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Stability analysis for pod yield and its component traits in some peanut genotypes

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Abstract

Eight peanut genotypes were grown at two locations during four successive summer seasons from 2014 to 2017 to give eight environments in order to evaluate yield stability. Significant genotype × environment interaction was detected for all traits. Results revealed that peanut genotypes Sohag116, Sohag119 and Sohag120 were superior in their mean performance for yield and yield components, The regression coefficient value was approached unity in genotypes VAC-R92, Sohag nos. 116, 119 and 120 also, pod weight and seed weight, genotypes Sohag nos. 116 and 119 as well as number of pods and number of seeds plant^{-1} genotypes Giza 6, Line 9, VAC-R92 and Sohag 119 as well as shelling percentage, genotypes Sohag 112, Line 9, Introduction 508 and Sohag 120 as well as 100-pod weight, genotypes Sohag 112, Introduction 508 and VAC-R92 for 100-seed weight genotypes Sohag 112, Line 9, Introduction 508 and Sohag 116 for pod yield fed^{-1}., where the value of bi almost approached unity, indicating average response to the fluctuating environmental conditions prevailed. Genotypes VAC-R92, Sohag nos. 116 and 120 had the highest pod weight plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1} and seed weight plant^{-1} among the tested genotypes, as they had high mean of pods (50.19) over population average mean of pods plant^{-1} (46.5) peanut genotypes VAC-R92, Sohag nos. 119 and 120 for 100- pod weight (g), genotypes Sohag nos. 116 and 119 for 100-seed weight (g), genotypes Sohag nos. 116, 19 and 120 for pod yield fed^{-1} (ard.). These genotypes are suitable especially for favorable growing seasons as they had nearest (bi) value to 1. genotype Sohg112 recorded the highest number of pods plant^{-1} over the grand mean, whereas genotypes Sohag nos. 116 and 120 gave highest shelling percentage, genotype Sohag116 gave the highest 100-pod weight and Sohag120 gave the highest number of seeds plant^{-1} indicated that these genotypes are fitted, for less favorable locations as they had low (bi) value (b<1). Such genotypes can be utilized in a breeding program for transferring stability characters in to high yielding cultivars peanut as genotype 8 which was the best one.

Key words: *Peanut, Stability, Pod yield, Yield components.*

Introduction

Groundnut or peanut (*Arachis hypogaea* L.*)*, a segmental allopolyploid, self-pollinated legume. Popularly known as peanut, groundnut or poor man's cashew. It is widely cultivated as legume/oil crop in more than 114 countries including tropical to temperate region (**Abo-Elezz *et al*., 2010)**. It is an important oil, food and feed legume, where kernels are rich in oil (48-50 %) and protein (25-28%). It stated that global groundnut production increased marginally in last decade by just 0.4% only (**Janila *et al*., 2013**). Since Asian and African countries accounts for the 93% of global groundnut production, where cultivation is predominantly under rainfed and resource poor conditions (**Knauft and Gorbet, 1993)**. The lower productivity in groundnut is mainly due to various biotic and abiotic stresses. Yield is a complex character resulting from interplay of various yield contributing characters, which have positive or negative association with yield and among themselves also. The consistent performance of a genotype over a range of environments is essential for a wide stability of a variety. Stability of genotypes depends upon maintaining expression of certain morphological and physiological attributes and allowing others to vary, resulting in G×E interactions. G×E interaction has a masking effect on the performance of a genotype and hence the relative ranking of the genotype do not remain the same over number of environments. Stability of genotypes to environmental fluctuations is important for stabilization of crop production both temporally and spatially. Estimation of phenotypic stability, which involves regression analysis, has proven to be a valuable tool in the assessment of varietal adaptability. Stability analysis is useful in the identification of stable genotypes and in predicting the responses of various genotypes over changing environments (**Eberhart and Russell, 1966; Finlay and Wilkinson, 1963)**. It is generally agreed that the more stable genotypes adjust their phenotypic responses to provide some measure of uniformity in spite of environmental fluctuations (**Patil *et al.*, 2014**). Therefore, an attempt has been made in present study to evaluate different groundnut genotypes across the different locations to know the role of G×E interactions and also to analyze the stability of genotypes for different traits.

