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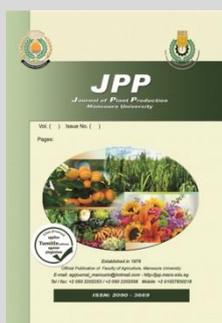
Graphical Presentation of some Peanut Genotypes by Comparing Two Patterns of Biplot Analysis

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ABSTRACT

The present work was carried out at the Agriculture Research Station of Shandwell during the two successive seasons of 2018 and 2019 to assess the yield potential of 20 peanut genotypes. Genotype by trait biplot (GT) and genotype by yield*trait (GYT) analyses were automated to obtain information on genotypes for selection based on multiple traits (nine traits), and appreciate the relationships between these attributes. Applying biplot analyses to the multiple trait data revealed that genotype by yield*trait (GYT) graphically facilitated visual, more effective and clear in providing information about the superior genotypes and the relationships between the yield and its components genotype compared to trait biplot (GT). Also, ranking genotypes was tested by a superiority index that collective yield and other target traits with the GYT biplot. In the GYT biplot, yield-trait combinations clearly appeared that the best genotypes defined for all traits, whereas in the genotype \times trait (GT) biplot, the best genotypes were not known for all traits. The promising genotypes being No. 7, 16 and 17 are clearly observed using the GYT biplot technique.

Keywords: Peanut, selection, GT biplot graph, GYT biplot graph.

INTRODUCTION

Peanut (*Arachis hypogea* L.) is an important oil and protein crop, which is grown mainly in semi-arid tropic and sub-tropic areas of 109 countries around the world (Siva *et al.*, 2014). It is grown for oil extraction and also as a food product (Pasupuleti *et al.*, 2013). The peanut seeds are directly consumed as raw or crushed for edible and industrial oil uses (Murali and Janila, 2017).

Peanuts are ranked as the fourth in oilseed crops in the world after soybeans, rapeseed, and cotton. It is also an important oilseed crop for the production of vegetable oils (Arioglu, 2014). In Egypt, there is a great shortage in edible oils so that almost 90% of the consumption needs are currently imported (Zaher *et al.*, 2017).

Samaha *et al.* (2019) mentioned that groundnut successfully cultivated in the newly reclaimed sandy soils which commonly suffer from deficiency or unavailability of most the micronutrient.

Egypt has given great attention to plant groundnut because its ability for growing in the newly reclaimed sandy soil conditions.

Extremely necessary to increase the total production of oilseed crops including peanut either by increasing their yield per feddan or by increasing their acreage of cultivation or by a combination of both to bridge the gap between consumption and production.

In GT biplot analysis, several attributes of the genotypes can be presented graphically, and thus, relations among several genotypes and attributes can be visually assessed and compared (Yan *et al.*, 2001). Therefore, researchers commonly prefer the GT biplot method due to ease of interpretation and assessment (Yan, 2014). This

method does not answer for decided the effect of combining all the traits on yield under multiple environmental conditions, while the relationship between each trait and yield can be determined.

A genotype by yield*trait (GY*T) biplot is unprecedented method was proposed by Yan and Frégeau-Reid (2018) to tackle the problem of genotype evaluation on multiple traits. It is based on the following conceptualizations: 1) Yield is the most important trait and all other target traits are important only when combined with high yield, 2) The superiority of a genotype should be judged by its weight based on combining yield with other target traits, rather than the individual traits.

In this approach, trait can be any breeding objective other than yield; it may be an agronomic trait, a grain quality, processing quality, or nutritional quality trait, or a disease resistance. Compared to existing methods, this approach is graphical, objective, effective, and straightforward (Zhou *et al.*, 2018 and Seyni and Abdoua, 2019).

Genotype selection based on multiple traits is a key issue in plant breeding; it has been dependent on setting a subjective weight for each trait in index selection. Also, when trying to improve one trait in breeding programs, the breeder may disable another trait. For this purpose, the genotype by yield*trait (GYT) biplot approach assessment all the traits together and provides more accurate results. Therefore, peanut breeders must distinguish the importance of the traits and their positive or negative association with the crop yield.

The goals of this investigation were using the GT and GYT biplot techniques to study the relationship between different agronomic traits of twenty peanut

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genotypes as well as to select superior genotypes based on multiple traits and observe the advantages of the GYT biplot compared to GT biplot.

MATERIALS AND METHODS

The current study was carried out at Shandwell Agricultural Research Station during the two successive seasons of 2018 and 2019. The yield potential of twenty peanut genotypes was evaluated where the code and origin of genotypes are shown in Table 1. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Plot area was 9.6 m² (4 rows, 4 m long and 60 cm apart). Distance between hills within rows was 15 cm with one plant left per hill after thinning. All agricultural practices were applied according to the recommendations for Shandwell location.

