

**Multivariate analyses of yield and its components in some peanut  
genotypes**

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**ABSTRACT (ARIAL, BOLD, 11 FONT, LEFT ALIGNED, CAPS)**

**Aims:** for proposing a statistical approach to select of the most promising genotypes for breeding program, in wich crop? Please clarify it.

**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 1<sup>st</sup> factor explained 42.039% of the total variance and recorded high heritability coupled with high genetic advance %. Anova results 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 (ARIAL, BOLD, 11 FONT, LEFT ALIGNED, CAPS)

Peanut (*Arachis hypogaea* L.) is a main summer oil crop grown in sandy soils. Besides 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.

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] and [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] and [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. Material and methods (arial, bold, 11 font, left aligned, caps)**

### **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 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/feddann. P was added during soil preparation. N and k were splitted in 3 equal amounts added at sowing, 30 and 45 days after sowing.

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

| Soil characters | Physical analysis |       | Chemical analysis |      |      |                  |      |      |                               |      |      |
|-----------------|-------------------|-------|-------------------|------|------|------------------|------|------|-------------------------------|------|------|
|                 | 2018              | 2019  | character         | 2018 | 2019 | Cations Mg/100g  |      |      | Anions Mg/100g                |      |      |
|                 |                   |       |                   |      |      | character        | 2018 | 2019 | character                     | 2018 | 2019 |
| Sand%           | 60.32             | 70.12 | PH                | 7.7  | 8.1  | Na <sup>+</sup>  | 0.52 | 1    | Cl <sup>-</sup>               | 0.23 | 0.42 |
| Silt%           | 28                | 19    | N <sub>ppm</sub>  | 30   | 40   | K <sup>+</sup>   | 0.09 | 0.08 | So <sub>4</sub> <sup>-</sup>  | 0.27 | 2.37 |
| Clay%           | 10.68             | 10.88 | P <sub>ppm</sub>  | 8    | 8.6  | Ca <sup>++</sup> | 0.30 | 1.50 | HCo <sub>3</sub> <sup>-</sup> | 0.59 | 0.69 |
| Soil texture    | Sandy loam        |       | K <sub>ppm</sub>  | 496  | 488  | Mg <sup>++</sup> | 0.19 | 0.90 |                               |      |      |

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 from oil crops res. Department, fcrl, were used (table 2).

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

| Code no. | Name           | Origin      | Pedigree                            |
|----------|----------------|-------------|-------------------------------------|
| G1       | GIZA 6 (CHECK) | EGYPT FCRI* | 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.P12                                   |
| 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     | (RABUT33-1XNCAC316)X(53-68XRABUT33-1)F7B1 |
| G16 | INTR. 501 | CHINA       | TIANHU3                                   |
| G17 | INTR. 504 | BOLIVIA     | R.C.M444                                  |
| G18 | INTR.508  | U.S.A       | N.C17                                     |
| G19 | INTR. 510 | AUSTRALIA   | VIGINA BUNCH                              |
| G20 | INTR. 514 | ARGENTINA   | KRAPOVICKAS                               |

\*FCRI: FIELD CROP RESEARCH INSTITUTE (OIL CROP RESEARCH), AGRICULTURAL RESEARCH CENTER.

## 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 [\*\*].

The cluster analysis was performed using a measure of similarity levels and euclidean distance [17].

Estimates of genetic, genotype by season and error variance components ( $\sigma^2_g$ ,  $\sigma^2_{gs}$  and  $\sigma^2_e$ ) were computed. Broad-sense heritability was estimated with these components as suggested by [18]. 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 [19]

### 3. Results and discussion

Results revealed that the studied twenty peanut genotypes differed significantly for all traits in each season, except plant height the 1<sup>st</sup> 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 Tables (3). Results appeared that the studied genotypes significantly differed for all traits in over seasons [20]. 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 [21] 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 [22].

Results revealed that genotypes 18 (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) 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 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 2 (Ismailia 2), genotypes 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 (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.

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

| Code | Genotype | Plant | No. of | No. of | 100-pod | 100-seed | Shelling | Oil | Seed | Seed |
|------|----------|-------|--------|--------|---------|----------|----------|-----|------|------|
|------|----------|-------|--------|--------|---------|----------|----------|-----|------|------|

|     |                | height<br>(cm) | branches | pods  | weight<br>(g) | weight<br>(g) | percentage<br>% | content<br>(%) | yield/<br>plant (g) | yield<br>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             |
|     | Season (S)     | 4.98           | 0.18     | NS    | 5.04          | NS            | NS              | 0.85           | 5.06                | NS               |
|     | Genotype(      |                |          |       |               |               |                 |                |                     | 0.23             |
|     | G              | 6.80           | 1.09     | 12.85 | 25.58         | 1.32          | 5.00            | 3.46           | 15.07               |                  |
|     | S*G            | 9.62           | 1.54     | 18.18 | NS            | NS            | 7.07            | 4.89           | 21.31               | 0.32             |

### 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 [23] Therefore, factor analysis procedure was carried out with undertaking for investigation the prerequisites as follows:

#### 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 [24]. 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 [25]. 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 ( $\pm 1$ ) 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 [23]. Here, analysis was performed for all traits and results were interpreted.

