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Performance and Stability of Seed Yield and Oil % for Six Soybean Genotypes

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Abstract

Plant breeders are extremely concerned with genotype × environment (GxE) interaction. It caused more challenging to discover superior genotypes and restrict the advantages of selection. Three adjacent trials were carried out depending on planting date in 2019 and 2020 seasons. Three replicates in each sowing date and season were used in the split-plot design of the trial. The three densities were devoted in the main-plots. In the sub-plot, six soybean genotypes were cultivated. Utilizing various techniques, evaluate the seed weight/plant performance, quantify the GxE interaction, and look into the stability of the evaluated genotypes. The results revealed that the studied genotypes responded differently to environmental circumstances, as indicated by highly significant mean squares for genotypes, environments, and GxE interaction. Also, very significant results for the terms of predictable (linear) and unpredictable (non-linear) interaction components support the finding that the examined soybean genotypes varied greatly in terms of their relative stability. The greatest seed weight/ plant were produced by Giza111 followed by H1 L3genotypes in both seasons that out-yielded the grand mean over environments for seed weight/ plant. Giza 22 in both seasons contains large percentage of oil. The genotype H6 L198 was stable phenotypically because, had S^2di values which were not significantly different from zero and bi = 1 for oil%. Also, it was average stable under the studied environments. According AMMI and GGE biplot analysis, the genotype Giza 22 followed by Giza 111 was more stable for the studied traits. Thus the mention genotypes is favorable to grow in various environment

Keywords: Soybean, Sowing date, Plant density, AMMI, GGE biplot.

Introduction

The soybean is one of the most important agricultural legumes, supplies oil, a component of medications, and high-quality protein for both people and animals (**Pagano and Miransari, 2016**). Soybean may also improve soil by fixing atmospheric nitrogen (**Ngalamu *et al.*., 2013**). It will benefit the subsequent crop. Hence, developing stable, high-yielding genotypes is one of the most crucial goals to increase soybean production and area. There is constant research being done on novel techniques to boost production, and the planting area needed to fulfil the rising demand for this commodity on a worldwide scale is always expanding. (**Masuda and Goldsmith, 2009**). For soybeans to grow and develop healthily and keep their yield potentiality, the ideal planting date is necessary. How planting date impacts soybean seed output is significantly influenced by genetic and environmental variables (**Egli and Cornelius, 2009**). The optimal planting date and its impact on the many kinds under investigation were determined by several researches. The relationship between the planting date and the protein and oil content of seeds **Bajaj *et al.*., (2008), Muhammad *et al.* (2009), El-Hosary et al. (2015) and Morsy et al. (2017).**

The genotype and geographic location may affect the ideal plant density to achieve the best yield. In America, the ideal plant density is from 30 to 50 plants/ m^2 (**Zuffo, 2018**). **Kang *et al.*. (1998)** reported the greatest output in South Korea at 33 to 53 plants m^{-2}. The statistics shown above clearly shows that the ideal plant density for soybeans may vary based on the area.

In soybeans, plant density modifies leaf area, which impacts light absorption and canopy photosynthesis. Due to enhanced light interception, the narrow row of soybeans produces a larger yield than the broader row of soybeans (**Board *et al.*., 1992**).

The assessment of genotypes under varied environments is one of the most crucial steps in the majority of applied plant breeding programmes (years, sowing dates and plant density). A genotype's yield performance frequently differs from one environment to another due to its quantitatively inherited traits, resulting in a strong genotype ×

environment (GxE) interaction. The use of mean seed yield across environments as a gauge of genotype performance is dubious when the (GxE) interaction is considerable (**Ablett *et al.*, 1994**) and **El-Hosary *et al.* (2015)**. Only the presence, significance, and degree of stability can be determined using the combined analysis of variance. If a genotype has a high mean yield and the capacity to avoid significant yield volatility in a variety of conditions, it is said to be stable. Several researchers, including **Ablett *et al.* (1994), Radi *et al.* (1993), Al-Assily *et al.* (1996) and (2002**) described the significance of (GxE) in stability study of soybean.

Modeling the (GxE) interaction may be used to determine stability using a variety of statistical techniques. Nonetheless, approaches based on regression models and variance measurements are those that are most frequently utilized. **Yates and Cochran (1938)** first suggested using regression statistics as a stability parameter; this idea was later rediscovered by **Finlay and Wilkinson (1963)**, and then it was further developed by **Eberhart and Russell (1966). Tai (1971)** also provided two stability factors that were comparable to those of **Eberhart and Russell (1966)**.

Mean performance, slope of the regression line, and deviation from regression are the three metrics used by the regression technique to describe stability. According to the statistics used to parameterize the variance component measurements as stability parameters, yield performance varied depending on the environment or the contribution of each genotype to the overall (GxE) interaction.

Examining the yield components that are strongly connected with yield is a contemporaneous option to the AMMI and GGE biplot analysis as doing so enables the breeder to simultaneously adjust yield by enhancing other particular associated features. The inability to assess the relative significance of the direct and indirect impacts of the factors that drive grain production, however, limits estimates based on simple correlations.

Therefore, the objectives of this work were to evaluate the stability of six soybean genotypes and to examine the effect of seasons, sowing dates and plant density for mean performance and stability of seed yield/ plant and oil% across the aforementioned environments.

Materials and Methods

The present study was carried out at the experimental farm, Mattana Agricultural Research Station, at an altitude of 99 masl and at 25.67°N, 32.71°E, Luxor Governorate, Egypt during the period of 2019 and 2020 summer seasons.

The soybean genotypes used in this study consisted of two Egyptian commercially cultivars i.e. Giza 22and Giza 111, in addition four local promising lines selected from the soybean Breeding program of legume department research. Names, origin and pedigree of the studied six soybean genotypes are presented in **Table 1**.

Table 1. The name, pedigree, origin and growth habit of the six tested soybean genotypes.

Genotype code	Cultivar name	Pedigree	Origin	Growth habit
G1	H1 L3	H20 X Gassoy	Egypt	Indeterminate
G2	H4 L4	DR101 x Lamar	Egypt	Indeterminate
G3	H6 L198	Toano x Nena	Egypt	Indeterminate
G4	H18 L54	Dekabig x Crawford	Egypt	Indeterminate
G5	Giza 22	Crawford x Forest	Egypt	Indeterminate
G6	Giza111	Crawford x Celest	Egypt	Indeterminate

Meteorological data in seasons 2019 and 2020 were obtained from the Agro-Meteorological Station at mattana from April to September, the average temperatures in the first season were 32, 34, 35, 35, 33 and 35°C and relative humidity were 51.2, 57.6, 58.2, 51.4, 51.7 and 50.4%, respectively. Comparable data in the second season 2020 at the same location from April to September, the average temperatures in the first season were 34, 34, 35, 34, 31 and 26.2°C and relative humidity were 51.2, 57.6, 58.2, 51.4, 51.7 and 50.4%, respectively.

Field trial

In each season, three separate experiments were conducted according to the sowing date. Thus, three adjacent experiments were designated and sown on 15th April, 1st May, and 15th May, representing the early, optimum and late sowing dates. In each sowing date, the three plant populations densities i.e. 70000, 140000 and 210000 plants/ fed were achieved. The experimental design was laid out in a split-plot design with three replicates in each sowing date and season. The Three aforementioned plant population densities were distributed randomly in the main-plots, whereas the six soybean genotypes were assigned randomly in the sub-plots. Each plot included three ridges that were each 3 m long and spaced 60 cm apart. The seed was inoculated with soybean inoculums. Three weeks following planting, plant thinning was carried out to produce optimum plants per hill. The area's customary cultural techniques for producing soybeans with high seed yields were followed. At harvest, seed weight/plant and oil% were measured. Which seed oil was

extracted using the soxhlet extraction device and petroleum ether (40 to 60 c) as a solvent was identified by the oil percentage. 60 g of pumpkin seeds, 100 g of pumpkin seeds, and 100 g of milk thistle seeds were obtained for oil extraction since 20 g of oil was required for further analysis. Using a rotating vacuum evaporator, the extracted oil was separated from the organic solvent.

