT biplot model.

Graph was divided into many sectors (8) by perpendicular lines from origin point to the polygon sides. Presences of secondary color of testa fall on the origin center point, pointing to identification performance of all/most secondary testa color. Three genotypes (Line 389, Line 22, and Line 240 Line 91) that allocated with three traits (seed main color of testa, embryo shape and presence of secondary color of testa) in the same sector of right the graph were closely related **[4, 5, 35, 38]**. Therefore, these 3 genotypes cleared mostly similarity for these 3 seed morphological traits (as mixture testa main color, broad embryo shape and Present secondary testa color). However, seed shape trait with (Line 409 Line 327, Line 91) genotypes in the same sector presented same mixture shape.

From obvious results, seed traits (visual assessment) may be used to distinguish the tested genotypes under investigation **[4, 5]**.

Based on comparison GT biplot, comparison of genotypes under morphological traits were performed **(Figure 7b)** to detect the desirable tolerant genotypes. The biplot used the average environment (traits) coordinates (AEC) method **[38]** to determine the stable seed performance genotypes across multiple traits. Then, ranks of the seed traits were Line 389, and Line 22 followed by Line 240 showed the same desirable performance.

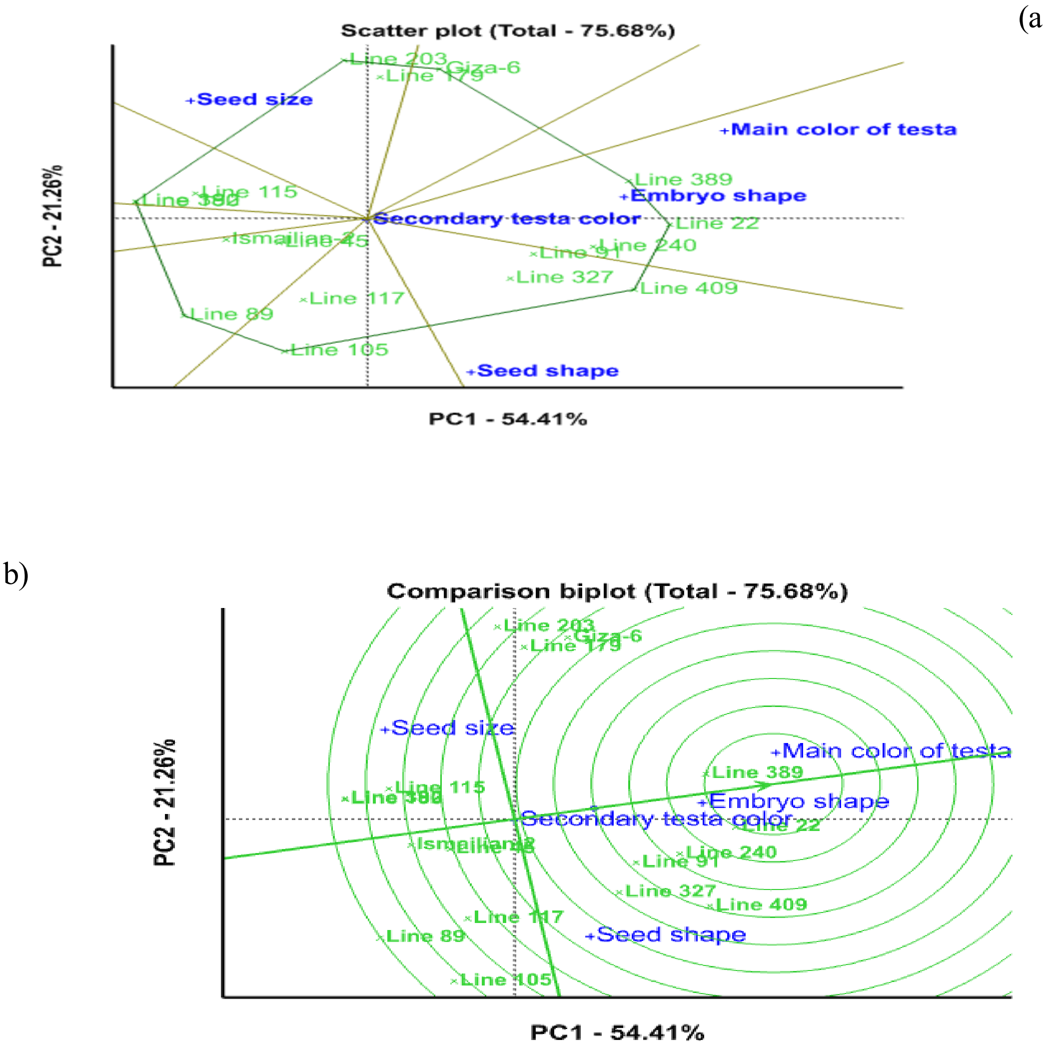


Figure (7): GT (genotype and traits) biplot (a- polygon view and b- comparison) for describing of groundnut genotypes based on morphological traits.

3.4.2. Selection genotypes under multiple agronomic traits

Small circle on the Average-Tester Axis (ATA) that passes through the origin and the average traits indicated to the position of the average trait and the arrow pointed to the average trait direction. Ranking based on the genotype assumed scaling discriminated high mean yield depending on the gain of multiple traits **[20]**. The best nominee genotypes were expected to have high performance pods yield across all test traits.

In **Figure (8a)**, polygon-view of 18 groundnut genotypes by yield traits in which-won-where and comparison (GT) biplot illustrated the status of genotypes in terms of traits and the relationship between them. Biplot graph used to compare different genotypes (G) under different yield traits (T) with detect its relationship. In this of groundnut seed yield traits, GT-biplot of data mean performance explained 89.20% of the total variation. The first and two principal components (PC1 and PC2) explained 73.07 % and 16.13%, respectively. This relatively high proportion reflected the complexity of the relationships among the genotypes and the observed associated traits.

