

Performance of Some Faba Bean Genotypes (*Vicia faba* L.) and its Stability Using GGE-Biplot Analysis

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ABSTRACT

The present study was carried out at three locations, i.e., Sakha, Sids, and Mataana Agricultural Research Stations, within two successive seasons (2020/2021 and 2021/2022), to evaluate eighteen promising faba bean genotypes derived from eleven crosses along with two commercial varieties, Giza 843 and Sakha 1. GGE model pattern analysis was used to determine stable faba genotypes for seed yield and to conceive of the relationships between environments and genotypes. Results of the combined analysis revealed that there were highly significant differences for genotypes and locations, indicating high genetic variability between genotypes and wide differences between locations. Comparing the check cultivars, Giza 843 had wide adaptability and produced a higher seed yield under Middle and Upper Egypt conditions, while Sakha 1 was superior under Sakha conditions. The new genotype G6 ranked first under all conditions and exceeded the average of the commercial cultivars by 9.8, 8.5, 11.6, and 10.0% under Sakha, Sids, Mataana, and the grand mean, respectively. GGE results revealed that the first principal components (PC1 and PC2) explained 83.57% of the total variation. The most stable genotypes were G6, G13, G15 and the check cultivar G1. These results suggested the release of G6 as a new faba bean cultivar for its wide adaptation and high productivity.

KEYWORDS: Faba bean, performance, stability, GGE-biplot, GT-biplot.

1. INTRODUCTION

Faba bean (*Vicia faba* L.) is the main food legume crop in Egypt. It is a primary source of protein in the diet of mass. Included in the

crop rotation will keep the soil fertile and productive through biological N₂ fixation. The cultivated area of faba bean in Egypt during the 2021/2022 season was 125.000 feddan with an

average seed yield of 9.6 ardab/feddan (Economic Affairs Sector 2022).

Improving seed yield is a major objective in faba bean breeding programs. A successful breeding program depends on a selection of individuals that have desirable traits. The yield of faba bean, similar to the other crops, is a complex trait and controlled by many factors that are correlated to each other i.e. pods per plant and 100-seed weight which are important traits for increasing seed yield (Loss *et al.*, 1997). Environmental variation has a major effect on the variation of yield (up to 80% or higher) (Temesgen *et al.*, 2015). Plant breeders evaluate different genotypes under different environmental conditions aiming to identify genotypes that are compatible with these environments, especially with the occurring climate changes (Mohammed *et al.*, 2023).

Genotypes and GE interaction are more relevant for genotypes evaluation and selection and they must be considered simultaneously when selecting a genotype; in other words, an ideal genotype should have both high mean yield performance and high stability across environments (Dyke *et al.*, 1995, Gedif and Yigzaw, 2014). Hence, evaluating genotypes across different ranges of environments and years helps to select either consistently yielding genotypes across environments and years or specifically best-performing cultivars a few environments (specific adaptation).

Genotypes and GE interactions are of major importance for breeders, given that they reduce the association between phenotypic and

genotypic values across environments (Chandrika *et al.*, 2015). GGE is considered the most suitable model for multi-environment analysis for genotype evaluation and test environment evaluation which provides differentiates power versus representativeness (Gurmu *et al.*, 2012). The Leguminous Crops Research Department established a breeding program for the faba bean crop using crossing to create variations through hybridization between local genotypes and some imported genotypes. Segregation generations are cultivated and then superior lines are selected for their high-yield potential and evaluated in several locations. This work aimed to evaluate these promising lines at three different locations to study the genotype-environment interactions using GGE biplot techniques to determine the most convenient genotype of faba bean.

2. MATERIAL AND METHODS

The present study was carried out at Sakha (31.08808° N, 30.94588° E), Sids (28.92001°N, 30.9891° E), and Mataana (25.69676° N, 32.64426°E) Agricultural Research Stations, representing North, Middle and Upper Egypt during the two successive seasons 2020/2021 and 2021/2022 for examine the performance and stability of seed yield of twenty faba bean genotypes (eighteen promising faba bean genotypes were selected from F₆ generation that derived from eleven crosses as well as two commercial cultivars Giza 843 and Sakha 1). Table 1 presents the genotype's name, and pedigree.