Materials and Methods

The experiments were carried out during four successive summer seasons of 2014, 2015, 2016 and

2017 at Assuit and Shandweel agricultural research station. Eight peanut genotypes were used for this experiment. The name and origin of genotypes are shown in Table (1). 6 Soil samples were collected from each experimental area (Ass., Sh.) from the upper soil layer (30 cm). The samples from each experimental area were mixed together to make combined sample for each location. Each combined samples was subjected to lab analysis to determined physical and chemical properties of soil as presented in Table (2). The experiment was laid out in a randomized complete block design (RCBD) with three replications at eight environments (2 locations x 4 years). Plot area was 9.6 m^2 (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. Cultural practices were done according to recommendations. The two guarded inner rows were harvested to determine the following characteristics: pod weight $plant^{-1}$(g), number of pods $plant^{-1}$, number of seeds $plant^{-1}$, seed weight $plant^{-1}$ (g), shelling percentage (%), 100-seed weight (g), 100-pod weight (g) and pod yield fed^{-1}. (ardab), where (one ardab = 75 kg and one feddan = 4200 m^2). Data of yield components were recorded on ten guarded plants per plot.

Table 1. Name and Origin of the eight peanut genotypes**.**

No	Genotype	Pedigree	Origin
1	Giza6 (G1)	A commercial cultivar	Egypt
2	Sohag112 (G2)	A line selected from H7 x VAC-R92	Egypt 1998
3	Line9 (G3)	A line selected from L 382 x Giza5	Egypt
4	Introduction 508 (G4)	Not available	USA
5	VAC-R92 (G5)	Not available	USA
6	Sohag116 (G6)	A line selected from H9 x NC-7	Egypt 1998
7	Sohag119 (G7)	A line selected from Intr.500 x L262	Egypt 1998
8	Sohag120 (G8)	A line selected from Intr.500 x NC-7	Egypt 1998

Table 2. Some physical and chemical properties of experimental soils of Assuit (Ass.) and Shandweel (Sh).

Years	**Texture**		**Ca^{++}**		**EC dsm**		**Soil ph**		**Organic matter (O.M)**		**Available nutrients in soil (ppm)**					
											N		**P**		**K**	
	Ass.	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**	**Ass.**	**Sh.**
2014	**sandy**	**Clay loam**	**2.16**	**7.6**	**0.42**	**0.087**	**8.10**	**7.8**	**0.27**	**1.1**	**0.5**	**15**	**8.31**	**18**	**11.7**	**82**
2015	**sandy**	**Clay loam**	**2.10**	**7.9**	**0.39**	**0.09**	**8.50**	**7.9**	**0.22**	**1.3**	**0.3**	**18**	**8.32**	**19**	**11.9**	**77**
2016	**sandy**	**Clay loam**	**2.00**	**7.8**	**0.35**	**0.086**	**8.55**	**7.7**	**0.21**	**1.1**	**0.4**	**16**	**8.28**	**19**	**12.1**	**80**
2017	**sandy**	**Clay loam**	**2.18**	**7.7**	**0.40**	**0.089**	**8.47**	**7.9**	**0.25**	**1.2**	**0.4**	**17**	**8.30**	**18**	**12.0**	**79**

Homogeneity test was used to satisfy the assumption of homogeneity of variances before running the combined analysis on the eight genotypes and eight environments (two locations and four years) according to Bartlett's test.

A combined analysis of variance across locations was computed assuming replications and locations effects as random and genotypes as fixed variable **(Steel *et al.*, 1997**). Mean comparisons for these traits were done according to **Duncan's** Test at $P < 0.05$ **(Duncan, 1955).**

Stability analysis

The stability analysis was done following **Eberhart and Russel (1966)** model which interprets the variance of regression deviations as a measure of cultivar stability and the liner regression coefficient (b) as a measure of environmental index. In this model, mean (μ) and environmental index (Ij) are used as dependent and independent variables respectively to compute the regression coefficient. According to this model, an ideal genotype should have high mean (μ>X), a unit regression coefficient (bi=1) and no deviation from linearity ($S^2di=0$).

The basic model for the Eberhart and Russel (1966) model is:

$$Yij = \mu i + \beta iIj + \delta ij,$$

Where,

Y_{ij}= genotypic mean of i^{th} genotype at j^{th} environment. μi= mean of i^{th} genotype over all environments bi= regression coefficient which measures the response of i^{th} genotype to environments I_j= environmental index as mean of all genotypes at j^{th} environment minus the overall mean, and δij= deviation from regression coefficient of i^{th} genotype at j^{th}

Results and Discussion

Bartlett's test indicated homogenous error variance for the traits in each of eight environments and allowed to proceed further for pooled analysis across environments. Genotype, environment variances and genotype × environment interaction were significant for all traits except number of pods plant^{-1}for genotypes Table (3).

