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Multivariate Analyses of Yield and Its Components in Some Peanut Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. Authors AAES and MAA were sown the peanut crop under recommendation cultural practices, collect data of yield and its components and managed the literature searches. Author ZEG designed the experiments, put the idea of this study, performed the statistical analysis, tabulated results and wrote the first draft of the manuscript with result explanation. Then, all authors read and approved the final manuscript.

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ABSTRACT

Aims: For proposing a statistical approach to select of the most promising genotypes for peanut breeding program.
Place and Duration of Study: Twenty peanut genotypes were evaluated at Matana Agricultural Station Research, Luxor governorate, Egypt during 2018 and 2019.
Study Design: In a randomized complete block design with three replications.
Methodology: Analysis of variance (ANOVA), correlation coefficients, factor analysis, cluster method and some genetic parameters for seed yield and its components were calculated.
Results: Results revealed that significant differences among the tested genotypes for the eight studied traits. Correlation coefficients indicated that seed yield was significantly correlated with all traits except plant height. Meanwhile, factor analysis was used to remove multi-collinearity problems, to simplify the complex relationships and to reduce variables number (into three extracted factors). 100-seed weight, number of branches/plant, 100-pod weight and seed oil content (%) with seed yield/plant traits which present in the 1st factor explained 42.039% of the total variance and recorded high heritability coupled with high genetic advance %. ANOVA results

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for factor scores obtained (native best multi-traits data) revealed that genotypes varied significantly.
Conclusion: Factor and cluster analysis agreed in grouping Ismailia 2, Intr. 267, Intr. 182, Intr. 332 and Sohag 107 to be promising genotypes to increase peanut seed yield, whereas genotypes Intr. 504 and intr. 510 could be utilized to increase peanut seed oil content %. Then, the utilization of a factor score as a variable in ANOVA analysis was more appropriate rather than the original data. Consequently, factor scores (as a native data) would be more agreeable to selection and can be employed in plant breeding programs.

Keywords: Correlation; factor scores; cluster; heritability; selection.

1. INTRODUCTION

Peanut (*Arachis hypogaea* L.) is a main summer oil crop grown in sandy soils. Beside it is an important cash crop for the growers due to high yielding potentiality in such soils. Peanut is grown on 27.34 million hectares in the world, producing 46.75 million metric tons pods yield with an average productivity of 1520 kg/ha [1]. The cultivated area of peanut is 60 thousand hectare in Egypt, producing 210 thousand metric tons pods yield with an average productivity of 3200 kg/ha [1].

Releasing new high yielding varieties is the main target of the breeders, achieved either by crossing and selection in the segregating generation or via selection of high yielding entries from well adapted new accessions under local conditions. In addition, good quality characters especially pod and seed characters that fulfilling export needs, are also a plus in selecting the most superior entry over a range of environmental conditions that represent the peanut growing areas in Egypt.

Hence, it was proposed through the present study to establish peanut genotypes by collecting the morphological data from different experimental years. The studied peanut genotypes were processed for a clustering analysis basing on the statistical integration of their pre-harvest, post-harvest and biochemistry parameters.

Multivariate analyses have been extensively used to summarize and describe variation pattern in population genotypes of crop. These statistical methods can easily select important traits and reduce the data size to explore the relationships between traits, their variations and also show their relationships with the factors as factor analysis. Also, can extract dataset statistically, clustering similar vectors into classes by clustering analysis, using (hierarchical) method [2].

In peanut breeding programs, selection of promising genotypes are based on various characteristics, most importantly the final seed yield and quality. Relationships among yield and yield-components also play an important role [3,4,5,6]. In the present paper, to detect yield-contributing traits having influence on seed yield, factor analysis is commonly applied.

Heritability and genetic advance are very useful biometrical tools for breeders in determining the direction and magnitude of selection. High heritability alone is not enough to make efficient selection in the advanced generations and unless accompanied by substantial amount of genetic advance. Correlation measures the level of dependence among traits, but it is often very difficult to determine the actual mutual effects among traits if correlation values are similar for certain pairs of traits, direct effects for some of them and especially indirect effects via other traits can differ for some traits [7,8,9,6].

The objectives of this study therefore, were to evaluate and determine the genetic diversity in twenty peanut genotypes, identify the correlated yield traits that sort the genotypes into different groups, suggest the best genotypes could be used in improvement breeding program by using multivariate techniques for classification of variation.

2. MATERIALS AND METHODS

2.1 Experimental Procedures

A field experiments were conducted for two consecutive seasons: 2018 and 2019, at Matana Agricultural Station Research, Luxor governorate (located between latitude 36-25 north, and 33-32 east), Egypt. The soil properties are illustrated in Table 1. In each season, a randomized complete block design with three replications was used for laying out the field experiments. Each replication was divided into twenty plots, to which the

Table 1. Some physical and chemical analysis of the Matana experimental soil

Soil characters	Physical analysis		Character	Chemical analysis							
				2018	2019	Cations Mg/100 g			Anions Mg/100 g		
	2018	2019				Character	2018	2019	Character	2018	2019
Sand%	60.32	70.12	PH	7.7	8.1	Na^{+}	0.52	1	Cl^{-}	0.23	0.42
Silt%	28	19	N_{ppm}	30	40	K^{+}	0.09	0.08	So_4^{-}	0.27	2.37
Clay%	10.68	10.88	P_{ppm}	8	8.6	Ca^{++}	0.30	1.50	HCo_3^{-}	0.59	0.69
Soil texture	Sandy loam		K_{ppm}	496	488	Mg^{++}	0.19	0.90			

genotypes were assigned randomly. Cultural practices were carried out as recommendation packages. Sowing was carried out on ridges 60 cm apart and 20 cm between hills. NPK was added at 30/30/24 kg/feddan. P was added during soil preparation. N and k were splitted in 3 equal amounts added at sowing, 30 and 45 days after sowing.

At harvest, 10 plants were randomly taken from each plot to record plant height (cm), number of branches/plant, number of pods/plant, 100-pod weight (g), 100-seed weight (g), shelling percentage%, seed yield/plant (g), seed yield (ton/fed) and seed oil content (%). The estimation of oil content was done according to [10]. Twenty peanut genotypes obtained from Oil Crops Research Department, Field Crop Research Institute (FCRI) were shown in Table 2.