Table 1. Faba bean genotypes, number of the selected line, purpose, origin, and their pedigree

Crosses	No. of selected lines	Pedigree	Purpose	Origin
x- 1931	1	(Giza 40 x Misr 2) x (Giza 716 x T.W)	Earliness	ARC- Egypt
x- 2143	1	Giza 429 x Nubaria 2	<i>Orbanche</i> tolerant +drought	ARC- Egypt
x- 2199	1	Sakha 2 x Rinamora	Foliar diseases	ARC- Egypt
x- 2200	1	Sakha 3 x Rinamora	Foliar diseases	ARC- Egypt
x- 2214	1	Sakha 4 x PN52104 LT. 10/11	Foliar diseases	ARC- Egypt
x- 2206	1	Giza 716 x PN58133 LS. 10/11	Foliar diseases	ARC- Egypt
x- 2213	1	Sakha 1 x PN52104 LT. 10/11	Foliar diseases	ARC- Egypt
x- 2220	1	Sakha 1 x PN52123 LT. 10/11	Foliar diseases	ARC- Egypt
x- 2218	3	Giza 843 x PN52123 LT. 10/11	<i>Orbanche</i> tolerant	ARC- Egypt
x-2237	2	OPYTL-32/2012 x Misr 3	<i>Orbanche</i> tolerant	ARC- Egypt
x- 2238	5	OPYTL-26/2012 x Giza 843	<i>Orbanche</i> tolerant	ARC- Egypt

Total 18

Table 2. Genotypes and Code of the Twenty Faba bean genotypes used in this study

No.	Genotypes	No.	Genotypes
G1	Giza 843	G11	2238/239/2018
G2	Sakha 1	G12	2238/249/2018
G3	2214/37 5/2017	G13	2238/254/2018
G4	2220/379/2017	G14	2238/2432018
G5	1931/415/2009	G15	2143/633/2015
G6	2199/318/2016	G16	2200/398/2016
G7	2206/358//2017	G17	2218/200/2017
G8	2213/373/2017	G18	2218/211/2017
G9	2237/242/2018	G 19	2218/214/2017
G10	2238/238/2018	G20	2237/233/2018

All materials were grown in a randomized complete block design (RCBD) with three replicates. The experimental plot consisted of five ridges, each ridge was 3 m long and 60 cm apart (the plot size was 9 m²). The sowing took place on the first week of November in all locations. All agriculture practices were carried out at all sites following standard recommendations. At harvest, five guarded plants were taken from each plot to

determine the means of the number of branches per plant, number of pods per plant, seed yield per plant (g), 100-seed weight (g), and seed yield (ard./fed.). The three middle ridges of each plot were harvested to determine seed yield/ardab feddan (1 ardab= 155 Kg and 1feddan = 4200 m²). The maximum and minimum temperatures during the 2020/2021 and 2021/2022 growing seasons show in Table (3).

Table 3. Mean maximum and minimum air temperatures during the two growing seasons at Sakha, Sids, and Mataana Agricultural Research Stations

Months	Air temperature (°C) 2020/2021					
	Sakha		Sids		Mataana	
	Max	Min	Max	Min	Max	Min
November	25.76	15.79	25.03	13.57	27.03	12.68
December	23.48	11.73	22.90	10.23	25.60	10.32
January	22.05	9.95	22.02	7.84	24.04	7.43
February	22.25	9.73	22.34	8.04	24.90	8.34
March	23.35	10.30	25.11	9.70	29.98	11.75
April	29.84	12.09	31.07	12.89	34.77	15.69
Months	Air temperature (°C) 2021/2022					
	Sakha		Sids		Mataana	
	Max	Min	Max	Min	Max	Min
November	28.57	16.50	28.41	14.94	30.56	15.01
December	20.51	10.87	19.72	8.53	22.53	8.71
January	17.60	6.96	16.71	4.50	19.08	4.71
February	19.90	7.98	19.88	6.44	22.93	6.36
March	20.78	8.18	22.00	7.06	26.88	9.13
April	31.45	13.43	33.32	15.19	37.67	18.47

Source: Central Lab. for Agricultural Climate

2.1. Statistical analysis procedures

Analysis of variance (ANOVA) among genotypes was done in each location separately

then the combined analysis of locations and seasons was performed whenever homogeneity of mean squares was detected according to

(Gomez and Gomez, 1984). The least significant difference (LSD) test was used for mean separation at 5% probability.