At harvest, ten plants of the middle two rows were taken randomly to determine the yield components as follows:

Plant height (cm) (PH) was measured from the ground level (at the base of the plant) to the top of the highest point including the terminal leaflet using a graduated metre stick, number of branches/plant (NB), Number of pods/plant (NP), 100-pod weight (g) (PW) were measured. Whole plot was harvested and the pods were air dried to calculate seed yield and 100-seed weight (g) (SW), mass of unshelled pods (Pod yield, ardeb/feddan) (PY) and mass of shelled seeds were taken and used to determine the shelling percentage(Sh %). So, shelling percentage was calculated as follows:

$$\text{(Mass of shelled seeds/ Mass of unshelled pods) x 100}$$

And oil percent (O %) was determined according to methods described by AOAC. (2005). Seed oil yield per faddan were calculated by multiplying oil% by seed yield fad⁻¹.

Statistical analysis

Levene test was firstly run as a routine statistical step, prior to the combined analysis to confirm the homogeneity of individual error terms (Levene, 1960). Least significant difference (LSD) test was used to detect the significant differences among the proper items at probability level of 0.05. Data were subjected to a combined analysis of variance for randomized complete block design over the two seasons as outlined by Steel *et al.* (1997).

Yan and Rajcan (2002) used the genotype by trait (GT) biplot, which is an application of the GGE biplot to study the genotype by trait data. Because the traits were measure in different units, the biplot procedure was generated using the standardized values of the trait means.

The adjusted mean values of the traits were used for the analysis of genotype by trait and trait associations. These mean values were standardized to mean zero and unity variance in order to minimize biases due to differences in scales of traits according to the formula suggested by Yan and Frégeau-Reid (2018):

$$P_{ij} = \frac{T_{ij} - T_j}{S_j}$$

P_{ij} is the standardized value of genotype (i) for trait or yield-trait combination (j) in the standardized table, where T_{ij} is the authentic value of genotype (i) for trait or yield-trait collection (j) in the GT or GYT table, (T_j) is the

mean across genotypes for trait or yield-trait combination j, and s_j is the standard deviation for trait or yield-trait combination j.

The GT biplot (Figure 1) was created by plotting the PC1 scores against the PC2 scores for each genotype and each trait resulting from Singular Value Decomposition (SVD) of the standardized GT data. SVD decomposes the GT table into genotype eigenvalues, trait eigenvalues, and singular values:

$$P_{ij} = (d\lambda_1 \alpha \zeta_{i1}) (\lambda_{11} - \alpha \tau_{1j}/d) + (d\lambda_2 \alpha \zeta_{i2}) (\lambda_{21} - \alpha \tau_{2j}/d) + \epsilon_{ij}$$

Where ζ_{i1} and ζ_{i2} are the eigenvalues for PC1 and PC2, respectively, for genotype i; τ_{1j} and τ_{2j} are the eigenvalues for PC1 and PC2, respectively for trait j; and ϵ_{ij} is the residual from fitting the PC1 and PC2 for genotype i on trait j; λ_1 and λ_2 are the singular values for PC1 and PC2, respectively. α is the singular value partitioning factor.

A GYT biplot was generated the same way as a GT biplot except that the term “trait” was replaced by the term “yield*trait” (used interchangeably with the term “yield-trait combination”).

The genotype by yield*trait (GYT) data (Table 4) was obtained as follows: the value for yield*trait combination was obtained by multiplying the pods yield value (Y) with the trait value for each genotype (e.g., Y*PH, Y* NB, Y* NP, Y* PW, Y* SW, Y* Sh % and Y* O %). These values reflect how grain yield and traits content were combined in a genotype. Previous characters which had larger values means more desirable in peanut crop. To rank the tested peanut genotypes, the Superiority Index (weight of selection criteria) was computed for each genotype as the average over the standardized data of yield-trait combination values. Data collected were subjected to excel and subsequently analyses using GENSTAT statistical package 15th edition.

Table 1. The name, pedigree and origin of the studied genotypes

Genotypes	Code	Pedigree	Country
1	G1	Egyptian variety	Egypt
2	G2	Egyptian variety under registration	Egypt
3	G3	From sohag	Egypt
4	G4	From sohag	Egypt
5	G5	From sohag	Egypt
6	G6	Florigiant	U.S.A
7	G7	Shullamit	F.a.w Italy
8	G8	57-422	Senegal
9	G9	R.M.P 12	Upper volta
10	G10	58-344	Senegal
11	G11	Mount Makulu Red	Zambia
12	G12	Faizpur	Icrisat
13	G13	Exotic 3-5	Icrisat
14	G14	N-C-17	U.S.A
15	G15	(Robut33-1Xncac316) x (53-68xRobut33-1) F781	Icrisat
16	G16	Tianhu3	China
17	G17	R.C.m444	Bolivia
18	G18	n.c.17	U.S.A
19	G19	Vigina Bunch	Australia
20	G20	Krapovickas	Argentina

RESULTS AND DISCUSSION

Mean performance

The results of Levene test proved homogeneity of separate error variances for all studied traits that permits to apply combined analysis.

The combined ANOVA revealed insignificant interaction effect (season x genotype) for all investigated traits. When the interaction effect was insignificant, it is meaning that the peanut genotypes had similar attitude in the two growing seasons. In accordance, it is enough to present their combined averages across the two seasons without showing its seasonal averages. It may also mean that the genotypes are fixed, and they are not affected by environmental conditions because they are at the last stage of the breeding program. Based on the abovementioned results, the combined mean values of the traits were presented in Table 2.

