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Annals of Agricultural Science, Moshtohor (ASSJM)
https://assjm.journals.ekb.eg/

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Original Article Vol. 61(2) (2023), 307 – 318 DOI:10.21608/ASSJM.2023.316883

Evaluation Yield Performance and Stability of Six Soybean Genotypes

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Abstract

Plant breeders are very concerned about the presence of genotype-environment (G x E) interaction since it might make it more difficult to identify superior genotypes and limit the benefits of selection. In each season of 2019 and 2020, three separate experiments were conducted according to sowing dates. The trial design was laid out in a split-plot design with three replicates in each of the sowing dates and seasons. The densities were located in main plots, while, six soybean genotypes were grown in a sub-plot. To evaluate the plot yield performance, quantify (GxE) interaction and screen genotype using various stability techniques. Significant mean squares for genotypes, environments, and (GxE) interaction were found, revealing that genotypes responded differently to the various environmental factors. The terms of predictable (linear) and unexpected (non-linear) interaction components were highly significant further supports the fact that the tested soybean genotypes varied greatly in their relative stability. The most plot weight was generated by Giza 22 and H18 L54 that out-yielded the grand mean across studied environments. The genotype H18 L54 was stable phenotypically because, it had S^2d_i values not significantly different from zero and bi = 1. Also, it was averagely stable under the studied environments. According to AMMI and GGE biplot analysis, The genotype H18 L54 was more stable as located nearest to the origin and with above-average mean descending ranked as follows: Giza22 > H18 L54, whereas the remaining genotypes had below-average mean yield. The mention genotypes seemed to be ideal across various environments.

Keyword: Soybean, Sowing date, Plant density, AMMI, GGE biplot

Introduction

One of the most significant agricultural legumes is soybean [*Glycine max* (L.) Merrill (2n = 40)], which provides oil, the component of medicines, and high-quality protein for both human and animal use (**Pagano and Miransari, 2016**). In addition, soybean may enhance the soil by fixing atmospheric nitrogen (**Ngalamu *et al.*, 2013**), which will help the following crop. Thus, one of the most important objectives to enhance soybean output and area is the creation of stable, high-yielding genotypes. The planting area required to meet the growing demand for this crop globally is always expanding, and there is intense research being done on new ways to increase yield (**Masuda and Goldsmith, 2009**). For soybeans to grow and develop healthily and keep their potential for high grain yields, the ideal planting date is crucial. Genetic and environmental factors strongly influence how planting date affects soybean seed production (**Egli and Cornelius, 2009**). Numerous studies identified the ideal sowing date and its implication on different varieties investigated. Also, how the sowing date relates to the oil and protein 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 the USA, the ideal plant density is from 30 to 50 plants per square meter (**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 show 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 in a variety of conditions is one of the crucial last phases in the majority of applied plant breeding efforts (years, Sowing dates, and plant density). A genotype's yield performance typically differs from one environment to another due to its quantitatively inherited features, resulting in a considerable genotype × environment (GxE) interaction. The use of mean seed yield over environments as a gauge of genotype performance is

dubious whenever the (GxE) interaction is substantial (**Ablett *et al,* 1994**) and **Morsy et al. (2017)**. 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 **Radi *et al.* (1993), Ablett *et al.* (1994), Al-Assily *et al.* (1996) and (2002**) described the significance of (GxE) in the 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)**.

The three metrics employed by the regression approach to characterize stability are mean performance, the regression line's slope and its departure from the mean. According to the statistics utilised to parameterize the variance component measurements as stability parameters, the yield performance varied depending on the environment or genotype. Contributions 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 seed 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 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 commercial cultivars *i.e.* Giza 22 and Giza 111, in addition to four local promising lines selected from the soybean Breeding program of legume department research. Names, origins and pedigree of the studied six genotypes of soybeans are shown in **Table 1**.

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

Genotype code	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 typical temperature range 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 of 2020, the average temperatures at the same site from April to September 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. Three plant population densities were achieved. The experimental design was laid out in a split-plot design with three replicates in each sowing date and season. The three plant populations densities) 70000, 140000 and 210000 plants/ fed) 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, the plot pod's weight in kilogram was measured.

