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Sequential Path Analysis for Determining the Interrelationships between Yield and its Components in Peanut

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THE CURRENT work was carried out at the Agriculture Research Station of East Al-Eweinat, New Valley Governorate to evaluate the yield potential of 16 peanut genotypes during 2016 and 2017 growing seasons. The used experimental design was a randomized complete block design with three replicates. Correlation coefficients were computed between pod yields and its related attributes as well as normal and sequential path analysis models were automated to obtain information on the direct and indirect effects of important traits affecting pod yields for using them as selection criteria in future peanut breeding programs. Results showed that genotypes 7, 11 and 16 produced the heaviest pod yields while genotypes 13 and 15 recorded the lowest pod yields. Concerning the normal path analysis model, several undesirable symptoms were obtained indicating the presence of multicollinearity problem. Subsequently, the poor estimators of normal path analysis model, as a result of multicollinearity, enough to reject the normal form of path analysis. Statistically, more precise results were obtained using the sequential path analysis model. Results revealed that the pod yields depended primarily upon pod weight per plant and number of pods per plant as first-order variables accounted for nearly 98% of the variation in pod yields. The maximum positive direct effects were obtained by pods weight per plant (0.91) followed by number of pods per plant (0.14) indicting that the indirect selection for pod yields through these traits would be effective for peanut improvement. The second-order path analysis showed that seeds weight per plant had the considerable positive direct and indirect effects toward each of number of pods per plant and pods weight per plant. In fact, the sequential path analysis gave a somewhat different picture from what the normal model path analysis did.

Keywords: Peanut, Selection criterion, Sequential path analysis.

Introduction

Peanut *(Arachis hypogaea* L.) is an important oil, food and feed crop all over the world. It is cultivated in over 100 countries, with over 95 % of cultivated area in Asia and Africa. The peanut seeds are directly consumed as raw or crushed for edible and industrial oil uses (Murali & Janila, 2017). The area cultivated with peanut in Egypt during 2016 season was about 58,000 hectare (feddan= 0.42 hectare) (FAO, 2016). Lately, this crop has been given great attention due to its proportionality for growth in the newly reclaimed sandy areas in Egypt. New reclaimed areas in Egypt are mostly sandy soils and usually deficient in organic matter and poor in plant nutrients.

Stamatov (2015) proved that the yield of peanuts is a complex polygenic characteristic and its components are of strong relations among

them. Direct selection for pod yield would not be a reliable approach owing to its quantitative inheritance that constituted by number of yield attributes. Plant yield components develop sequentially with developing components under the control of earlier-developing components (Simane et al., 1993; Agrama, 1996). There may be difficulties in interpretation of the actual contribution of each variable because the effects are mixed or confounded because of collinearity.

Clear Information on contribution of each component attributes that influence the complex trait would come out through the study of correlation coefficient and causation of path coefficient analysis (Ashutosh et al., 2016). A true picture of the correlation coefficient between the yield attributes and pod yield and information on relative importance of direct and indirect effects of these attributes on pod yield is the pre-requisite for crop improvement to attain the goal of augmented production by increasing the yield potential of crop (Shankar et al., 2018).

Path analysis is an integral part of structural equation modeling has proven to be popular in recent decades for the study of association in quantitative traits as illustrated by Dewey & Lu (1959). Among path analysis models, it can distinguish two types: (i) Simple models, in which all traits except for the dependent one are set up at the same ontological level, (ii) Complex models, in which traits are set up at different levels.

Dewey & Lu (1959) introduced simple path analysis models which continue for some time but now the most popular approach appear to be the complex path analysis models. A simple reason for this change is that complex models can be representative of biological processes in complex biological systems. Because of the way they are formulated, complex models are also referred to as sequential models where they reflect sequential development of crop.

Sequential models of path analysis aim to help researchers to understand relations among traits that develop in subsequent stages during plant ontogenesis. As with any statistical model, such sequential models should be representative of biological processes that they are built to analyze (Kozak & Azevedo, 2014). The assessment of the genetic diversity in crop species is of interest for the conservation of genetic resources, broadening of the genetic base and practical applications in breeding programs. In applied plant breeding, success of the programs may be anticipated to its genetic variability of different selection method is known. The correlation and path analysis provides information on genetic association of yield and different yield contributing characters, which in turn are useful in developing breeding strategies (Jadhav, 2017).

Kozak & Azevedo (2011) discussed how sequential models should be interpreted, and built in terms of model formulation. These models must reflect the biological processes they are to represent. Thus, model formulation obviously affects whether an interpretation is biologically correct or not.