2.2 Statistical Analyses

Analysis of variance was carried out for the data in each season. Bartlett's homogeneity test was used to satisfy the assumption of homogeneity of variances before running the combined analysis across the two seasons to test significant differences among the twenty genotypes. Then, a combined analysis of variance across the two seasons was computed for the variances homogeneity traits, assuming replications and seasons effects as random and genotypes were considered as fixed variable [11].

Data over both seasons of seed yield and its components were subjected to simple correlation coefficients according to [12].

After Bartlett's test of sphericity (less than 0.05), determinant collinearity (higher than 0.00001) and KAISER-MEYER-OLKIN (KMO'S test) measure of sampling adequacy tests (higher than 0.50 and close to 1.0), the factor analysis method [13] consists in the reduction of a large number of correlated variables to a much smaller number of variables called factors. After extraction, the matrix of factor loading was submitted to a varimax orthogonal rotation, as applied by [14]. The array of communality, the amount of variance accounted by the common factors together, was estimated by the highest correlation coefficient in each array as suggested by [15]. Factors with Eigen values greater than 1 out of 8 factors were employed in ANOVA analysis [16]. The proportion of variance in the set of variables accounted for by a factor is the sum of square loading for the factor (variance of factor) divided by the number of variables (if rotation is orthogonal). These analyses were conducted by using SPSS software [17].

The cluster analysis was performed using a measure of similarity levels and Euclidean distance [18].

Table 2. Name, origin and pedigree for twenty peanut genotypes used in the experiments

Code no.	Name	Origin	Pedigree
G1	Giza 6 (check)	Egypt *	Egyptian variety
G2	Ismailia 2	Egypt *	Egyptian variety under registration
G3	Sohag 104	Egypt *	Line 245 x Geregory
G4	Sohag 107	Egypt *	Nc12 x Geregory
G5	Sohag 110	Egypt *	Line 292 x Geregory
G6	Intr. 182	U**.S.A.**	Florigiant
G7	Intr. 242	**FAO**	Shullamit
G8	Intr. 259	Senegal	57-422
G9	Intr. 267	Upper Volta	R.M.P 12
G10	Intr. 288	Senegal	58-344
G11	Intr. 332	Zambia	Mount Makulu Red
G12	Intr. 335	Icrisat	Faizpur
G13	Intr. 336	Icrisat	Exotic 3-5
G14	Intr. 342	U**.S.A.**	Nc-17
G15	Intr. 425	Icrisat	(Robut33-1xNcAc316)x(53-68xRobut33-1)F7B1
G16	Intr. 501	China	Tianhu3
G17	Intr. 504	Bolivia	R.C.M 444
G18	Intr.508	U**.S.A.**	N.C. 17
G19	Intr. 510	Australia	Vigina Bunch
G20	Intr. 514	Argentina	Krapovickas

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

Estimates of genetic, genotype by season and error variance components (σ^2_g, σ^2_{gs} and σ^2_e) were computed. Broad-sense heritability was estimated with these components as suggested by [19]. Expected genetic advance (GA %) for each trait was calculated as a proportion of the general mean to allow comparison among traits for potential improvement through selection [20].

3. RESULTS AND DISCUSSION

Results revealed that the studied twenty peanut genotypes differed significantly for all traits in each season, except plant height the 1st season. Significance of mean performances due to different sources of variability for studied traits in some separate analysis and other combined ones are given in Table 3. Results appeared that the studied genotypes significantly differed for all traits in over seasons [21]. Combined analysis of variance among two seasons revealed the significance of the seasons on plant height, number of branches, 100-pod weight/plant, seed oil content % and seed yield/plant. Therefore, it could be established that the environment significantly affected the performance of the studied peanut genotypes. These results are in agreement with those obtained by [22] who pointed that climatic conditions vary from year to year at the same location. However, insignificant effects of seasons on the performance of some important traits such as number of pods/plant, 100-seed weight/plant, shelling percentage and seed yield (ton/fed) due to the evaluation for two seasons under the same location has led to narrower environmental fluctuation.

Results showed that genotype x season interaction had significant effects on all studied traits except 100-seed weight. All traits in both seasons revealed high significant differences among the studied genotypes. This indicates the presence of sufficient variability. The similar results were observed for plant height, no. branches, oil content % and seed yield by many authors [23].

Results revealed that genotypes18 (Intr.508) and 1 (Giza 6) possessed the tallest plants (83.85 and 82.23 cm) whereas; genotypes 8 (Intr. 259) and 11 (Intr. 332) exhibited the shortest plants (65.01 and 66.10 cm). For number of branches per plant, genotypes 2 (Ismailia 2) and 9 (Intr. 267) showed the profuse branches (11.10 and 10.62) whereas the genotypes 17 (Intr. 504) and 19 (Intr. 510) possessed the lowest branches/ plants (7.12 and 7.32). Genotypes 2 (Ismailia 2), 6 (Intr. 182) and 14 (Intr. 342) possessed the highest pod number/ plant (93.08, 86.61 and 84.39 pod) whereas; 19 (Intr. 510) and 18 (Intr.508) genotypes exhibited the lowest ones (55.04 and 58.94 pod). The highest 100-pods per plant and 100-seed weight (257.98 and 245.70 - 30.63 and 29.74 g) was recorded for 2 (Ismailia 2) and 9 (Intr. 267), respectively, whereas the lowest values (146.93 and 141.54 – 146.93 and 141.54 g) was scored for genotypes 17 (Intr. 504) and 19 (Intr. 510), respectively. Regarding to shelling percentage, genotypes 7 (Intr. 242) and 2 (Ismailia 2) possessed the highest values (68.66 and 67.53 cm) whereas genotypes 19 (Intr. 510) and 15 (Intr. 425) exhibited the lowest values (58.26 and 59.96). On the other hand, 17 (Intr. 504) and 19 (Intr. 510) exhibited the highest values of seed oil content % which gave (57.80 and 56.13%, respectively), but genotypes 2 (Ismailia 2) and 6 (Intr. 182) revealed the lowest values for this trait (33.54 and 34.86%, respectively). The highest seed yielder genotypes in combined across the two seasons were genotypes 2 (Ismailia 2), 6 (Intr. 182) and 9 (Intr. 267) which gave (169.70, 133.03 and 129.40 g/plant – 2.83, 2.26 and 2.16 ton/fed) for seed yield/plant and seed yield (ton/fed), respectively. Meanwhile, the lowest one was 17 recording (68.29 g and 1.32 ton/fed) for seed yield/plant and seed yield (ton/fed), respectively.