2.2. GGE Biplot technique

GGE (genotype + genotype by environments interaction effect) biplot graphs display two-way data considering the first two principal components (PC2 and PC1). This technique was employed to explain the interaction between the evaluated twenty faba bean genotypes and the six environments (three location X two seasons) in the same graph to assess the adaptability or stability of seed yield ard./fed. trait as described by (Yan and Tinker, 2005). GT biplot (genotypes – traits biplot) was performed on the twenty genotypes and the five studied traits using method of (Yan *et al.*, 2000). All statistical analysis was performed by GenStat 21th Ed statistical software (GENSTAT, 2009).

3. RESULTS AND DISCUSSION

Results of statistical analysis expressed as mean squares for the various traits: Number of branches per plant, pod number per plant, seed yield per plant (g), 100-seed weight (g), and seed yield ard./fed. are presented in Table (4). Highly significant differences were estimated for genotype and location and their interactions for all studied traits except no. of branches for the interaction. While the seasonal effect and its interactions with genotypes and locations were insignificant in most cases this may be a result of no significant changes in weather during the two seasons (Table 3). Mean Square of genotypes and locations were higher than other sources of variance for all traits, indicating high genetic variability between evaluated genotypes and wide variation between locations Table (4).

Table 4. Combined analysis of variance over seasons (S), locations (L) and (G) genotypes.

Source	df	No. of branches /plant	No. of pods/ plant	Seed yield/ plant	100-seed weight	Seed yield (ard./fed.)
L	2	4.2617**	358.71**	2276.51**	266.63**	14.839**
S	1	1.1903 ^{NS}	0.982 ^{NS}	638.45**	1986.33**	1.599 ^{NS}
L.S	2	1.8661 ^{NS}	75.576**	586.5**	389.75**	2.292 ^{NS}
Residual	12	0.6514	8.499	36.16	31.1	1.539
G	19	2.5819**	168.86**	2160.07**	1172.21**	39.346**
L.G	38	0.2783 ^{NS}	7.196**	189.27**	147.22**	3.866**
S.G	19	0.2631 ^{NS}	10.064**	44.31**	68.56**	4.97**
L.S.G	38	0.1415 ^{NS}	4.259 ^{NS}	52.92**	46.53**	1.718 ^{NS}
Residual	228	0.3619	4.14	21.54	26.51	1.756

NS. *, ** insignificant and significant at 0.05 and 0.01 levels, respectively

The mean number of branches, pods, and seed yield/plant of the twenty faba bean genotypes are present in Table (5). The number of branches/plant was in the range between 3.4 to 4.7 for the genotype G 20 (2237/233/2018) and G 6 (2199/318/2016), respectively. The highest number of branches was shown in Sids while the interaction between genotype and locations was insignificant. The number of pods per plant is an important selection criterion for the development of high-yielding faba bean genotypes and is strongly influenced by the environment (Abdalla *et al.*, 2015). The mean of no. pods were higher under Sakha conditions with a mean value of 28.35. The genotypes G 6 (2199/318/2016), G 13 (2238/254/2018), G 15

(2143/633/2015) produced the highest number of pods/plant 34.0, 32.5 and 31.6, that exceeded the average of check cultivars by 10.8%, 6.1% and 3% for first check (Giza 843), 8.1%, 12.8% and 9.7% for second check (Sakha 1) respectively. Regarding seed yield/plant highly significant differences were recorded among all sources of variances. The plant productivity was high (80.76g) under Sakha conditions, while the mean seed yield/plant was low (72.25g) under Mataana conditions. The promising new genotypes G6 (2199/318/2016) and G 13 (2238/254/2018) significantly occupied the first rank under Sakha conditions and mean of the three locations with mean values of 102.75, 102.1 and 95.4, 93.3g, respectively. They share

the first rank with G15, G10, G1 under Sids conditions and with G1 (the check cultivar Giza 843), G15, G17 under Matanna conditions. On the side, the smallest value (55.0g) recorded by Genotype G 20 (2237/233/2018).

