

Genotype $\times$ environment interaction and yield stability of Egyptian cotton genotypes under soil moisture deficit conditions

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Abstract

Using univariate and multivariate stability statistics, the current study attempts to evaluate the 27 cotton genotypes that are stable and adaptive under normal irrigation and drought stress conditions. The combined ANOVA and AMMI model study of seed cotton yield (SCY) showed that the $G \times E$ interaction is the largest factor and that there was significant variation among genotypes, environment, and GEI. PC1, PC2, and PC3 were also highly significant. In the 2023 and 2024 seasons, the grand mean of SCY was reduced by drought stress, with values of 2.12% and 6.19%, respectively, compared to normal irrigation. G17 and G18 genotypes with highest SCY by Y_i , b_i , S_{di}^2 , W_i^2 , D^2 , σ_i^2 , and CV_i statistics and G4, G27, and G26 genotypes with the high to moderate SCY by ASTAB, ASI, ASV, MASI, MASV, Za, and WAAS statistics were most stable genotypes. For rW_i^2 , rS_{di}^2 , rD^2 , $r\sigma_i^2$, and rCV_i statistics, as well as for AMMI-based stability statistics under study, all possible pairs had positive significant rank correlation coefficients. The genotypes G17, G12, G8, and G20 by the AMMI model and the genotypes G17, G23, G18, G9, and G4 by GGE biplot analysis are more stable and produce higher mean SCY. Based on the mean response and most stability statistics, the genotypes G17, G18, and G4 were determined to be the most stable and optimal. The test environment E4 was thought to be the most discriminating test environment, making it ideal for choosing genotypes that are widely acclimated to drought stress in Egypt.

Keywords: *Gossypium barbadense* L.- Stability Statistics- $G \times E$ interaction- AMMI -GGE-Crop resilience

1. Introduction

Egyptian Cotton (*Gossypium barbadense* L.) is one of the most important strategic crops in Egypt. In the 2021 season, the cultivated area was about 312.8 thousand feddan (126.6 thousand hectares) (CATGO 2024). In the April 2025 report, area, yield, and production of the 2024 season in Egypt were 0.13 million hectares, 712 kilograms per hectare, and 0.43 million 480 lb. bales, respectively (USDA 2025). The Egyptian extra-long-staple cotton varieties (ELS) are famous in the world for their high fiber quality. Also, it's important for oil manufacture, animal feed industries, which are fully needed specially to minimize importing these products which cost the Egyptian economy a lot by

hard currency Soliman (2018) and Bakheit. *et al.* (2022). One of the biggest complicated issues of any breeding program is identifying the highest yielding and stable/resilient genotype across a wide range of environmental conditions. However, unpredictable climatic fluctuations significantly affect the resilience and productivity of cotton genotypes and consequently should consider the stability of yield performance for releasing new cultivars (Darwish *et al.*, 2022). Drought is a major abiotic stress that adversely affects growth, phenology, yield, and fiber quality. The problem will become more critical in future climate change scenarios because of the frequent occurrence of high temperatures and water deficits (Pettigrew, 2008). Water stress at the flowering stage causes a decrease in seed cotton yield, mostly because of square and young boll shedding (Rahman *et al.*, 2008). The cotton genotypes under water deficit

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stress conditions showed a decrease in seed cotton yield up to 62 % in comparison to the genotypes that have been well watered Mahdy *et al.* (2021). Plant breeders can obtain improvement in a variety of stability by determining the factors which are responsible for genotype stability or genotype $\times$ environment. The tolerance/resistance of a genotype to abiotic stress is crucial for its stable performance. Thus, it is essential to identify the various factors responsible for genotype $\times$ environment interactions Riaz *et al.* (2019). Genotype by environment interaction (GEI) is an altered performance of a genotype or a given trait across environments. GEI illustrates that not only the genetic potential of a genotype but also, its interaction with environmental factors (soil type, climate fluctuations, planting methods, management technology, etc.) affect the phenotypic expression the genetic background. Promising genotypes need to be evaluated in the multi-environmental test over several years to determine their stability and the extent of adaptation. However, Eberhart and Russell (1966) postulated that genotype/s with minimal interaction with the environmental indices could be regarded as stable genotypes. The common parametric parameter used for detecting the nature of GEI is the linear regression model of Eberhart and Russell (1966) in which b_i give information about adaptability, and S_{di}^2 is used as a measure of the stability of performance. The elucidation of GEI is an important task to allocate the proper selection procedure either direct or indirect selections of potential genotypes for crop improvement programs. Indirect selection for a given trait requires repetitive field trials in different locations and years and needs suitable statistical methods to the extent of the performance, adaptability, and stability of genotypes. The selection of stable genotypes for diverse environments is considered a possible way to minimize GEI in any crop production system. Perfect knowledge of the investigated environments is significant to the analysis of GEI. The model of Eberhart and Russell (1966) is commonly used for the analysis of $G \times E$ interaction, in which the b_i parameter is a measure of response (adaptability), and S_{di}^2 is a

parameter of stability of performance, as well as coefficient of variation, CV_i Francis and Kannenberg (1978), the eovalence (W_i), measures the extent of $G \times E$ due to each genotype Wricke (1962). In addition to that, the additive main effect, and the multiplicative interaction analysis (AMMI) Crossa (1990) are widely used for GEI study, as used to measure stability and adaptability. Stable genotypes show superior performance and stability in yield across several environments (Becker and Leon 1988). Therefore, these investigations were conducted to evaluate the stability and adaptability of 27 advanced breeding lines in the F_5 and F_6 generations, analyze genotype-by-environment interactions using univariate and multivariate stability methods to identify lines with superior performance under normal and stressed irrigation conditions, provide insights into breeding strategies that enhance drought tolerance and yield stability in Egyptian cotton, and select the best lines for effective selection in future breeding programs.

2. Materials and Methods

Twenty-seven advanced breeding lines were evaluated in four field trials during the 2023 and 2024 seasons at the Experimental Farm of the Faculty of Agriculture, Minia University, Egypt. These cotton breeding lines descended from nine of the fifteen Egyptian cotton crosses, originating from a diallel cross among six elite cotton genotypes in 2015 season (Taha *et al.*, 2018) and developed and assessed under different sowing dates and irrigation regimes (Asaad *et al.*, 2023). In each season, two separate trials were conducted using two irrigation regimes, as normal (N) watering (using two weeks intervals) and stressed one (S) (with three-week intervals irrigation). Each trial was conducted as RCBD with three replications with two-ridge plots, each was four meters long and 65 cm wide (5.2 m²). The seeds were dry planted at one side of the ridge in hills distanced 25 cm; seedlings were thinned to two plants /hill after six weeks from planting. All other recommended agronomic and cultural practices for cotton production at El-Minya region were adopted in all trials.

Seed cotton yield (SCY) was recorded using ten guarded plants chosen randomly from each plot to estimate the stability parameters.