**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 <sup>**</sup>  | 0.34 <sup>**</sup> |                     |                      |                     |                     |
| 100-seed weight     | 0.06         | 0.67 <sup>**</sup>  | 0.32 <sup>**</sup> | 0.73 <sup>**</sup>  |                      |                     |                     |
| Shelling percentage | 0.05         | 0.09                | 0.32 <sup>**</sup> | 0.20 <sup>*</sup>   | 0.28 <sup>**</sup>   |                     |                     |
| Oil content         | -0.09        | -0.45 <sup>**</sup> | -0.08              | -0.43 <sup>**</sup> | -0.51 <sup>**</sup>  | 0.08                |                     |
| Seed yield/ plant   | 0.07         | 0.69 <sup>**</sup>  | 0.33 <sup>**</sup> | 0.67 <sup>**</sup>  | 0.81 <sup>**</sup>   | 0.25 <sup>**</sup>  | -0.52 <sup>**</sup> |
| 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.

### 3.1.2 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.

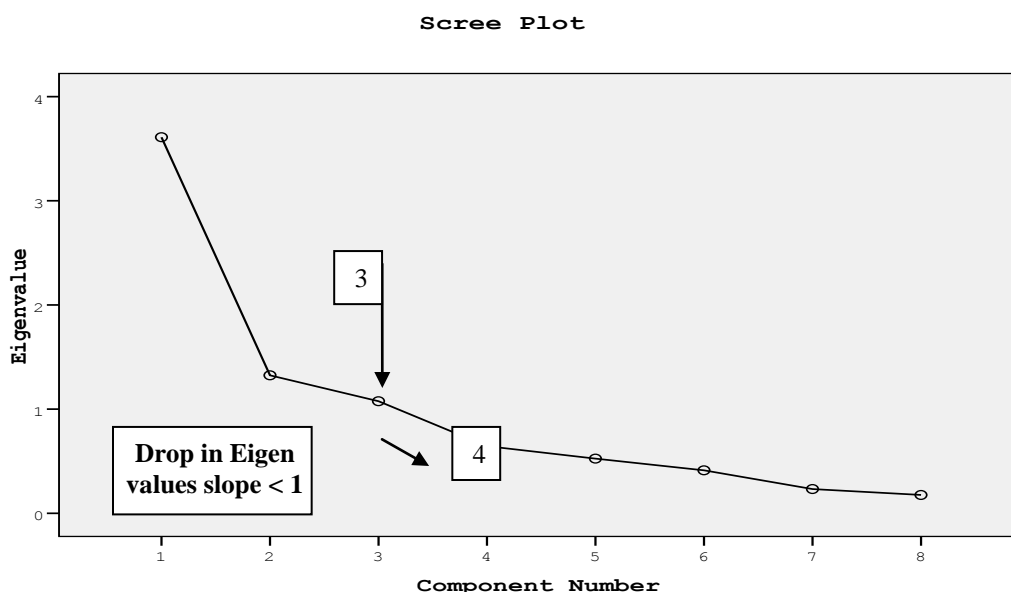
The Kaiser-Meyer-Olkin Measure of Sampling Adequacy (KMO's test) estimate was 0.821 (high value) higher than 0.50 and close to 1.0, indicating the proportion of variance in your variables might be caused by underlying factors. Generally indicates that a factor analysis may be useful with these data.

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 **Figure (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.



**Figure (1):** The scree plot graph showing Eigen values in response to number of components for the estimated variables of peanut.

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 1<sup>st</sup> factor. Furthermore, communality values for variables were high. For example, communality for 100-seed weight was 84.60%, 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 [26].

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 1<sup>st</sup> selected factor, existence yield traits in this factor suggested that there were not significant loss in the yield amount.

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 [27]. Factor score coefficients in Table 5 were confirming the previous 3 factor results and it was used to obtain factor score values.