Table 3. Combined analysis of variance of evaluated genotypes over different environments.

Source of Variance	df	Pod weight plant^{-1}	No. of pods plant^{-1}	No. of seeds plant^{-1}	Seed weight plant (g)	Shelling %	100- pod weight (g)	100- seed weight	Pod yield fed^{-1} (ardab)
Genotypes(G)	**7**	**3790.91****	**112.67**	**1779.13****	**1883.01****	**16.97****	**8342.00****	**617.66****	**121.58****
Environments(E)	**7**	**3878.68****	**714.19****	**839.00****	**1611.21****	**4.46***	**2979.43****	**431.88****	**247.88****
G x E	**49**	**390.35****	**100.91****	**203.099***	**167.13****	**3.45***	**668.24****	**37.76***	**4.37***
Pooled error	**128**	**62.78**	**23.57**	**41.82**	**26.66**	**1.39**	**157.19**	**8.49**	**3.11**
Total	**191**								

* and ** significant at 0.05 and 0.01 probability levels, respectively.

The existence of significant difference among the genotypes was the representation of the difference of genetic potentiality of the genotypes for the evaluated characteristics; also, the existence of significant difference among the studied environments represents the significant variety effect in the additive structure of data for the evaluated characteristics among the environments. Similar results were reported by **Minimol *et al.* (2001), Mahasi *et al.* (2006) and Zerihun *et al.* (2011).**

Mean performance of genotypes for eight studied traits is shown in Table (4). Results revealed that the means values varied from 83.60 to 123.35 g with an average of 97.88 g for pod weight plant^{-1}, from 43.78 to 50.19 with an average of 46.5for number of pods plant^{-1}, from 65.52 to 83.91 with an average of 73.67 for number of seeds plant^{-1}, from 53.28 to 81.81 with an average of 63.62 g for seed weight plant^{-1}, from 63.63 to 66.42 with an average of 64.93 for shelling percentage %, from 186.98 to 245.36 with an average of 202.47 g for 100- pod weight, from 81.51 to 97.27 with an average of 86.13 g for 100-seed weight, and from 21.44 to 27.64 with an average of 25.61 ardab for pod yield fed^{-1}. The genotype Sohag 120 produced the highest values for all studied traits. Regarding the environments, (Table 4), there were significant effects on the studied traits, indicating a wide range of environmental effects. Assuit environment (4) had the highest mean values of environments for pod weight plant^{-1}, number of seeds plant^{-1}**,** Seed weight plant^{-1} (g) and100- pod weight, and Assuit environment (3) had the highest mean values of environments for pod yield fed.$^{-1}$, Meanwhile, Shandweel environment (6) had the highest mean values of environments for 100- seed weight. The reverse trend was true for different traits and environments. In this connection, some investigators emphasized that environments had great effects on peanut genotypes traits Therefore, Assuit environments were the best environment. Similar results were reported by **(Abd El-Rahman *et al*. (2016)** and **Minde *et al.* (2017).**

The mean squares due to genotype were highly significant for all the studied characters except number of pods plant^{-1} (Table 5), which revealed the presence of substantial amount of variation among the groundnut genotypes. The significant mean squares for environment (linear) for various traits were also reported by **Habib *et al.* (1986) and Patil *et al.* (2014)**. Variance due to genotypes × environment (linear) was significant for pod weight plant^{-1}, No. of seeds plant^{-1}, seed weight plant (g) and pod yield fed^{-1} (ardeb). Significance of variance due to environment (linear) was observed for all the characters studied except shelling percentage and 100-pod weight (g), (Table 5). The higher magnitude of mean squares for environment (linear) compared to genotypes × environments (linear) indicated that linear response of environment accounted for the major part of total variation for all studied characters and may be responsible for high adaptation in relation to yield and other traits. Therefore, prediction of performance of genotypes over environments would be possible for the various characters. Similar findings were reported by **Thaware (2009)**, **Pradhan *et al.* (2010), Habib *et al.* (1986) and Patil *et al.* (2014).** Variance due to pooled deviation was significant for all studied characters indicating that genotypes differed considerably with respect to their stability. The significant pooled deviation (Non-linear) for various traits were also reported by **Senapati *et al.* (2004), Chuni Lal *et al.* (2006) and Patil *et al.* (2014)**. Interactions of genotypes with environments obtained as the environment + genotype × environments (e + g×e) were significant for all characters (Table 5), which suggested the distinct nature of environments and genotype × environment interactions in phenotypic expression. The significant environment + (genotype × environment) interactions for various traits were also reported by **Joshi *et al.* (2003) and Patil *et al.* (2014).**

Table 4. Mean performance of studied traits over different environments.