The mean values of plant height for peanut genotypes across the two seasons were varied between 34.77 and 40.53 cm., number of branches between 6.50 and 8.37, number of pods between 43.86 and 72.41, weight of 100 pods between 170.80 and 239.70 gm, 100 seed weight between 75.33 and 109.50 gm, shelling % between 59.37 and 76.41, pod yield between 17.00 and 23.68 ardad/feddan and Oil % between 32.16 and 57.76.

Mean values over two seasons showed that genotypes No. 20, 5 and 16 have the tallest plants recording 40.50, 40.53 and 39.83 cm, respectively, while the shortest plants were obtained by genotypes No. 1, 9 and 14 recording 34.77, 35.18 and 35.63 cm, respectively.

There were significant differences among the entries considering number of branches, where the highest values were gained by genotypes No. 13, 20 and 9 recording 8.37, 8.27 and 8.05, respectively while the two genotypes No. 3 and 1 have the lowest values recording 6.50 and 6.57 over the two seasons.

The maximum number of pods was recorded by genotypes No. 17 (72.41), 7 (62.80) and 20 (61.70) while genotypes No. 3, 4 and 8 recorded the lowest values being 43.86, 51.50 and 51.85, respectively.

Genotypes No. 3, 2 and 4 gave the heaviest weight of 100 pods (239.70, 233.50 and 231.30 gm, respectively) as compared to genotypes No. 17, 6 and 20 which recorded the lightest weight of 100 pods (170.80, 180.00 and 188.20

gm, respectively). In the same context, the heaviest weight of 100 seeds was scored by genotypes No. 2, 3 and 4 recording 109.50, 102.17 and 93.83 gm, respectively while genotypes No. 13, 6 and 19 gave the lowest weight of 100 seeds being 75.33, 79.50 and 83.00 gm, respectively.

There were significant differences among the entries considering shelling percentage where genotypes No. 1, 20 and 11 gave the high shelling percentage values being 76.41, 76.24 and 76.24 %, while genotypes No. 3, 4 and 9 recorded the lowest values being 59.37, 60.00 and 62.31% across the two seasons. Gabisa *et al.*, (2017) reported that the shelling percentage is the indication of pod filling efficiency and high shelling percentage values indicate effective pod filling.

The pod yield is the final expression of the many individual physiological processes, which have interacted with the weather and environment during the growth. However, a part of this variation is usually due to the environment and different genetic backgrounds. It is obtained that genotypes No. 17, 7 and 20 produced the heaviest pod yield (23.68, 23.00 and 21.67, respectively Ardad/feddan) While, genotypes No. 3, 6 and 15 have the lowest values of pod yield (17.00, 17.67 and 18.33, respectively Ardad/feddan).

Regarding the Oil %, it is obvious that the genotypes No. 12, 19, and 1 gave the maximum values being 57.76, 56.08, and 55.22 %, respectively without significant differences among them while the minimum values were observed by genotypes No. 4, 15 and 3 being 28.67, 32.16 and 33.76 %, respectively across the two seasons.

It is worth mentioning that the high yielder genotype No. 3 was characterized by high pod weight per plant, weights 100 pods and seeds per plant while high yielder genotype No. 20 occupied the first order for most yield components which are plant height, number of branches per plant, pod yield and shelling percentage (Mohammad *et al.*, 2018 and Tirkey *et al.*, 2018).

From the current results, it is concluded that the used material genotypes could be good sources of for genetic studies and breeding programmes. These results agreed with those obtained by Makweti (2018), Samaha *et al.*, (2019) and Mahmoud *et al.*, (2020).

Table 2. Mean values of pod yield and its related characters across two seasons.

Genotypes	Pod yield and its related characters							
	PH	NB	NP	PW	SW	Sh %	PY	Oil %
G1	34.77	6.57	56.68	192.8	83.83	76.41	19.33	55.22
G2	37.62	7.25	49.12	233.50	109.50	76.15	22.04	48.97
G3	37.85	6.50	43.86	239.70	102.17	59.37	17.00	33.76
G4	38.43	7.40	51.50	231.30	93.83	60.00	21.17	28.67
G5	40.53	7.10	53.59	205.30	90.00	75.15	19.00	51.34
G6	35.58	7.22	58.10	180.00	79.50	63.21	17.67	55.07
G7	37.37	7.38	62.80	211.70	86.17	65.65	23.00	35.87
G8	39.03	7.73	51.85	203.00	92.00	71.94	20.17	51.85
G9	35.18	8.05	54.09	194.80	83.33	62.31	19.33	51.52
G10	38.38	7.32	56.37	206.20	86.67	69.32	21.83	48.68
G11	37.15	7.73	52.89	195.80	90.67	76.24	18.67	47.64
G12	38.98	7.42	51.97	216.70	94.83	69.50	20.67	57.76
G13	36.65	8.37	59.50	179.20	75.33	71.52	19.00	52.87
G14	35.63	7.25	52.38	218.70	91.00	74.28	19.17	52.55
G15	37.63	7.52	54.03	191.70	90.17	68.28	18.33	32.16
G16	39.83	7.65	60.69	196.50	95.50	67.15	22.67	38.31
G17	39.73	7.23	72.41	170.80	89.67	68.34	23.68	46.52
G18	37.13	7.07	53.97	202.50	89.33	73.70	20.50	49.85
G19	36.63	7.57	58.81	212.70	83.00	66.13	20.83	56.08
G20	40.50	8.27	61.70	188.20	86.17	76.33	21.67	47.32
Mean	37.73	7.43	55.82	203.56	89.63	69.55	20.29	47.10
L.S.D _{0.05%}	2.63	0.83	4.53	17.96	10.587	7.43	3.43	0.01