Garcia Del Moral et al. (1991, 2003 and 2005) indicated that Path analyses were very useful in clarifying the effects of yield components and phenology on grain yield formation, which were not accurately reflected by simple correlation analyses, thus providing helpful information for breeders.

If one aims to form a sequential path analysis model, one assumes that some traits develop earlier in ontogeny and affect other traits that develop later. In Egypt, on peanut, no references were found to use sequential path for exploring the interrelationships among yield components. Consequently, the present investigation was carried out to: 1- obtain information on the association of pod yields and its component traits, interrelationships among themselves and to assess their relative importance. The second goal is, to identify the direct and indirect effects of important plant traits on pod yields for using them as selection criteria in future breeding programmers.

Materials and Methods

Experimental design and plant materials
The materials of the present study comprised 16 peanut genotypes grown in a randomized complete block design with three replications during 2016 and 2017 growing seasons at the Agriculture Research Station of East Al-Eweinat, New Valley Governorate. The aimed genotypes were selected as promising items from the local breeding program of peanut. The name and pedigree of the studied genotypes are listed in Table 1. Peanut seeds (2-3 seeds)

were deposited in rows 4m length, 60cm width and 20cm spacing between plants within rows and then the plants were thinned after complete emergence (one week from planting) to one plant/hill. The recommended doses of chemical fertilizers NPK were applied. Before cultivation, peanut seeds were treated with *Bradyrhizobium* spp. to enhance the number of bacterial nodules/plant. Sprinkler irrigation was used for applied water management during experiment periods.

Before cultivation, soil samples at 0-30cm depth were collected during the two study seasons. The mechanical and chemical analyses of the experimental soil were applied according to Jackson (1973) and Chapman & Pratt (1978). Details of soil properties of the experiment site during the two seasons of the study are shown in Table 2.

All required cultural practices were followed for raising good healthy crop. After maturity, a random sample of 10 guarded plants from each genotype in each replication were taken to determine the characters of plant height (PH) (cm), number of branches per plant (NOB), number of pods per plant (NOP), number of seeds per plant (NOS), 100-seed weight (100 SW) (g), 100-pod weight (100 PW) (g), seeds weight per plant (SW) (g), pods weight per plant (PW) (g), pod yields (PY) (ardab/fed), and harvest index% (HI) that was calculated as the ratio between 100-seed weight and 100-pod weight. At harvest, each experimental unit was manually harvested, weighted and converted to the unit of ardab per feddan (ardab = 75kg and one feddan = 4200m²).

Statistical analysis

Firstly the datasets were tested for homogeneity of individual error terms by Levene test as proposed by Levene (1960). Regular analysis of variance of Randomized Complete Block Design (RCBD) was run as outlined by Gomez & Gomez (1984). Simple correlation coefficients between various pairs of the studied characters were computed according to Gomez & Gomez (1984).

TABLE 1. Genotype Code, pedigree and Origin of the studied groundnut genotypes .

Genotype code	Pedigree	Origin
1	Hybrid 2 Family 1 Int (Florigiant x TG 16)F10 X (Grogory)	Malawi ,U.S.A
2	Hybrid 1 Family 1(GA 186-28)X Int (Florigiant x TG 16)F10	Malawi
3	Hybrid 2 Family 2 Int (Florigiant x TG 16)F10 X (Grogory)	Malawi ,U.S.A
4	Hybrid 3 Family 1 Int (Florigiant x TG 16)F10 X L0cal (Giza 6)	Malawi ,Egypt
5	ICGM # 340	Malawi
6	Hybrid 1 Family 2 Int (Florigiant x TG 16)F10 X (GA 186-28)	Malawi ,U.S.A
7	Span Cross	U.S.A
8	Local genotype	Egypt
9	Hybrid 3 Family 2 Int (Florigiant x TG 16)F10 X L0cal (Giza 6)	Malawi ,Egypt
Giza 6	Giza 6 Varity	Egypt
11	Int (Florigiant x TG 16)F10	Malawi
12	Hybrid 3 Int (Florissant) X (Giza 6) L0cal	U.S.A ,Egypt
13	Local genotype	Egypt
14	Mutation 28 (Giza 6 Radiation)10 Kr	Egypt
15	Hybrid 1 Int (Florissant) X (GA 186-28)	U.S.A, U.S.A
16	Hybrid 2 Int (Florissant) X (Grogory)	U.S.A, U.S.A

According to the data of the Egyptian Oil Crops Research Department, ARC.

TABLE 2. Some physical and chemical properties of representative soil samples of the experimental site before sowing for 2016 and 2017 seasons.