The genotypes on the right side of the ordinate had higher mean across yield traits. Meanwhile, other lower ones fall on the left side. Most desired yield traits (pods yield, ard/fed, pods weight/plant, number of pods/plant and seeds weight/plant) allocated with some genotypes (Line 389, Line 22, and Line 91) in the same right sector of the graph, pointing to found large positive association. Then, these genotypes may be distinguished under growth and considered as the best productivity. However, neighbor sector, genotype Line 117 could be distinguished by increase shelling percentage. Meanwhile, the other traits (plant height, number of branches and oil %) were placed near the origin, which pointed to not any discriminating criteria.

Based on GT graph **(Figure 8b)** for comparison of the genotypes with the ideal one and presenting the relationship among the studied groundnut genotypes using the pods yield and its related traits. Similar results were found in most cases by **[4]** in lupine.

Comparison GT biplot illustrated that Line 389 genotype fall on the first central circle, followed by (Line 22 and Line 91) indicating to high pods yield and relative performance stability for other traits compared to the rest of tested genotypes **(Figure 8b).** Genotype that potted on nearest points to the centric circle was the ideal one. Obviously, genotype (Line 389) was the ideal genotype, recording the highest stable pods yield traits performance. However, genotypes Line 22, Line 91 and Line 240 were located close to the ideal genotype or around the center of concentric circle, referring their potential for specific adaptability with better pods yield performances for most pods yield traits. As well as, Line 117 had specific adaptability with better pod yield performances (especially shelling %). Meanwhile, genotypes Line 45, Line 89 and Line 105 assumed the farthest points to the centric circle, indicating to their relatively poor performance toward these traits.

Therefore, pods yield followed by number of pods and seeds per plant and seeds weight/plant was the most discriminating trait **(Figure 8b)**. Meanwhile, traits of plant height, number of branches per plant and oil % were non-discriminating and less representative traits.

Similarly, **[38]** reported that some genotypes were stable, representative and discriminating among traits for the performance of studied groundnut genotypes.