Statistical analysis

1- Analysis of variance

Each environment underwent a systematic study of variance in split-piece design according to **Gomez and Gomez (1984).** Prior to joint analysis, **a Bartlett test (1937)** was performed to determine whether variances were homogeneous based on the homogeneity of the individual error components. In light of this, a pooled study of variance across 18 environments was appreciated. In this study, environments (groups of years, sowing dates, and plant densities) were considered random effects, while genotypes were generally considered fixed effects. We were able to investigate the stability of the yield performance of the tested genotypes due to the identification of significant genotype-environment (GxE) interactions. **Zobel *et al.* (1988)** was used to separate one degree of freedom for the non-additive component to examine the presence of multiplicative (GxE) interaction in the two-way data.

2- Stability analyses

Two mathematical techniques used in parametric procedures are regression modeling and variance measures in multivariate analysis. **Eberhart and Russell (1966).** and **Tai (1971)**. introduced the regression technique. The regression model suggested by Eberhart and Russell (1966) provides the linear regression coefficient, b, and the deviation from the regression mean square, S2d, as indications of the genotype response to the environmental variable. If the regression coefficient (b value) is not significantly different from unity, the genotype is classified as environment-adapted. Tai (1971) also provided two stability factors that were comparable to those of **Eberhart and Russell (1966).** Tai method statistics measure, in terms of the size of the error variance, respectively, the linear response of environmental factors and deviation from the linear response. The parameters for genotypic stability are the two parts. The parameters of α and λ could be regarded as modified forms of b and S2d, respectively.

The GGE—biplot technique, which combines two concepts (**Gabriel, 1971**) and the GGE concept, was used to visually examine the multi-environment yield trails (MEYTs) data (**Yan *et al.* 2000**). The method uses a biplot to display the variables (genotype and genotype by environment interaction), which are other factors of variation. This work used genotype-focused scaling for both the visualizing for genotypic comparison and the visualizing for environmental comparison. Moreover, symmetric scaling provided the clearest representation of the MEYTs yield data's which—won—where pattern (**Yan and Rajcan, 2002**). The additive effect means and multiplicative interaction AMMI model was performed using the Genotype x Environment Analysis with R for Windows) Version 4.1 (2017-08-3) software.

Results and Discussion

The results presented in Table 2 show the main effect of different sowing dates and plant density rates and interactions between them on seed weight/ plant and oil% of soybean in the 2019 and 2020 seasons.

Average values of seed weight/ plant as affected by studied sowing dates showed a significant decrease in seed weight with delay in sowing dates. The highest seed weight mean values reached 43.23 and 50.78 in the 2019 and 2020 seasons, respectively. Meanwhile, the decrease in seed weight percentages at the late sowing date reached 2.48% and 33.49% in 2019 and 13.07% and 46.24% in the 2020 season, respectively when soybean planted on 1st May and 15th Jun as compared with the early sowing date 15th April in each season, respectively.

As for, oil%, as affected by studied sowing dates, showed an insignificant effect in oil%. The highest oil% mean values reached 41.89% in the 2020 season.

The main effect of plant density affected decreased significantly seed weight/ plant of soybean with decreased density. However insignificant differences were found between 140000 and 210000 plant/ fed. There was a significant interaction effect due to the sowing date and plant density. The highest increase in the seed weight of soybean in the first season (53.85) was detected in the early sowing date with low plant density, followed by the combination between the early sowing date and plant density of 140000 plants/ fed. (50.99), Meanwhile, the lowest value of seed weight was shown when soybean was planted on 15th Jun 2020 with 210000 plants/ fed. In each plant density, it can be noted that the values of seed weight decrease significantly by delay in the sowing date, Also the seed weight loss was observed in each sowing date by increasing plant density in the studied seasons.

The main effect of plant density affected an increase significantly oil% of soybean with increased density percentage estimated by 2.24% and 5.24% in 2019; 2.56% and 4.08% in 2020 when increase plant density from 70000 to 140000 and 210000 plants/ fed, respectively. Meanwhile, There was an insignificant interaction effect due to the sowing date and plant density Results in **Table 3** illustrate the main effect of studied genotypes for seed weight/

plant and oil%. The main effect of genotypes shows a pattern of Giza111< H18 L54 < H1 L3< Giza 22 <H6L198< H4 L4 and average seed weights were 57.58, 57.53, 45.73, 44.97, 40.51, and 39.88, respectively in the first season 2019. Meanwhile, the pattern was Giza111< H1 L3< H18 L54 < H6L198<Giza 22 < H4 L4 and average seed weights were 49.16, 47.85, 39.80, 38.61, 35.73, and 32.27, respectively at 2020.

Table 2. The main effect of different sowing dates and plant density rates and interactions between them on seed weight/ plant and oil% of soybean in the 2019 and 2020 seasons.

Seed weight/ plant								
Plant density (Plants per fed.)	**S1 15th April 2019**	**S2 1st May 2019**	**S3 15th may 2019**	**Mean**	**S1 15th April 2020**	**S2 1st May 2020**	**S3 15th Jun 2020**	**Mean**
70000	53.85	47.78	61.71	54.44	50.51	42.82	29.06	40.8
140000	43.25	37.77	51.79	44.27	50.99	40.36	30.33	40.56
210000	32.6	40.93	59.64	44.39	50.83	49.24	22.49	40.85
Mean	43.23	42.16	57.71		50.77	44.14	27.3	
			2019				**2020**	
	item		**LSD5%**		**item**		**LSD5%**	
	Sowing date (S)		0.99		Sowing date (S)		3.07	
	Plant density (D)		0.99		Plant density (D)		3.07	
	SxD		1.31		SxD		4.04	
Oil%								
Plant density (Plants per fed.)	**S1 15th April 2019**	**S2 1st May 2019**	**S3 15th may 2019**	**Mean**	**S1 15th April 2020**	**S2 1st May 2020**	**S3 15th Jun 2020**	**Mean**
70000	38.78	39	38.94	38.91	40.12	40.34	40.28	40.25
140000	40.22	40.17	40.11	40.17	41.32	41.28	41.23	41.28
210000	41.11	40.72	41	40.94	42.01	41.72	41.94	41.89
Mean	40.04	39.96	40.02		41.15	41.11	41.15	
			2019				**2020**	
	item		**LSD5%**		**item**		**LSD5%**	
	Sowing date (S)		0.71		Sowing date (S)		0.66	
	Plant density (D)		0.71		Plant density (D)		0.66	
	SxD		0.94		SxD		0.87	

It can be concluded that the three genotypes Giza 111, H18L54, and H1L3 seemed to be the best varieties which give the highest values for seed weight. Meanwhile, the genotype H4L4 showed low values for seed weight/ plant in both seasons. The interaction between genotypes and plant density for seed weight/plant is presented in Table 3. A significant decrease in seed weight/plant was observed associated with a decrease in plant density for most genotypes. The same order pattern for genotypes was found in each plant density in the two seasons. The highest values were detected by the genotype H18 L54 followed by Giza 111 in the three plant densities in the first seasons. Meanwhile, the genotype H4L4 with 240000 plants / fed exhibited a low value for seed weight.

Regarding oil%, the main effect of genotypes shows a pattern of Giza 22< H4 L4< H6L198< H18 L54 < Giza111< H1 L3. In each season and average oil% were 42.15, 40.33, 40.07, 39.52, 39.52, and 38.44, respectively in the first season of 2019 and 42.87, 41.40, 41.19, 40.74, 40.74, and 39.87 in the second season. It can be concluded that the three genotypes Giza 22 seemed to be the best varieties which give the highest values for oil%. Meanwhile, the genotype H1L3 showed low values for oil% in both seasons. The interaction between genotypes and plant density for oil% is presented in Table 3. A significant increase in oil% was observed associated with an increase in plant density for all genotypes. The same order pattern for genotypes was found in each plant density in the two seasons. The highest values were detected by the genotype Giza 22 in the third plant density in the first and second seasons. Meanwhile, the genotype H1L3 with 70000 plants / fed exhibited a low value for oil%.

Table 3. The main effect of studied genotypes and plant density and the interaction between them in the two studied seasons for seed weight/ plant and oil%.