Table 1. Code, name and pedigree of 27 Egyptian cotton lines

Code	Name	Pedigree
G1	1×6 EN-104	
G2	1×6 EN-208	(Giza 90) × {[(G83×G80) ×G89] × Australian}
G3	1×6 EN-302	
G4	3×6 ES-102	
G5	3×6 ES-207	Giza 95×{[(G83×G80) ×G89] × Australian}
G6	3×6 ES-308	
G7	4×5 LN-104	
G8	4×5 LN-205	Karashanky × [G90 ×C. B58]
G9	4×5 LN-308	
G10	5×6 LS-109	
G11	5×6 LS-202	[G90 ×C. B58] × {[(G83×G80) ×G89] × Australian}
G12	5×6 LS-308	
G13	2×3 ES-109	
G14	2×3 ES-210	Giza 94×Giza 95
G15	2×3 ES-302	
G16	2×5 LN-106	
G17	2×5 LN-210	Giza 94× [G90 ×C. B58]
G18	2×5 LN-302	
G19	3×5 LS-103	
G20	3×5 LS-201	Giza 95× [G90 ×C. B58]
G21	3×5 LS-306	
G22	1×5 ES-109	
G23	1×5 ES-205	Giza 90× [G90 ×C. B58]
G24	1×5 ES-308	
G25	2×4 LS-101	
G26	2×4 LS-208	Giza 94×{[(G83×G80) ×G89] × Australian}
G27	2×4 LS-304	

2.1. Soil Physical Analysis

The mechanical analyses of experimental soil were conducted in the soil lab of the Soil Sciences Dept. Fac., Agric., Minia University, revealed that the soil texture of the experimental site is clay loam.

The percentages of clay, silt, and sand were 53.5, 36.5, and 10.0, respectively with pH 7.8. The soil moisture percentages during the 2023 and 2024 summer seasons are presented in Table 2.

Table 2. Soil moisture percentages during two summer seasons

Season	2023		2024	
Trial	Normal (E ₁)	Drought (E ₂)	Normal (E ₃)	Drought (E ₄)
Field capacity (F.C%)	37.9	36.8	39.8	36.9
Wilting point (WP%)	13.5	13.1	14.2	13.8
Available water (AW%)	24.4	23.7	25.6	23.7

2.2. Statistical Analysis

A combined analysis of variance due to 27 Egyptian cotton genotypes over 4 environments (2 irrigation intervals $\times$ 2 growing seasons) was performed according to Gomez and Gomez (1984). Additive Main Effects and Multiplicative Interaction Model (AMMI) (Gauch 1988) was used to evaluate the effects of genotypes, four environments (normal irrigation and drought stress situations in the 2023 and 2024 growing seasons), and their interaction on seed cotton production. For these parameters, statistical tests of significance were determined using F-tests. To encompass a wide range of stability study methodologies, univariate and multivariate stability statistics were selected. The stability statistics were performed in accordance W_i^2 Wricks's (1962) ecovalance; b_i : Regression coefficient (Finlay and Wilkinson 1963); b_i and S_{di}^2 : Deviation from regression (Eberhart and Russell 1966); D^2 : Genotypic stability (Hanson 1970); σ_i^2 : Stability variance (Shukla 1972); CV_i : Coefficient of variation (Francis and Kannenberg 1978); ASTAB: AMMI based stability parameter (Rao and Prabhakaran 2005); ASI: AMMI stability index (Jambhulkar *et al.*, 2017); ASV: AMMI-stability value (Purchase *et al.*, 2000); MASI: Modified AMMI stability index (Ajay *et al.*, 2018); MASV: Modified AMMI stability value (Ajay *et al.*, 2019); Za: Absolute value of the relative contribution of IPCs to the interaction (Zali *et al.*, 2012); WAAS: Weighted average of absolute scores (WAAS) (Olivoto *et al.*, 2019). Also, adaptability and phenotypic stability analyses were carried out graphically using the AMMI (Zobel *et al.*, 1988) and genotype (G) main effect plus genotype-by-environment (GE) interaction (GGE) biplot (Yan *et al.*, 2000) models after the significance of the G $\times$ E interaction was established. To gain a better

understanding of the relationships between the stability methods and all potential pairwise comparisons of seed cotton yield, Spearman's rank correlation coefficient was employed. PBSTAT-GE 3.0.3 was the software used for statistical analysis (Suwarno *et al.*, 2025).

3. Results and Discussion

3.1. Combined ANOVA with AMMI analysis

According to the combined ANOVA with AMMI analysis that is shown in Table 3, there was a significant variation for the effects of genotypes ($p < 0.05$), environments, and genotype $\times$ environment interaction (GEI) ($p < 0.01$) on seed cotton yield/plant. Using AMMI analysis of variance, Lingaiah *et al.* (2020) and Sheeba *et al.* (2025) have previously demonstrated the substantial effects of genotypes, environments, and their interactions on seed cotton yield. These results indicated that both 27 genotypes of cotton and the existing four environmental conditions (two growing seasons under normal irrigation and drought conditions) influenced seed cotton yield/plant. Finding the optimum genotypes for adaptability to the examined growing seasons under drought stress conditions is made easier by the fact that the testing years varied and contributed to the variation of the genotypic performance for these variables (Yehia *et al.*, 2023a). The GEI sum of squares (41.26%) showed the greatest component among all the sums of squares for both normal irrigation and drought stress conditions over the two growing seasons, followed by the environments (26.07%) and genotypes (22.25%) under study. This implies that there were notable differences in the responses of the genotypes over time, which led to variations in the seed cotton yield. These differences can aid in the selection of the best genotypes for drought

stress conditions. Three main component axes (PCs) were obtained from the sum of squares of the GEI component. The SS for GEI showed that the three main components (PC1, PC2, and PC3) were highly significant, with respective values of 47.86%, 34.95%, and 17.19%. According to Alishah *et al.* (2021), the first two main components accounted for 81.0% of the variation

in the GEI. According to Yehia *et al.* (2023a), this illustrates not just the fluctuation between years but also the adequate and desired genetic variety among different genotypes under drought conditions. This information could be utilized to increase cotton yields in Egypt's drought-prone regions.