Table 6 presents mean performances of the evaluated genotypes for 100 seed weight, and seed yield ard./fed. Mean of 100-seed weight (g) showed the superior of genotypes, G6 (2199/318/2016), G13 (2238/254/2018), G15 (2143/633/2015) and G1 (Giza 843) with mean values of 96.5, 95.2, 93.7 and 93.6 g, respectively, whereas the lowest 100-seed weight (64.8g) was recorded by G20 (2237/233/2018). This is agreed with (Abdalla *et al.*, 2017) detected highly significant additive genetic variance for pods/plant, seed yield/plant, and 100-seed weight and reported that selection could be favored for improving this trait. Also, (Kanoosh and Al-Falahy, 2020) found that seed yield/plant, number of branches/plant, and number of pods/plant desirable characteristics to improve the faba bean genotypes.

Concerning seed yield ard./fed the faba bean genotypes G6 (2199/318/2016) showed wide adaptability and recorded high seed yield under all conditions as well as their mean, followed by G13 under all locations but significantly was not in the first rank at the mean of all environments. Genotype G6 exceeded the average of the check cultivars (Giza 843 and Sakha 1) by 9.8, 8.5, 11.6, and 10.0% under Sakha, Sids, Mataana, and the grand mean, respectively. The other genotypes ranked differ under the evaluated locations. G15 was among the ideal genotypes under both Sids, Mataana, and the grand mean but under Sakha, conditions came in the second rank. The same trend was recorded by the check cultivar G1 (Giza 843) indicating that both of these genotypes suitable for Middle and Upper Egypt. On the other hand, the check cultivar G2 (Sakha 1) was superior under only Sakha conditions. However, faba bean genotypes produced higher seed yield ard./fed. under both Sakha and Sid than Mataana.

The highly significant differences among faba bean genotypes and the superiority

of new lines on commercial cultivars were in harmony with many previous authors (El-Emam and Rabie, 2015).

3.1. GGE biplot

GGE biplot analysis of multi-environment trial (MET) data can help researchers to better understand their target environment, establish less cost-effective breeding and testing strategies, and identify superior genotypes that are widely or specifically adapted. It was suggested by (Yan and Tinker, 2005) to estimate genotype effect (G) and genotype by environment interaction effect (GE) in multi-environment trials. GGE biplot is erected based on the first (73.86%) and second (9.71%) components (PC1 and PC2) of principal components analysis (PCA). In this study, PC1 and PC2 explained 83.57 % of the total variation.

3.2. Scatter plot

GGE biplot was constructed based on grain yield ardab/fed. trait for the twenty genotypes under six environments *i.e.* Sakha, Sids, and Mattana during the 2020 and 2021 seasons (SA1, SA2, SDS1, SDS2, MAT1, and MAT2, respectively). The angle between environment vectors provides information on the correlation between environments. An acute angle indicates a positive correlation, a right angle indicates no correlation and an obtuse angle indicates a negative correlation between the environments. The scatter plot of the GGE biplot (Fig. 1) with the origin point represents a virtual genotype that has average performance for seed yield ardab/feddan in each environment. The scatter plot shows that there is a positive correlation between four environments (SA1, SA2, SDS1, and SDS2) while MAT1 and MAT2 were separated in other positive correlations this means that data of both locations (Sids and Sakha) were in harmony because approximately 482 km apart between Mataana and the nearest location Sids.