Soil property	Seasons	
	2016	2017
Sand (%)	73.32	72.45
Silt (%)	18.46	19.13
Clay (%)	8.22	8.42
Texture grade	Sandy loam	Sandy loam
EC (1:1 extract) (ds m^{-1})	1.87	1.92
pH (1:1 suspension)	7.62	7.54
Total CaCO$_3$ (%)	8.65	8.72
Organic matter (%)	0.057	0.063

Sequential models of path analysis aim to help researchers to understand relations among traits that developing in subsequent stages during plant ontogenesis as proposed by Agrama (1996).

In the current investigation, sequential path analysis was implemented to organize the explanatory variables into first, second order paths (Fig. 1) on the basis of their respective contributions to total variation of pod yields (PY) as a responsible variable. The statistical analysis and its responding path diagram of sequential path analysis were automated using R studio statistical software version 3.6.1. According to the proposed model, the explanatory variables were grouped to overcome the multicollinearity phenomenon expressed as minimum variance inflation factor (VIF) (lower than 10) and to record maximum direct effects.

Pods weight (PW) and number of pods per plant (NOP) was considered the first-order explanatory variables among various yield characters study (Fig. 1). Consecutively, the procedure was again performed separately taking the independent variables (PW and NOP) as dependent variables to find out second-order variables for these two response variables, which shall be, consequently, third-order variables regarding pod yields. The conventional path analysis model allows studying the relationships between all studied traits (yield components as explanatory variables) and the pod yields as responsible variable as proposed by Dewey & Lu (1959).

Results and Discussion

The results of Levene test proved homogeneity of separate error variances for all studied traits

that permits to apply combined analysis.

Mean performance

Results of the combined analysis of variance indicated that there were significant differences between the two seasons and among the aimed peanut genotypes for all studied characters as shown in - 3. Regarding the interaction effect between seasons and genotypes, significant and highly significant (0.05 probability level) differences were obtained for all traits except for number of pods per plant (NOP), number of seeds per plant (NOS), seeds weight (SW), 100-pod weight (100 PW) and harvest index (HI). When the interaction effect between genotypes and seasons was insignificant, it is meaning that the peanut genotypes had similar behavior in the two growing seasons. In accordance, it is enough to present the combined averages across the two seasons without showing its seasonal averages. On the contrary, since the genotype x season interactions was significant, it is indicated that peanut genotypes were differently responded to the environmental conditions suggesting the importance of assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment. In this case, it the mean values should be displayed presented separately for the two seasons in addition to their combined data.

Results indicated that the 2nd season had higher mean values for all traits compared to the 1st season, except for 100 - pods weight representing seasonal differences. The 2nd season was characterized by optimum environmental conditions during the vegetative growth which was reflected on peanut yield and related characters.

Results in Table 3 appeared the mean performance across the two seasons. It is revealed that genotypes 4, 6, 3, and 14 being (69.17, 67.33, 66.50 and 66.08cm, respectively) had the tallest plants while the shortest plants were obtained by genotypes 5 and 10 being (54 and 56.83cm). Regarding the number of branches per plant, it is obvious that the genotypes 3, Giza 6, 11 and 12 gave the maximum values (9.07, 8.17, 8.70 and 8.87, respectively) without significant differences among them while the minimum values were observed by genotypes 9 and 15 being (5.77 and 5.60).

TABLE 3. Mean values of pod yields and its attributes for sixteen peanut genotypes as affected by seasons, genotypes and their interaction effect.