Table 3. Combined ANOVA with AMMI analysis for seed cotton yield/plant (g) of 27 genotypes evaluated across normal irrigation and drought stress conditions during two growing seasons

S.O.V.	Df	Sum squares	Percent	Mean squares	F value	Pr(>F)
Environment (E)	3	4912.50	26.07	1637.50**	38.20	0.00
Replication/E	8	342.93	1.82	42.87**	5.50	0.00
Genotype (G)	26	4192.33	22.25	161.24*	1.62	0.05
G x E	78	7774.79	41.26	99.68**	12.78	0.00
PC1	28	3721.27	47.86	132.90**	17.04	0.00
PC2	26	2717.13	34.95	104.51**	13.40	0.00
PC3	24	1336.39	17.19	55.68**	7.14	0.00
Residuals	208	1622.43		7.80		

Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$

3.2. Mean Performance

When comparing the average values of genotypes with LSD under normal irrigation and drought conditions in both the 2023 and 2024 growing seasons, the results of the seed cotton yield/plant in Table 4 showed a highly significant variability in the genotype performances. The findings showed that drought stress reduced the seed cotton output/plant of the majority of genotypes examined and that drought stress conditions affected seed cotton production in comparison to normal watering conditions. These findings suggested that whereas certain genotypes exhibited excellent behavior, as seen by their great capacity to seed cotton yield/plant even under drought conditions, other genotypes suffered more adverse effects from drought conditions. The drought stress conditions significantly decreased the grand mean of seed cotton yield/plant, where values of 2.12% and

6.19% compared to under normal irrigation conditions in the 2023 and 2024 growing seasons, respectively. Yehia *et al.* (2023a), Soliman *et al.* (2024), Shani *et al.* (2025), and Zhangjin *et al.* (2025) reported similar findings. In the 2023 and 2024 growing seasons, the G14 and G16 genotypes under normal irrigation conditions and the G18 and G4 under drought conditions had a maximum seed cotton yield/plant, respectively. In both irrigation conditions, the greatest mean performances were noticed by the genotypes G14 and G17 in the 2023 and 2024 growing seasons, respectively. According to Thillainathan and Fernandez (2002), yield stability could result from reliable results in many settings (sites and/or years). The varying yield ranking of genotypes across environments demonstrated that the GEI impact was of the crossover type (Yan and Hunt 2001).

Table 4. Seed cotton yield/plant (g) of 27 selected genotypes across normal irrigation and drought stress conditions during two growing seasons

Genotypes*	2023 summer season			2024 summer season		
	Normal (E1)	Drought (E2)	Mean	Normal (E3)	Drought (E4)	Mean
G1	66.67	53.87	60.27	63.60	53.67	58.63
G2	67.97	55.47	61.72	50.20	53.17	51.68
G3	50.60	44.13	47.37	55.53	45.47	50.50
G4	67.97	55.73	61.85	55.67	65.40	60.53
G5	65.33	53.73	59.53	45.87	43.47	44.67
G6	61.44	62.73	62.09	47.00	49.87	48.43
G7	54.33	61.20	57.77	62.53	50.80	56.67
G8	65.70	62.07	63.88	59.87	49.33	54.60
G9	63.37	61.53	62.45	62.00	60.33	61.17
G10	50.19	65.33	57.76	45.60	46.33	45.97
G11	65.33	67.73	66.53	57.53	46.67	52.10
G12	64.60	62.07	63.33	61.80	52.00	56.90
G13	63.91	56.00	59.96	56.53	53.40	54.97
G14	76.40	63.80	70.10	47.67	54.33	51.00
G15	56.54	60.27	58.41	51.67	44.27	47.97
G16	56.40	56.67	56.53	74.07	45.33	59.70
G17	67.58	67.73	67.66	68.93	56.67	62.80
G18	58.60	69.67	64.13	61.33	62.73	62.03
G19	52.67	68.33	60.50	59.40	53.40	56.40
G20	60.56	59.33	59.94	54.07	53.67	53.87
G21	57.63	59.07	58.35	62.47	47.93	55.20
G22	65.12	54.40	59.76	63.60	54.80	59.20
G23	71.59	58.47	65.03	62.80	56.07	59.43
G24	62.15	54.73	58.44	64.33	47.27	55.80
G25	66.33	58.60	62.47	65.67	51.47	58.57
G26	63.50	57.60	60.55	64.53	53.67	59.10
G27	64.58	66.67	65.63	62.93	51.00	56.97
Grand Mean	62.48	59.89		58.79	51.94	
LSD 0.05	4.18	3.76		3.45	3.84	
CV (%)	4.89	4.60		4.30	5.41	
P-value	0.00	0.00		0.00	0.00	

*The genotypes key names can be found in Table 1

3.3. Stability statistics

Both yield and performance stability should be considered at the same time in order to optimize the advantages of GEI and improve the precision and refinement of genotype selection (Darwish *et al.* 2022). Therefore, stability statistics can be utilized as a compromise method to select genotypes with a moderate yield and good stability, as well as to find genotypes that are adapted to hard growth circumstances (El-Hashash and Agwa 2018) and (Al-Ashkar *et al.* 2015). As illustrated in Table 5, stability analyses of seed cotton yield/plant for 27 cotton genotypes under four environment conditions (two growing years

and two irrigation conditions) were conducted using various stability univariate and multivariate approaches. The G3 genotype produced the lowest average of 48.93 g of seed cotton per plant in four different conditions, while the G17 genotype produced the highest average of 65.23 g. When the mean response was employed as the initial criterion for evaluating the genotypes under both normal irrigation and drought conditions in both growing seasons, 14 genotypes outperformed the grand mean (58.28 g). The genotypes with the greatest seed cotton yield/plant (Y_i) values performed better in a variety of conditions. In contrast to the genotypes G3, G10, and G5 under environmental conditions, the genotypes G17,

G18, G23, G9, G27, and G4 by Y_i statistic recorded the highest values and indicated the most stable genotypes. According to Eberhart and Russell (1966), the best measure of phenotypic stability is a genotype with a regression coefficient, b_i , equal zero, whose yields were almost the same in every environment. Under the four environments, a significant difference was observed in the majority of genotypes by deviation from regression (S_{di}^2) and some genotypes by regression coefficient (b_i). These results imply that genotypes had already responded differently to environmental changes. The genotypes with the best cotton yield performance, G17 and G23, had b_i values near unity, while the genotypes with moderate cotton yield performance were G2, G6, and G12. In both growing seasons, these genotypes showed particular adaptation to every environment under both irrigation conditions. With b_i less than one and nearly equal to unity, genotypes G1, G26, and G22 produced moderate seed cotton yield performance and were suited to both irrigation scenarios. Since the most stable genotype is G17, with a b_i value near unity, this b_i can be regarded as a biological (static) definition of stability (Eberhart and Russell 1966). With the lowest S_{di}^2 values and a substantial difference from zero, the genotypes G17 and G27 demonstrated outstanding seed cotton yield performance. The G17 genotype offered a good mix of stability and yield. Conversely, the genotypes G9, G12, and G8 exhibited the lowest S_{di}^2 values and a moderate performance in seed cotton yield. In general, when $b_i = 1$ is combined with $S_{di}^2 = 0$ or a minimum value, the genotypes are more stable. As a result, when this pair is linked to high or low mean yield, respectively, genotypes are often either well-adapted or poorly adapted across all habitats. These results are similar to Alishah *et al.* (2021), Baraki *et al.* (2024) and Deho *et al.* (2021). When compared to other genotypes, the most stable