Table 5. Mean performance of number of branches/plant, number of pods/ plant and seed yield/plant (g) for studied genotypes over locations and seasons

No.	Populations	Number of branches/plant				Number of pods/ plant				Seed yield/plant (g)			
		Sakha	Sids	Mataana	Overall	Sakha	Sids	Mataana	Overall	Sakha	Sids	Mataana	Overall
1	Giza 843	4.50	4.90	4.20	4.50	31.45	32.15	28.35	30.70	93.50	96.05	86.30	92.00
2	Sakha 1	4.55	4.60	3.85	4.30	31.60	29.15	25.70	28.80	89.25	88.85	80.40	86.20
3	2214/37 5/2017	3.55	3.80	3.30	3.60	27.20	25.15	23.35	25.20	67.70	62.70	60.65	63.70
4	2220/379/2017	3.45	3.95	3.95	3.80	24.85	24.05	22.20	23.70	79.40	74.40	70.30	74.70
5	1931/415/2009	3.60	3.90	3.30	3.60	25.95	25.15	22.70	24.60	65.00	60.00	60.80	61.90
6	2199/318/2016	4.65	4.95	4.50	4.70	35.40	35.30	31.20	34.00	102.75	94.65	82.50	93.30
7	2206/358//2017	3.75	3.80	4.00	3.90	27.85	27.30	24.65	26.60	79.20	83.10	73.30	78.50
8	2213/373/2017	3.80	4.10	3.85	3.90	23.35	23.95	22.00	23.10	85.30	81.60	63.55	76.80
9	2237/242/2018	3.50	3.80	3.75	3.70	27.20	26.90	23.15	25.80	76.40	71.40	66.85	71.60
10	2238/238/2018	4.20	4.55	4.05	4.30	27.00	30.15	24.65	27.30	85.80	97.05	70.50	84.50
11	2238/239/2018	3.95	4.25	3.90	4.00	27.10	26.65	23.50	25.80	71.40	66.40	70.40	69.40
12	2238/249/2018	3.50	3.80	4.00	3.80	25.75	24.00	22.85	24.20	72.70	67.70	67.45	69.30
13	2238/254/2018	4.60	4.85	4.40	4.60	34.10	33.85	29.40	32.50	102.10	98.60	85.35	95.40
14	2238/2432018	4.20	4.75	3.85	4.30	31.60	30.00	26.00	29.20	92.75	70.60	69.50	77.60
15	2143/633/2015	4.60	4.85	4.45	4.60	33.45	31.65	29.75	31.60	93.95	95.35	84.95	91.40
16	2200/398/2016	3.70	4.00	4.00	3.90	26.70	26.00	23.70	25.50	68.10	63.10	74.20	68.50
17	2218/200/2017	3.85	4.30	4.35	4.20	24.15	25.35	27.35	25.60	82.40	76.70	82.75	80.60
18	2218/211/2017	3.65	3.95	3.95	3.90	27.00	26.20	23.80	25.70	75.80	77.30	71.90	75.00
19	2218/214/2017	3.55	4.60	3.90	4.00	28.50	27.00	24.35	26.60	74.65	83.85	66.95	75.20
20	2237/233/2018	3.20	3.50	3.60	3.40	26.75	26.10	23.30	25.40	56.95	51.70	56.35	55.00
	Mean	3.92	4.26	3.96	4.05	28.35	27.80	25.10	27.10	80.76	78.06	72.25	77.03
L.S.D 0.05	L				0.19				0.67				1.38
	G	0.72	0.86	0.43	0.39	2.56	2.27	2.17	1.34	5.40	5.20	5.41	3.05
	LxG				ns				2.38				5.37

Table 6. Mean performance of 100-seed weight (g)/plant and seed yield (ard./fed.) for studied genotypes over locations and seasons