Seed weight/ plant

	2019				2020			
	Plant density (Plants per fed.)				Plant density (Plants per fed.)			
Genotype	70000	140000	210000	Mean	70000	140000	210000	Mean
H1 L3	49.79	39.69	47.71	45.73	51.65	45.74	46.17	47.85
H4 L4	49.18	35.46	35.01	39.88	35.96	34.78	29.06	33.27
H6 L198	42.11	37.52	41.89	40.51	39.29	36.96	39.57	38.61
H18 L54	65.42	54.84	52.33	57.53	37.1	40.16	42.14	39.8
Giza 22	58.38	38.15	38.39	44.97	33.01	35.48	38.71	35.73
Giza111	61.78	59.96	51	57.58	47.76	50.25	49.47	49.16
Mean	54.44	44.27	44.39		40.8	40.56	40.85	

2019		2020	
item	LSD 5%	item	LSD 5%
Genotype (G)	1.13	Genotype (G)	3.04
Plant density (D)	0.33	Plant density (D)	3.07
GxD	1.48	GxD	3.99

Oil%

	2019				2020			
	Plant density (Plants per fed.)				Plant density (Plants per fed.)			
Genotype	70000	140000	210000	Mean	70000	140000	210000	Mean
H1 L3	36.67	38	40.67	38.44	38.45	39.51	41.65	39.87
H4 L4	39.56	40.67	40.78	40.33	40.77	41.68	41.76	41.4
H6 L198	39.22	40.33	40.67	40.07	40.49	41.41	41.66	41.19
H18 L54	38.56	39.67	40.33	39.52	39.94	40.89	41.4	40.74
Giza 22	41.33	42.11	43	42.15	42.23	42.84	43.55	42.87
Giza111	38.11	40.22	40.22	39.52	39.6	41.32	41.31	40.74
Mean	38.91	40.17	40.94		40.25	41.28	41.89	

2019		2020	
Item	LSD 5%	item	LSD 5%
Genotype (G)	0.7	Genotype (G)	0.65
Plant density (D)	0.71	Plant density (D)	0.66
GxD	0.92	GxD	0.86

Results of **Table 4** show that the interaction between genotypes and sowing date was significant in both studied seasons for the seed weight/ plant and oil%.

The genotypes Giza 11 and H18L54 showed the highest values for seed weight/ plant in the early sowing date in the inaugural season, while, the genotype, H18L54 give the low values for seed weight/ plant when planted on 15th Jun 2020. For the third-order interactions, the finest standards for seed weight/ plant were in the inaugural season when planted variety H18L54 with a plant density of 70000 plants/ fed. On the other hand, the low value for the mentioned trait was detected in the second season, when planted H18 L54 in a late sowing date with 210000 plants/ fed in the second season.

The genotype Giza 22 showed the highest values for oil% in the optimum sowing date in the first season, while, the genotype, H1 L3 give the low values for oil% when planted on 15th Jun 2019 (Table 4).

For the third-order interactions, the highest values for plot weight were in the first season when planted variety Giza 22 with a plant density of 200000 plants/ fed. On the other hand, the low value for the mentioned trait was detected in the second season, when planted H1L1 in a late sowing date with 70000 plants/ fed in the first season.

Table 4. The interaction between genotypes, plant density, and sowing dates for seed weight/plant in seasons 2019 and 2020.

	Seed weight/ plant											
	Sowing date in 2019											
	S1 15th April 2019 Plant density (Plants per fed.)			Mean	S2 1st May 2019 Plant density (Plants per fed.)			Mean	S3 15th may 2019 Plant density (Plants per fed.)			Mean
Genotype	70000 (E1)	140000	210000		70000 (E4)	140000	210000		70000 (E7)	140000	210000	

		(E2)	(E3)			(E5)	(E6)			(E8)	(E9)	
H1 L3	51.37	38.40	25.20	38.32	42.37	27.70	46.67	38.91	55.63	52.97	71.27	59.96
H4 L4	37.72	32.88	30.11	33.57	53.49	32.17	33.41	39.69	56.33	41.32	41.50	46.38
H6 L198	38.25	31.60	26.72	32.19	51.57	40.93	43.55	45.35	36.51	40.04	55.40	43.98
H18 L54	83.33	62.39	33.88	59.86	43.61	37.50	45.81	42.31	69.33	64.62	77.31	70.42
Giza 22	52.18	34.44	43.98	43.53	48.45	43.91	32.67	41.68	74.51	36.09	38.53	49.71
Giza111	60.23	59.81	35.71	51.92	47.19	44.39	43.47	45.02	77.93	75.67	73.83	75.81
Mean	53.85	43.25	32.60	43.23	47.78	37.77	40.93	42.16	61.71	51.79	59.64	57.71
					Sowing date in 2020							
	S1 15th April 2020 Plant density (Plants per fed.)			**Mean**	**S2 1st May 2020 Plant density (Plants per fed.)**			**Mean**	**S3 15th Jun 2020 Plant density (Plants per fed.)**			**Mean**
	70000 (E10)	**140000 (E11)**	**210000 (E12)**		**70000 (E13)**	**140000 (E14)**	**210000 (E15)**		**70000 (E16)**	**140000 (E17)**	**210000 (E18)**	
H1 L3	69.35	56.23	63.20	62.92	42.03	35.36	50.67	42.69	43.57	45.62	24.63	37.94
H4 L4	38.94	45.24	35.91	40.03	42.83	36.84	31.41	37.03	26.11	22.25	19.87	22.74
H6 L198	43.03	40.95	32.87	38.95	48.90	40.60	59.55	49.68	25.93	29.33	26.29	27.18
H18 L54	38.05	51.55	60.44	50.01	40.94	41.83	51.53	44.77	32.31	27.11	14.45	24.62
Giza 22	40.17	39.53	53.71	44.47	40.79	44.91	42.60	42.76	18.09	22.00	19.81	19.96
Giza111	73.51	72.44	58.81	68.26	41.43	42.63	59.69	47.91	28.35	35.68	29.92	31.32
Mean	50.51	50.99	50.83	50.77	42.82	40.36	49.24	44.14	29.06	30.33	22.49	27.30
	item		**2019 LSD 5%**					**Item**		**2020 LSD 5%**		
	Sowing date (S)			0.99				Sowing date (S)		3.07		
	SxG			1.48				SxG		3.99		
	SxD			1.48				SxD		3.99		

Table 4. Cont.

	Oil%											
					Sowing date in 2019							
	S1 15th April 2019 Plant density (Plants per fed.)			**Mean**	**S2 1st May 2019 Plant density (Plants per fed.)**			**Mean**	**S3 15th may 2019 Plant density (Plants per fed.)**			**Mean**
Genotype	**70000 (E1)**	**140000 (E2)**	**210000 (E3)**		**70000 (E4)**	**140000 (E5)**	**210000 (E6)**		**70000 (E7)**	**140000 (E8)**	**210000 (E9)**	
H1 L3	36.00	38.00	42.00	38.67	38.00	39.00	39.00	38.67	36.00	37.00	41.00	38.00

H4 L4	39.00	41.00	40.67	40.22	40.00	40.00	40.67	40.22	39.67	41.00	41.00	40.56
H6 L198	39.00	41.00	41.00	40.33	39.33	39.67	40.00	39.67	39.33	40.33	41.00	40.22
H18 L54	38.67	40.00	40.33	39.67	38.00	38.00	39.67	38.56	39.00	41.00	41.00	40.33
Giza 22	40.00	41.00	42.00	41.00	44.00	44.33	45.00	44.44	40.00	41.00	42.00	41.00
Giza111	40.00	40.33	40.67	40.33	34.67	40.00	40.00	38.22	39.67	40.33	40.00	40.00
Mean	38.78	40.22	41.11	40.04	39.00	40.17	40.72	39.96	38.94	40.11	41.00	40.02
					Sowing date in 2020							
	S1 15th April 2020 Plant density (Plants per fed.)			**Mean**	**S2 1st May 2020 Plant density (Plants per fed.)**			**Mean**	**S3 15th Jun 2020 Plant density (Plants per fed.)**			**Mean**
	70000 (E10)	**140000 (E11)**	**210000 (E12)**		**70000 (E13)**	**140000 (E14)**	**210000 (E15)**		**70000 (E16)**	**140000 (E17)**	**210000 (E18)**	
H1 L3	37.88	39.49	42.69	40.02	39.51	40.30	40.32	40.04	37.95	38.74	41.94	39.54
H4 L4	40.30	41.97	41.65	41.31	41.13	41.13	41.69	41.32	40.88	41.93	41.94	41.58
H6 L198	40.28	41.97	41.92	41.39	40.62	40.88	41.13	40.88	40.57	41.38	41.94	41.30
H18 L54	40.00	41.13	41.38	40.84	39.51	39.57	40.88	39.99	40.30	41.97	41.94	41.40
Giza 22	41.18	41.92	42.75	41.95	44.37	44.63	45.15	44.72	41.13	41.97	42.75	41.95
Giza111	41.11	41.43	41.65	41.39	36.87	41.16	41.13	39.72	40.84	41.38	41.13	41.12
Mean	40.12	41.32	42.01	41.15	40.34	41.28	41.72	41.11	40.28	41.23	41.94	41.15
			2019							**2020**		
	item		**LSD 5%**					**Item**		**LSD 5%**		
	Sowing date (S)		0.71					Sowing date (S)		0.66		
	SxG		0.92					SxG		0.86		
	SxD		0.92					SxD		0.86		
	SxDxG		1.21					SxDxG		1.13		