genotypes are the ones with the lowest W_i^2 , σ_i^2 , D^2 , and CV_i values. Based on the W_i^2 and σ_i^2 statistics, the genotypes G12, G8, G17, G13, and G20 registered the minimum values and, thus, were more stable. While, the genotypes G9, G20, G18, and G13 recorded the lowest D^2 , and CV_i values, therefore, they were more stable. These genotypes selected by four the previously stability parameters had high to moderate seed cotton yield. Baraki *et al.* (2024) identified the best and most stable genotype by σ_i^2 , W_i^2 , S_{di}^2 , and CV_i parameters. The minimum values of ASTAB, ASI, ASV, MASI, MASV, Za, and WAAS statistics indicate that the genotypes would be more stable across environments. Based on the ASI, ASV, MASI, Za, and WAAS parameters, G4, G26, and G27 had the high seed cotton yield and the most stable genotype simultaneously because they had low their values under studied environments. The lowest values of ASTAB and MASV parameters were observed for genotypes G4, G9, G13, and G26; thus, they were stable across environments and with high to moderate seed cotton yield. Our results are similar to the results by Taleghani *et al.* (2023), who stated there is equal potential for identifying stable genotypes by these AMMI model parameters. Although the majority of AMMI model parameters contain a dynamic concept of stability, only a few of them, like MASV, helped identify stable high-yielding genotypes, according to Pour-Aboughadareh *et al.* (2022). Generally, the Y_i , b_i , S_{di}^2 , W_i^2 , and σ_i^2 parameters ranked the genotype G17 as more stable with high seed cotton yield. While most stability parameters ranked the genotypes G9, G26, G13, G20, G4, and G27 as more stable genotypes with high to moderate seed cotton yield. Most stability parameters under study are associated with dynamic stability because they are related to the high cotton yield genotypes.

Table 5. Mean response and stability methods for seed cotton yield/plant of 27 cotton genotypes investigated under normal irrigation and drought conditions (four environments).

Genotypes	Y_i	b_i	S_{di}^2	W_i^2	D^2	σ_i^2	CV_i	ASTAB	ASI	ASV	MASI	MASV	Za	WAAS
G1	59.45	0.99 ^{ns}	34.58 ^{**}	74.36	154.75	25.44	11.24	2.43	0.57	1.62	0.57	3.07	0.14	0.77
G2	56.70	1.06 ^{ns}	54.71 ^{**}	114.87	205.42	40.02	13.78	7.24	0.98	2.81	0.98	5.28	0.24	1.36
G3	48.93	0.41 ^{ns}	33.11 ^{**}	92.86	90.84	32.10	10.64	3.93	0.41	1.18	0.50	2.65	0.16	0.86
G4	61.19	-0.16 ^{**}	58.62 ^{**}	204.08	122.44	72.14	10.51	0.20	0.09	0.26	0.11	0.48	0.03	0.17
G5	52.10	1.81 [*]	43.59 ^{**}	132.22	327.93	46.27	18.91	0.75	0.29	0.83	0.30	1.52	0.09	0.47
G6	55.26	1.12 ^{ns}	54.97 ^{**}	116.03	214.68	40.44	14.45	9.36	1.39	3.98	1.40	4.22	0.30	1.74
G7	57.22	0.62 ^{ns}	32.54 ^{**}	79.04	107.24	27.12	9.76	1.48	0.38	1.08	0.39	2.14	0.11	0.61
G8	59.24	1.56 ^{ns}	-2.53 ^{ns}	19.35	180.19	5.64	11.87	9.51	1.42	4.06	1.42	4.15	0.28	1.62
G9	61.81	0.26 [*]	-2.23 ^{ns}	34.24	11.28	11.00	2.03	0.62	0.32	0.92	0.33	1.10	0.08	0.46
G10	51.86	0.77 ^{ns}	106.62 ^{**}	221.76	270.51	78.51	17.74	5.59	0.56	1.61	0.64	3.70	0.17	0.87
G11	59.32	1.95 [*]	17.61 ^{**}	94.77	309.64	32.79	16.00	5.77	0.82	2.34	0.83	4.64	0.21	1.16
G12	60.12	1.22 ^{ns}	-1.74 ^{ns}	4.75	117.93	0.38	9.24	3.42	0.82	2.34	0.82	2.94	0.19	1.12
G13	57.46	0.83 ^{ns}	7.32 [*]	21.70	78.73	6.48	7.86	0.80	0.28	0.79	0.30	1.11	0.08	0.46
G14	60.55	1.73 ^{ns}	140.18 ^{**}	317.60	501.54	113.01	20.59	1.33	0.52	1.49	0.52	1.64	0.12	0.68
G15	53.19	1.34 ^{ns}	14.63 ^{**}	41.46	170.87	13.60	12.99	2.08	0.51	1.47	0.52	2.70	0.14	0.79
G16	58.12	1.31 ^{ns}	156.73 ^{**}	324.51	449.91	115.50	20.43	1.84	0.48	1.36	0.48	2.72	0.11	0.60
G17	65.23	1.15 ^{ns}	6.40 [*]	19.44	122.82	5.67	8.80	2.38	0.61	1.74	0.62	2.35	0.17	0.94
G18	63.08	-0.11 ^{**}	30.32 ^{**}	141.15	65.96	49.49	7.47	1.47	0.44	1.26	0.45	1.95	0.13	0.72
G19	58.45	0.40 ^{ns}	71.40 ^{**}	170.10	166.80	59.91	12.40	1.00	0.42	1.21	0.42	1.65	0.11	0.61
G20	56.91	0.63 ^{ns}	4.17 ^{ns}	21.75	51.61	6.50	6.24	1.29	0.26	0.74	0.30	1.66	0.09	0.50
G21	56.77	1.09 ^{ns}	19.60 ^{**}	44.90	139.30	14.83	10.98	3.13	0.65	1.85	0.67	2.60	0.19	1.04
G22	59.48	0.78 ^{ns}	27.22 ^{**}	62.58	113.23	21.20	9.54	8.07	0.71	2.04	0.81	3.81	0.26	1.39
G23	62.23	1.20 ^{ns}	23.95 ^{**}	55.48	164.98	18.64	10.98	4.34	0.80	2.30	0.83	2.86	0.22	1.21
G24	57.12	1.38 ^{ns}	30.14 ^{**}	74.01	208.43	25.31	13.57	3.41	0.83	2.39	0.83	2.85	0.19	1.10
G25	60.52	1.34 ^{ns}	15.86 ^{**}	43.96	173.55	14.49	11.52	2.45	0.65	1.86	0.65	2.55	0.17	0.96
G26	59.83	0.88 ^{ns}	13.28 ^{**}	32.66	97.18	10.43	8.55	0.91	0.04	0.12	0.17	0.96	0.04	0.21
G27	61.30	1.46 ^{ns}	6.99 [*]	31.98	178.27	10.18	11.47	1.62	0.04	0.12	0.22	1.28	0.06	0.28

Y_i : Mean response; W_i^2 Wricks's (1962) ecovalance; b_i : Regression coefficient (Finlay and Wilkinson 1963); b_i and S_{di}^2 : Deviation from regression (Eberhart and Russell 1966); D^2 : Genotypic stability (Hanson 1970); σ_i^2 : Stability variance (Shukla 1972); CV_i : Coefficient of variation (Francis and Kannenberg 1978); ASTAB: AMMI based stability parameter (Rao and Prabhakaran 2005); ASI: AMMI stability index (Jambhulkar *et al.* 2017); ASV: AMMI-stability value (Purchase *et al.* 2000); MASI: Modified AMMI stability index (Ajay *et al.* 2018); MASV: Modified AMMI stability value (Ajay *et al.* 2019); Za: Absolute value of the relative contribution of IPCs to the interaction (Zali *et al.* 2012); WAAS: Weighted average of absolute scores (WAAS) (Olivoto *et al.* 2019). Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$; ns: indicate the non-significant difference. The genotypes and environment key names can be found in Tables 1.