From the obvious results, it could be concluded that genotype 2 (Ismailia 2) followed by genotypes 6 (Intr. 182) and 9 (Intr. 267) showed the highest number of branches per plant, 100-pods weight, 100-seeds weight, seed yield/plant and seed yield (ton/fed) coupled with the lowest oil content (%). These results reflect that the selection prospects within these genotypes to improve the performance through breeding program.

3.1 Factor Analysis

Factor Analysis model was used to create a set of independent variables that are uncorrelated, avoiding multi-collinearity and fit the dependent variable as well as the original independent variables with no-influenced correlation matrix by sample size [24]. Therefore, factor analysis procedure was carried out with undertaking for investigation the prerequisites as follows:

Table 3. Mean performance of some yield traits for the twenty peanut genotypes (combined across 2018 and 2019 seasons)

Code	Genotype	Plant height (cm)	No. of branches	No. of pods	100-pod weight (g)	100-seed weight (g)	Shelling percentage%	Oil content (%)	Seed yield/ plant (g)	Seed yield ton/fed*
G1	Giza 6 (check)	82.23	9.23	77.47	197.86	25.66	66.57	47.52	115.51	1.86
G2	Ismailia 2	75.49	11.10	93.08	257.98	30.63	67.53	33.54	169.70	2.83
G3	Sohag 104	70.43	9.22	76.52	207.41	26.22	60.64	46.96	119.80	1.98
G4	Sohag 107	71.68	9.90	73.84	222.85	27.05	65.89	38.80	123.90	2.13
G5	Sohag 110	71.18	9.55	79.02	214.97	26.90	64.78	42.45	120.75	2.05
G6	Intr. 182	69.37	10.35	86.61	227.51	28.13	62.00	34.86	133.03	2.16
G7	Intr. 242	70.18	8.87	76.74	187.36	25.09	68.66	48.86	111.13	1.84
G8	Intr. 259	65.01	8.35	77.55	182.61	23.37	63.03	50.89	102.75	1.80
G9	Intr. 267	75.96	10.62	79.07	245.70	29.74	66.34	36.70	129.40	2.26
G10	Intr. 288	70.26	8.62	67.23	185.52	23.36	63.72	50.89	111.78	1.79
G11	Intr. 332	66.10	9.85	75.02	219.09	27.52	62.68	40.74	124.51	2.08
G12	Intr. 335	68.51	8.23	64.11	159.96	20.76	61.59	55.43	83.89	1.36
G13	Intr. 336	69.32	8.23	68.31	180.24	23.21	64.57	52.14	80.85	1.74
G14	Intr. 342	78.40	7.75	84.39	169.65	22.59	62.35	55.09	88.79	1.58
G15	Intr. 425	81.23	8.30	70.45	170.49	23.23	59.96	52.07	108.27	1.79
G16	Intr. 501	72.77	9.08	70.37	188.23	25.16	63.11	48.86	113.58	1.91
G17	Intr. 504	68.04	7.12	70.04	141.54	17.57	58.52	57.80	68.29	1.32
G18	Intr.508	83.85	7.92	58.94	183.38	22.77	62.63	52.75	88.55	1.70
G19	Intr. 510	77.07	7.32	55.04	146.93	18.55	58.26	56.13	72.67	1.36
G20	Intr. 514	70.29	8.43	75.44	187.22	23.62	65.24	51.47	107.97	1.80
LSD	Season (S)	4.98	0.18	*NS*	5.04	*NS*	*NS*	0.85	5.06	*NS*
	Genotype(G	6.80	1.09	12.85	25.58	1.32	5.00	3.46	15.07	0.23
	S*G	9.62	1.54	18.18	*NS*	*NS*	7.07	4.89	21.31	0.32

**fed: Meaning feddan = 4200 m^2*

Table 4. Correlation coefficients among studied traits of peanut genotypes and some tests for ability analysis of factor (Determinant, KMO's and Bartlett's test)

Traits	Plant height	No. of branches	No. of pods	100-pod weight	100-seed weight	Shelling percentage	Oil content
No. of branches	0.19*						
No. of pods	-0.11	0.15					
100-pod weight	-0.13	0.47**	0.34**				
100-seed weight	0.06	0.67**	0.32**	0.73**			
Shelling percentage	0.05	0.09	0.32**	0.20*	0.28**		
Oil content	-0.09	-0.45**	-0.08	-0.43**	-0.51**	0.08	
Seed yield/ plant	0.07	0.69**	0.33**	0.67**	0.81**	0.25**	-0.52**
Determinant = 0.029		KMO's test = 0.821			Bartlett's Test = **		

**, ** and ns indicates significant at the 0.05 and 0.01 level of probability and insignificant, respectively*

3.1.1 Correlation coefficients

Correlation coefficient matrix estimates was shown in Table 4. The estimates of correlation coefficient showed that number of branches and pods per plant, weight of 100-pods and 100-seeds and shelling percentage had a highly significant and positive correlation with seed yield per plant (r= 0.69**, r= 0.33**, r= 0.67**, r= 0.81** and r= 0.25**, respectively). These findings indicate that selection for each or all of these traits, thereupon high shelling percentage would be accompanied by high seed yielding ability in peanut. These findings are in agreement with those obtained by [4] and [25]. Meanwhile, seed yield was negative and significant association with oil content (r= -0.52**). Then, selection for peanut seed yield is an adversely direction for oil content, indicating that the highest peanut oil content genotypes were having less seed potentiality as compared to those get lowest. [4] pointed out that correlation coefficients between peanut seed yield and its oil content% was negative value but insignificant.

In fact, selection decisions based only on correlation coefficients may not always be effective because it measures the association between a pair of traits neglecting the complicated interrelationships among all traits [26]. Therefore, the correlation procedure may not provide a deep imagine about the importance of each component in the structure of peanut seed yield. The factor analysis can efficiently play this vital role.