The stability analysis

In Table (5), the pooled analysis of variance is displayed. For mention traits, very significant mean squares resulting from the interaction of genotypes and environments show that genotypes vary greatly between environments. Environment + (genotype × environment) interaction was partitioned into the environment (linear), genotype × environment (linear) interaction (sum of squares due to regression, bi), and unexplained deviation from regression (pooled deviation mean squares, S2d). Significant genotype × environment (linear) mean squares were detected for the studied characters indicating the linearity response of different genotypes to different environmental conditions when they test for pooled deviations. Nonetheless, the extremely significant pooled deviation for all characteristics under investigation shows that deviation from linear regression plays a substantial role in determining the degree of each genotype under investigation. These findings supported those made earlier by **Silva *et al.* (2022).** Between the examined genotypes, environments, and genotypes environments interaction for plot weight, they discovered extremely significant differences.

Table 5. Mean squares of stability analysis of seed weight/ plant and oil% for six genotypes across eighteen environments.

SOV	Df	seeds weight/ plant	oil%
Genotype	5	738.96**	22.43**
Environment+ G*E	102	192.66**	2.12**
Environment	17	691.83**	5.78**
Genotype x Env.	85	92.82**	1.38**
a) Env . (linear)	1	11761.06**	98.30**
b) V x Env. (linear)	5	264.59**	2.30**
c) pooled deviations	96	68.40**	1.11**
Genotypes			
H1 L3	16	82.11**	1.05**
H4 L4	16	34.39**	0.17**
H6 L198	16	67.78**	0.15**
H18 L54	16	87.28**	0.63**
Giza 22	16	87.17**	2.54**
Giza111	16	51.70**	2.10**
poled error	180	0.15	0.001

Phenotypic and genotypic stability

Three parameters—mean performance across contexts, linear regression, and deviations from regression function—were used to assess the phenotypic stability of the six genotypes under investigation. Table 6 lists the analyzed characteristics' phenotypic stability parameters. The findings make it abundantly evident that the regression coefficient (bi) for every genotype varied considerably from zero for every characteristic.

In the same context, the genotypic stability technique was performed according to **Tai (1971)**, who separated the genotype x environment interaction effect of the ith genotypes into two statistical parameters namely α and λ. These statistics α and λ measure the linear response to environmental effects and the deviation from the linear response in terms of the magnitude of the error variance, respectively. Genotypic stability parameters of the studied traits are presented in **Table 6**.

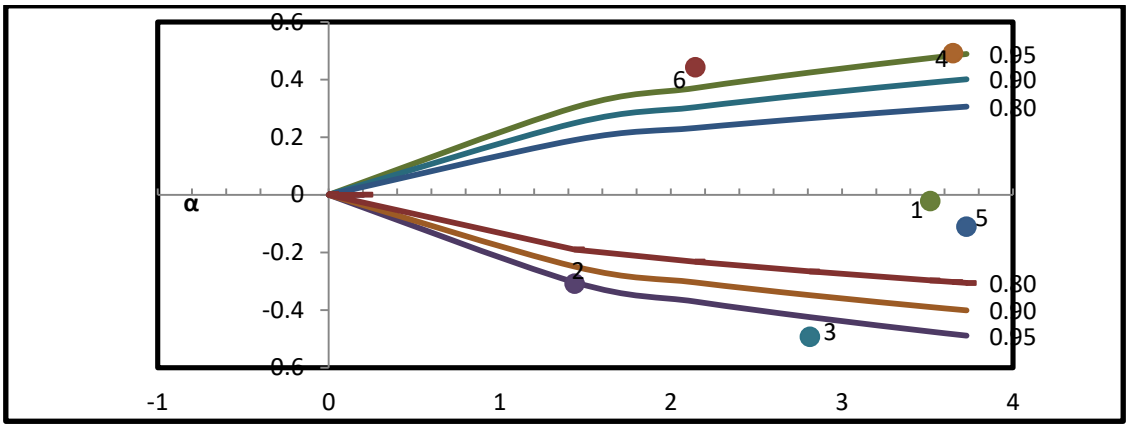
Table 6. Estimation of stability and adaptability parameters of all studied traits.

	seed weight/ plant					oil%				
	Eberhart and russell,1966			**Tai,1971**		**Eberhart and russell,1966**			**Tai,1971**	
Genotype	**MEAN**	**b i**	**S^2 di**	**α**	**Λ**	**MEAN**	**b i**	**S^2 di**	**α**	**Λ**
H1 L3	46.79	0.98	81.966**	-0.02	3.52	39.16	1.72	1.045	-2.45	30.13
H4 L4	36.57	0.71	34.239**	-0.31	1.44	40.87	0.75	0.165	0.86	4.04
H6 L198	39.56	0.54	67.632**	-0.49	2.81	40.63	0.84	0.151	0.54	2.37
H18 L54	48.67	1.45	87.133**	0.49	3.65	40.13	0.95	0.627	0.17	5.68
Giza 22	40.35	0.9	87.027**	-0.11	3.73	42.51	0.71	2.544**	1	26.07
Giza111	53.37	1.41	51.554**	0.44	2.14	40.13	1.04	2.100*	-0.13	18.71
Mean	44.22					40.57				
LSD 5%	3.98					0.51				

** refer to Significant at 0.05 probability levels.

For the Seed weight/ plant, Table 6 listed averages across environments and phenotypic stability metrics. The mean seed weight/ plant, bi and S2di parameters for the 6 genotypes. The genotypes showed different responses to differences among the environments. The bi values significantly differed from zero and did not differ significantly from unity in all genotypes except, H18 L54 and Giza111. Also, all genotypes had significant S2di values from zero, indicating that these genotypes had the most stable performance. According to Eberhart and Russell (1966). However, genotypes, H1 L3, H18 L54, and Giza111 gave the highest mean values, but there were unstable across the studied environments because S2di were significant. Graphical analysis Fig. 9 showed could be useful in identifying stable genotypes. The genotype H4 L4 was genetically stable for seeds weight/ plant across the environments. Meanwhile, the mentioned genotypes gave the lowest mean values compared with the grand mean. But, it exhibited the above stability. Such genotypes can be used as a source for stability to be crossed with high seeds weight/ plant and practicing selection for genotypes with high yield and sound stability. Fig. 1 also provides a visual overview that is helpful in identifying the genotypes that are genetically stable. One could see that H1 L3 and Giza 22 had stability values on average that did not substantially deviate from 0 at any of the probability levels at P = 0.90. Also, for the

genotypes, the statistics were not substantially different from =1, showing that they were generally stable in the contexts under study. The seed weight/plant stability of the other genotypes was unstable.



Tai's stability statistics for seed weight/plant of six soybean genotypes across 18 settings are shown in fig. 1.
Notes: 1- **H1 L3**, 2- **H4 L4**, 3- **H6 L198**, 4- **H18 L54**, 5- **Giza 22** and 6- **Giza111**

Table 6 provides means across environments as well as phenotypic and genotypic stability characteristics. For all genotypes save H1 L3, a negligible regression coefficient (bi) from unity was found.
Regarding, the second stability parameter (S2d) the genotypes H4 L4, H6 L198, and H18 L54 exhibited insignificant and low deviation from regression, at the same time the mean value of oil% for H4 L4 and H6 L198 over the average mean, indicating that more phenotypically stable with high mean.
The values of α and λ for oil% are displayed in Table 35 and graphically illustrated in **Figure 2**. The results of the study showed that the genotypes H18 L54 and Giza111 had average stability. Meanwhile, the genotypes H4 L4 and Giza 22 had below-average stability α < 0 and λ =1.