Trait	Env. code	Assuit				Shandweel				Mean
		2014	2015	2016	2017	2014	2015	2016	2017	
	Genotypes	Env.1	Env.2	Env.3	Env.4	Env.5	Env.6	Env.7	Env.8	
Pod weight plant^{-1}	Giza 6	81.190	94.30	100.16	101.96	79.250	99.350	80.92	92.12	91.16de
	SOHAG112	85.82	87.44	92.163	90.00	78.40	103.02	77.907	85.69	**87.56ef**
	LINE9	84.78	97.70	94.17	105.89	67.87	75.50	69.55	73.33	**83.60f**
	INTRO. 508	90.63	88.93	97.94	123.27	84.53	92.10	78.54	92.01	**93.49cd**
	VAC-R92	98.78	75.18	91.33	146.08	93.90	110.39	89.99	107.10	**101.59b**
	SOHAG116	101.75	92.34	133.67	137.27	72.93	118.24	75.88	115.96	**106.01b**
	SOHAG119	102.86	78.93	105.02	116.02	74.57	101.63	82.77	108.60	**96.29c**
	SOHAG120	**147.10**	**93.58**	**110.17**	**144.21**	**113.75**	**133.76**	**106.45**	**137.73**	**123.35a**
	Mean	**99.12c**	**88.55d**	**103.08bc**	**120.59a**	**83.15e**	**104.25b**	**82.75e**	**101.57bc**	**97.88**
No. of pods plant^{-1}	Giza 6	46.41	52.67	53.47	49.95	36.89	44.47	35.62	44.55	**45.50bc**
	SOHAG112	42.92	43.73	59.50	41.59	45.66	51.83	43.37	49.10	**47.22b**
	LINE9	40.24	58.00	51.55	46.13	36.67	39.77	34.85	43.29	**43.81c**
	INTRO. 508	52.22	46.39	56.07	56.22	36.92	39.17	36.79	44.83	**46.07bc**
	VAC-R92	46.53	34.46	46.93	62.78	45.12	49.20	43.34	52.81	**47.65ab**
	SOHAG116	42.80	37.73	63.74	58.08	35.92	52.72	36.02	55.22	**47.78ab**
	SOHAG119	46.84	39.53	51.09	50.19	33.68	43.91	37.89	47.07	**43.78c**
	SOHAG120	**60.87**	**42.00**	**49.19**	**55.16**	**43.41**	**51.47**	**45.51**	**53.89**	**50.19a**
	Mean	**47.35c**	**44.32d**	**53.94b**	**52.52b**	**39.28e**	**46.57cd**	**39.18e**	**48.85a**	**46.5**
No. of seeds plant^{-1}	Giza 6	67.16	76.27	86.47	80.08	61.37	66.51	62.64	70.89	**71.43c**
	SOHAG112	71.74	69.85	77.69	66.02	64.90	67.41	65.21	71.81	**69.33c**
	LINE9	66.33	81.19	78.44	77.97	54.38	52.74	56.44	56.65	**65.52d**
	INTRO. 508	74.33	73.69	80.77	86.40	63.93	63.10	64.17	72.21	**72.33c**
	VAC-R92	75.73	60.08	77.20	99.37	68.95	79.57	69.15	79.50	**76.19b**
	SOHAG116	75.02	68.88	109.48	96.15	55.04	86.88	56.72	88.21	**79.55b**
	SOHAG119	71.55	65.97	86.75	82.02	52.30	73.38	58.79	77.69	**71.06c**
	SOHAG120	**93.32**	**66.96**	**80.06**	**95.93**	**76.44**	**90.57**	**73.58**	**94.42**	**83.91a**