Abbreviations: PH: Plant height (cm), NB: Number of branches/plant, NP: Number of pods /plant, PW: Pod weight per plant (g), SW: 100-pod weight (g), Sh %: shelling percentage PY: Pod yield (ardab/fed) and O %: Oil percent.

GT Biplot graph

1. Genotype comparison (Polygon "which-won-where"):

Yan and Rajcan (2002) and Yan and Tinker (2005) reported that, the biplot graphs can be used to compare genotypes on the basis of multiple traits (pod yield and its related characters) and to identify genotypes that are particularly good in certain part or side and therefore can be nominee for selection and hybridization in peanut breeding program.

The polygon view of a biplot is the best way to visualize the relationship patterns between genotypes and traits (Yan and Kang, 2003).

The biplot graph (Fig. 1) presents the relationship among the aimed peanut genotypes using the pod yield and its related attributes. The GT biplot of the mean performance of the peanut data explained 58.97 % of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 34.82% and 24.15%, respectively.

GT biplot generated and shown in (Figure 1) that name is "which-won-where". Figure dividing with thick axes from the centre and separating each zone with two thick lines, the sectors obtained were indicated by correlative numbers (1, 2, 3, etc). The genotypes and traits mightily related when they are located in the same sector, (Yan and Tinker, 2006; Kendal *et al.*, 2016 and Kendal, 2019). These lines divided the genotypes-traits combinations into 4 of 7 sectors. Sector without traits indicate that the genotypes falling in these sectors including the vertex genotype, for instance genotypes No. 6 (vertex genotype), 1, 9 and 11 had low values for all the traits studied. Also, the genotype placed on a vertex is the most performers for the trait placed within the corresponding sector (Yan and Fréreau-Reid, 2018).

The perpendicular lines to the polygon sides facilitate comparison between neighbouring vertex genotypes. It is obvious that genotype No.17 recorded high values of plant height (PH), Number of pods (NP), Number of branches (NB) and pod yield (PY). In addition, genotypes No. 20, 16, and 7 located in the same sector and reflected similar behaviour toward the same traits. It is noted that the points of these genotypes and traits placed into one sector and the angles among them were acute reflecting the positive associations among them.

The vertex genotype No.13 was the best genotype in terms of shelling percentage Sh % and oil percentage O%. On the other hand, the three genotypes No. 6, 1 and 9 recorded the lowest values of PH, NB, NP and PY because obtuse angles were found between these genotypes and these characters.

Because the genotypes No. 5, 8, 10, 12, 15, 18 and 19 were spread near the original point, they had moderate values of most studied traits. Finally, the four genotypes No. 2, 3, 4 and 14 were recorded highest values for 100-pod weight (PW) and 100-seed weight (SW).

Consequently, the distance between the genotype and the biplot origin is the vector length of a genotype which measures the genotype's peculiarity (i.e. how it differs from an average genotype). Genotypes with long vectors are those that have extreme levels for one or more traits. Such genotypes could be either selected for further

trials or for parent's instance genotypes No.3, 16, 17, and 13.

The genotype by trait (GT) biplot has been utilized to study trait relationships and genotype evaluation in several crop species. Similar results were reported for soybean (Yan and Rajcan, 2002 and Kocaturk *et al.*, 2019), bean (Hirpa *et al.*, 2013), cowpea (Oladejo *et al.*, 2011), durum and bread wheat (Akcura, 2011 and Gab Alla *et al.*, 2018).

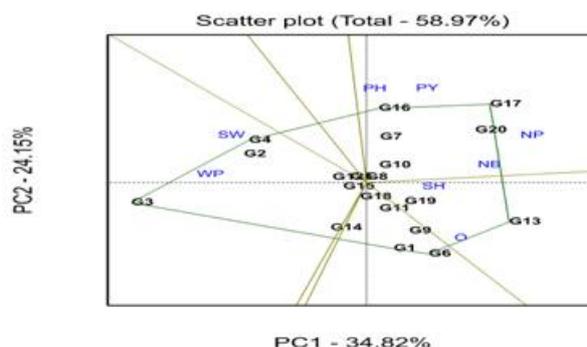


Fig. 1. Polygon view which-won-where (GT) biplot showing which genotype had the highest values for which traits for 20 peanut genotypes across two seasons.