Characters	PH	NOB	NOP	PW	NOS	SW	100 SW	100 PW	HI	PY
Seasons (S)										
2016/17	61.15	6.50	26.25	48.54	31.85	32.91	103.59	192.73	55.03	14.58
2017/18	63.88	7.96	31.34	53.21	37.08	39.81	107.86	172.59	75.51	16.26
F-test	*	*	*	*	**	**	*	**	**	*
Genotypes (G)										
1	63.50	7.90	30.44	55.31	39.25	42.19	107.55	179.41	66.18	16.59
2	59.67	7.27	26.17	45.30	31.33	33.83	108.58	166.33	75.16	14.36
3	66.50	9.07	31.83	53.17	32.23	33.18	100.81	169.21	60.13	16.28
4	69.17	7.80	30.68	48.74	36.70	35.66	95.38	164.96	63.52	14.81
5	54.00	6.73	34.25	53.63	40.78	41.61	104.38	174.18	70.55	16.26
6	67.33	6.73	32.92	52.22	42.57	42.33	100.99	168.93	71.25	15.81
7	58.33	5.93	31.30	56.56	36.05	38.42	106.54	182.72	60.40	16.95
8	65.50	5.80	27.58	53.34	28.05	31.67	112.69	199.79	57.02	16.00
9	63.50	5.77	25.87	46.09	28.57	31.50	109.82	181.66	63.38	13.99
Giza 6	56.83	8.17	29.27	54.22	32.32	35.67	110.04	181.31	64.64	16.43
11	59.33	8.70	33.67	55.61	42.92	43.36	100.63	163.76	69.74	16.85
12	65.50	8.87	26.33	51.24	30.43	35.60	114.29	195.56	64.61	15.37
13	60.25	7.18	22.37	44.69	31.23	34.35	112.37	203.35	70.13	13.41
14	66.08	7.08	25.47	47.17	32.98	32.34	100.29	197.66	62.63	14.48
15	62.50	5.60	19.70	40.80	27.40	31.98	111.15	216.63	62.13	12.24
16	62.17	7.13	32.80	55.96	38.63	38.08	96.05	177.11	62.84	16.86
L.S.D. Value at 0.05	5.28	1.07	4.22	5.38	5.5	6.08	6.25	30.25	10.15	1.35
Significant of Interaction S x G	*	**	NS	**	NS	NS	**	NS	NS	**

- PH: Plant height (cm), NOB: Number of branches per plant, NOP: Number of pods per plant, PW: Pod weight per plant (g), NOS: Number of seeds per plant, SW: Seed weight per plant (g), 100 SW: 100-seed weight (g), 100 PW: 100-pod weight (g), HI: Harvest index%, PY: Pod yield (ardab/fed)

- *: Significant, **: Highly Significant and NS : Not significant.

The heaviest of 100-seed weight were recorded by genotypes 12, 8. 13 and 15 were without significant differences among them. They gave values being (114.29, 112.69, 112.37 and 111.15gm, respectively) for 100-seed weight. Meanwhile, the lightest weights of 100-seed weight were belonged to genotype 4 with values (95.38gm). These results indicated that the peanut genotypes that characterized by high 100-seed weight often have lower values of number of seeds per plant and seeds weight reflecting the compensatory effects among yield components in peanut crop.

The pod yield is the ultimate expression of the many individual physiological processes, which have interacted with the weather and environment during the growth. Variation in pod yields among studied peanut genotypes was relatively high as shown in Table 3. However, a part of this variation is usually due to the environment and different genetic backgrounds. Genotypes 7, 11 and 16 produced the highest values for pod yield recording 16.95, 16.85 and 16.86 ardab per feddan, respectively while genotypes 13 and 15 recorded the lowest pod yield being 13.41 and 12.24 ardab per feddan, respectively.

It is worth mentioning that the high yielder genotype 7 was characterized by high pods weight per plant as well as elite genotype 11 occupied the first order for most yield components which are number of branches per plant, pods and seeds per plant and pods and seeds weight per plant. Also, the superior genotype 16 had the highest values of number of pods per plant and pods weight per plant (Mohammad et al., 2018; Tirkey et al., 2018).

The interaction effect between seasons x genotypes was significant for plant height, number of branches per plant, pod yields per plant, pods weight per plant, and 100-seed weight as shown in Table 4. These results indicated that peanut genotypes responded differently to the environmental conditions suggesting the importance of assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment.

Results indicated that genotypes 4, 6 and 14 had the tallest plants (73, 70 and 73.83cm, respectively) in the 2nd season, whereas, the

minimum values of plant height were recorded by genotypes 5, 7 and 13 (53, 54 and 54.67cm, respectively) in the 1st season. For number of branches per plant, the highest values were obtained by genotypes 3 and 11 recording 10.67 and 10.07, respectively, while the lowest values were observed by genotypes 8 and 15 recording 5.40 and 5.27, respectively in the 2nd season.

Results showed that the highest values of pods weight per plant and pod yields were obtained by genotypes 1, 7, 11 and 16 recording (60.28 g and 18.08 ardab), (60.12g and 18.04 ardab), (60.22g and 18.40 ardab) and (60.92g and 18.28 ardab), respectively, in the 2nd season. However, the lowest pods weight per plant and pod yields were produced by genotypes 4, 9 and 15 recording (42g and 12.63 ardab), (42g and 12.60 ardab) and (40.33g and 12.10 ardab), respectively, in the 1st season. This result indicates that the pods weight per plant is the most important determinant for pod yields. Regarding the trait of 100-seed weight, the heaviest weights were obtained by genotypes 12 and 13 recording 119.81 and 118.11 g, respectively, in the 2nd season while the lightest weights were observed by genotypes 4 and 16 recording 87.55 and 86g, respectively, in the 1st season. These results agreed with those obtained by Zayton et al., (2014), Awadalla & Abbas (2017), El-Metwally et al. (2018), Afify et al. (2019), Mekdad (2019).