3.4. Rank correlation among mean yield and stability statistics

Data in Table (6) displays the Spearman's rank correlation coefficients, which were computed for every pair of stability statistics and seed cotton yield. A significant and perfect rank correlation coefficient ($r=1.00$) was noticed between rW_i^2 and $r\sigma_i^2$, rASI and rASV, and rZa and rWAAS statistics. These results indicated the ranks of genotypes by these stability parameters were identical. The rY_i exhibited positive and significant rank correlation coefficients with rCV_i parameter (moderate). Positive associations between rY_i and other stability statistics under study were observed (from low to very low). For rW_i^2 , rS_{di}^2 , rD^2 , $r\sigma_i^2$, and rCV_i statistics, as well as for rASTAB, rASI, rASV, rMASI, rMASV, rZa, and rWAAS statistics, all possible pairs had significant rank correlation coefficients in a positive direction ($P < 0.05$ or 0.01). The statistics rb_i and rD^2 had significant positive rank correlation coefficients with rASI, rASV, and rMASI statistics ($P < 0.05$). The rb_i and rMASV parameter is positively and significantly correlated with rD^2 and rCV_i

parameters ($P < 0.05$ or 0.01). The significant positive correlation between these stability statistics indicates their close relationship with each other and suggests that these parameters would play close similar roles with effective in stability ranking of genotypes, and *vice versa*. Therefore, their parameters can be used to select high yielding and stable genotypes in seed cotton yield. These methods should not be treated as separate procedures (Lin *et al.* 1986). According to Mekbib (2002), the non-significant association between mean yield and stability parameters implies that stability parameters offer information that average yield alone cannot supply. According to Ajay *et al.* (2018), AMMI-based stability measurements showed a positive and significantly correlation with mean yield, suggesting that it has a dynamic concept of stability. The strong positive association between stability models suggests that they provide comparable data regarding genotype rankings for stability in various environments. Thus, any of these parameters, or any combination of them, can be utilized to choose stable and high-yielding genotypes (Yehia *et al.*, 2023b).

Table 6. Rank correlation among seed cotton yield and stability statistics for 27 genotypes across four environments

Statistics	rY_i	rW_i^2	b_i	rS_{di}^2	rD^2	$r\sigma_i^2$	rCV_i	rASTAB	rASI	rASV	rMASI	rMASV	rZa
rW_i^2	0.23 ^{ns}												
b_i	0.03 ^{ns}	-0.14 ^{ns}											
rS_{di}^2	0.32 ^{ns}	0.95 ^{**}	-0.13 ^{ns}										
rD^2	0.26 ^{ns}	0.48 [*]	0.73 ^{**}	0.50 ^{**}									
$r\sigma_i^2$	0.23 ^{ns}	1.00 ^{**}	-0.14 ^{ns}	0.95 ^{**}	0.48 [*]								
rCV_i	0.41 [*]	0.59 ^{**}	0.62 ^{**}	0.62 ^{**}	0.97 ^{**}	0.59 ^{**}							
rASTAB	0.25 ^{ns}	-0.06 ^{ns}	0.32 ^{ns}	0.00 ^{ns}	0.35 ^{ns}	-0.06 ^{ns}	0.33 ^{ns}						
rASI	0.09 ^{ns}	-0.03 ^{ns}	0.41 [*]	0.01 ^{ns}	0.42 [*]	-0.03 ^{ns}	0.37 ^{ns}	0.85 ^{**}					
rASV	0.09 ^{ns}	-0.03 ^{ns}	0.41 [*]	0.01 ^{ns}	0.42 [*]	-0.03 ^{ns}	0.37 ^{ns}	0.85 ^{**}	1.00 ^{**}				
rMASI	0.13 ^{ns}	-0.05 ^{ns}	0.40 [*]	-0.01 ^{ns}	0.40 [*]	-0.05 ^{ns}	0.36 ^{ns}	0.90 ^{**}	0.99 ^{**}	0.99 ^{**}			
rMASV	0.32 ^{ns}	0.07 ^{ns}	0.31 ^{ns}	0.12 ^{ns}	0.41 [*]	0.07 ^{ns}	0.42 [*]	0.93 ^{**}	0.87 ^{**}	0.87 ^{**}	0.89 ^{**}		
rZa	0.18 ^{ns}	-0.06 ^{ns}	0.33 ^{ns}	-0.02 ^{ns}	0.32 ^{ns}	-0.06 ^{ns}	0.30 ^{ns}	0.94 ^{**}	0.95 ^{**}	0.95 ^{**}	0.97 ^{**}	0.90 ^{**}	
rWAAS	0.15 ^{ns}	-0.07 ^{ns}	0.32 ^{ns}	-0.03 ^{ns}	0.31 ^{ns}	-0.07 ^{ns}	0.29 ^{ns}	0.93 ^{**}	0.95 ^{**}	0.95 ^{**}	0.97 ^{**}	0.89 ^{**}	1.00 ^{**}

Statistically significant differences at ^{*} $p \leq 0.05$ and ^{**} $p \leq 0.01$; ns: indicate the non-significant difference.

3.5. AMMI biplot

In this study, 27 cotton genotypes were examined for drought tolerance over a two-year period under both normal irrigation and drought stress using the AMMI biplot, as shown in Figure 1. The first two PCs contributed 82.8% of the overall variability in the data, where PC1 and PC2 explained 47.9% and 34.9% of the total variance of 27 genotypes and four environments, respectively. Jamil *et al.*

(2022), Rehman *et al.* (2022), Sadabadi *et al.* (2018), and Shaker *et al.* (2019) also found similar findings. As a result, PC1 and PC2 can be used to identify drought-tolerant genotypes during normal irrigation and drought stress conditions in both growing seasons. Genotypes that gathered and positioned close to the biplot origin were the most stable and made fewer contributions to GEI (Yehia *et al.* 2023b). The genotypes G17, G12, G8, and G20 are close to the biplot origin with lower GEI,

so they are stable across all environments, followed by the genotypes G13, G21, and G27 (Figure 1). On the other hand, because they are farther from the origin and contribute more to GEI in all environments, the genotypes G10, G24, and G16 are unstable. The mean phenotypic performance of all genotypes in various conditions was represented by the origin of the biplot (Abro *et al.*, 2022). When environment and genotype are placed near each other in the biplot, there is a positive connection, indicating particular adaptation (Silveira *et al.*, 2013 and Sheta *et al.*, 2024). For instance, the G16 and G18 genotypes with E3 and E2, respectively, showed the particular adaption. The E1 environment produced the

longest vectors and the largest cotton production, followed by the E2 and E3 environments. This suggests that the GEI determination is significantly influenced by these environments. For the E4 environment, short vectors were seen nearer the biplot origin and closer to zero. Furthermore, the angle that separates the E1 and E4 habitats is less than 90 degrees. As a result, these settings are more stable and less interactive, which almost ensures that every genotype will function better there. Ashwini *et al.* (2020), Sheeba *et al.* (2025) and Yehia *et al.* (2023b) have found similar results for AMMI biplot analysis of cotton genotypes.