The traits codes are PH: Plant height, NB: Number of branches, NP: number of pods, 100WP: 100-pod weight, 100SW: 100-seed weight, Sh%: shelling percentage and (O %): oil percentage.

2. Trait relations (vector graph):

The evaluation genotypes based on multiple traits and identifying those are superior in the desired variables this is essential attention in method Genotype by trait and these can be used as parents in breeding programs or even as possible commercial genotypes. A quick and practical visualization of the genetic correlation between traits is also provided by this analysis. Yan and Tinker (2006) and Oral *et al.*, (2018) reported the less important traits can be detected and identified as the most suitable to indirectly select a favourable and complex trait such as yield.

The method for interpreting a GT biplot was described by Yan and Rajcan (2002) and Yan and Tinker (2006) as a graph bi-directionally which can be explained in different ways. The correlation between two properties it is expressed by the cosine of the angle between the vectors. Thus, when angle smaller than 90° indicates a positive correlation, an angle greater than 90° indicates a negative correlation, and an angle of 90° indicates that there is not any correlation between the two traits. Also, the vector length of a trait indicates how well the trait is represented in the biplot; a relatively short vector indicates that the variation of the trait across genotypes is either small or not well represented in the biplot because of its weak or absence of correlation with other traits.

The averages values across two seasons presented in Table 2 were used to generate GT biplot and visualizing Figure 2.

The following observations can be made about Figure 2 according to these items described in the GT biplot technique. A strong positive association between Pod yield, plant height (PH), Number of pods (NP), Number of branches (NB) and Shelling percentage (Sh) as indicated by the acute angles (< 90°) that mean

dependency of these characters on each other. The observed positive associations of previous characters with pod yield were in conformity with the results of Amarsinghe *et al.*, (2016), Afify *et al.*, (2019) and Mahmoud *et al.*, (2020).

However, Shelling percentage (Sh) indication of pod filling efficiency and high shelling percentage values indicate effective pod filling. 100-seed weight (SW) recorded highly positive association with 100-pod weight (WP) as shown by acute angles ($< 90^\circ$) between their vectors. Similar findings were reported by Kadam *et al.*, (2018) and Mohammad *et al.*, (2018).

On the other hand, the strong negative associations between 100-seed weight (SW) and 100-pod weight (WP) with the traits of number of pods (NP), number of branches (NB), shelling percentage (Sh) and Oil percent (O %) were shown by the large obtuse angles ($> 90^\circ$) among their vectors. Near zero correlation between pod yield and each of 100-seed weight (SW) and Oil percent (O %) as indicated by the near perpendicular vectors among them ($r = \cos 90 = 0$).

Safari *et al.*, (2013), Ajay *et al.*, (2017) and Makweti (2018) observed similar association with yield contributing characters. The largest variation explained by the biplot from the abovementioned results, came from pod yield, plant height, 100-seed weight, 100-pod weight, number of pods and Oil percent, as indicated by the relative length of their vectors. It is noted that the interrelationships among these traits that are most relevant to peanut breeding. Safari *et al.*, (2013), Ajay *et al.*, (2012 and 2017) and Makweti (2018) had used GT bi-plot to identify superior cultivars after analyzing various yield components in groundnut that reflected 52-65% of the total variation of the data among various peanut cultivars. They attributed this low proportion of variation to complex relationships among different traits.

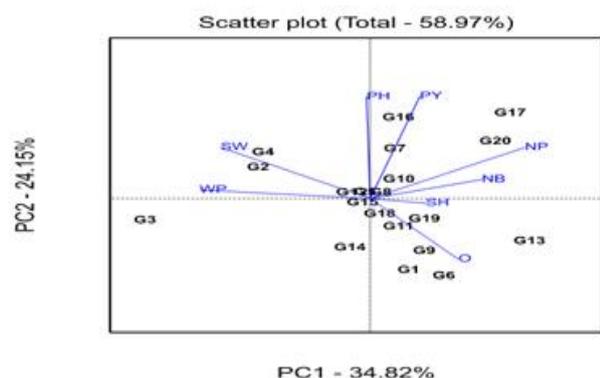


Figure 2. Vector view genotype by trait biplot, showing the interrelationship among measured traits for 20 peanut genotypes across two seasons.

The traits codes are PH: Plant height, NB: Number of branches, NP: number of pods, 100WP: 100-pod weight, 100SW: 100-seed weight, Sh%: shelling percentage and (O %): oil percentage.

Genotype by yield*trait (GYT) biplot

1. Genotype comparison (Polygon "which-won-where"):

Yan and Frégeau-Reid (2018) proposed GYT biplot to tackle the problem of genotype evaluation on multiple traits. It is depending on the following concepts, 1) Yield is the most important trait and all other target traits are

important only when combined with high yield. 2) The superiority of a genotype should be judged by its levels in combining yield with other target traits, rather than by its levels in individual traits. A GYT biplot was generated the same way as a GT biplot except that the term "trait" was replaced by the term 'yield*trait' (used interchangeably with the term "yield-trait combination"). This technique is used to distinguish genotypes according to their features over yield-trait combinations and show trait profiles.