Simple correlations coefficient
The coefficients of correlation between all pairs of the studied traits were computed and graphically illustrated in Fig. 1. It is obvious that the data distribution of each variable is shown on the diagonal. The bi-variate scatter plots with a fitted line between the all studied traits are displayed below diagonal while the value of the correlation plus the significance level as stars was shown above diagonal.

Results shown in Fig 1 presented that pod yields (PY) was positively and highly significant (P<0.01) associated with number of pods per plant (r =0.88**), pods weight per plant (r =0.99**), number of seeds per plant (r =0.63*) and seeds weight per plant (r =0.63**). Fortunately, the associations among the aforementioned characters were positive and significant; therefore, the selection of any one of them would contain the others. But the character of number of pods per plant was visually easier to apply in the field

compared to the pods weight and number of seeds per plant. However, the character of 100-pod weight recorded significant and negative association (r = -0.57*) with pod yields per plant. On the other hand, pod yields had negative but non-significant associations with plant height and 100-seed weight. The negative associations between each of 100-pod weight and 100-seed weight with pod yields per plant indicated that there some pods may be empty or contain atrophic seeds. Also, the negative association of plant height toward pod yields indicated that more shooting growth may be badly affects the pod yield.

TABLE 4. Effect of interaction between season and peanut genotypes on plant height, number of branches, pods weight, 100- seed weight and pod yields.

Genotype (G)	PH		NOB		PW		100 SW		PY	
	2016/17	2017/18	2016/17	2017/18	2016/17	2017/18	2016/17	2017/18	2016/17	2017/18
1	62.33	64.67	6.53	9.27	50.33	60.28	106.42	108.68	15.10	18.08
2	60.33	59.00	6.07	8.47	53.00	37.60	112.50	104.67	15.93	12.78
3	64.00	69.00	7.47	10.67	50.67	55.67	98.41	103.21	15.20	17.37
4	65.33	73.00	6.53	9.07	42.00	55.48	87.55	103.20	12.63	16.98
5	53.00	55.00	5.87	7.60	50.67	56.59	100.94	107.83	15.33	17.18
6	64.67	70.00	6.93	6.53	50.00	54.44	112.33	89.66	14.97	16.64
7	54.00	62.67	5.87	6.00	53.00	60.12	106.78	106.30	15.87	18.04
8	69.67	61.33	6.20	5.40	51.33	55.35	110.17	115.20	15.40	16.61
9	63.33	63.67	5.60	5.93	42.00	50.18	108.90	110.75	12.60	15.39
10	55.67	58.00	6.53	9.80	50.33	58.11	107.39	112.70	15.10	17.77
11	61.33	57.33	7.33	10.07	51.00	60.22	90.31	110.95	15.30	18.40
12	63.33	67.67	8.73	9.00	50.33	52.15	108.78	119.81	15.10	15.64
13	54.67	65.83	5.73	8.63	45.00	44.37	106.64	118.11	13.50	13.31
14	61.33	70.83	5.60	8.57	45.67	48.67	97.98	102.61	13.70	15.27
15	66.00	59.00	5.93	5.27	40.33	41.26	116.34	105.96	12.10	12.38
16	59.33	65.00	7.13	7.13	51.00	60.92	86.00	106.11	15.43	18.28
LSD $_{0.05}$	7.47		1.51		7.60		8.84		1.91	