Results revealed that significant differences in the correlation coefficients magnitude and direction without recording complete (±1) or no (0) correlation. Plant height exhibited insignificantly positive low correlation value with seed yield (r= 0.07), so it may exclude this trait. These prerequisites are according to [24]. Here, analysis was performed for all traits and results were interpreted.

3.1.2 Factor analysis tests ability

Table 4 shows test results that indicate the suitability of peanut data for structure detection as Determinant value for Multi-collinearity absence, KMO's test for sampling adequacy and Bartlett's test for identity matrix [16].

Determinant is a collinearity statistics used to determine the probably continuous factor analysis. Recorded value was 0.029 (higher than 0.00001), meaning no multi-collinearity among the studied peanut data. Then, results of the factor analysis probably are very useful.

The Kaiser-Meyer-Olkin Measure of Sampling Adequacy (KMO's test) estimate was 0.821 (high value) higher than 0.50 and close to 1.0, indicating the proportion of variance in your variables might be caused by underlying factors. Generally indicates that a factor analysis may be useful with these data.

A significance level (less than 0.05) of Bartlett's test of sphericity test, meaning the hypothesis that correlation matrix is an identity matrix, which would indicate that the studied variables are unrelated and therefore unsuitable for structure detection and factor analysis may be useful in these data.

According the previous tests, continuous factor analysis probably is very useful for the studied peanut data to determine the best yield traits.

3.1.3 Factor analysis

The Eigen value of each component in the initial solution is plotted in Fig. 1. The scree plot helps

to utilize the optimal number of components by determining the last big drop in Eigen values slope lower than one. Generally, the last big drop occurs between the third and fourth components, so using the first three components is a best choice.

Data in Table 5 presents the results obtained from the factor analysis of the studied peanut traits (Eigen value, % of variance and cumulative variance % of components) before and after rotation. Factor analysis revealed that only 3 of the 8 original factors had Eigen values greater than one and were selected as the best factors. These first three factors together explained 75.124% (6.01 Eigen values/8 variables) of the variance among the genotypes.

Regarding to the first factor including seed yield/plant, 100-seed weight, number of branches/plant, 100-pod weight and seed oil content (%) with Eigen value of 3.363 accounted for only 42.039% of the variance. These five traits recorded the highest effective values (loading) in the 1st factor. Furthermore, communality values for variables were high. For example, communality for 100-seed weight was 0.846, indicating that 84.60% of the variance in 100-seed weight is accounted for by Factor 1, 2 and 3. The second factor that accounted for 18.925% of the total variance is mainly loaded by shelling percentage % and number of pods/plant with Eigen value 1.514. The third factor with Eigen value 1.133 that accounted for just 14.160% of the total variance is mainly described by plant height. These results were similar for those obtained by [27].

All the eight traits were included in the three selected factors. But only some of traits possessed high loads within each factor. For the selected three factors, Table 5 presents factor loading and factor score coefficients. Factors were interpreted from the variables that were highly correlated with them. The bold italic marked loading values indicate the highest correlations between variables and corresponding factors. The greater loading meaning the variables is pure measure of factor. For instance, seed yield/plant, 100-seed weight, number of branches/plant, 100-pod weight and seed oil content (%) which showed the highest correlation with Factor 1 were considered as a group. Meanwhile, shelling percentage % and number of pods/plant traits possessed the highest loads in factor 2. Similarly, factor 3 showed highest association with only plant height. Seeing the 1st selected factor, existence yield traits in this factor suggested that there were not significant loss in the yield amount.

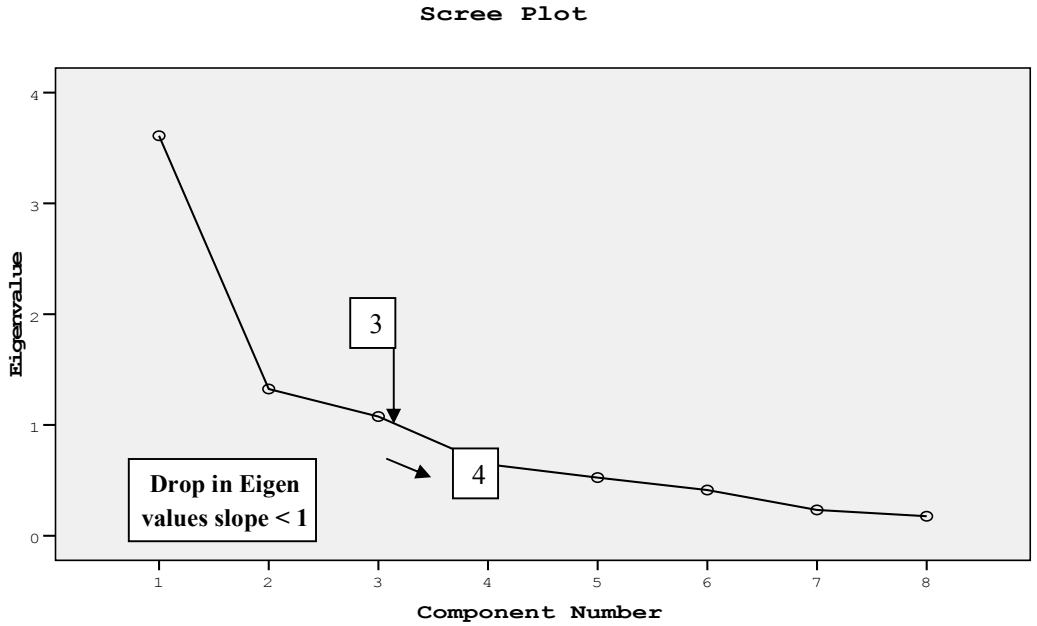

Fig. 1. The scree plot graph showing Eigen values in response to number of components for the estimated variables of peanut

The rotated component matrix helps to determine what the components represent. This suggests that it could be focused on seed yield, 100-seed weight, number of branches, 100-pod weight and oil content % in further analyses, but you can do even better by saving component scores [28]. Factor score coefficients in Table 5 were confirming the previous 3 factor results and it was used to obtain factor score values.