Therefore, the GYT biplot technique was used to determine when the value of a trait of any genotype was low and grain yield was high or vice versa and whether the results were affected by the combination or if there was any change in their ranking. As a result, when trait and yield values entered the combination, data changed as did cultivar ranking. Therefore, a greater value is always desirable in the GYT Table.

In the GYT, data in each column consist of a yield-trait combination. The standardized GYT values and superiority index of 20 peanut genotypes across two seasons are shown in Tables 3 and 4.

For example, Y*Ph is the combined level of pod yield and plant heights, which is a measure of how pod yield and plant heights content were combined in a genotype. Either low pod yield or low plant heights content would affect this combined value and the genotype will thereby be judged unfavourably. The same is true for other yield-trait combinations.

The diagrams have been explained previously in detail in the GT part, so we will provide the results directly, Polygon "which-won-where" (Fig. 3) presents the relationship among the aimed peanut genotypes using the pod yield-trait combinations across the two growing seasons. The GYT biplot of the mean performance of pod yield and its components data explained 81.09% of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 63.71% and 17.38 %, respectively.

The polygon was constructed by connecting the markers of the genotypes that are farthest away from the biplot origin so that all other genotypes are contained in the polygon. For each polygon side, a line was drawn to start from the biplot origin and to be perpendicular to the polygon side. These lines divided the yield-trait combinations into 5 sectors out of which 3 sectors are without traits. Sector without traits indicate that the genotypes falling in these sectors including the vertex genotype, had low values for all the traits studied. These genotypes were G1, G3, G5, G6, G9, G11, G13, G14 and G15.

It is obvious that genotype No.17 (vertex genotype) had wins for pod yield combining with each of plant height (Y*Ph), number of pods (Y*NP), number of branches (Y*NB), shelling percentage (Y*Sh) and oil percentage (Y*O). As well as, genotypes 10, 12, and 20 located in the same sector and reflected similar behaviour toward the same pod yield-trait combinations. That it is meaning a superior genotype for high pod yield and its attributes with respect to the value of superiority index (Table 4), genotype No. 17 ranked as the first one among the tested genotypes which confirmed the previous results obtained by GY*T biplot graph. According to superiority index

(Table 4), the abovementioned genotypes (G10, G12 and G20) were ranked as 7, 8 and 5, respectively.

In the second sector G7 and G16 are existing with Y*100PW and Y*100SW gathering, while vertex genotype 'G2' is the winning cultivar for the combination located in same sector. Furthermore, genotypes 8, 14, 18 and 19 located closer to the centre of the axis had values close to the grand mean of the most studied pod yield-trait combinations (Fig. 3). The superiority index ranks genotypes with the means overall traits (Figure 3, Table 4); elevated values of SI (1.24) indicate the best genotype (G17) and low values of SI (-1.40) indicate a weak genotype (G6). Several researchers reported similar results to the present finding on different crop species, such as soybean (Malek *et al.*, 2014), bean (Payasi, 2015), oats (Yan and Frégeau-Reid, 2018), Sesamum (Seyni and Abdoua, 2019), bread wheat (Abd-ElHamid *et al.*, 2019), durum wheat (Kendal, 2019) and Lance *et al.* (2020).

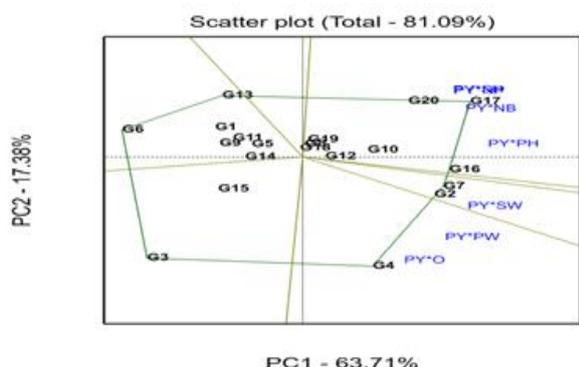


Figure 3. The "which-won-where" view of the genotype by yield*trait (GYT) biplot to highlight genotypes with outstanding profiles. [The traits codes are Y*PH: Plant height, Y*NB: Number of branches, Y*NP: number of pods Y*100WP: 100-pod weight, Y*100SW: 100-seed weight, Y*Sh%: shelling percentage and (Y*O): oil percentage.

2.Trait relations (vector graph):

Graph can be bi-directionally interpreted in different ways (Yan and Rajcan, 2002; Yan and Tinker, 2006; Dogan *et al.*, 2016). The relationships and among pod yield combining in Figure 4 are visualized.

Figure 4 showed that all pod yield-trait combinations head for to correlate positively with each other because they have the yield component, shown by the acute angle represent between their vectors. This is an important priority of the GYT biplot technique (Fig. 4) compared to the GT biplot (Fig. 2). Based on Fig. 4, genotypes have the chance to be ranked in a more meaningful way.