PH: Plant height (cm), NOB: Number of branches per plant, PW: Pod weight per plant (g), 100 SW: 100-seed weight (g), PY: Pod yield (ardab/fed).
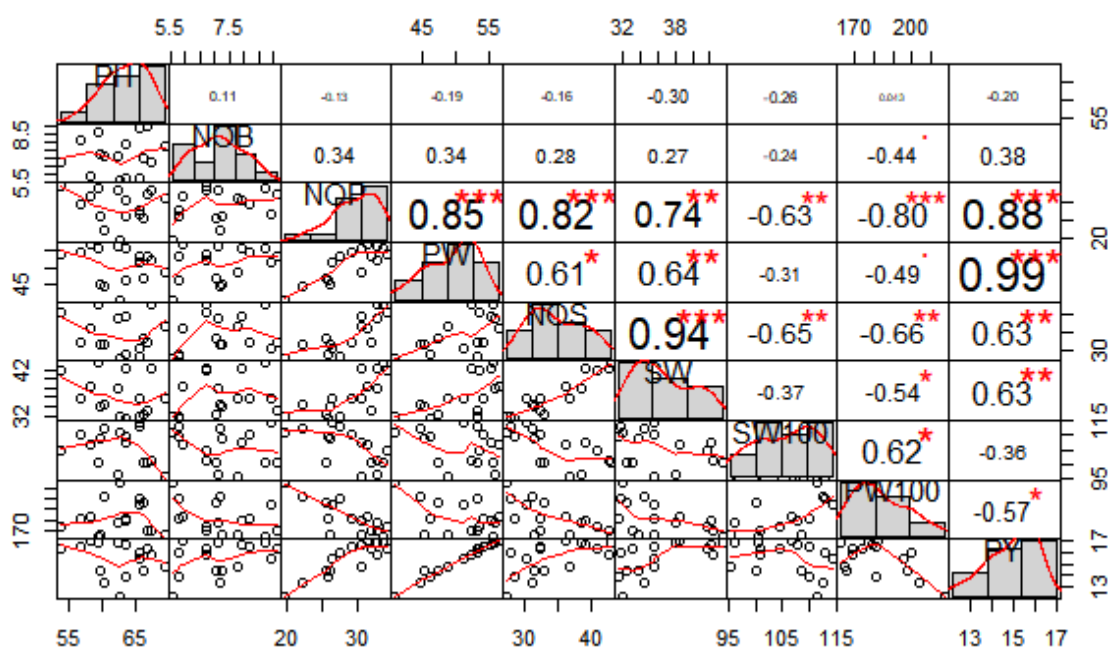
Fig .1. Correlation matrix of pod yield and its related attributes [PH: Plant height, NOB: Number of branches per plant, NOP: Number of pods per plant, PW: Pod weight per plant NOS: Number of seeds per plant, SW: Seed weight per plant 100 SW: 100-seed weight, 100 PW: 100-pod weight, PY: Pod yield per plant].

The interrelationships among yield component traits revealed that seed weight per plant recorded positive and significant association with number of pods per plant (r =0.74**), pod weight per plant (r = 0.64**) and number of seeds per plant (r =0.94**). These results indicated to the existence of high multicollinearity among yield components and consequent leading to inability to confirm actual contribution of each component to the total pod yield due to mixed or confounded effects. The number of pods per plant had positive and highly significant association with pod weight per plant (r =0.85**), number of seeds per plant (r =0.82**) indicating that dependency of these characters on each other. Seed weight recorded positive non-significant associations with number of branches (r =0.27), and negative non-significant associations with plant height (r = -0.30). The other correlation coefficients had no significant and were trivial values. Ashutosh et al. (2016), Mahesh et al. (2018), Mohammad et al. (2018) and Afify et al. (2019) observed similar associations of pod yield per plant with other yield contributing characters. Also, the observed positive associations between each of number of pods per plant and number of branches per plant with pod weight per plant were in conformity with the results obtained by Amarasinghe et al. (2016),

Tirkey et al. (2018) and Vitthal et al. (2018). From the abovementioned results, it is evident that pods weight per plant and number of pods per plant are considered the main determinant of pod yields because they emerged as major components toward pod yields. Accordingly, the breeders should be aware the nature of interrelationships among the yield components.

Normal and Sequential path analyses

Although correlation coefficients give information regarding the association of different component traits, it does not give the complete picture especially when the causal factors are interrelated and interdependent, consequently path analysis is used as a tool to understand the magnitude and direction of the direct and indirect contribution of component traits to yield.

The direct and indirect effects for the studied traits using the normal path analysis (original model) and alternative model (Sequential path analysis) are shown in Table 5. The coefficient of determination (R^2), standard error and variance inflation factor (VIF) values of the path coefficients are also listed in Table 5 to discuss the validity and goodness of fit for the proposed models.

TABLE 5. Coefficient of determination (R^2), Direct and indirect effects, standard error and variance inflation factor (VIF) values for the predictor variables in normal and sequential path analysis models.