**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 | <b>0.870</b>             | 0.271        | 0.029        | 0.831       | 0.870   | <b>0.245</b>              | 0.064        | 0.023        |
| 100-seed weight   | <b>0.869</b>             | 0.301        | 0.008        | 0.846       | 0.869   | <b>0.240</b>              | 0.085        | 0.006        |
| No. of branches   | <b>0.798</b>             | 0.049        | 0.248        | 0.701       | 0.798   | <b>0.251</b>              | -0.074       | 0.204        |
| 100-pods weight   | <b>0.765</b>             | 0.265        | -0.280       | 0.735       | 0.765   | <b>0.219</b>              | 0.055        | -0.251       |
| Oil content %     | <b>-0.757</b>            | 0.259        | -0.016       | 0.640       | -0.757  | <b>-0.292</b>             | 0.311        | 0.023        |
| Shelling          | 0.029                    | <b>0.861</b> | 0.177        | 0.773       | 0.861   | -0.132                    | <b>0.645</b> | 0.216        |
| No. of pods       | 0.222                    | <b>0.685</b> | -0.270       | 0.591       | 0.685   | -0.029                    | <b>0.453</b> | -0.199       |
| Plant height      | 0.072                    | -0.008       | <b>0.942</b> | 0.893       | 0.942   | 0.001                     | 0.047        | <b>0.836</b> |
| Eigen value       | <b>3.363</b>             | <b>1.514</b> | <b>1.133</b> | <b>6.01</b> |         |                           |              |              |

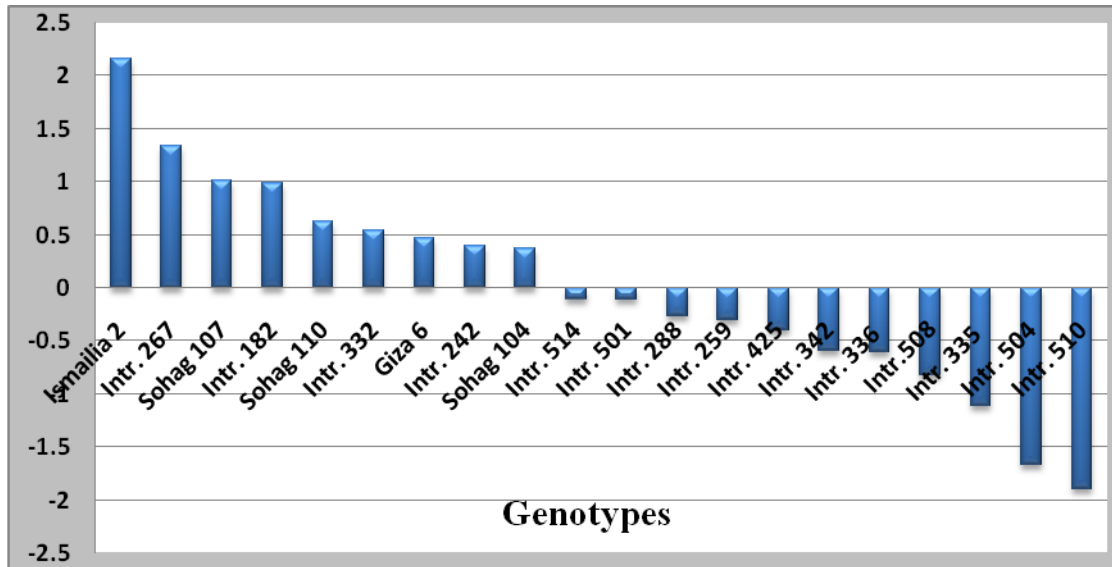
|                     |               |               |               |               |
|---------------------|---------------|---------------|---------------|---------------|
| <b>Variance%</b>    | <b>42.039</b> | <b>18.925</b> | <b>14.160</b> | <b>75.124</b> |
| <b>Cumulative %</b> | <b>42.039</b> | <b>60.964</b> | <b>75.124</b> |               |

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

Concerning factor score values for the 1<sup>st</sup> 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 Figure (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 Figure (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 would have better chance to get a promising genotypes with higher desired yield (seed or oil).



**Figure 2:** Dendrogram showing the classification of twenty peanut genotypes based on extracted Factor scores 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 average linkage procedure. The tested genotypes were classified according to seed and oil yield and its related traits and were classified as illustrated in dendrogram (**Figure 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.

**Table (5):** 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 |

Regarding, the second main cluster comprised of three sub-clusters (b<sub>1</sub>, b<sub>2</sub> and b<sub>3</sub>). The sub-cluster (b<sub>1</sub> and b<sub>2</sub>) 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<sub>3</sub>) 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, Sohag 104 and Giza 6) surpassed Giza6 (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 [26], [27] and [28]. Meanwhile, sub-cluster (a<sub>3</sub>) genotypes (Sohag 110, Sohag 104 and Giza 6) considered as the medium in both seed yield and oil%.