However, the relationships between the two traits in the GT biplot technique (Fig. 2) are not the same as for GYT (Fig. 4). For example, there is strong negative associations between each of 100-seed weight (SW) and 100-pod weight (WP) with traits of number of pods (NP), number of branches (NB), shelling percentage (Sh) and Oil percent (O %) (Fig.2). On the other hand, the GYT biplot technique appeared non-same relationship.

In groundnut, genotypes are only preferred by farmers when they have high pod yield: however, high

yield has been affected by combining many traits. Thus, the GYT biplot presented breeders the opportunity to estimate genotypes and identify both superior genotypes and the superiority index. The GYT methodology appears all the factors determining the effect of each trait that affects high efficiency used by breeders.

If the varieties are registered with a selection based on combining traits, with yield, they will then be quite stable in terms of all traits and yield for similar environments. For this purpose, the GYT biplot has been recently developed and used by researchers to evaluate the values obtained from combining multiple traits with yield and multiple environments in breeding studies. The GYT biplot approach has been reported as a comprehensive and effective method; it classifies genotypes according to their levels in the combination with target characteristics and graphically ranks genotypes for their strengths, weaknesses, and in different crops (Yan and Frégeau-Reid, 2018).

Finally, the GT biplot technique was drawn Figures (1 and 2) using the data in Table 2, while the GYT biplot technique was applied Figures (3 and 4) using the data in Table 3. The peanut industries demand peanut products that have the best processing properties, while farmers supplicate for highly productive and high quality varieties. As in other groundnut products, it is very difficult to identify both high yield and high quality varieties, and this situation becomes more complicated when different environmental problems are combined. These complex problems can be solved by using the GYT biplot.

The examination of genotypes depended on the SI and GYT combination; it is showed that poor and strong cultivars can be determined by GYT and that this technique (Figures 3 and 4) is better than the GT biplot (Figures 1 and 2). On the other hand, in the GTY biplot, genotypes No. 17 and 20 are stable for all traits and genotypes No. 2 and 16 are superior for quality traits, which are 100-seed weight (SW) and 100-pod weight (WP). Therefore, this investigation found that the GYT biplot technique is a convenient method to determine the most suitable genotypes for all traits in peanut genotypes. Yan and Frégeau-Reid (2018), (Seyni and Abdoua, 2019), (Kendal 2019) and (Lance *et al.*, 2020) reported similar results to the present findings on different and other crop species.

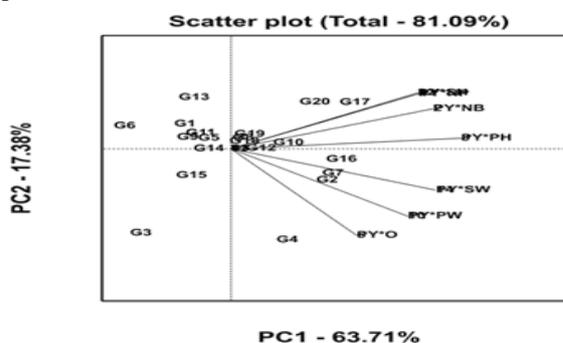


Figure 4. Relationship of genotype × yield × trait (GYT) biplot across two seasons

The traits codes are Y*PH: Plant height, Y*NB: Number of branches, Y*NP: number of pods Y*100WP: 100-pod weight, Y*100S W: 100-seed weight, Y*Sh%: shelling percentage and (Y*O): oil percentage.

Table 3. Genotype by yield*trait (GYT) data for 20 Peanut genotypes across two seasons

Genotypes	Y*Ph	Y*NB	Y*NP	Y*100PW	Y*100SW	Y*Sh	Y*O
G1	672.10	127.00	1095.62	3726.82	1620.43	1477.01	1067.40
G2	829.14	159.8	1082.60	5146.34	2413.38	1678.35	1079.30
G3	643.45	110.5	745.62	4074.9	1736.89	1009.29	573.92
G4	813.56	156.66	1090.26	4896.62	1986.38	1270.2	606.94
G5	770.07	134.9	1018.2	3900.70	1710.00	1427.85	975.46
G6	628.70	127.58	1026.63	3180.60	1404.77	1116.92	973.09
G7	859.51	169.74	1444.4	4869.10	1981.91	1509.95	825.01
G8	787.24	155.91	1045.81	4094.51	1855.64	1451.03	1045.81
G9	680.03	155.61	1045.56	3765.48	1610.77	1204.45	995.88
G10	837.84	159.80	1230.56	4501.35	1892.01	1513.26	1062.68
G11	693.59	144.32	987.46	3655.59	1692.81	1423.40	889.44
G12	805.72	153.37	1074.22	4479.19	1960.14	1436.57	1193.90
G13	696.35	159.03	1130.50	3405.00	1431.27	1358.88	1004.53
G14	683.03	138.98	1004.12	4192.48	1744.47	1423.95	1007.38
G15	689.76	137.84	990.37	3513.86	1652.82	1251.57	589.49
G16	902.95	173.43	1375.84	4454.66	2164.99	1522.29	868.49
G17	940.81	171.21	1714.67	4044.54	2123.39	1618.29	1101.59
G18	761.17	144.94	1106.39	4151.25	1831.27	1510.85	1021.93
G19	763.00	157.68	1225.01	4430.54	1728.89	1377.49	1168.15
G20	877.64	179.21	1337.04	4078.29	1867.30	1654.07	1025.42
Mean	766.78	150.87	1138.54	4128.08	1820.48	1411.78	953.79
SD	90.86	17.51	206.62	514.07	243.85	172.13	180.29