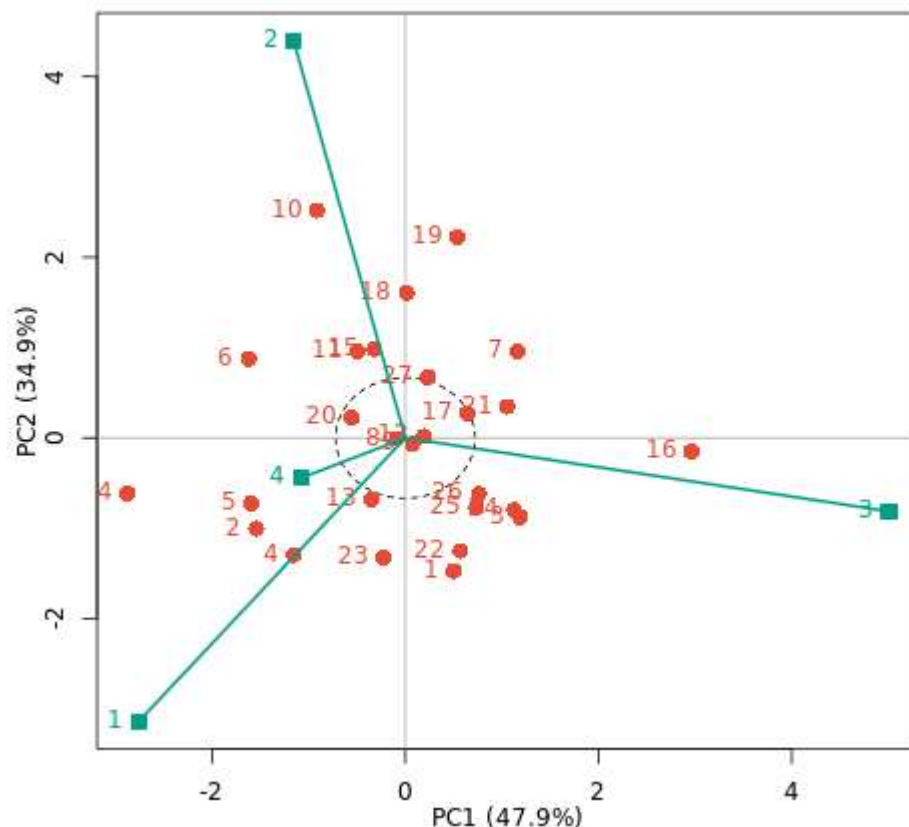


Figure 1. AMMI biplot of PC1 vs PC2 for seed cotton yield with 27 cotton genotypes (red color) and four environments (green color). The genotypes and environment key names can be found in Tables 1 and 4, respectively.

3.6. GGE Biplot Analysis

The PC1 and PC2 generated by applying singular value decomposition to environment-centered yield data were plotted to form the GGE biplot (Yan *et al.*, 2000). Using average PCAs in all settings, genotype yield stability was evaluated using the

average environment coordination (AE) technique, which is based on genotype-focused singular value partitioning (SVP). The GGE biplot provides valuable information about the genotypes and environments being studied and is a straightforward method for evaluating the impact

of genotype on the environment in cotton (Sadabadi *et al.*, 2018). GGE biplot of PC1 and PC2 explained 37.2% and 30.1%, respectively, and collectively, they explained 67.3% of the total G+GE variation under normal irrigation and drought stress conditions in both growing seasons. PC1 and PC2 were used to plot the GGE biplot for seed cotton yield, which explained 96.4% of the total GEI variation and 70.2% and 26.2% of the variance, respectively (Sheeba *et al.*, 2025). Six genotypes, namely G3, G5, G10, G14, G16, and G17 formed the polygon vertices under normal and drought irrigation conditions in both growth seasons, and they are spread out from the biplot origin in all directions, while, the polygon includes

every other genotype. (Figure 2). Some genotypes with no environmental vectors for seed cotton yield were discovered at the polygon's vertex by Ali *et al.* (2017) and Yehia *et al.* (2023b). For the environments that fell into each sector, the genotype at its vertices is the ostensibly highest cotton yield. As a result, genotype G16 did best in the E3 environment, whereas G4, G17, and G23 provided the highest cotton production in the E1, E2, and E4 environments. Because no environment fit within the sectors of genotypes G3, G10, and G15, they were the poorest of all the settings compared to the genotypes at the vertices, those inside the polygon are less environmentally friendly.