Statistical analysis

1- Analysis of variance

Each environment underwent a regular study of the variance of the split-plot design according to **Gomez and Gomez (1984).** Prior to doing the combined analysis, **the Bartlett test (1937)**. was run to determine whether the variances were homogeneous based on the homogeneity of the individual error components. In light of this, a combined study of variance across 18 environments was developed. In the present study, environments (combinations of years, sowing dates, and plant density) were regarded as random effects whereas genotypes were deemed to be fixed effects overall. We were able to investigate the stability of yield performance for the tested genotypes thanks to the identification of significant GxE interactions. **Zobel *et al.* (1988)** was used to separate one degree of freedom for a 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 measures of variance multivariate research. **Tai (1971)**. and **Eberhart Russell (1966).** and 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, S^2d, as indications of the genotype response to the environmental variable. If the regression coefficient (b value) is not substantially different from one, the genotype is classified as environment-adapted. **Tai (1971)**. also provided two stability factors that were comparable to those of **Eberhart and Russell (1966).** The statistics α and λ in Tai method measure were refer to the linear response of environmental effects and deviation from the linear response in terms of the magnitude of the error variance, respectively. The two components are defined as genotypic stability parameters. In fact, 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 show the variables (genotype and genotype by environment interaction), which are also the causes 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 means to effect 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 studied traits of soybean in the 2019 and 2020 seasons.

Table 2. The main effect of different sowing dates and plant density levels as well as interactions between them on plot weight of soybean in 2019 and 2020 seasons.

	Plot weight (Kg/ plot)							
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	2.20	1.76	1.77	1.91	1.83	1.76	1.31	1.63
140000	2.57	2.29	2.24	2.37	2.38	2.28	1.74	2.14
210000	2.08	2.81	2.66	2.51	2.43	2.81	1.21	2.15
Mean	2.28	2.29	2.22		2.22	2.29	1.42	
			2019				**2020**	
	item		**LSD5%**		**Item**		**LSD5%**	
	Sowing date (S)		0.28		Sowing date (S)		0.36	
	Plant density (D)		0.28		Plant density (D)		0.36	
	SxD		0.36		SxD		0.47	

The maximum values of plot weight were detected when soybean planted on an optimum date (1st May) reached 2.29 and 2.29 days in the 2019 and 2020 seasons, respectively. The early date (15th April) came second order; as it achieved plot weight reached 2.28 and 2.22 kg/plot in the 2019 and 2020 seasons, respectively. However, deficiency occurs in plot weight with a delay in planting date.

The main effect of plant density affected increased significantly plot weight of soybean with increased density percentage estimated by 23.90% and 31.67% in 2019; 30.71% and 31.74% in 2020 when increase plant density from 70000 to 140000 and 210000 plants/ fed, respectively.

There was a significant interaction effect due to the sowing date and plant density. The highest increase in the plot weight of soybean (2.81 kg) was detected in the optimum sowing date with high plant density at the two seasons, followed by the combination between the early sowing date and growth at 140000 plant density (2.57), in the first season. Meanwhile, the lowest value of plot weight (1.21) was shown when soybean was planted in 15th Jun 2020 with 240000 plants/ fed.

Results in Table 3 illustrate the main effect of the studied genotypes. The main effect of genotypes shows a pattern of Giza 22< H18 L54 < H1 L3< H4 L4< Giza111 <H6 L198 and average plot weights were 2.95, 2.29, 2.27, 2.15, 1.96, and 1.96, respectively in the first season 2019. Meanwhile, the pattern was Giza 22< H18 L54< Giza111< H1 L3< H4 L4< H6 L198, and average plot weights were 2.40, 2.28, 1.97, 1.95, 1.66, and 1.58, respectively at 2020.

It can be concluded that the variety Giza 22 and genotype H18L54 in both seasons give the highest values for plot weight. Meanwhile, genotype H6 L198 showed low values for plot weight in both seasons.