No.	Populations	100-Seed weight (g)				Seed yield (ard./fed.)			
		Sakha	Sids	Mataana	Overall	Sakha	Sids	Mataana	Overall
1	Giza 843	96.10	96.10	88.60	93.60	13.00	13.30	12.90	13.05
2	Sakha 1	83.60	91.30	83.60	86.10	13.60	12.50	10.40	12.13
3	2214/37 5/2017	76.60	73.50	70.80	73.60	10.90	11.10	9.10	10.37
4	2220/379/2017	76.80	87.30	79.60	81.20	10.10	11.20	9.20	10.13
5	1931/415/2009	79.00	76.50	76.10	77.20	9.40	9.60	8.50	9.15
6	2199/318/2016	100.40	100.40	88.90	96.50	14.60	14.00	13.00	13.85
7	2206/358//2017	76.50	84.50	78.70	79.90	10.10	10.90	8.70	9.88
8	2213/373/2017	84.30	78.90	80.80	81.30	9.80	10.60	11.30	10.57
9	2237/242/2018	76.90	77.70	79.70	78.10	10.20	9.20	9.80	9.73
10	2238/238/2018	82.30	93.90	76.50	84.20	10.80	12.30	11.00	11.35
11	2238/239/2018	79.80	79.70	78.60	79.30	10.90	10.80	10.00	10.53
12	2238/249/2018	80.60	75.60	77.50	77.90	10.40	10.70	9.30	10.08
13	2238/254/2018	98.70	96.80	90.00	95.20	13.40	12.90	12.40	12.88
14	2238/243/2018	88.70	72.00	77.80	79.50	12.70	10.90	10.20	11.27
15	2143/633/2015	95.80	95.30	90.20	93.70	13.10	13.90	12.80	13.27
16	2200/398/2016	79.60	77.40	72.10	76.30	11.00	11.20	10.70	10.93
17	2218/200/2017	68.10	69.50	84.50	74.00	9.10	9.00	11.10	9.70
18	2218/211/2017	78.00	81.40	75.80	78.40	9.80	9.80	8.90	9.48
19	2218/214/2017	82.60	78.60	73.00	78.10	9.20	8.80	10.80	9.58
20	2237/233/2018	62.60	59.70	72.30	64.80	8.80	8.50	9.00	8.75
	Mean	82.35	82.31	79.76	81.45	11.05	11.06	10.46	10.83
L.S.D 0.05	L				1.28				0.29
	S				1.57				0.35
	G	6.06	5.63	6.06	3.38	1.38	1.53	1.65	0.87
	SxL				2.20				0.49
	SxG				4.80				1.23
	LxG				5.88				1.50
	SxLxG				8.32				2.13

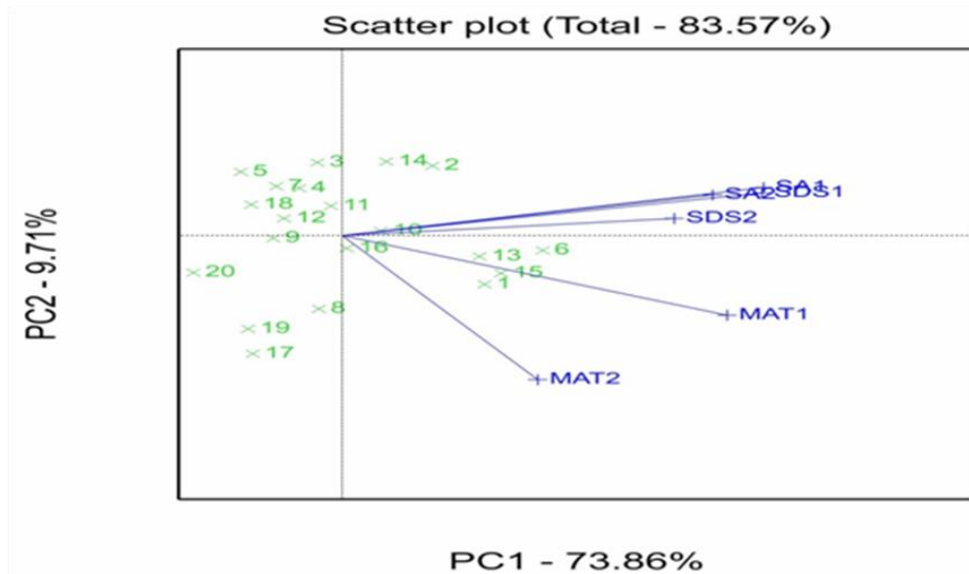


Figure 1. Scatter plot of GGE biplot for the evaluated faba bean genotypes across the six environments for seed yield (ard./fed.).