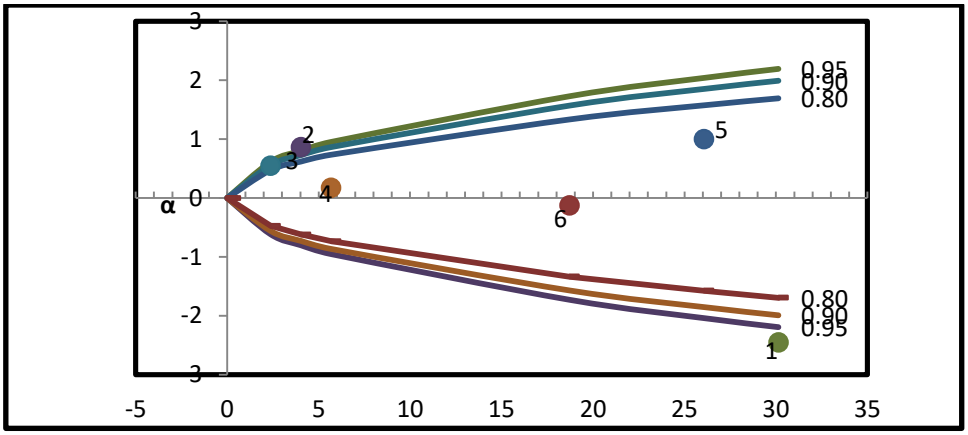


Fig. 2. Distribution of Tai's stability statistics for oil% of six soybean genotypes across 18 environments.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.
AMMI: Analysis of multiplicative interactions and additive main effects.

AMMI is a hybrid model that uses a two-way data structure's additive and multiplicative elements. Principal component analysis (PCA) is then applied to the interaction portion of the model to a new set of coordinate axes that more thoroughly explains the interaction pattern and the estimation carried out using the least squares principle. The model first separates the additive variance from the multiplicative variance. This test may be used to determine the number of multiplicative terms to be preserved in a multiplicative model by comparing the mean square for axis n against an estimate of the error term. The AMMI analysis has been shown to be successful because it captures a sizable portion of the GxE sum of squares, distinguishing main effects from interaction effects that offer various opportunities for agricultural researchers, and the model frequently provides an agronomically relevant interpretation of the data. The outcomes of the AMMI analysis can be represented visually as biplots, where the genotype and environment scores of the first two or three bilinear (multiplicative)

components are represented by vectors in space, with beginning points at the origin and end points specified by the scores. Usually, the environmental and genotype scores of the first and second bilinear terms are plotted. The distance between two genotype vectors (their endpoints) is indicative of the amount of interaction between the genotypes. The cosine of the angle between two genotypes (or environment) vectors approximates the correlation between the genotypes (or environments) with respect to their interaction. Acute angles indicate a positive correlation, with parallel vectors (in exactly the same directions) representing a correlation of 1. Negative correlations are represented by obtuse angles, with a correlation of -1 being opposite directions. Directions' perpendicularity suggests a correlation of 0. From orthogonal projections of the environmental vectors on the line specified by the direction of the corresponding genotype vector, one may compute the relative amounts of interaction for a specific genotype over environments. Environmental vectors having the same direction as the genotype vectors have positive interactions (that is these environments favored these genotypes), whereas vectors in the opposite direction have negative interactions.

AMMI biplot with the first two components is presented in **Fig. 3**, With regard to seeds weight/ plant results that environment, genotype, and interaction mean squares reached to be significant. Revealing that all sources of variance are important in analysis however, the contribution of genotypes, environments and the interaction principal component axis (IPCA) were 15.83%, 50.38%, and 33.79%, respectively of the variances in the treatments and (IPCA1 and IPCA2) together had a total variance of (70.56%) of the interaction.

AMMI biplot with the first two components is presented in Fig. 3, with this model we can explain 70.55 % of the total variability. Fig. 3 illustrated that the highest mean values for seed weight/ plant were detected by G6- Giza111 followed by G4- H18 L54, then G1- H1 L3, where, the places of those genotypes are located on the left. Meanwhile, the low mean values were exhibited by the two genotypes, G2- H4 L4, G3- H6 L198, and G5- Giza 22 and they are located on the right. We can observe that the environments that classify in a form similar are E10 with E11, E9, and E8. Also, E12 was closely related to E2, E1, and E7. Meanwhile, E4, E14 E5, and E3 indicate that for many cycles in the same environment with the same genotypes, we can discard any of the environments without losing precision in the results. Another thing that we can observe in the biplot is the behavior of the genotypes in each environment, the high mean value for genotype G6- Giza 111 has better seed weight/ plant than other genotypes, especially in the environment E8; the genotypes G4- H18 L54 ranked the second genotype for seed weight/plant. It seemed to behave better in the mentioned trait than other genotypes in the environments E12, E2,E 1, and E7; Meanwhile, the genotypes G1-H1 L3 ranked the third genotype across all studied environments and have better in seed weight/-plant than other genotypes.
especially in the environments E10, E11 and E9.

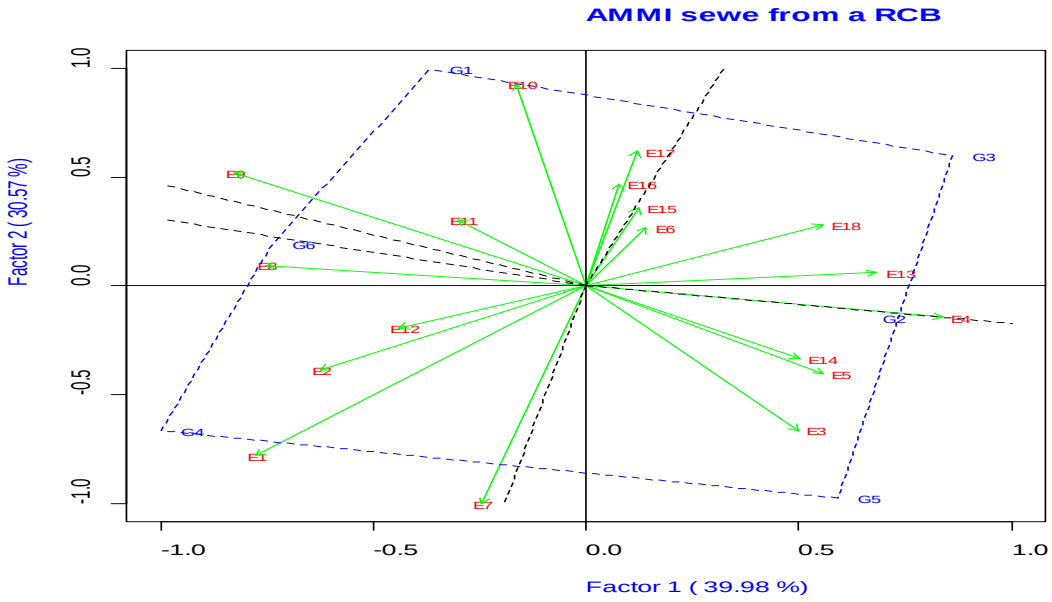


Fig. 3. AMMI biplot with the first two components for seed weight/ plant.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

AMMI is a hybrid model that uses a two-way data structure's additive and multiplicative elements. Principal component analysis (PCA) is then applied to the interaction portion of the model to

a new set of coordinate axes that more thoroughly explains the interaction pattern and the estimation carried out using the least squares principle. The model first separates the additive variance from the multiplicative variance. This test may be used to determine the number of multiplicative terms to be preserved in a multiplicative model by comparing the mean square for axis n against an estimate of the error. The AMMI analysis is efficient because it captures a sizable portion of the GxE sum of squares, clearly distinguishing main effects from interaction effects that offer various opportunities for agricultural researchers, and the model frequently offers an agronomically relevant interpretation of the data. The outcomes of the AMMI analysis can be represented graphically as biplots, where the genotype and environment scores of the first two or three bilinear (multiplicative) terms are represented by vectors in space, with starting points at the origin and end points determined by the scores. The first and second bilinear terms' environmental and genotype scores are often shown. The level of interaction between the genotypes is shown by the separation between two genotype vectors' ends. The correlation between two genotypes' (or environments') vectors regarding their interaction can be approximated by the cosine of the angle between them. Parallel vectors (moving in the same direction) show a correlation of 1, whereas acute angles show a positive correlation. Negative correlations are represented by obtuse angles, with a correlation of -1 being opposite directions. Directions' perpendicularity suggests a correlation of 0. Using orthogonal projections of the environmental vectors on the line specified by the direction of the corresponding genotype vector, one may compute the relative quantities of interaction for a certain genotype over environments. Positive interactions (i.e., environments preferred these genotypes) result from environmental vectors moving in the same direction as the genotype vectors, whereas negative interactions result from environmental vectors moving in the opposite way.