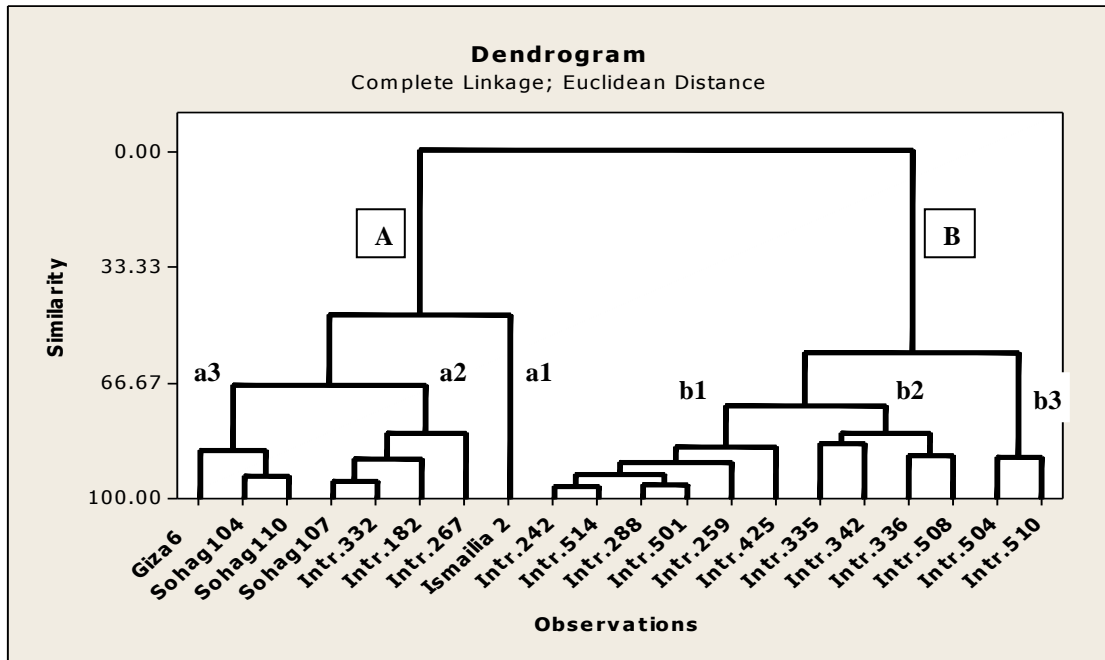
Then, present study exhibited the presence of considerable genetic diversity among the tested genotypes which will be useful for selecting superior and promising peanut genotypes on the basis of their phenotypic expression to use them in breeding programs to improve the desired commercially important 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 [26], [27] and [28].

### 3.3 Genetic analysis

Estimates of variance components (environmental,  $\sigma^2_e$ ; genetic, phenotypic,  $\sigma^2_g$ ;  $\sigma^2_{ph}$ ) 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 %) [19]. Genetic parameters were estimated to compare the variation among various studied peanut traits. Estimates of variance components ( $\sigma^2_e$ ,  $\sigma^2_g$ ,  $\sigma^2_{ph}$ ), genotypic and phenotypic (GCV, PCV %) coefficient of variability, broad-sense heritability and expected genetic advance as percentage of mean (GA %) are presented in Table (6).

In the majority, the variations among these peanut genotypes were due to genetic factors rather than environmental ones, as indicated by higher genetic variances [29] and [30].





**Figure (3).** Cluster analysis showing the relationship among twenty peanut genotypes based on all studied yield traits.

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 [30].

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 ( $\sigma_g^2$ ) were the highest component comparing with others (environment  $\sigma_e^2$  and interaction  $\sigma_i^2$  variance) for all traits except shelling percentage that had highest  $\sigma_i^2$  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.

**Table 6.** 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%    |
|---------------------|---------------------|------------|------------|---------------|-------------|-------|-------|--------|
|                     | $\sigma_e$          | $\sigma_l$ | $\sigma_g$ | $\sigma_{ph}$ |             |       |       |        |
| 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 |

Genotypic ( $\sigma^2g$ ), genotypes  $\times$  years ( $\sigma^2l$ ), error ( $\sigma^2e$ : variance)

Concerning to the high values of heritability coupled with high values of genetic advance (as % of mean), results in Table (6) 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 [31], [32], [7] and [6] for seed yield and its component traits. In contrast, low heritability and genetic advance were reported by [29] 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 [33] and [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 [29]).

#### 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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