(a

(b

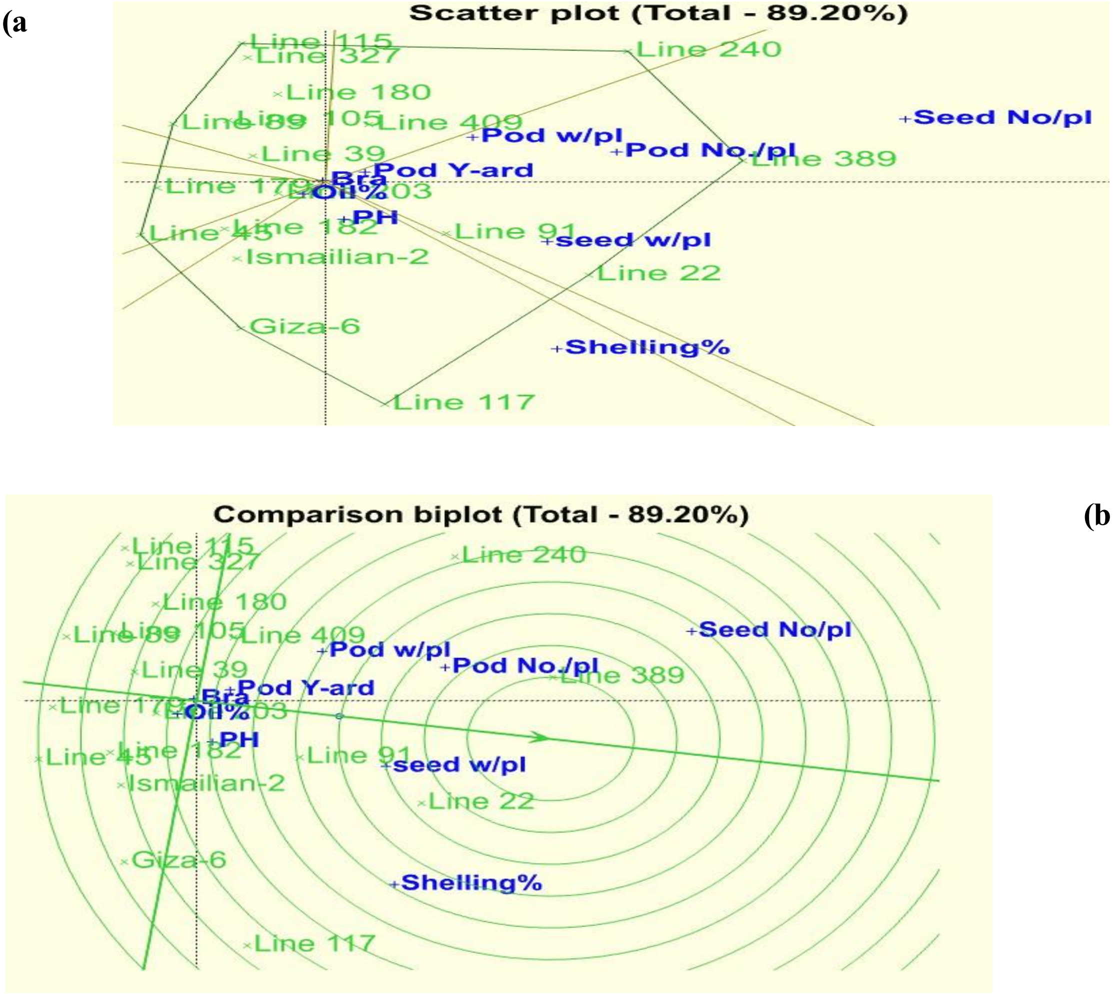


Figure (8): Polygon view of the Agronomic yield traits, describing groundnut genotypes comparison on the basis of GT-biplot.

Plant height, (PH); number of branches / plant, (Bra); number of pods/plant (Podno); number of seeds/plant (Sno); pods weight/plant, (PWP); seeds weight/plant, (SWP); pods yield, ard/fed (PodY); shelling percentage (Shl%) and seeds oil content (Oil %).

IV. Conclusion

This study investigated genetic diversity in the groundnut collection and growing under Egyptian conditions. It was conducted to evaluate 16 promising peanut genotypes with to commercial check varieties (Giza 6 and Ismalian 2), based on the morphological and agronomical traits. By evaluating the novel peanut lines, they showed a wide variance concerning the different studied traits. Some of them had agro-morphological and genetic parameters traits that are close to each other. The genetic variation observed demonstrated the possibility of genetic improvement of groundnut for increased productivity and adaptation to local conditions to establish an efficient improvement program.

V. Conflict of interest

The authors declare that they have no conflict of interest.

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