The interaction between genotypes and plant density for plot weight is presented in Table 3. Significant interactions between plant density and genotypes were detected. A significant increase in plot weight was observed associated with an increase in plant density for each genotype. 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 three plant densities (210000 plant/ fed) in the first seasons. Meanwhile, the genotype H6 L198 with 700000 plants / fed exhibited a low value for plot weight.

Table 3. The main effect of studied genotypes and plant density and the interaction between them in the two studied season for plot weight.

Plot weight (Kg/ plot)								
	2019				2020			
	Plant density (Plants per fed.)				Plant density (Plants per fed.)			
Genotype	70000	140000	210000	Mean	70000	140000	210000	Mean
H1 L3	1.77	2.34	2.71	2.27	1.38	2.05	2.42	1.95
H4 L4	1.75	2.32	2.38	2.15	1.47	1.76	1.77	1.66
H6 L198	1.82	1.94	2.11	1.96	1.26	1.79	1.68	1.58
H18 L54	1.85	2.46	2.54	2.29	1.86	2.41	2.56	2.28
Giza 22	2.69	2.99	3.19	2.95	2.07	2.66	2.48	2.40
Giza111	1.58	2.15	2.17	1.96	1.77	2.14	2.00	1.97
Mean	1.91	2.37	2.51		1.63	2.14	2.15	
			2019				2020	
	item		LSD 5%		item		LSD 5%	
	Genotype (G)		0.30		Genotype (G)		0.34	
	Plant density (D)		0.28		Plant density (D)		0.36	
	GxD		0.40		GxD		0.45	

Results of Table 4 show that the interaction between genotypes and sowing date was significant in both studied seasons for the plot weight. The genotype Giza 22 showed the highest values for plot weight in the early sowing date in the first season, while, the genotype, H18 L54 give the low values for plot weight when planted on 15th Jun 2020. 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 140000 plants/ fed. On the other hand, the low value for the mentioned trait was detected in the second season, when planted H6L198 in a late sowing date with 210000 plants/ fed in the second season.

Table 4. The interaction between genotypes, plant density and sowing dates for plot weight in season 2019 and 2020.

Genotype	Plot weight (Kg/ plot)											
	Sowing date in 2019											
	S1 15th April 2019			Mean	S2 1st May 2019			Mean	S3 15th may 2019			Mean
	Plant density (Plants per fed.)				Plant density (Plants per fed.)				Plant density (Plants per fed.)			
	70000 (E1)	140000 (E2)	210000 (E3)		70000 (E4)	140000 (E5)	210000 (E6)		70000 (E7)	140000 (E8)	210000 (E9)	
H1 L3	2.06	2.60	1.92	2.19	1.58	2.06	3.65	2.43	1.67	2.35	2.55	2.19
H4 L4	2.10	2.43	2.15	2.23	1.57	1.97	1.98	1.84	1.58	2.55	3.02	2.38
H6 L198	2.07	2.03	1.75	1.95	1.53	1.78	2.05	1.79	1.87	2.02	2.53	2.14
H18 L54	2.07	2.75	2.07	2.29	1.94	2.49	3.15	2.53	1.55	2.15	2.40	2.03
Giza 22	3.27	3.42	3.20	3.29	2.41	3.00	3.27	2.89	2.38	2.55	3.08	2.67
Giza111	1.65	2.20	1.37	1.74	1.54	2.44	2.78	2.25	1.55	1.80	2.35	1.90
Mean	2.20	2.57	2.08	2.28	1.76	2.29	2.81	2.29	1.77	2.24	2.66	2.22
	Sowing date in 2020											
	S1 15th April 2020			Mean	S2 1st May 2020			Mean	S3 15th Jun 2020			Mean
	Plant density (Plants per fed.)				Plant density (Plants per fed.)				Plant density (Plants per fed.)			
	70000 (E10)	140000 (E11)	210000 (E12)		70000 (E13)	140000 (E14)	210000 (E15)		70000 (E16)	140000 (E17)	210000 (E18)	
H1 L3	1.60	2.65	2.49	2.25	1.59	2.02	3.65	2.42	0.95	1.50	1.13	1.19
H4 L4	1.63	1.64	2.07	1.78	1.57	1.93	1.98	1.83	1.20	1.70	1.25	1.39
H6 L198	1.23	1.90	1.90	1.68	1.53	1.81	2.05	1.80	1.02	1.66	1.08	1.26
H18 L54	2.32	2.69	3.00	2.67	1.94	2.48	3.15	2.52	1.32	2.05	1.55	1.64
Giza 22	2.33	3.21	3.03	2.86	2.41	3.00	3.27	2.89	1.47	1.77	1.15	1.46
Giza111	1.88	2.22	2.08	2.06	1.54	2.44	2.78	2.25	1.88	1.76	1.12	1.59
Mean	1.83	2.38	2.43	2.22	1.76	2.28	2.81	2.29	1.31	1.74	1.21	1.42
			2019							2020		
	item		LSD 5%					item		LSD 5%		
	Sowing date (S)		0.28					Sowing date (S)		0.36		
	SxG		0.40					SxG		0.45		
	SxD		0.40					SxD		0.45		
	SxDxG		0.52					SxDxG		0.59		