AMMI biplot with the first two components is presented in **Fig. 3**, about seeds, weight/ plant results showed that mean squares of treatments, genotypes, and environments were highly significant reveling that all sources of variance are important in analysis, however, genotypes, environment and interaction principal component axis (IPCA) contributed with 15.83%, 50.38% and 33.79% in treatments variances, the (IPCA1 and IPCA2) together with had a total (70.56%) variances of the interaction.

AMMI biplot with the first two components is presented in Fig. 3, with this model we can explain 70.55 % of the total variability. Fig. 3 illustrated that the highest mean values for seed weight/ plant were detected by G6- Giza111 followed by G4- H18 L54, then G1- H1 L3, where, the places of those genotypes are located on the left. Meanwhile, the low mean values were exhibited by the two genotypes, G2- H4 L4, G3- H6 L198, and G5- Giza 22 and they are located on the right. We can observe that the environments that classify in a form similar are E10 with E11, E9, and E8. Also, E12 was closely related to E2, E1, and E7. Meanwhile, E4, E14 E5, and E3 indicate that for many cycles in the same environment with the same genotypes, we can discard any of the environments without losing precision in the results. Another thing that we can observe in the biplot is the behavior of the genotypes in each environment, the high mean value for genotype G6- Giza 111 has better seed weight/ plant than other genotypes, especially in the environment E8; the genotypes G4- H18 L54 ranked the second genotype for seed weight/plant. It seemed to behave better in the mentioned trait than other genotypes in the environments E12, E2, E 1, and E7; Meanwhile, the genotypes G1-H1 L3 ranked the third genotype across all studied environments and have better in seed weight/ plant than other genotypes
especially in the environments E10, E11 and E9.

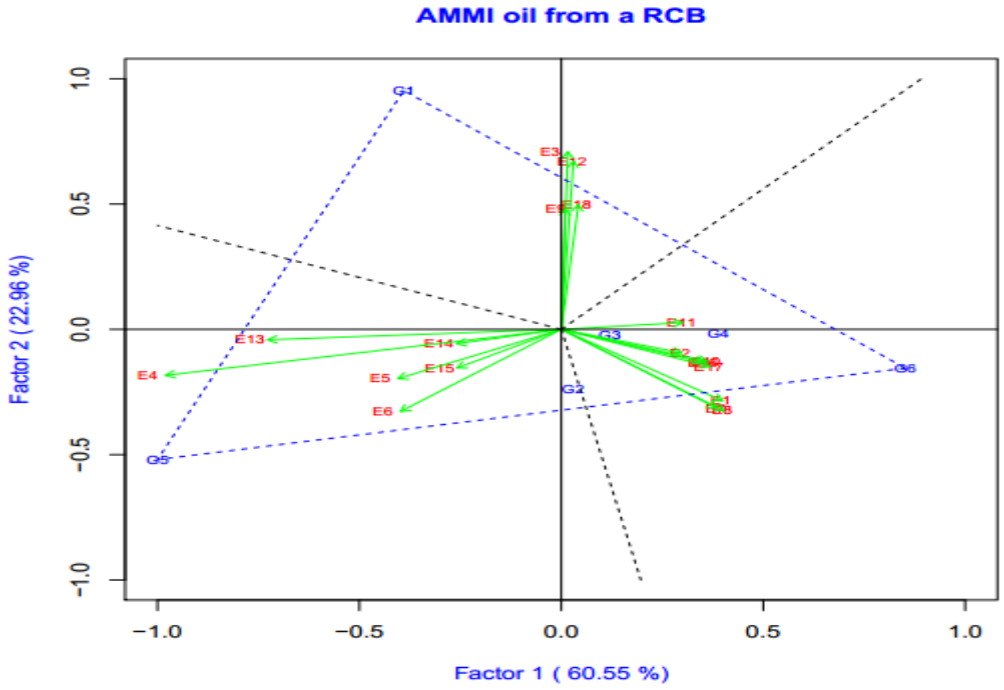


Fig. 4. AMMI biplot with the first two components.

Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.

Environments: E1 to E18 were identified and presented in Table 4.

Biplot analysis for GGE Mega-environments (which-won-where) illustrated that, the ideal genotype or genotypes for each environment are shown in the polygon view of the GGE biplot for seed weight/plant in Figure 5. The best or worse genotypes in some or all settings, with the exception of the left bottom quadrant, are those found near the vertices of a polygon. This gives the researcher a clear and convincing explanation for suggesting genotypes that are suitable for that specific environment. Moreover, it implies that the genotypes may be evaluated in those select mega-environments and still produce reliable yield data. The GGE biplot also provided data that is crucial for decision-making and drawing inferences about certain relationships between environments and genotypes.

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The first (PC1) and second (PC2) principal components, which together account for 43.55% and 27.31% of the overall variation of the standardized data, are both responsible for the GGE-biplot model's 70.68% explanation of variation. The intricacy of the interaction between genes and environment is reflected in the relative percentage of variation (70.68%) for GxE interaction. Analyses of which won where or which is best for what. For the potential presence of many mega-environments in an area, it is vital to analyses the which-won-where pattern of multi-environment yield trails (Yan 2001).

The polygon believes that a biplot is the most useful tool for understanding a biplot and for visualising the interaction patterns between genotypes and environments (Yan *et al*.., 2007). Regarding (Fig. 5), the surroundings fall into one of the four sectors that the rays created by dividing the biplot into two. The top genotypes for each sector in this interpretation of the GGE-biplot have greater yields than the other genotypes in all settings that belong to the sector (**Yan and Rajcan, 2002**) and **Morsy *et al*. (2017)**.

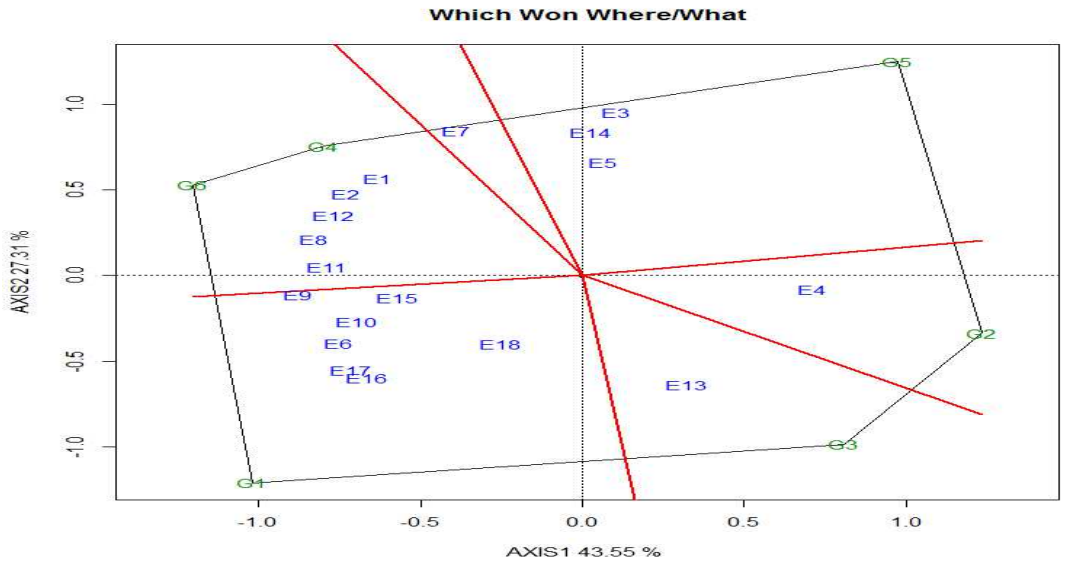

Fig. 5. Polygon view of the GGE-biplot for the which one – where the pattern for 6 soybean genotypes were grown across 18 environments for seed weight/ plant.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