	Mean	**74.40bc**	**70.36d**	**84.61a**	**85.49a**	**62.16e**	**72.52cd**	**63.34e**	**76.43b**	**73.67**
Seed weight plant^{-1} (g)	Giza 6	53.09	62.51	67.32	67.09	51.79	63.27	53.33	60.48	**59.86d**
	SOHAG112	56.43	57.10	59.05	58.64	50.59	65.51	49.44	54.38	**56.39e**
	LINE9	53.78	64.04	60.89	68.07	42.89	46.01	43.61	46.97	**53.28f**
	INTRO. 508	59.77	58.09	62.89	77.71	54.34	60.32	51.26	60.27	**60.58d**
	VAC-R92	63.26	48.83	59.69	94.48	59.16	73.79	57.69	68.01	**65.62c**
	SOHAG116	68.22	59.89	88.11	88.25	46.78	78.67	48.97	74.02	**69.11b**
	SOHAG119	64.95	52.12	68.53	74.30	47.47	65.32	54.47	71.17	**62.29d**
	SOHAG120	**94.76**	**62.75**	**73.59**	**94.75**	**75.68**	**89.09**	**71.36**	**92.50**	**81.81a**
	Mean	**64.29c**	**58.17d**	**67.51b**	**77.91a**	**53.59e**	**67.75b**	**53.77e**	**65.97bc**	**63.62**
Shelling percentage (%)	G1	65.45	66.27	67.21	65.79	65.34	63.69	65.92	65.69	**65.67b**
	SOHAG112	65.75	65.30	64.08	65.19	64.53	63.63	63.48	63.44	**64.43d**
	LINE9	63.37	65.66	64.71	64.29	63.24	60.94	62.71	64.09	**63.63e**
	INTRODUCE5	65.74	65.35	64.27	63.02	64.31	65.45	65.27	65.49	**64.87cd**
	VAC-R92	63.93	64.94	65.38	64.71	63.01	66.86	64.10	63.51	**64.56cd**
	SOHAG116	67.06	64.68	65.99	64.32	64.11	66.52	64.55	63.81	**65.13bc**
	SOHAG119	63.38	66.00	65.28	63.99	63.67	64.26	65.82	65.53	**64.74cd**
	SOHAG120	64.43	67.04	66.77	65.70	66.55	66.63	67.05	67.19	66.42a
	Mean	64.89bc	65.66a	65.46ab	64.63c	64.35c	64.75c	64.86bc	64.85bc	64.93
100-pod weight (g)	Giza 6	175.13	181.05	188.19	204.30	214.91	223.47	227.27	206.83	**202.64d**
	SOHAG112	200.03	199.97	154.91	216.30	171.74	198.72	179.63	174.49	**186.98e**
	LINE9	210.80	171.50	183.28	229.67	185.02	189.91	199.77	169.38	**192.42e**
	INTRO. 508	173.91	191.61	177.47	219.15	229.20	234.89	213.76	205.39	**205.67d**
	VAC-R92	212.23	221.54	195.73	233.23	208.50	224.51	207.84	202.66	**213.28c**
	SOHAG116	237.56	250.30	210.86	236.16	203.26	224.90	210.85	209.95	**222.98b**
	SOHAG119	219.13	201.97	206.68	231.07	221.41	231.67	218.37	230.55	**220.11bc**
	SOHAG120	**241.58**	**223.57**	**224.35**	**261.15**	**262.70**	**260.13**	**233.89**	**255.54**	**245.36a**
	Mean	**208.79b**	**205.19b**	**192.69c**	**228.88a**	**212.09b**	**223.52a**	**211.42b**	**206.85b**	211.18