The analysis of stability

Table 5 is displayed the pooled analysis of variance. Very significant mean squares resulting from the interaction of genotypes and environments for plot weight were found, showing that genotypes significantly differed across various environments. Environment (linear), genotype (linear) interaction (sum of squares due to regression, bi), and unexplained departure from regression were the three divisions of the environment + (genotype environment) interaction (pooled deviation mean squares, S^2d). Significant mean squares due to genotype × environment (linear) were detected for the studied trait 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).**

Also, they discovered that the genotypes, environments, and genotypes environments interaction for yield weight all differed in extremely significant ways.

Table 5. Mean squares of stability analysis of all studied traits for six genotypes across eighteen environments.

SOV	df	plot weight (Kg/ plot)
Genotype	5	1.91**
Environment+ G*E	102	0.31**
Environment	17	1.34**
Genotype x Env.	85	0.11**
a) Env . (linear)	1	22.72**
b) V x Env. (linear)	5	0.40**
c) pooled deviations	96	0.07**
Genotypes		
H1 L3	16	0.07**
H4 L4	16	0.10**
H6 L198	16	0.04**
H18 L54	16	0.06**
Giza 22	16	0.09**
Giza111	16	0.09**
poled error	180	0.03

** refer to Significant at 0.05 probability levels.

Phenotypic and genotypic stability

Three parameters *i.e.* mean performance across environments, linear regression, and deviations from regression function were used to assess the phenotypic stability of the six genotypes under investigation. Table 6 lists the phenotypic stability parameters for the investigated characteristics. The findings make it abundantly evident that all genotypes' regression coefficients (bi), which reflect plot weight, varied considerably from zero.

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. Table 6 lists the genetic stability parameters for the traits under investigation.

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

Genotype	plot weight (Kg/ plot)				
	Eberhart and russell, 1966			Tai, 1971	
	MEAN	bi	$S^2 d_i$	α	λ
H1 L3	2.11	1.48	0.07	0.48	11.79
H4 L4	1.91	0.71	0.101	-0.29	17.16
H6 L198	1.77	0.69	0.04	-0.31	6.83
H18 L54	2.28	1.02	0.058	0.02	9.88
Giza 22	2.68	1.28	0.089	0.29	15.19
Giza111	1.97	0.81	0.085	-0.19	14.59
Mean	2.12				
LSD 5%	0.13				

Table 6 provides the means across environments and the phenotypic stability factors for the plot weight. Ratios of regression (bi) substantially varied from 0 for all genotypes. However, bi they differed greatly from one for genotypes H1 L3 and Giza 22. With remaining to the secondary stability criterion (S2d) each genotype of soybean had a large departure from the regression, indicating that genotypes except H1 L3 and Giza 22 would be classified as stable. Regarding, the remaining crosses, results suggest that these genotypes were stable because they had S2di values that weren't significantly different from 0 and bi = one, and genotype H18 L54 the heavier plot weighed against the average of all genotypes.