Concerning factor score values for the 1st selected factor that were used as a variable in univariate analysis of variance (ANOVA) to screen the studied genotypes based on the most yield-effective traits. There is no study included the same traits and statistical model as in this investigation. Therefore the results were discussed with indirectly related studies. Also as expected, the collinearity statistics show that the factor scores are uncorrelated. This means that more of the factors are identified as statistically significant, which can affect final results of the model that only includes significant effects [16]. This model built can employ analysis of variance (ANOVA) for the first factor scores (FS) as (variable) that extracted from the best set of affecting dependent seed yield trait. Hence, results in Fig. 2 showed classification for the 20 genotypes. This histogram revealed the relative rank of genotypes with the direction additively of peanut seed yield. Genotypes that have high seed yielding, recorded high (FS) values plotted in the positive direction. Meanwhile, negative (FS) values indicate to low seed yielding means.

From histogram of Fig. 2, it was clear that there were nine genotypes existed in positive area recorded positive (FS) values for seed yield-related traits. These genotypes were ranked as G2 (Ismailia 2), G9 (Intr. 267), G4 (Sohag 107), G6 (Intr. 182), G5 (Sohag 110), G11 (Intr. 332), G1 (Giza 6), G7 (Intr. 242) and G3 (Sohag 104), recording 6 genotypes over G1 (check genotype, Giza 6) and only two genotypes were put in order lower than G1 (Giza 6 check). On the other hand, genotypes G19 (Intr. 510), G17 (Intr. 504) and G12 (Intr. 335) scored the best grad in oil content %, based on the reverse correlation (previously) between seed yield and oil content %. Therefore, G2 (Ismailia 2), G9 (Intr. 267), G4 (Sohag 107), G6 (Intr. 182), G5 (Sohag 110) and G11 (Intr. 332) considered as the best seed yield genotypes, contrary oil content % genotypes were G19 (Intr. 510), G17 (Intr. 504) and G12 (Intr. 335).

From the previous results, the (FS) explained help in selecting genotypes with higher positive (FS) values for seed yield components. Thus, it would have better chance to get promising genotypes with higher desired yield (seed or oil).

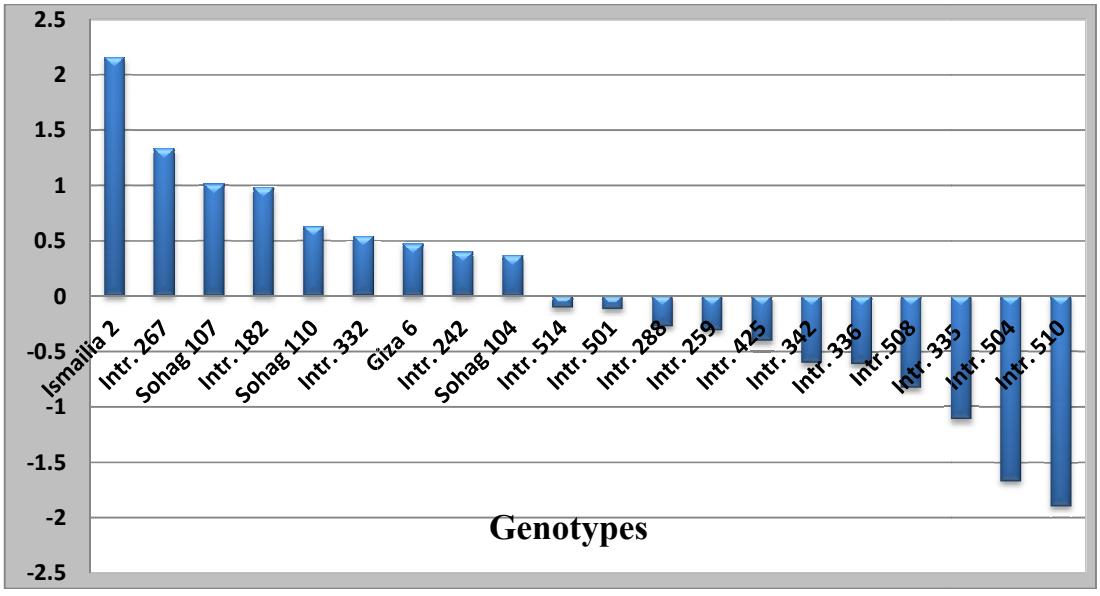

Fig. 2. Dendrogram showing the classification of twenty peanut genotypes based on extracted Factor scores (FS) of first factor concluding the best yield traits

3.2 Cluster Analysis

Cluster analysis is an effective procedure for extracting the structured relationships among genotypes and provides a hierarchical classification of them. Hierarchical cluster analysis for discriminating the investigated 20 genotypes obtained with the complete linkage procedure. The tested genotypes were classified according to seed and oil yield and its related traits and were classified as illustrated in dendrogram (Fig. 3). Each classified cluster and its mean estimates for seed yield (per plant and ton/fed.) and oil content % are present in Table 5. Therefore, all classified cluster were describe and discussed.

Obviously, dendrogram (Fig. 3) and Table 6 illustrated the genotypes into two major clusters namely; A and B. However, the first main cluster divided into three sub-clusters which could be named, a_1, a_2 and a_3. Some genotypes were grouped in the same sub-cluster. Only one genotype (G2, Ismailia 2) was consisted as sub-cluster (a_1) that had the highest seed yield (169.70 g/plant, 2.83 ton/fed) coupled with the lowest oil content (33.54%) at all. Followed by sub-cluster (a_2) grouping (4) genotypes (Intr. 267, Intr. 182, Intr. 332 and Sohag 107) that recorded (127.71 g/plant, 2.16 ton/fed and 37.78%) for seed yield and oil %, respectively. The sub-cluster (a_3) contained three genotypes (Sohag 110, Sohag 104 and Giza 6), registering 118.69 g/plant, 1.96 ton/fed and 45.64% for seed yield and oil %, respectively.