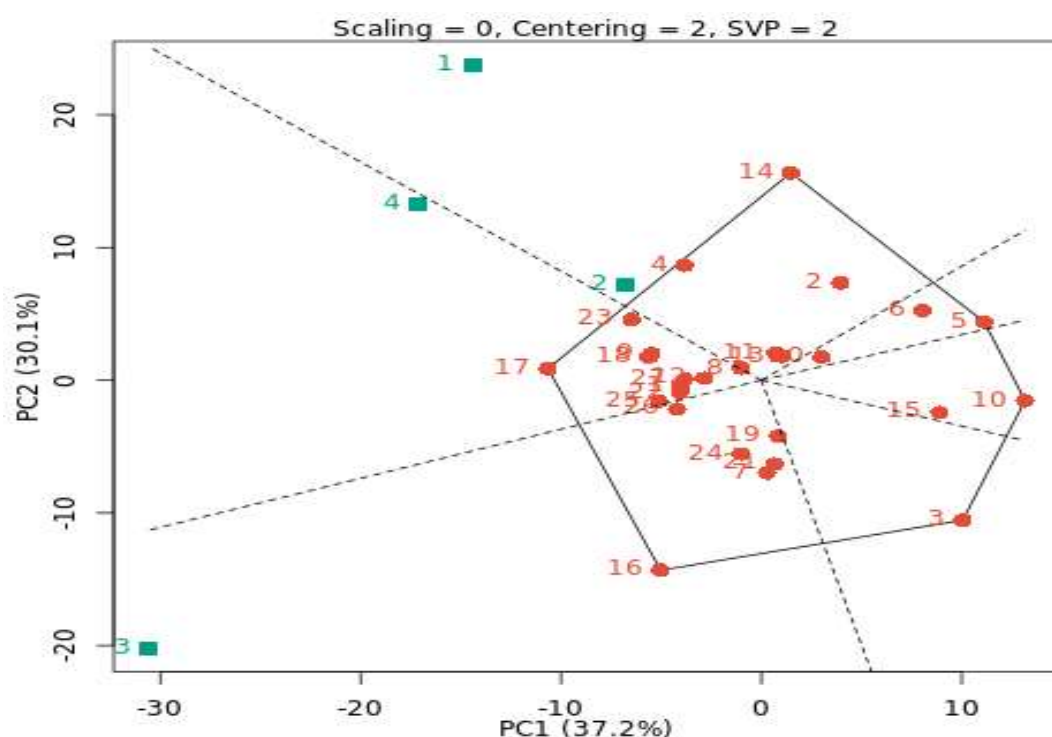


Figure 2. GGE biplot polygon of "which-won-where" for seed cotton yield with 24 cotton genotypes (red color) and four environments (green color). The genotypes and environment key names can be found in Tables 1 and 4, respectively.

A basic set of representative and discriminating test environments can be found with the aid of the GGE biplot of the discriminativeness vs. representativeness view, which is a helpful tool for assessing test environments. It is crucial to identify test environments, accurately define genotype differences, and supply the information needed for plant breeders to make an election. According to Yan *et al.* (2007), the test environment E4 is more indicative of other test environments since it has

the lowest angles with AE, followed by the environments E2 and E1 (Figure 3). Small and medium angles with AE, as well as medium and long vectors, respectively, were found in test environments E1 and E4, suggesting that these environments are ideal and have the best capacity to distinguish between genotypes, encouraging the selection of superior genotypes. According to Yan and Rajcan (2002), the genotype that is closest to the graph of the ideal environment is the most

desired. Therefore, in both growth seasons and under both irrigation regimes, the most productive and stable genotypes are G17, G23, G18, and G4. Strong positive correlations were observed among E1, E2, and E4 environments because the angles between them are acute, while E3 had a moderate positive correlation with the E4 and E2 environments and a slight one with the E1 environment. Ashwini *et al.* (2020) found that all environments had a medium sharp angle with the abscissa, suggesting a favorable relationship with environments. The similarity (covariance) of the two environments is determined by their length vectors and the cosine of their angle (Yan and

Tinker 2006). Consequently, the ray's lines separated the environments into two groups: the E3 environment was part of the second group, while the E1, E2, and E4 environments were part of the first group. Our findings that the environment was the most important determinant in genotype yield performance are consistent with the findings of Abro *et al.* (2022), Iqbal *et al.* (2022), and Yehia *et al.* (2023b). The dataset has been filtered using GGE Biplot based on genotype and environmental knowledge, especially about varietal maturity (McPherson 2022).

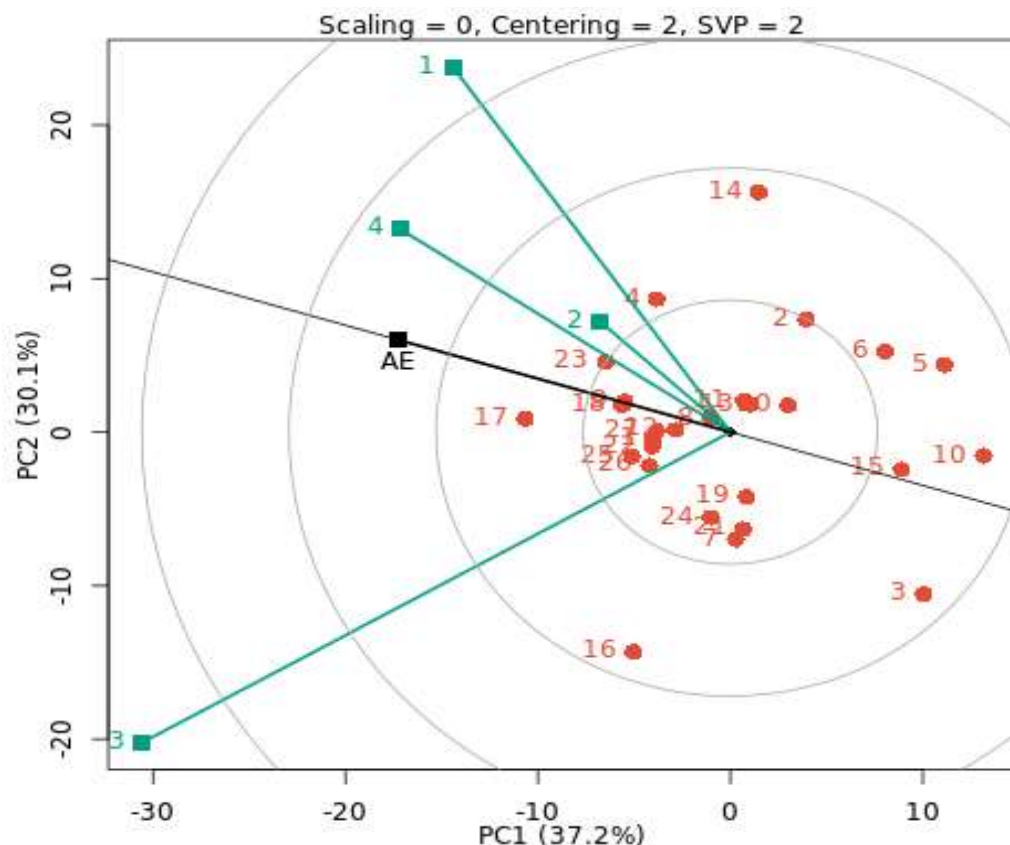


Figure 3. GGE biplot of discriminativeness vs. representativeness for seed cotton yield with 24 cotton genotypes (red color) and four environments (green color). The genotypes and environment key names can be found in Tables 1 and 4, respectively.

One noteworthy aspect of the GGE biplot graph is the depiction of genotypes that combine high mean performance and stability. The arrow sign on the AE indicates that the genotypes are classified based on their average seed cotton yield (Figure 4). From G17 to G11 genotypes had above-average

means, whereas from G13 to G3 genotypes had below-average means. While genotypes G3, G10, and G5 recorded the lowest seed cotton output throughout environments, genotypes G14, G18, G4, and G16 produced better seed cotton yields in E1, E2, E4, and E3 environments, respectively.

The most stable genotypes were G18 and G9, which had a near-zero projection onto the AE ordinate and were situated nearly on the AE abscissa. The G17, G18, G23, G9, and G4 genotypes are more stable and produce higher mean seed cotton yields than the other genotypes. The genotypes G3 and G10, on the other hand, perform below average in the contexts being studied and are more changeable and unstable.