Fig. 1 gives a graphic summary useful in identifying the genetically stable genotypes. It could be noticed that the average stability in the figure contained only genotype H18 L54 with α values for stability not significantly differing from = 0 at all degrees of probability at P =0.90. Also, the λ Statistics did not considerably differ from λ=1 for the genotypes showing that they average stability under the research environments. The different genotypes

were unsteady for this quality. Also, there was evidence of phenotypic stability for the H4 L4, Giza 22, and Giza111. However, the genotypes, H4 L4, and Giza111 showed an average of stability, and the genotype Giza 22 exhibited below stability.

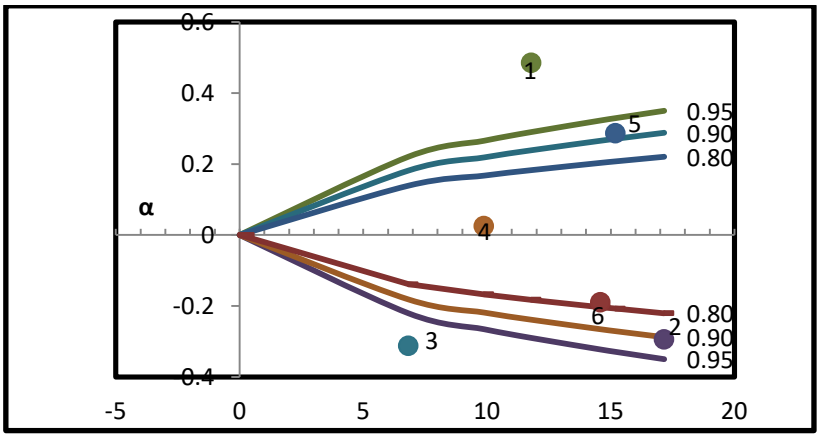

Fig. 1. Distribution of Tai's data on stability for plot weight across 18 conditions for six soybean genotypes.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.

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 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 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. 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. 2, with this model we can explain 75.26 % of the total variability. The genotypes more stable are the nearest to the origin (G4- H18 L54) in consequence their behavior across all environments is similar. Also, Fig. 2 illustrated that the highest mean values for plot weight were detected by G1- H1 L3, G4- H18 L54, and G5- Giza 22, 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 and G3- H6 L198, and they are located on the right. We can observe that the environments that classify in a form similar are E1 with E3, E7, E8, E9, and E18. Also, E16 was closely related to E17, and 13. Meanwhile, E4, E10, and E16 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 Genotypes G2- H4 L4 and G3- H6 L198 have better flowering dates than other genotypes in the environments E9, E8, E7, and E18; the genotypes G4- H18 L54 and G6- Giza111 have better in flowering date than other genotypes in the environments E10, E 14; Meanwhile, the genotypes G1-H1 L3 and G5- Giza 22 have better in plot weight than other genotypes, especially in the environments E11, E12, and E2.