Response variable	Predictor variables	R^2	Direct effect	Indirect effect	SE	VIF
Normal path analysis						
PY	NOP	0.99	- 0.087	0.793	0.048	<u>28.894</u>
	PW		1.012	-0.022	0.026	<u>11.028</u>
	PH		-0.039	-0.239	0.011	1.427
	NOB		0.023	0.354	0.043	1.598
	NOS		0.277	0.348	0.072	<u>97.283</u>
	SW		-0.286	0.346	0.073	<u>63.833</u>
	100-Sw		0.073	-0.249	0.023	<u>13.785</u>
	100-pw		-0.151	-0.725	0.006	6.234
Sequential path analysis						
PY	NOP	0.98	0.140	0.740	0.014	3.676
	PW		<u>0.910</u>	0.080	0.017	3.676
NOP	PH	0.77	0.034	-0.163	0.060	1.161
	NOB		-0.035	0.379	0.228	1.277
	SW		<u>0.442</u>	0.293	0.099	1.607
	100-pw		<u>-0.581</u>	-0.219	0.014	1.603
PW	PH	0.46	-0.043	-0.146	0.091	1.161
	NOB		0.134	0.203	0.348	1.277
	SW		<u>0.507</u>	0.135	0.151	1.607
	100-pw		<u>-0.157</u>	-0.333	0.021	1.603

PH: Plant height, NOB: Number of branches per plant, NOP: Number of pods per plant, NOS: Number of seeds per plant, 100 SW: 100-seed weight, SW: Seed weight per plant, PW: Pod weight per plant, 100 PW: 100-pod weight, PY: Pod yield per plant.

Concerning the original model of path analysis, several undesirable symptoms were obtained indicating the presence of multicollinearity problem. The highest VIF values (above 10) for some basic yield characters *i.e.* pods weight/plant (11.03), number of pods/plant (28.89), number of seeds/plant (97.28), seeds weight/plant (63.83) and 100- seed weight (13.79) are clear indicators that the assumption of orthogonality (independence) among the yield related characters is violated. Already, highly significant correlation coefficients were detected between these yield components as stated before in Table 4. Accordingly, the estimation of path coefficients (direct or indirect) was adversely influenced by the negative effects of multicollinearity case.

The path coefficients were obviously fluctuated recording very small values (close to be zero) and other inflated values exceeded 1. For example, the direct effect for pod weight/plant (1.012) was more than 1. Gravois & Helms (1992) reported that if the path coefficient is above 1, this reflect bad effect of multicollinearity. Only, pod weight/plant had the highest direct effect on pod yield while the direct effects of the other traits were low direct effects values. Carvalho et al. (1999) stated that the variances of path coefficients may become too large in the presence of multicollinearity making the estimation unreliable.

Statistically, the aforementioned poor estimators of path analysis, as a result of

multicollinearity, enough to reject the normal form of path analysis and give the justification to find an alternative model can overcome the above obstacles. Kozak & Kang (2006) pointed out that applying the ordinary model of path analysis as described by Dewey & Lu (1959) would become out of date compared to the modern models as sequential path analysis.

The advantage of sequential path procedure is its ability to overcome the bad results of collinearity problems and identifying the actual contribution of each component in different path components. The proposed path analysis model makes the direct and indirect effect for all studied traits less than 1 unlike the original model. Also, all variance inflation factor values (VIF) became lower than 10 indicating that the collinearity problem was solved. Consequently, the sequential path analysis model is more valid and considered an effective remedial tool to overcome the multicollinearity dilemma. Therefore, throughout the remainder part of this paper, the discussion will be focused only on the results of the statistically valid model (ridge path analysis).

Sequential path analysis illustrated in (Fig. 2) gave a better understanding of the interrelationships between components and their relative contribution to pod yield. One headed arrow between two variables denotes standardized regression coefficients (direct effect of independent variable toward the dependent variable). Double headed arrow for the dependant variable represents the residual variance $(1-R^2)$ indicating the part of the dependant variable that did not explained by the predictors. The double-headed dotted arrows between two variables indicate to linear correlation coefficient.