The trait abbreviations are: Ph: Plant height; NB: Number of branches; NP: Number of pods; 100WP: Weight of 100 Pods; 100 SW: Weight of 100 Seed; Sh: Shelling percent; O: Oil Percent; Y Pod yield. SD: Standard deviation.

Table 4. Estimates of standardized yield*trait (GYT) data and superiority index for the genotypes across two seasons

Genotypes	Y*PH	Y*NB	Y*NP	Y*100WP	Y*100SW	Y*Sh%	Y*OIL	Mean superiority index	Ranking
G1	-1.04	-1.36	-0.21	-0.78	-0.82	0.38	-0.88	-0.67	18
G2	0.69	0.51	-0.27	1.98	2.43	1.55	0.01	0.99	4
G3	-1.36	-2.31	-1.90	-0.10	-0.34	-2.34	0.49	-1.12	19
G4	0.51	0.33	-0.23	1.50	0.68	-0.82	2.59	0.65	6
G5	0.04	-0.91	-0.58	-0.44	-0.45	0.09	-0.70	-0.42	12
G6	-1.52	-1.33	-0.54	-1.84	-1.70	-1.71	-1.14	-1.40	20
G7	1.02	1.08	1.48	1.44	0.66	0.57	1.72	1.14	2
G8	0.23	0.29	-0.45	-0.07	0.14	0.23	-0.53	-0.02	19
G9	-0.95	0.27	-0.45	-0.71	-0.86	-1.20	-0.66	-0.65	17
G10	0.78	0.51	0.45	0.73	0.29	0.59	0.00	0.48	7
G11	-0.81	-0.37	-0.73	-0.92	-0.52	0.07	-0.51	-0.54	14
G12	0.43	0.14	-0.31	0.68	0.57	0.14	-0.81	0.12	8
G13	-0.78	0.47	-0.04	-1.41	-1.60	-0.31	-0.80	-0.64	16
G14	-0.92	-0.68	-0.65	0.13	-0.31	0.07	-0.75	-0.45	13
G15	-0.85	-0.74	-0.72	-1.19	-0.69	-0.93	1.08	-0.58	15
G16	1.50	1.29	1.15	0.64	1.41	0.64	1.28	1.13	3
G17	1.92	1.16	2.79	-0.16	1.24	1.20	0.54	1.24	1
G18	-0.06	-0.34	-0.16	0.05	0.04	0.58	-0.33	-0.03	11
G19	-0.04	0.39	0.42	0.59	-0.38	-0.20	-0.69	0.01	9
G20	1.22	1.62	0.96	-0.10	0.19	1.41	0.08	0.77	5
Mean	0	0	0	0	0	0	0	0	0
SD	1	1	1	1	1	1	1	1	1

The trait abbreviations are: PH: Plant height; NB: Number of branches; NP: Number of pods; 100WP: Weight of 100 Pods; 100 SW: Weight of 100 seed; Sh: Shelling percent; O: Oil Percent; Y: Pod yield. SD: standard deviation.

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العرض البياني لبعض التراكيب الوراثية لل فول السوداني بمقارنة نموذجين من تحليل المحاور الثنائية
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أجريت هذه الدراسة بمحطة البحوث الزراعية بشندويل خلال موسمي 2018 و 2019 لتقييم الأداء المحصولي لعدد 20 تركيب وراثي من محصول الفول السوداني. تم استخدام تقنية الأشكال البيانية لطريقة المحاور الثنائية باستخدام كل من أسلوب (التراكيب الوراثية – الصفات) و (التراكيب الوراثية والمحصول – الصفات) وذلك للحصول على معلومات تفيد في إنتخاب أفضل التراكيب الوراثية وكذلك في دراسة العلاقات المتداخلة بين الصفات تحت الدراسة . أظهرت النتائج أن طريقة المحاور الثنائية باستخدام أسلوب (التراكيب الوراثية والمحصول – الصفات) كانت أكثر نجاحا وفعالية ووضوحا في تحديد أفضل الأصناف ومعرفة العلاقات بين المحصول ومكوناته مقارنة بطريقة المحاور الثنائية (التراكيب الوراثية – الصفات). تم أيضا ترتيب التراكيب الوراثية باستخدام معامل التفوق والذي يعتمد في نفس الوقت على كل من المحصول وباقي الصفات بناءا على طريقة المحاور الثنائية (التراكيب الوراثية والمحصول – الصفات) اتضح من نتائج هذه الطريقة ان التراكيب الوراثية رقم 7،16،17 هم أفضل التراكيب الوراثية من ناحية المحصول ومكوناته.