Genotypes with below-average means are distinguished from those with above-average means by the AE ordinate (Abro *et al.*, 2022). Similarly, McPherson (2022) and Yasar (2023) have also used a GGE biplot of mean vs. stability for seed cotton yield to identify stable and high-yielding genotypes.

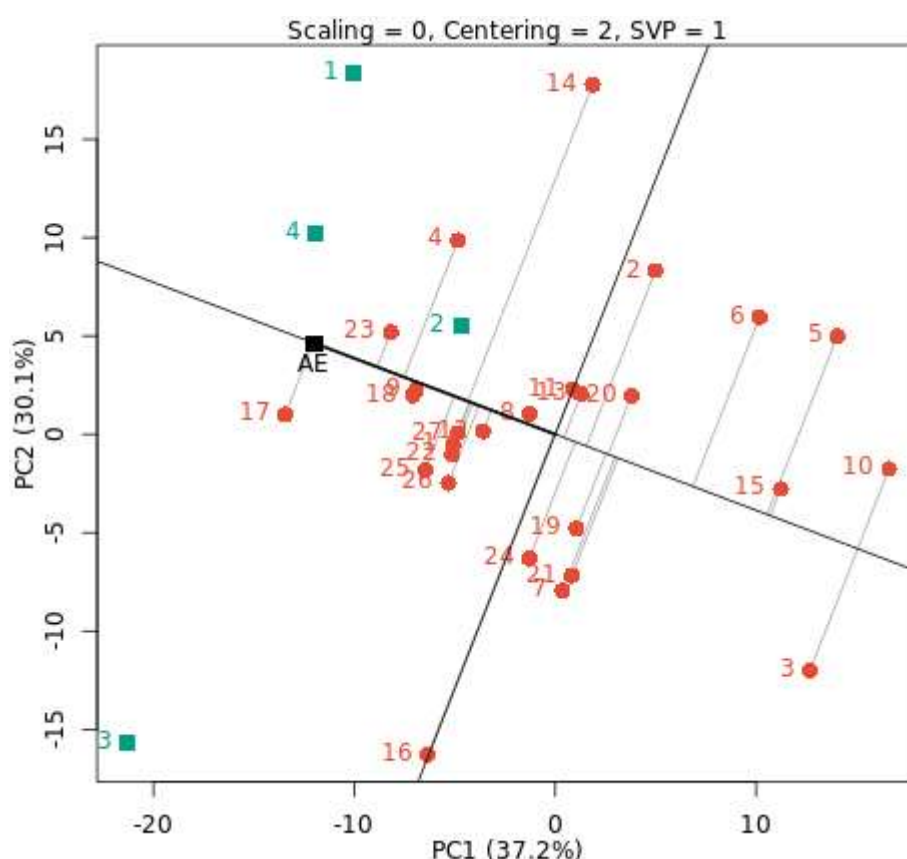


Figure 4. GGE biplot of mean vs. stability for seed cotton yield with 24 cotton genotypes (red color) and four environments (green color). The genotypes and environment key names can be found in Tables 1 and 4, respectively.

As shown in Figure 5, the ranking of the genotypes with above-average mean performance were G17, G18, G23, G9, G27, G4, G14, G25, G12, G26, G22, G1, G11, and G8 in all environments, and they are more stable with better mean cotton yield than the other genotypes. On the other hand, other genotypes were unstable with below-average mean

performance in all environments, where the rankings are G19, G16, G13, G7, G24, G20, G21, G2, G6, G15, G5, G10, and G3. According to Yasar (2023) and Yehia *et al.* (2023b), average yield and stability are necessary for the selection of superior cultivars of cotton.

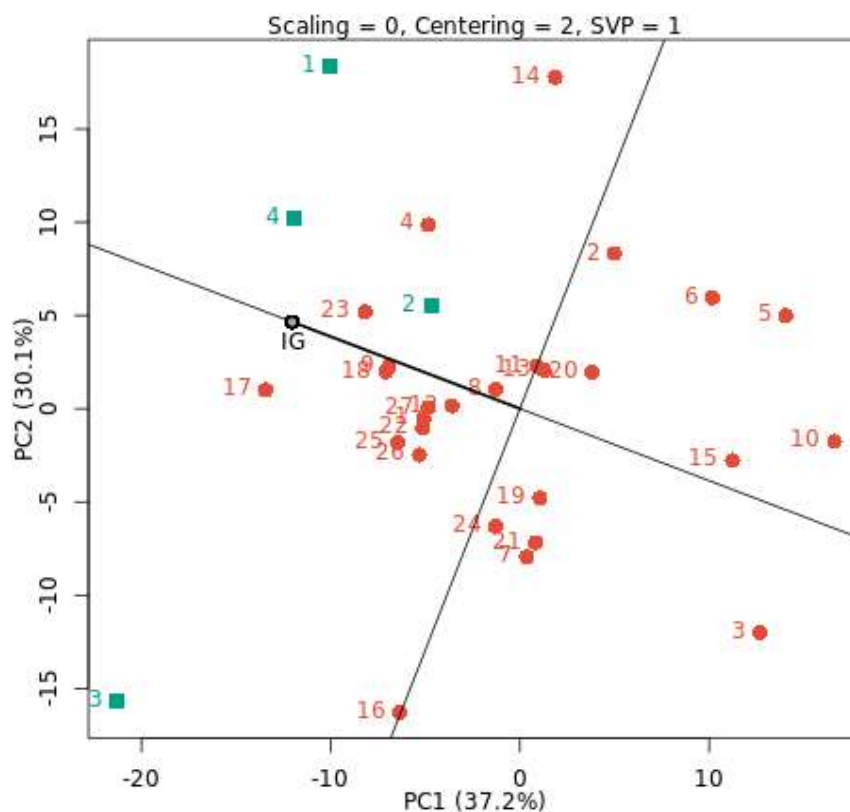


Figure 5. GGE biplot of ranking of the genotypes for seed cotton yield with 24 cotton genotypes (red color) and four environments (green color). The genotypes and environment key names can be found in Tables 1 and 4, respectively.

4. Conclusion

The phenotypic expression of seed cotton yield in this study has been significantly influenced by the environment and its interaction with the genetic structure of 27 genotypes. This has resulted in the genotypes providing significant responses to seed cotton yield based on normal irrigation and drought stress conditions. In general, based on the univariate and multivariate stability statistics, G17, G18, and G4 genotypes had high seed cotton yield and were the most stable genotypes. These genotypes were found to have a great deal of potential for high seed cotton yield and drought tolerance, which can be used as a source for drought tolerance in future breeding programs to develop a useful cotton genotype to address the climate change scenario in Egypt. The AMMI model, GGE biplot analysis, and other stability statistics helped identify these genotypes as having a great deal of potential for drought tolerance.

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

All authors of the manuscript have read and agreed to the publication that all authors have agreed to the submission to the journal

Availability of data and material

The data that support the findings of this study are available from the corresponding author upon reasonable request

Competing interests

The authors declare that they have no conflicts of interest

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Authors' contributions

All authors contributed equally to this study

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