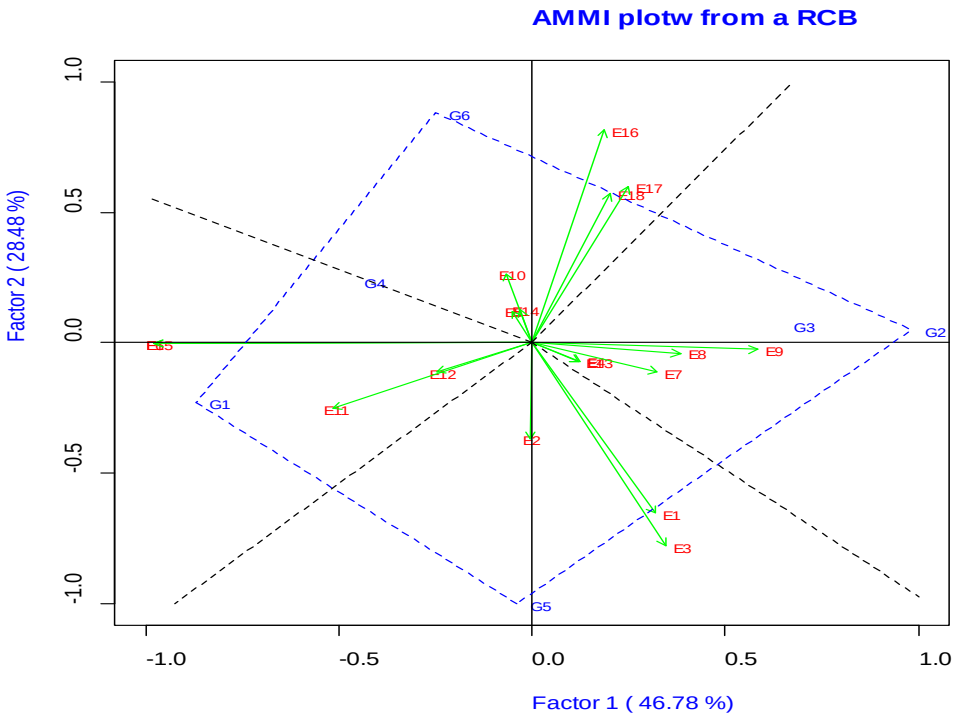

Fig. 2. AMMI biplot with the first two components.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

Biplot GGE analysis Mega-environments (which-won-where) the GGE biplot showing pot weight in polygon form the ideal genotype(s) for each habitat are shown in Fig. 3. 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 GGE-biplot model account for 96.37% of the total variation of the standardized data containing 76.43% and 56.91% variance attributable to the first (PC1) and second (PC2) principle component respectively. The relative percentage (19.52%) of variance for GEI reflects the complexity of the relationship between genotypes and the environment. Which–won–where or which–is–best for what analysis. Studying the which–won where a pattern of multi-environment yield trails is important for the possible existence of different mega–environments in a region (**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**). With respect to (**Fig. 3**). the rays divided the biplot into four sectors and the environments fail into one of them. A good feature of this view of GGE-biplot is that the top genotypes for each sector have a higher yield than the others in all environments that all fall in the sector, (**Yan and Rajcan 2002**). Four genotypes ~~i.e.~~ *i.e.* G5 and G4 located on the right of the original points. These results revealed that these genotypes had a high yield over the grand mean. Genotype G5 exhibited a high plot weight and ranked the first genotype in all environments (2.76 kg). This genotype recorded the highest average grain yield (large PC1 scores), but genotypes 1, 2, 3, and 6 were below average (PC1 scores < 0). Genotypes located at the left of the plot origin were less responsive than the vertex genotypes.