Three genotypes i.e. G5, G2, and G3 located on the right of the original points and these genotypes had a high yield over the grand mean. Genotype G6 exhibited a high seed weight/ plant and ranked the first genotype in all environments (53.37 g). This genotype recorded the highest average grain yield (large PC1 scores), but genotypes 2, 3, and 5 were below average (PC1 scores < 0). Genotypes located at the left of the plot origin were less responsive than the vertex genotypes. The biplot showed not only the average yield of genotype (PCA 1 effects) but also how it is achieved, (Kaya *et al*.., 2002)

Fig 6. genotypes and environments were shown in a GGE biplot on the same plot. The association between environments is revealed by the angle between environment vectors. A positive association is shown by an acute angle. Yet, a straight angle denotes a lack of association and an acute angle, a negative correlation. In order to clarify the positive associations between E3, E5, and E14 (group 1); E4 and E13 (group 2); E18, E16, E17, E6, E10, E15, and E9 (groups 1 through 4), see Figure 6. (group 3). A good link between the remaining settings was also discovered. There was an adverse link between the surroundings of groups 1, 2, 3, and 4, and vice versa.

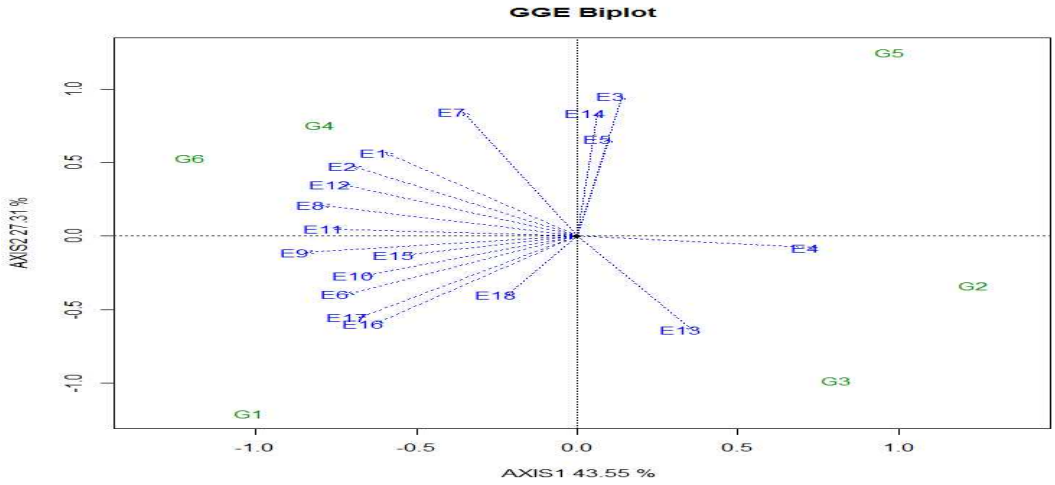

Fig. 6. Biplot of relationships among eighteen environments for seed weight/ plant.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

As seen in Fig. (7), the validity and goodness of fit of the GGE biplot approach were demonstrated by the 70.86% explanation of the two-way interaction table's overall variance by the first two principal components (PC1 and PC2). The Average Environment Coordinate is the straight line with a single arrow (abscissa) that goes through the biplot origin (AEC). The arrow's direction indicates that genotypes will do better on average. The average of the environment PC1 and PC2 scores is shown by the little circle that can be seen on this line. The biplot's average coordinates for each of the tested situations serve as its definition. The line (ordinate), which is perpendicular to the AEC line and crosses through the biplot origin, represents the stability itself.

So, it is accurate to say that the genotype located in the two directions that was closer to the AEC line had a more steady yield. As a result, the genotypes with above-average means are listed in the following order: G6 > G4 ,While, the remaining genotypes exhibited below-average mean seeds weight/plant, G6 outperformed G4. The genotypes positioned extremely close to the AEC line were reflecting their above-average stability whereas genotypes G1 and G3 exhibited below-average stability since it was somewhat put away from the AEC abscissa. This was true regardless of G4 and G6 the seeds weight/plant. In contrast, genotype 2 showed moderate environmental stability. In conclusion, the average environment vector's length was sufficient to choose genotypes based on the mean performance of seed yield. Regardless of the direction, represents a greater of the GEI genotypes which indicates that it is more variable and less stable across environments or vice versa. The current results are in a parallel line with those obtained by **Dehghani *et al*. (2006 and 2009),** Often, the GGE biplot graph is clear and easy to understand when few genotypes and environments are used. While, if many genotypes and environments are used, the graph becomes so crowded that could be difficult to visualize and interpret.

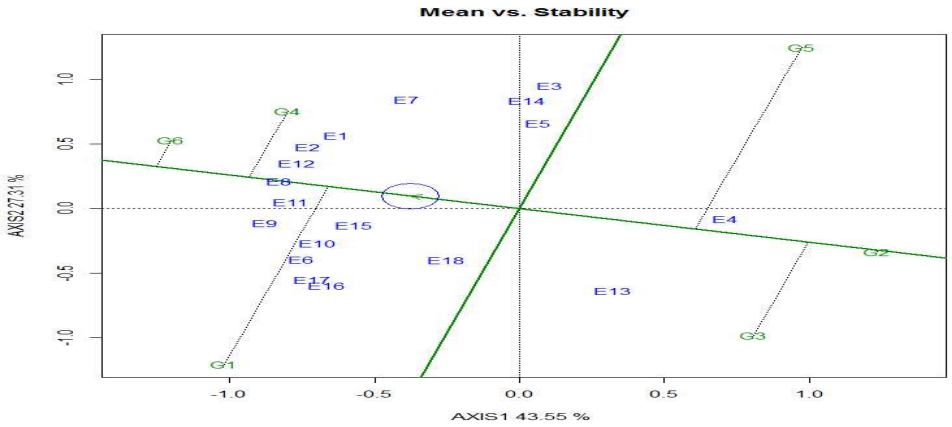

Fig. 7. The mean vs. stability view of the GGE biplot of six soybean genotypes for seed weight/ plant.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

Biplot GGE analysis Mega-environments (which-won-where), the ideal genotype(s) for each environment are shown in the polygon view of the GGE biplot for oil% in Figure 8. The best or worse genotypes in some or all environments, with the exception of the left bottom quadrant, are those found near the vertices of a polygon. This gives the researcher a clear and convincing explanation for suggesting genotypes that are suitable for that specific environment. Moreover, it implies that the genotypes may be evaluated in those select mega-environments and still produce reliable yield data. The GGE biplot also provided data that is crucial for decision-making and drawing inferences about certain relationships between environments and genotypes.

The first (PC1) and second (PC2) principal components, respectively, are responsible for 55.79% and 35.45% of the variance in the GGE-biplot model, which accounts for 91.24% of the total variation in the standardised data. The intricacy of the interaction between genes and environment is reflected in the relative percentage (91.24%) of variation for GEI. Analyses of which won where or which is best for what. For the potential presence of many mega-environments in an area, it is vital to analyse the which-won-where pattern of multi-environment yield trails (Yan 2001).

The polygon views a biplot as the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot (Yan *et al..*, 2007). Concerning (Fig. 8) the surroundings fall within one of the four sectors that the rays used to split the biplot into. The top genotypes for each sector in this interpretation of the GGE-biplot have greater yields than the other genotypes in all settings that are included in the sector (Yan and Rajcan 2002). The genotype G5 is located on the right of the original points. These results revealed that these genotypes had a high yield

over the grand mean. The genotype G5 exhibited a high oil% and ranked the first genotype in all environments (42.51%). This genotype recorded the highest average oil% (large PC1 scores), but genotype 1 was below average (PC1 scores < 0). Genotypes located at the left of the plot origin were less responsive than the vertex genotypes. The biplot showed not only the average yield of genotype (PCA 1 effects) but also how it is achieved, (Kaya *et al.*., 2002).