Regarding, the second main cluster comprised of three sub-clusters (b_1, b_2 and b_3). The sub-cluster (b_1 and b_2) consisted of six genotypes (Intr. 242, Intr. 514, Intr. 288, Intr. 501, Intr. 259 and Intr. 425) and four genotypes (Intr. 335, Intr. 342, Intr. 336 and Intr.508) respectively, that had the relatively high oil % (50.50% and 53.85%). Meanwhile, sub-cluster (b_3) included only two genotypes (Intr. 504 and Intr. 510) were characterized by the lowest seed yield and highest oil % (70.48 g/plant, 1.34 ton/fed and 56.97%) at all.

The previous results confirmed that cluster (A) genotypes (Ismailia 2, Intr. 267, Intr. 182, Intr. 332, Sohag 107, Sohag 110 and Sohag 104) surpassed Giza 6 (local check genotype) and was considered as the highest seed yield with the lowest oil % contrary cluster (B). Then, cluster (A) genotypes are related to each other, and are far from the rest genotypes of another (B) cluster [27,28,29]. Meanwhile, sub-cluster (a_3) genotypes (Sohag 110, Sohag 104 and Giza 6) considered as the medium in both seed yield and oil %.

Then, present study exhibited the presence of considerable genetic diversity among the tested genotypes which will be useful for selecting superior and promising peanut genotypes on the basis of their phenotypic expression to use them in breeding programs to improve the desired commercially important traits as seed yield and oil content %. The diversity among the peanut genotypes into groups with similar traits can be used to design a collection [27,28,29].

3.3 Genetic Analysis

Estimates of variance components (environmental, σ^2_e; genetic, phenotypic, σ^2_g; σ^2_{ph}) converted to their respective coefficients of variation (genetic, GCV %; phenotypic, PCV %) to permit comparisons between traits. Genetic variance relative to its mean and allow comparisons among traits with different units and scales and predict to available variability to be employed for genetic gain (GA %) [20]. Genetic parameters were estimated to compare the variation among various studied peanut traits. Estimates of variance components (σ^2_e, σ^2_g, σ^2_{ph}), genotypic and phenotypic (GCV, PCV %) coefficient of variability, broad-sense heritability and expected genetic advance as percentage of mean (GA %) are presented in Table 7.

In the majority, the variations among these peanut genotypes were due to genetic factors rather than environmental ones, as indicated by higher genetic variances [30,31].

Coefficient of variation extant indicated that high estimates of (PCV%) and (GCV%) were recorded for seed yield/plant (55.17 and 52.79%, respectively), 100- pod weight (40.09 and 38.57%, respectively), oil content% (38.41 and 37.58%, respectively) and followed by 100 - seed weight (33.87 and 33.51%, respectively). On the other hand, the lowest estimates in the remaining traits were observed for shelling percentage trait (14.67 and 7.59%, respectively). Generally, (PCV %) values were slightly higher than (GCV %) ones for all traits, reflecting influence of environment on the traits expression. In accordance, selection would be effective to improve these traits among the studied peanut genotypes the. Similar findings were reported by [31].

Table 5. Varimax rotated factor analysis results for eight studied peanut traits

Traits	Rotated component matrix			Communality	Loading	Factor score coefficients		
	Factor 1	Factor 2	Factor 3			Factor 1	Factor 2	Factor 3
Seed yield/ plant	0.870	0.271	0.029	0.831	0.870	0.245	0.064	0.023
100-seed weight	0.869	0.301	0.008	0.846	0.869	0.240	0.085	0.006
No. of branches	0.798	0.049	0.248	0.701	0.798	0.251	-0.074	0.204
100-pods weight	0.765	0.265	-0.280	0.735	0.765	0.219	0.055	-0.251
Oil content %	-0.757	0.259	-0.016	0.640	-0.757	-0.292	0.311	0.023
Shelling	0.029	0.861	0.177	0.773	0.861	-0.132	0.645	0.216
No. of pods	0.222	0.685	-0.270	0.591	0.685	-0.029	0.453	-0.199
Plant height	0.072	-0.008	0.942	0.893	0.942	0.001	0.047	0.836
Eigen value	3.363	1.514	1.133	6.01				
Variance%	42.039	18.925	14.160	75.124				
Cumulative %	42.039	60.964	75.124					

The bold italic marked: loading with the highest correlations between variables and corresponding factors.

Table 6. Cluster analysis summary of the 20 peanut genotypes for seed yield and oil %, showing the similarity, included genotypes and group average estimates

Cluster code	Group	Similarity	No. of genotypes	Included genotypes	Group average		
					Seed yield		Oil %
					Plant (g)	Ton/fed	
Cluster A	*a1*	47.14	1	(G2) Ismailia 2	*169.70*	*2.83*	33.54
	a2	81.34	4 (G9, G6, G11,G4)	Intr. 267, Intr. 182, Intr. 332 and Sohag 107	127.71	2.16	37.78
	a3	86.30	3 (G5, G3, G1)	Sohag 110, Sohag 104 and Giza 6	118.69	1.96	45.64
			Cluster A mean		138.70	2.32	38.99
Cluster B	b1	85.33	6 (G7, G20, G10, G16, G8, G15)	Intr. 242, Intr. 514, Intr. 288, Intr. 501, Intr. 259 and Intr. 425	109.25	1.82	50.51
	b2	81.44	4 (G12,G14, G13, G18)	Intr. 335, Intr. 342, Intr. 336 and Intr.508	85.52	1.60	53.85
	b3	88.10	2 (G17, G19)	Intr. 504 and Intr. 510	70.48	1.34	*56.97*
			Cluster B mean		88.42	1.59	53.78
			Grand mean		113.56	1.95	46.38

Table 7. Variance components, broad sense heritability (h^2), coefficients of variation (GCV % and PCV %) and genetic advance percent (GA %) for studied traits in peanut genotypes through the combined data

Trait	Variance components				h^2	GCV%	PCV%	GA%
	σ_e	σ_l	σ_g	σ_{ph}				
Plant height	35.00	10.92	161.91	207.83	0.78±0.07**	17.46	19.78	31.75
No. of branches	0.91	0.23	6.77	7.92	0.86±0.05**	29.23	31.60	55.70
No. of pods	124.90	33.70	444.33	602.93	0.74±0.08**	28.50	33.20	50.40
100-pod weight	494.90	-46.47	5588.35	6036.78	0.93±0.03	38.57	40.09	76.44
100-seed weight	1.32	0.15	67.71	69.17	0.98±0.01	33.51	33.87	68.29
Shelling percentage	18.92	44.49	23.16	86.57	0.27±0.19	7.59	14.67	8.09
Oil content	9.05	5.25	321.31	335.61	0.96±0.02	37.58	38.41	75.75
Seed yield/ plant	171.70	131.50	3296.33	3599.53	0.92±0.03**	52.79	55.17	104.07