Statistically, more precise results were obtained using the sequential path analysis model. Results in Table 5 and Fig. 2 revealed that the pod yield depended primarily upon pod weight per plant and number of pods per plant as first-order variables accounted for nearly 98% of the variation in pod yield. The maximum positive direct effects were obtained by pod weight per plant (0.91) followed by number of pods per plant (0.14) indicting that the indirect selection for pod yield through these traits would be effective for peanut improvement.
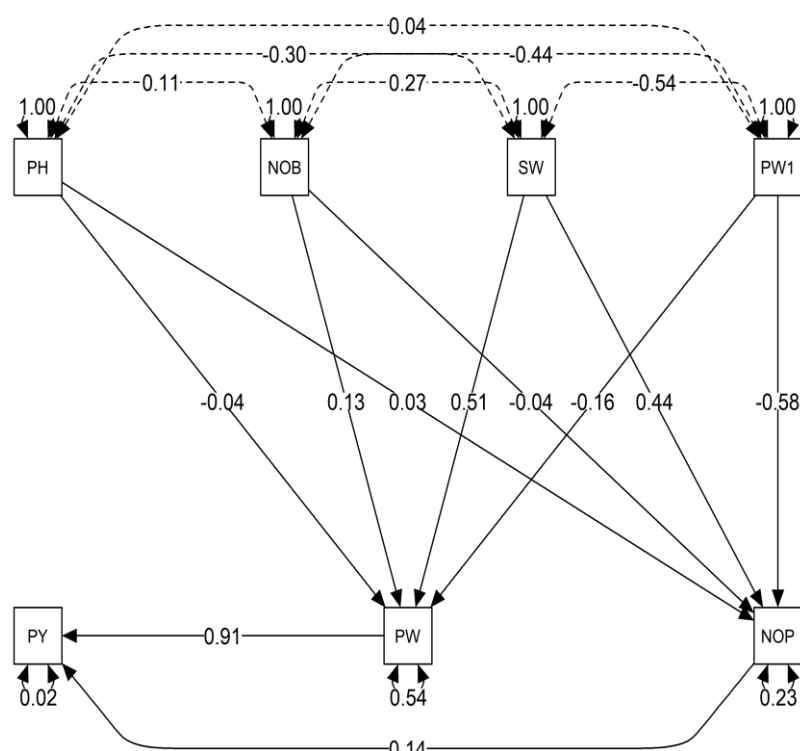

Fig. 2. Sequential path model illustrating cause-effect relationships among various characters contributing to pod yield [Plant height (PH), number of branches per plant (NOB), seed weight per plant (SW), 100-seeds weight (100 SW), number of pods per plant (NOP) and 100-pod weight (100 PW)].

The second-order path analysis showed that nearly 77% of the variation in number of pods per plant and 46% of the variation in pod weight per plant were explained by four characters namely plant height, number of branches per plant, seed weight per plant and 100 pod weights. Among these characters, plant height and seed weight per plant recorded positive direct effects while number of branches per plant and 100 pod weight showed negative direct effects on number of pods per plant (NOP). The negative direct effect of 100 pod weight toward number of pods per plant may be attributed to the compensation relationships among yield components. In the same order path analysis, the characters of plant height and 100 pod weight had negative direct effects while number of branches per plant and seed weight per plant showed positive direct effects on pod weight per plant (Table 5 and Fig. 2).

Considering the components of the indirect effects, number of branches and seeds weight per plant had positive indirect effects on number of pods per plant and pods weight per plant via other characters. These results appeared that seeds weight per plant had the considerable positive direct and indirect effects toward each of number of pods per plant and pods weight per plant. In fact, the sequential path analysis gave a somewhat different picture from what the normal model path analysis did. Using the normal model, it is obvious that direct effect of seed weight/plant toward pod yield was negative giving misleading conclusion.

The results of sequential path analysis will provide breeders with a set of key traits to target in selection programs to make the most progress in pod yields improvement instead of selection based on pod yields itself. The results were similar to those obtained by the Mohammadi et al. (2014), Amir & Hamid (2017) in wheat; Badu-Apraku et al. (2018) in maize; Kadam et al. (2018), Mahesh et al. (2018) and Tirkey et al. (2018) in ground-nut.

Conclusion

Peanut has been given great attention due to its proportionality for growth in the newly reclaimed sandy areas in Egypt. New reclaimed areas in Egypt are mostly sandy soils and usually deficient in organic matter and poor in plant nutrients.

In the current investigation, the results of Levene test proved homogeneity of separate error variances for all studied traits that permits to apply combined analysis. Results of the combined analysis of variance indicated that there were significant differences between the two seasons and among the aimed peanut genotypes for all studied characters. Regarding the interaction effect between seasons and genotypes, significant and highly significant (0.05 or 0.01 probability levels) differences were obtained for all traits except for number of pods per plant (NOP), number of seeds per plant (NOS), seeds weight (SW), 100-pod weight (100 PW), and harvest index (HI). It is indicated that peanut genotypes were differently responded to the environmental conditions suggesting the importance of assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment. Considering the components of the indirect effects, number of branches and seeds weight per plant had positive indirect effects on number of pods per plant and pods weight per plant via other characters. These results appeared that seeds weight per plant had the considerable positive direct and indirect effects toward each of number of pods per plant and pods weight per plant. In fact, the sequential path analysis gave a somewhat different picture from what the normal model path analysis did. Using the normal model, it is obvious that direct effect of seeds weight/plant toward pod yields was negative giving misleading conclusion. The results of sequential path analysis will provide breeders with a set of key traits to target in selection programs to make the most progress in pod yields improvement instead of selection based on pod yields itself.

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