3.3. Which-Won-Where

The “who won where” pattern of the multi-environment trial (MET) helps to identify which genotype performed the best in each environment and each mega-environment in the

region (Yan, 2001, Yan *et al.*, 2000). Polygon a convex hull (Fig. 2) has been drawn by connecting the farthest genotypes to form a polygon that compasses all genotypes. Sectors have been also added by drawing lines from the origin vertical to each side of the hull. Ellipses

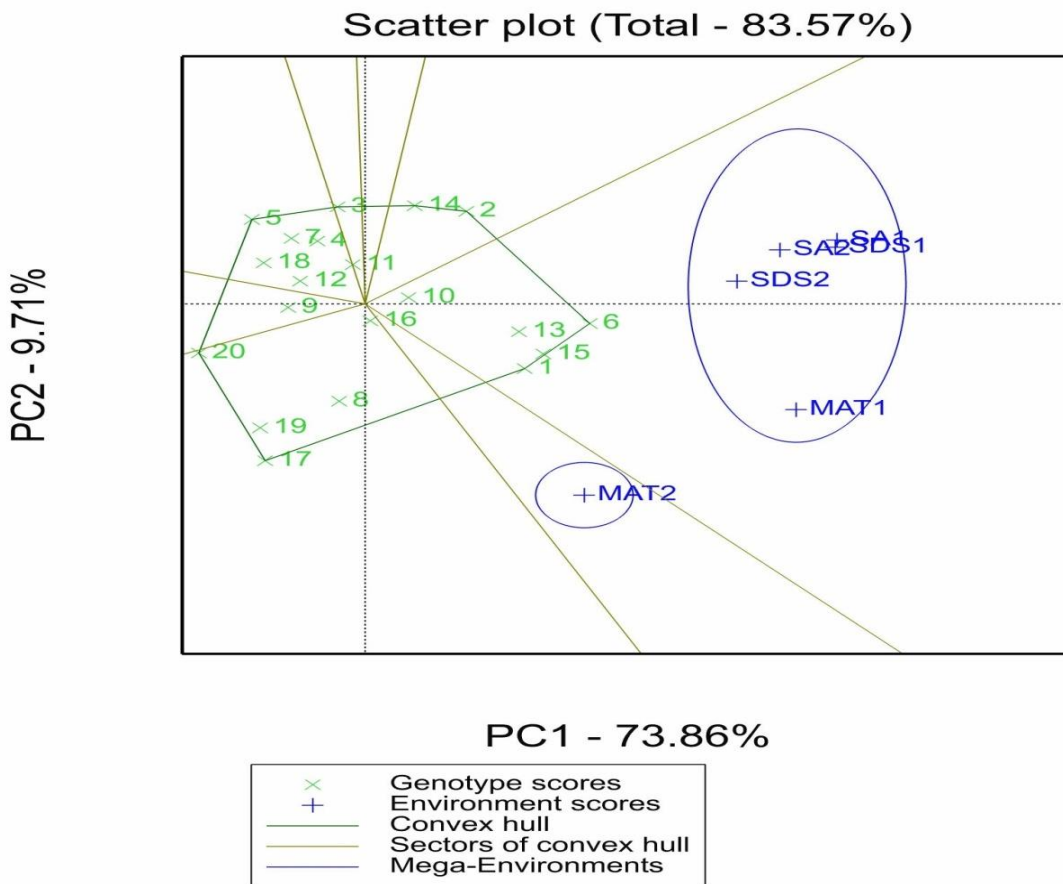


Figure 2. Which-Won-Where of GGE biplot for 20 genotypes of faba bean.

has been drawn around the environments with the same sector to form a mega environment. “Which - Won – Where” polygonal showed that there are two mega environments; the first mega environment (ME1) includes SA1, SA2, SDS1, SDS2, and MAT1 while the second mega environment (ME2) contains only one environment (MAT1). The first mega environment (ME1) includes the genotypes G6 (2199/318/2016), G13 (2238/254/2018), G15 (2143/633/2015) and G1 (Giza 843) which produced high yielding in most environments in addition to G 10 (2238/238/2018) and G16 (2200/398/2016). These results are in full agreement with those obtained by (Gurmu et al., 2012).