σ^2_g: Genotypic, σ^2_{ph}: phenotypic, σ^2_l: genotypes × years and σ^2_e: environmental variance

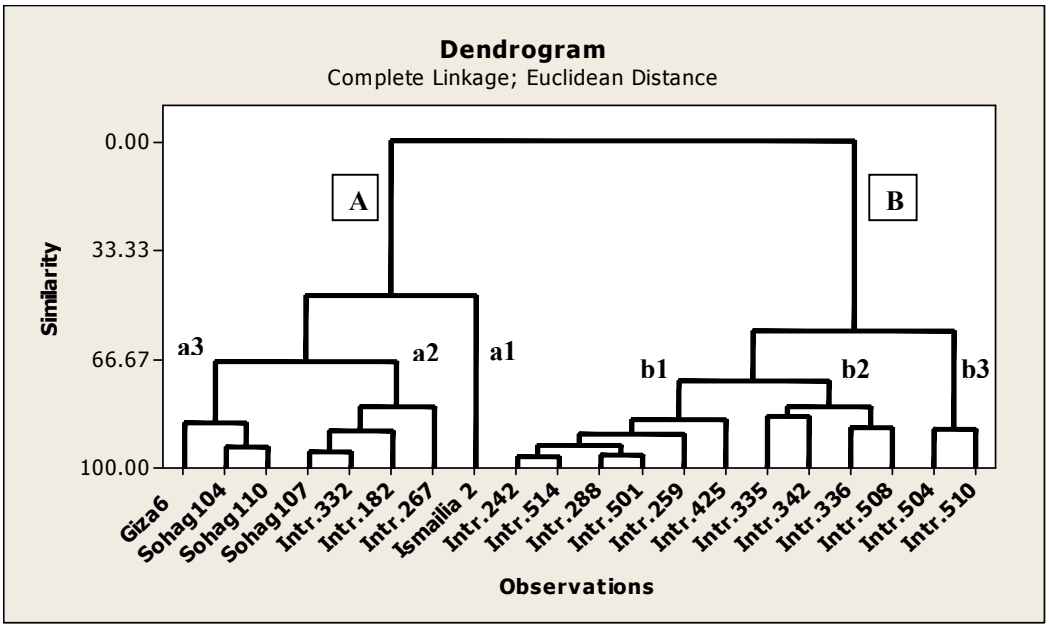

Fig. 3. Cluster analysis showing the relationship among twenty peanut genotypes based on all studied yield traits

Regarding heritability (h_b^2) estimates the results demonstrated that values were different for all studied traits (ranged from 0.27 for shelling percentage to 0.98 for seed yield/plant). Estimated components of variance contributing to (σ^2_g) were the highest component comparing with others (environment σ^2_e and interaction σ^2_i variance) for all traits except shelling percentage that had highest σ^2_i component. Then results demonstrated that heritability (h_b^2) estimates were high for all studied traits except this trait (shelling percentage) with value 0.27.

Concerning to the high values of heritability coupled with high values of genetic advance (as % of mean), results in Table 7 demonstrated high heritability with genetic advance for seed yield/plant (0.92 and 104.07%, respectively), 100- pod weight (0.93 and 76.44%, respectively), oil content% (0.96 and 75.75%, respectively) and followed by 100-seed weight (0.98 and 68.29%, respectively) and number of branches (0.86 and 55.70%, respectively). The previous results suggest the predominance of additive gene action, indicating phenotypic selection to be effective for these studied traits. Similar results were reported by [32,33,7,6] for seed yield and its component traits. In contrast, low heritability and genetic advance were reported by [30] for shelling percentage recording heritability estimate 0.27 along with low genetic advance 8.09%. Also, high heritability coupled with high genetic advance was observed for number of branches per plant by [34,8]. Plant height trait had moderate heritability (0.78) along with genetic advance % (31.75%). Peanut seed yield enhancement can perform from improvements in 100-pod weight, oil content%, 100-seed weight and number of branches. Meanwhile, shelling improvement was not significant which may be due to low genetic advance and low heritability estimate (as observed in the investigation of [30].

4. CONCLUSION

Present study was carried out during 2018 and 2019 crop season; statistical analysis was applied to various yield traits of the 20 genotypes. Correlation analysis indicated that seed yield was positively associated with plant height, branches, no. of pods, 100-pods, 100-seed and shelling percentage % except oil content %. Factor analysis reduced 8 traits into 3 factors. Factor 1 consisting of seed yield/plant, 100-seed weight, number of branches/plant, 100-pod weight and seed oil content (%) explained 42.039% of the total variance. Factor 2 that explained 18.925% of the total variance is loaded by shelling percentage % and number of pods/plant. However, Factor 3 comprising plant height accounted for 14.160% of the total variation. The extracted first factor scores was