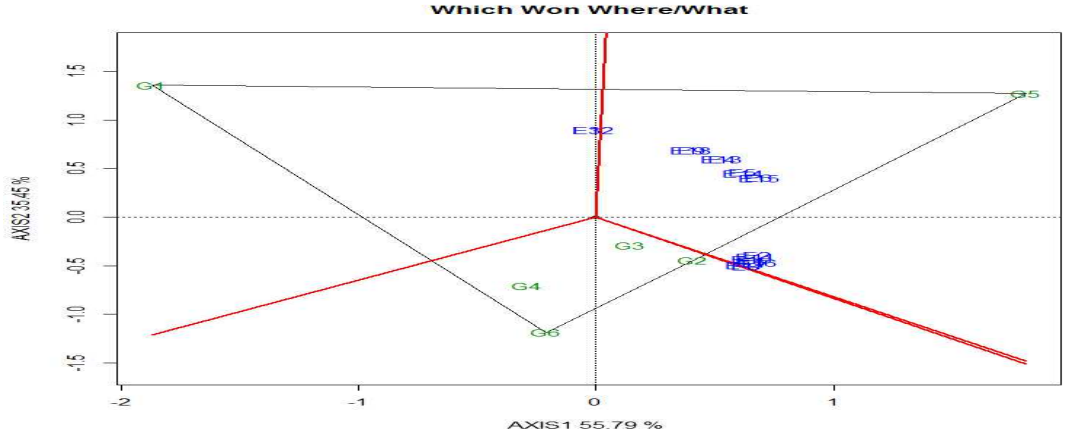

Fig. 8. Polygon view of the GGE-biplot for the which one – where the pattern for 6 soybean genotypes were grown across 18 environments for oil%.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

Fig 9. illustrated that, environments and genotypes in a GGE biplot are located on the same plot. The association between environments is revealed by the angle between environment vectors. A positive association is shown by an acute angle. Yet, a straight angle denotes a lack of association and an acute angle, a negative correlation. Thus fig 9 classified the correlation among environments into 2 groups and cleared the positive correlations between E3, E12, E9, E18, E14, E8, E5, E11, and E13 (group 1). Meanwhile, the other environments follow the other group. Also, a positive correlation between the remaining environments was found. And vice versa, there was a negative correlation between each of group 1 and 2 environments.

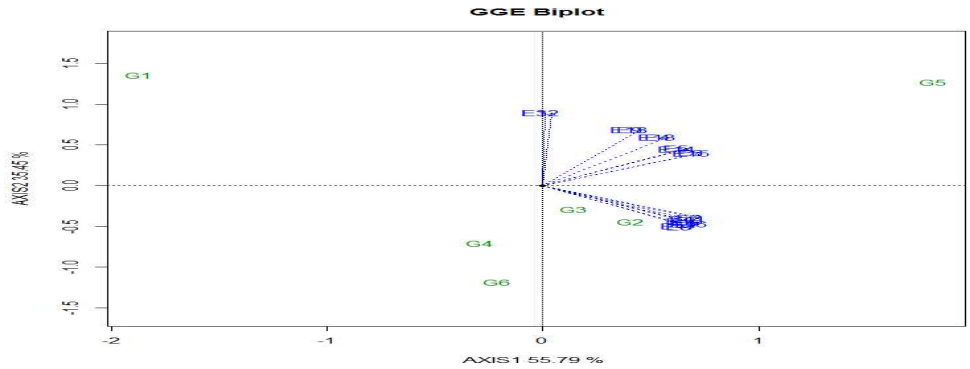

Fig. 9. Biplot of relationships among eighteen environments for oil%.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

As seen in Fig. (10), the validity and goodness of fit of the GGE biplot method were demonstrated by the 91.24% explanation of the total variation of the two-way interaction table by the first two principal components (PC1 and PC2). The Average Environment Coordinate is the straight line with a single arrow (abscissa) that goes through the biplot origin (AEC). The arrow's direction indicates that genotypes will do better on average. The average of the environment PC1 and PC2 scores is shown by the little circle that can be seen on this line. The biplot's average coordinates for each of the tested situations serve as its definition. The line (ordinate), which is perpendicular to the AEC line and crosses through the biplot origin, represents the stability itself. So, it is accurate to say that the genotype located in the two directions that was closer to the AEC line had a more steady yield. As a result, genotype 5 had above-average mean and stability, whereas the other genotypes exhibited below-average mean oil%.

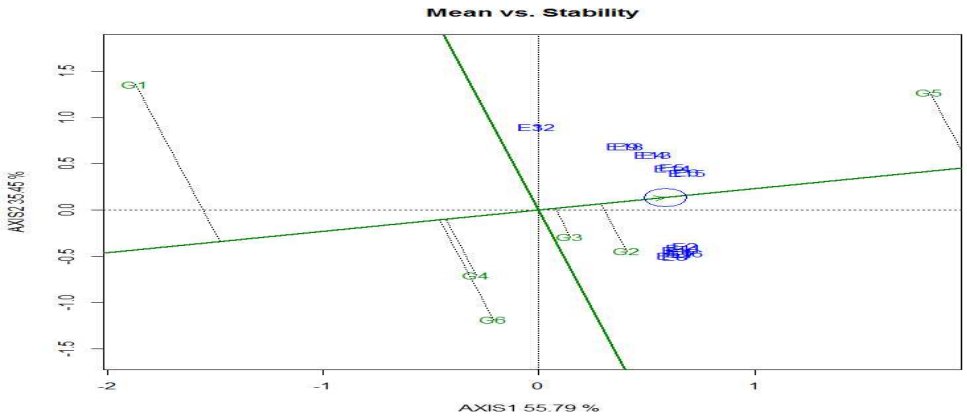

Fig. 10. The mean vs. stability view of the GGE biplot of the six soybean genotypes for oil%.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

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متوسط أداء وثبات محصول البذور ونسبة الزيت لستة تراكيب وراثية من فول الصويا

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يسبب وجود تفاعل البيئات مع التراكيب الوراثية (G x E) قلقًا كبيرًا لمربي النباتات لأنه قد يجعل من الصعب اكتشاف التراكيب الوراثية المتفوقة وتقييد مزايا الانتخاب. تم إجراء ثلاث تجارب متجاورة اعتمادًا على تاريخ الزراعة في موسمي 2019 و 2020. واستخدم تصميم القطع المنشقة فى ثلاث مكررات في كل تاريخ زراعة. تم وضع كثافات الزراعة فى القطع الرئيسية، بينما تم زراعة الست تراكيب وراثية من فول الصويا في القطعة المنشقة ، وذلك لتقييم أداء وزن محصول الحبوب/ نبات ونسبة الزيت في بذور فول الصويا. قدر حجم تفاعل التراكيب الوراثية× البيئة وقياس ثبات التراكيب الوراثية المقيمة باستخدام طرق ثبات مختلفة. أظهرت النتائج ان تباين كل من التراكيب الوراثية والبيئة والتفاعل بينهم معنوى مما يشير إلى أن التراكيب الوراثية المختبرة أظهرت استجابات مختلفة للظروف البيئية. أيضًا ، كانت تباين مكونات التفاعل (الخطي) وغير المتنبأ بها (غير الخطية) معنوي مما يؤكد أن التراكيب الوراثية لفول الصويا المختبرة تختلف اختلافًا كبيرًا في ثباتها النسبي. حقق الصنف جيزة 111 اكبر متوسط لوزن الحبوب/ نبات يليه التركيب الوراثي H1 L3 في كلا الموسمين وكل منهم حقق وزن قطعة اكبر من المتوسط العام لكل البيئات. كان التركيب الوراثي جيزة 22 اكثر ثباتا ظاهريًا لأنه يحتوي على اقل قيم S2di والتي لم تكن مختلفة بشكل كبير عن الصفر و bi = 1. وفقًا لتحليل AMMI و GGE biplot ، كان التركيب الوراثي جيزة 22 يليه الصنف جيزه 111 أكثر ثباتًا للصفتين تحت الدراسة. ولذلك يمكن زراعة التراكيب الوراثية السابقة تحت البيئات المختلفة حيث انها ثابتة.