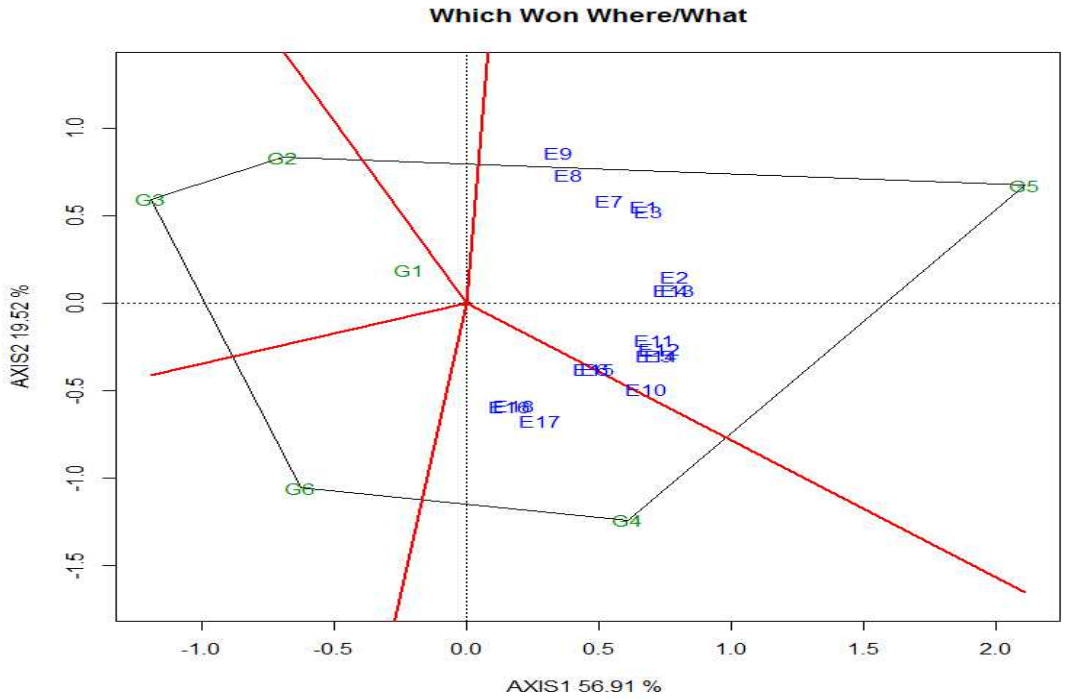

Fig. 3. Polygon view of the GGE-biplot for which one – where pattern for 6 soybean genotypes grown across 18 environments.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

Fig. 4 shows a GGE biplot that includes genotypes and environments in 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. The favorable connections between E9, E8, E7, E1, E3, E2, E14, and E13 (group 1) were therefore clearly shown in fig. 4. Moreover, a favorable association was discovered amongst the remaining settings (group 2). Each of the group1and group settings had a negative link with one another, and vice versa.

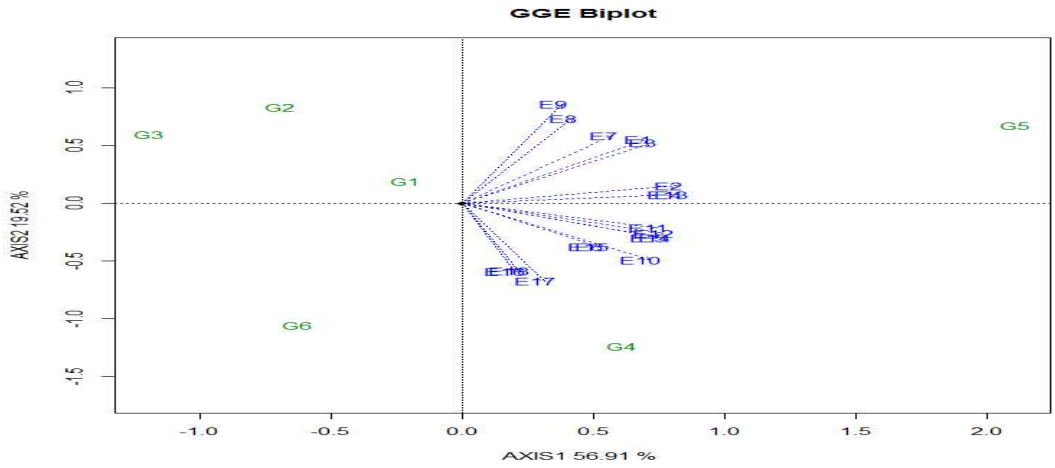

Fig. 4. Biplot of relationships among eighteen environments.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

As seen in Fig (5). The first two principal components (PC1 and PC2) explained 76.43% of the total variation in the two-way interaction table, demonstrating the validity and goodness of fit of the GGE biplot approach. 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 stable for yield.

Consequently, the genotypes with above-average mean are descending ranked as follows: G5 > G4, whereas the remaining genotypes had below-average mean yield. Concerning the stable genotype regardless of G1 and G2 plot weight, the genotypes located very close to the AEC line were reflecting their above-average stability while genotype G3 showed below-average stability because it was slightly placed away from AEC abscissa. In the conclusion, the length of the average environment vector was sufficient to select genotypes based on yield mean performance. 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*., (2008 and 2010**). When only a few genotypes and environments are employed, the GGE biplot graph is frequently unambiguous and simple to comprehend. But the graph becomes so cluttered when multiple genotypes and settings are used that it may be challenging to see and understand. In addition, **Bhartiya et al. (2017)** and **Vaezi et al. (2017)** reported on many winning genotypes in various (2017). According to **Melkamu et al (2015)**. the polygon vertices serve as markers for highly projected genotypes that indicate particular adaptability (2015). Compared to other genotypes, genotypes 5, 9, 1, and 6 are more adaptable. Similar to genotype, 25, 13, 17, 23, and 20, genotype 25 fared poorly in settings where the vectors were on the other side; not all testing locations.