Table 4. Continued.

Trait	Env. code Genotypes	Assuit 2014 Env.1	2015 Env.2	2016 Env.3	2017 Env.4	Shandweel 2014 Env.5	2015 Env.6	2016 Env.7	2017 Env.8	Mean
100-seed weight	Giza 6	79.15	81.98	78.17	83.88	84.48	95.31	85.27	85.33	**84.19de**
	SOHAG112	78.64	81.91	76.05	88.79	78.00	97.14	75.82	75.73	**81.51f**
	LINE9	81.34	78.74	77.63	87.28	78.92	87.37	77.29	83.01	**81.45f**
	INTRO. 508	80.42	78.85	77.86	90.09	85.02	96.03	79.88	83.49	**83.96e**
	VAC-R92	83.60	81.35	77.68	95.09	85.85	92.77	83.44	85.50	**85.66cd**
	SOHAG116	91.06	86.86	80.44	91.94	85.12	90.54	86.37	83.99	**87.04bc**
	SOHAG119	90.80	79.06	79.06	90.50	90.79	89.02	92.64	91.59	**87.93b**
	SOHAG120	**101.50**	**93.67**	**91.94**	**98.69**	**99.01**	**98.34**	**97.03**	**97.97**	**97.27a**
	Mean	**85.81c**	**82.81d**	**79.86e**	**90.79b**	**85.90c**	**93.32a**	**84.72c**	**85.83c**	86.13
Pod yield Fed.$^{-1}$(ardab)	Giza 6	22.91	23.55	28.76	25.11	23.16	20.32	20.91	19.69	**23.05de**
	SOHAG112	23.35	23.22	28.50	23.94	19.51	18.04	18.86	17.75	**21.65f**
	LINE9	24.02	23.58	28.21	22.88	19.67	17.54	17.83	17.75	**21.44f**
	INTRO. 508	24.05	23.11	28.92	24.36	23.71	17.67	17.93	17.00	**22.09ef**
	VAC-R92	21.77	23.19	28.45	26.66	25.49	22.26	21.06	20.37	**23.66cd**
	SOHAG116	26.82	24.54	31.30	26.61	22.96	23.06	21.53	20.44	**24.66c**
	SOHAG119	29.87	27.31	31.29	26.43	25.44	24.49	23.35	22.18	**26.29b**
	SOHAG120	27.98	27.57	33.29	28.66	27.47	26.48	25.84	23.86	27.64a
	Mean	**25.09bc**	**24.51c**	**29.84a**	**25.58b**	**23.43d**	**21.23e**	**20.91e**	**19.88f**	23.81

Table 5. Analysis of variance for pod yield and yield contributing traits under different environments

SOV	df	Pod weight plant^{-1}	No. of pods plant^{-1}	No. of seeds plant^{-1}	Seed weight plant (g)	Shelling %	100- pod weight (g)	100- seed weight	Pod yield fed^{-1} (ardeb)
Genotypes	**7**	**1263.67****	**37.58**	**279.67****	**627.66****	**5.65****	**2780.71****	**205.88****	**0.67****
Env. + (Genotypes x Env.)	**56**	**275.46****	**59.19****	**133.37****	**115.88****	**1.26**	**319.05***	**29.00****	**0.19****
Environment (linear)	**1**	**9050.49****	**1666.57****	**4151.31****	**3759.39****	**0.19**	**6952.14**	**1007.69****	**9.57****
Genotype x Environment (linear)	**7**	**234.85****	**38.211**	**142.22****	**100.84****	**0.48**	**111.66**	**17.29**	**0.04****
Pooled deviation	**48**	**98.57****	**28.77****	**48.37****	**42.17****	**1.11****	**211.1****	**10.32****	**0.019****
Giza6	**6**	**43.93**	**18.43****	**23.46**	**20.08***	**0.75**	**333.26****	**12.05****	**0.007**
Sohag112	**6**	**44.99**	**33.58****	**14.54**	**16.35**	**0.93****	**197.90****	**20.87****	**0.013**
Line9	**6**	**146.49****	**52.43****	**104.51****	**74.15****	**1.49****	**300.27**	**3.89**	**0.019**
Intr.508	**6**	**34.71**	**18.04****	**18.78**	**9.51**	**0.93**	**282.46****	**4.59**	**0.019**
VAC-R92	**6**	**154.38****	**51.78****	**73.64****	**66.78****	**1.49****	**52.03**	**3.26**	**0.047***
Sohag116	**6**	**90.34****	**20.44****	**45.21****	**36.64****	**1.64****	**312.10****	**7.27****	**0.012**
Sohag119	**6**	**37.47**	**3.09**	**10.35**	**17.32***	**0.69**	**64.84**	**24.09****	**0.025**
Sohag120	**6**	**236.22****	**32.31****	**96.48****	**96.51****	**0.94****	**145.95****	**6.53****	**0.009**
Pooled error	**128**	**22.74**	**7.8**	**14.06**	**9.63**	**0.46**	**50.14****	**2.89**	**0.017**

In the present investigation, model proposed by **Eberhart and Rusell (1966)** was used for analysis of G×E interactions. This model considered both linear (*bi*) and non-linear (S^2di) components of G×E interactions for the prediction of performance of the individual genotype. Higher mean performance of genotype for various characters along with regression coefficient (*bi*) as measures of responsive and deviation from regression (S^2di) as a measure of stability were used to assess the stability and suitability of performance over environments. The high mean performance of genotypes was taken on the basis of average performance of all genotype as population mean.