employed (as a variable) in ANOVA for evaluating the studied genotypes data to discriminate and screening the best or promising ones. Therefore, selection for the best promising genotypes is depending on the yield and most affecting yield traits not yield trait only according statistical analysis model. Concerning grouping genotypes Ismailia 2, Intr. 267, Intr. 182, Intr. 332 and Sohag 107 could be exploited for increase in peanut seed yield. Whereas, genotypes Intr. 504 and Intr. 510 be utilized for increase in peanut seed oil content %. Genotypes by environmental interactions are highly important in evaluating the peanut genotypes for high yielding with stable performance over years. The high estimates of GCV, h^2 and GA % were observed for seed yield per plant, oil content % and weight of 100-pod that were controlled by additive gene effects and selection would be useful for improvement of these traits.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. FAOSTAT. FAO STAT data of Food and Agriculture Organization of the United Nations; 2019.
2. Hair JF, William JR, Black C, Babin BJ, Anderson RE. Multivariate data analysis. Upper Saddle River, NJ: Pearson Prentice Hall. 7th Ed. Pearson Education Inc. and Dorling Kindersley Publishing Inc. 2006;6: 415.
3. Ayub K, Muhammad R, Khan MI, Tahir M. Genetic variability and criterion for the selection of high yielding peanut genotypes. Pakistan J. of Agric. Res. 2000;16(1):9-12.
4. Afify RR, El-Nwehy SS, Bakry AB, Abd El-Aziz ME. Response of peanut (*Arachis hypogaea* L.) crop grown on newly reclaimed sandy soil to foliar application of potassium nano-fertilizer. Middle East J. Appl. Sci. 2019;9(1):78-85.
5. John K, Madhavi Santhoshi MV, Rajasekhar P. Correlation and path analysis in groundnut (*Arachis hypogaea* L.) Int. J. Curr. Microbiol. App. Sci. 2019;8(12):1521-1529.
6. Kumar N, Ajay BC, Rathanakumar AL, Radhakrishnan T, Mahatma MK, Kona P, Chikani BM. Assessment of genetic variability for yield and quality traits in genotypes. Electronic J. of Plant Breed. 2019;10(1):196–206.
7. Patidar OP, Nadaf HL. An assessment of genetic variability and traits association among high oleic advanced breeding lines for yield and quality traits in groundnut (*Arachis hypogaea* L.). Electronic Journal of Plant Breeding. 2017;8(1):201-205.
8. Mahesh R. Hampannavar, Khan H, Temburne BV, Janila P, Amaregouda. Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.) J. of Pharmacognosy and Phyto-chemistry. 2018;7(1):870-874.
9. Tirkey SK, Ahmad E, Mahto CS. Genetic variability and character association for yield and related attributes in groundnut (*Arachis hypogaea* L.). Journal of Pharmacognosy and Phytochemistry. 2018;1:2487-2489.
10. AOAC. Official methods of analysis. Association of Official Analysis Chemist, 15th Ed. Washington, USA; 1990.
11. Steel RGD, Torrie JH, Dickey DA. Principles and procedures of statistics. McGraw Hill Book Co. Inc, New York, USA; 1997.
12. Snedecor GW, Cochran WG. Statistical methods. 7th Ed. Iowa State Univ. Press, Ames Lowa, USA; 1981.
13. Cattell RB. Factor analysis: An introduction to essentials. The purpose and underlying models. Biometrics. 1965;21:190–215.
14. Kaiser HF. The varimax criterion for analytic rotation in factor analysis. Psychometricka. 1958;23(3):187-200.
15. Seiller GJ, Stafford RE. Factor analysis of components in Guar. Crop Science. 1985;25:905–908.
16. Johnson RA, Wichern DW. Applied multivariate statistical analysis. Prentice Hall, Upper Saddle River, New Jersey, (USA). 2002;766.
17. SPSS. User's guide for SPSS for windows evaluation version 15.0, Statistical Program for Social Science, Inc. USA; 2006.
18. Everitt BS. Cluster analysis. Wiley, New York, USA; 1993.

19. Poehlman JM, Sleper DA. Breeding field crops. Fourth Edition. Iowa State University Pres. USA; 1995.
20. Gravois KA, Helms RS. Path analysis of rice yield and yield components as affected by seeding rate. Agron J. 1992;84:1–4.
21. Rao TV, Venkanna V. Studies on character association and path analysis in groundnut (*Arachis hypogaea* L.). Journal of Pharmacognosy and Phytochemistry. 2019;8(5):76-78.
22. Mekontchou T, Ngueguim M, Fobasso M. Stability analysis for yield and yield components of selected peanut breeding lines (*Arachis hypogaea* L.) in the North Province of Cameroon. Tropicultura. 2006;24(2):90-94.
23. Minimol JS, Datke SB, Deshmukh SN, Satpute GN. Genotype x environment interaction in groundnut (*Arachis hypogaea* L.). Ann. Pl. Physio. 2001;14(1):74-79.
24. Kline P. An easy guide to factor analysis. London: Routledge; 1994.
25. Mekdad AAA. Response of *Arachis hypogaea* L. to different levels of phosphorus and boron in dry environment. Egypt J. Agron. 2019;41(1):21-28.
26. Kang MS. Applied quantitative genetics. Kang Publ. Baton Rouge, LA, USA; 1994.
27. Makinde SCO, Ariyo OJ. Multivariate analysis of genetic divergence in twenty two genotypes of groundnut (*Arachis hypogaea* L.). J Plant Breed Crop Sci. 2010;2(7):192-204.
28. Ajay BC, Gowda MVC, Rathnakumar AL, Kusuma VP, Abdul Fiyaz R, Prasanna Holajjer, Ramya KT, Govindaraj G, Prashanth Babu H. Improving genetic attributes of confectionary traits in peanut (*Arachis hypogaea* L.) using multivariate analytical tools. J Agri Sci. 2012;4(3):247-258.
29. Gantait S, Gunri SK, Kundu R, Chatterjee S. Evaluation of genetic divergence in Spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. Plant Breed Biotech. 2017;5(3):163-171.
30. Ashutosh K, Gupta S, Sharma SR, Pradhan K. Genetic variability, correlation coefficient and path coefficient analysis for yield and component traits in groundnut. Indian Journal of Ecology. 2016;43(2):85-89.
31. Nagaveni K, Khan H. Genetic variability studies in terminal drought tolerant groundnut (*Arachis hypogaea* L.). Journal of Pharmacognosy and Phytochemistry. 2019;8(2):747-750.
32. Rao VT, Venkanna V, Bhadru D. Genetic analysis of yield and its components in groundnut (*Arachis hypogaea* L.). International Journal of Applied Biology and Pharmaceutical Technology. 2015; 6(1):223-225.
33. Patil SK, Shivanna S, Irappa BM, Shweta. Genetic variability and character association studies for yield and yield attributing components in groundnut (*Arachis hypogaea* L.). International Journal of Recent Scientific Research. 2015;6(6):4568-4570.
34. Korat VP, Pithia MS, Savaliya JJ, Sodavadiya PR. Studies on genetic variability in different genotypes of groundnut. Legume Research. 2009;32(3): 224-226.

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