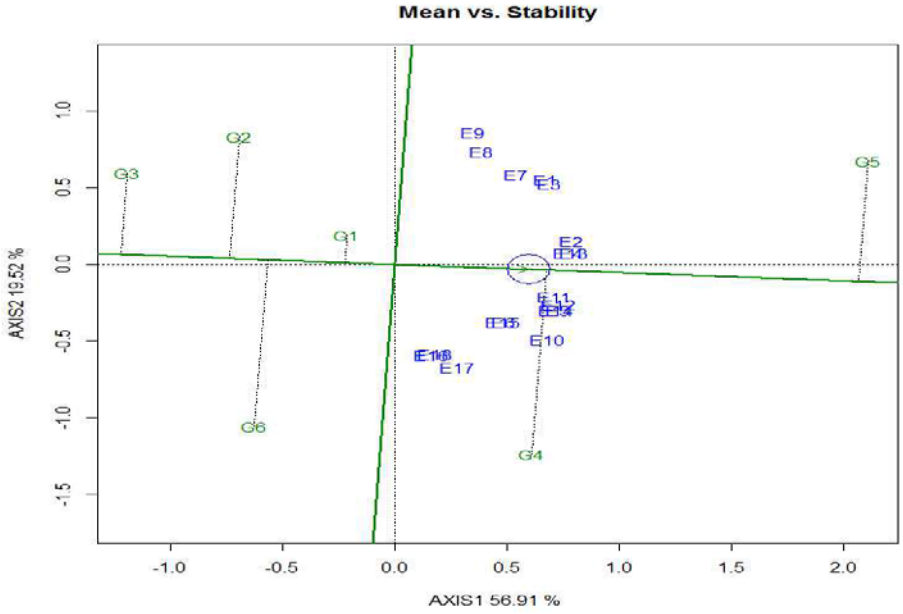

Fig. 5. Biplot of relationships among eighteen environments and stability of the six soybean genotypes.
Notes: 1- H1 L3, 2- H4 L4, 3- H6 L198, 4- H18 L54, 5- Giza 22 and 6- Giza111.
Environments: E1 to E18 were identified and presented in Table 4.

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تقييم إنتاجية تراكيب وراثية مختلفة من فول الصويا بطرق ثبات مختلفة

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يهتم مربى النبات بتقدير تفاعل البيئة مع التراكيب الوراثية لتحديد التراكيب الوراثية المتفوقة و الثابتة لأنتخابها. إجريت الدراسة فى موسمى 2019 و 2020 واقيمت ثلاث تجارب منفصلة حسب تاريخ الزراعة. وكان التصميم التجريبي قطاعات منشقة بثلاث مكررات في كل بيئة. حيث كانت كثافات الزراعة فى القطع الرئيسية بينما وزعت ستة تراكيب وراثية من فول الصويا في القطعة المنشقة ، . وذلك لتقييم أداء إنتاجية 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 22 اكبر متوسط لوزن القطعة يليه التركيب الوراثي H18 L54 في كلا الموسمين وكل منهم حقق وزن قطعة اكبر من المتوسط العام لكل البيئات. كان التركيب الوراثي H18 L54 اكثر ثباتا ظاهريًا لأنه يحتوي على اقل قيم S^2d_i والتي لم تكن مختلفة بشكل كبير عن الصفر و bi = 1. وفقًا لتحليل AMMI و GGE biplot ، كان التركيب الوراثي H18 L54 أكثر ثباتًا حيث كان أقرب موقع إلى الأصل ومع متوسط أعلى من المتوسط تنازليًا على النحو التالي: H18 L54 >Giza22 ، في حين أن التراكيب الجينية المتبقية كانت أقل من المتوسط المتوسط . التراكيب الوراثية المذكوره تعتبر مثالية عبر البيئات المدروسة.