The bi value was approached near unity in peanut genotypes VAC-R92, Sohag116, Sohag119 and Sohag120 for pod weight and seed weight, genotypes 6 and 7 for number of pods and number of seedsplant^{-1}genotypes 1, 3, 5 and 7 for shelling percentage , genotypes 2, 3, 4 and 8 for 100- pod weight ,genotypes 2, 4 and 5 for 100- seed weight genotypes 2, 3, 4 and 6 for pod yield fed^{-1}., where the value of bi almost approached unity, indicating average response to the fluctuating environmental conditions prevailed.

Genotypes 5, 6 and 8 had the highest pod weight plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1} and seed weight plant^{-1} among the tested genotypes, as they had higher means of pods plant^{-1} than overall mean value of (46.5). Peanut genotypes 5, 7 and 8 for 100- pod weight (g), genotypes 6 and 7 for 100- seed weight (g), genotypes 6, 7 and 8 for pod yield fed^{-1} (ard.). These genotypes are suitable especially for favorable growing seasons as they had high (bi) value (b>1). These results were in accordance with the **Pradhan *et al.* (2010) and Patil *et al.* (2014).**

Peanut genotype Sohag112 recorded the highest number of pods plant^{-1} over the grand mean (46.50), whereas genotypes 6 and 8 gave highest shelling percentage, genotype Sohag 116 gave the highest 100- pod weight and Sohag 120 gave the highest number of seedsplant^{-1}indicating that these genotypes are fitted, for less favorable locations as they had low (bi) value (b<1) these results agree with those reported by **Abd El-Rahman *et al.* (2016) and Hasan *et al.* (2018)**

Table 6. Estimates of stability parameters for eight peanut genotypes in all studied characters.

Genotypes	**Pod weight plant^{-1}**			**No. of pods plant^{-1}**			**No. of seeds plant^{-1}**			**Seed weight plant^{-1} (g)**		
	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d
Giza 6	91.16	0.56*	621.75	45.50	0.98**	309.26	71.43	0.88**	545.61	59.86	0.58*	280.52
SOHAG112	87.56	0.39	449.73	47.22	0.51	255.09	69.33	0.29	133.46	56.39	0.42	181.74
Line9	83.60	0.69	1424.92	43.81	0.74	427.23	65.52	0.87	1016.45	53.29	0.72	686.93
Intro.,508	93.49	0.96**	1243.51	46.07	1.29**	459.77	72.33	0.86**	497.36	60.58	0.89**	431.69
VAC-R92	101.59	1.38**	3091.43	47.65	0.84	458.75	76.19	0.96*	922.40	65.62	1.41**	661.84
Sohag116	106.01	1.79**	4197.83	47.78	1.86**	845.43	79.55	2.09**	2556.49	69.11	1.85**	870.68
Sohag119	96.29	1.12**	1644.58	43.78	1.09**	269.32	71.06	1.30**	944.26	62.29	1.09**	512.32
Sohag120	123.35	1.09	2752.12	50.19	0.68	289.93	83.91	0.73	852.57	81.81	1.03	485.25
Mean	97.88	1		46.50	1		73.66	1		63.62	1	
SE	3.75	0.29		2.03	0.37		2.63	0.31		2.45	0.29	
	Shelling %			**100- pod weight (g)**			**100- seed weight**			**Pod yield fed^{-1} (ard.)**		
	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d	$\bar{x}$	B_i	S^2_d
Giza 6	65.67	1.37	6.89	202.64	0.86	2643.05	84.19	0.98**	192.96	23.05	0.89**	60.51
Sohag112	64.43	0.32	5.72	186.98	1.37*	2807.56	81.51	1.51**	413.55	21.64	1.14**	98.11
Line 9	63.63	2.03	14.27	192.42	1.12	2892.38	81.45	0.86**	117.08	21.43	1.16**	104.20
Intro.,508	64.87	0.54	5.95	205.67	1.50*	3656.03	83.96	1.41**	277.04	22.09	1.26	122.01
VAC-R92	64.56	1.00	10.22	213.28	0.93**	1066.17	85.66	1.29**	231.02	23.66	0.76**	58.72
Sohag116	65.13	0.61	10.35	222.98	0.36	1989.13	87.04	0.72**	109.32	24.66	1.06**	85.64
Sohag119	64.74	1.60	7.45	220.10	0.75*	877.97	87.93	0.76	217.22	26.29	0.91**	68.48
Sohag120	66.42	0.55	6.02	245.36	1.10*	1934.40	97.27	0.46	65.99	27.64	0.82**	52.05
Mean	64.93	1		211.18	1		86.13	1		23.81	1	
SE	0.39	0.93		5.49	0.49		1.21	0.29		0.40	0.13	

The same letters in each column, on the basis of Duncan test have no significant differences at 5% level.

Conclusion

This information are of great importance for peanut breeders to choose a suitable genotype for fluctuating environments, i.e favorable or less favorable environments as well as to be cultivated under wide range of environments. Among the cultivars used in this study, genotypes Sohag nos. 116, 119 and 120 showed high mean performance for most studied characters, indicating stability across the environments and therefore, they could be used in a breeding programme for the development of high yielding stable genotypes across environments in the future

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تحليل الثبات في بعض التراكيب الوراثية للفول السوداني

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تمت زراعة ثمانية تراكيب وراثية من الفول السوداني في موقعين خلال أربعة مواسم صيفية متتالية من 2014 إلى 2017 لإعطاء ثمانية بيئات من أجل تقييم ثبات المحصول ومكوناته. أظهرت كل الصفات معنوية تفاعل التركيب الوراثي × بيئة. أوضحت النتائج أن التراكيب الوراثية سوهاج 116 ، 119 ، 120 كانت متفوقة بالنسبة للمحصول ومكوناته، وكانت قيم معامل الانحدار bi قريبة من الوحدة للتراكيب الوراثية VAC–R92 وسوهاج 116 ، 119، 120 لصفتى وزن القرون ووزن البذور للنبات، والتراكيب الوراثية سوهاج116 ، 119 لصفتى عدد القرون وعدد البذور للنبات، والتراكيب الوراثية جيزة 6 وسلاله 9 وVAC–R92 وسوهاج 119 لصفة نسبة التصافى، والتراكيب الوراثية سوهاج112 وسلالة 9 ومستورد 508 وسوهاج 120 لصفة وزن 100 قرن، والتراكيب الوراثية سوهاج 112 ومستورد 508 و VAC–R92 لصفة وزن 100 بذرة، والتراكيب الوراثية سوهاج112 وسلالة 9 ومستورد 508 وسوهاج116 لصفة محصول القرون للفدان؛ حيث تقترب قيمة معامل الانحدار bi تقريبا من الوحدة وأعطت التراكيب الوراثية VAC–R92 و سوهاج116 ، وسوهاج120 أعلى وزن وعدد قرون للنبات، وعدد وزن البذور بين التراكيب الوراثية التي تم اختبارها، حيث كان لديها متوسط عالى من القرون للنبات (50.19) أكثر من المتوسط العام لعشيرة الفول السوداني (46.5)، والتراكيب الوراثية VAC–R92، سوهاج119 وسوهاج120 لصفة وزن 100 قرن ، التراكيب الوراثية سوهاج 116 ، 119 لصفة وزن 100 بذرة (جم)، التراكيب الوراثية سوهاج 116 ، 119 ، 120 لصفة وزن محصول القرون للفدان بالاردب. هذه التراكيب الوراثية مناسبة بشكل خاص لموسم النمو حيث أن لها أقرب قيمة (bi) إلى الوحدة. سجل التركيب الوراثى للفول السوداني سوهاج 112 أعلى عدد قرون للنبات عن المتوسط العام ، في حين أعطى التركيبان الوراثيان سوهاج116 ، 120 أعلى نسبة تصافى، التركيب الوراثي سوهاج116 أعطى أعلى وزن 100 قرن، وأعطى سوهاج120 أعلى عدد من البذور للنبات، وقد أشارت النتائج إلى أن هذه التراكيب الوراثية تعتبرمناسبة في مواقع أقل تفضيلاً لأنها ذات قيمة (bi) منخفضة .(b<1). يمكن استخدام العديد من هذه التراكيب الوراثية في برامج التربية لنقل صفة الثبات إلى أصناف الفول السوداني ذات الإنتاجية العالية مثل التراكيب الوراثي سوهاج 120 والذي كان أفضلها.