3.4. Ranking biplot

The “Ranking Plot” is an effective tool for the visual evaluation of genotypes on both aspects (performance and stability). A superior genotype should have both high mean performance and high stability across a mega-environment. The stability of the genotypes is

graphically represented by the projection from the entry symbol to the ATA (Average Tester Axis), The genotypes are ranked along the ATA, with the arrow pointing to a greater value according to their mean performance across all locations. The perpendicular to the ATA that passes through the origin separates entries with below-average means from those with above-average means. The length of the line between the genotype and its orthogonal projection onto the biplot axis is a measure of genotype stability the short line showed high stability and the long line showed low stability. In that matter, GGE ranking biplot showed that G 6 (2199/318/2016), G13 (2238/254/2018), G15 (2143/633/2015) and G1 (Giza 843) were the highest yielding and most stable followed by G2 (Sakha 1), G10 (2238/238/2018), G14 (2238/2432018) and G16 (2200/398/2016) (Fig. 3). On the other side, G20 (2237/233/2018) was the poorest yielding genotype. These results are in agreement with those obtained by (Gurmu et al., 2012).

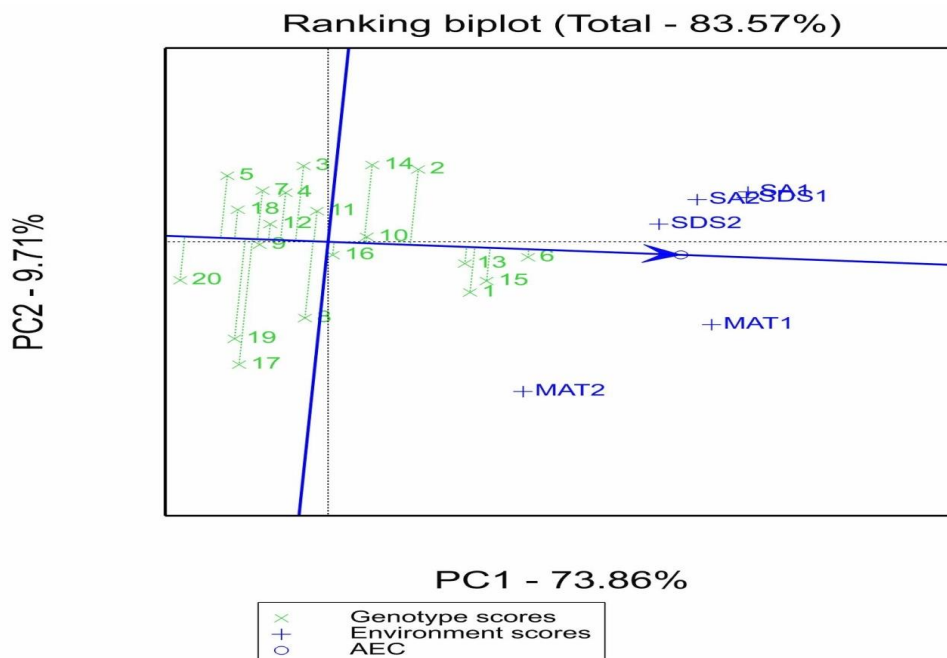


Figure 3. Ranking biplot for 20 genotypes of faba bean.

3.5. Genotype by trait (GT biplot)

The genotype–trait (GT) interaction is one of the GGE biplot methods of studying genotype–trait interaction data. GT biplot is a powerful method to identify cultivars and trait interactions (Stansluos *et al.*, 2023), in this

analysis, genotypes are considered as lines and traits as testers (Yan and Rajcan, 2002). It was attributed to data of mean performance overall in the test environments for the studied traits. GT biplot was generated using standardized data to remove the units followed by performing

PCA and plotting PC1 against PC2. GT biplot (Fig. 4) suggests a close positive association between 100-seed weight and seed yield/plant which ultimately affects the yield. Genotypes G1 (Giza 843), G6 (2199/318/2016), G13 (2238/254/2018), and G15 (2143/633/2015)

characterized by a higher 100-seed weight and seed yield/plant.

It showed the presence of sufficient variability (long vector for traits) and suitability for GT biplot, where interpreted 98.41% of the total variation which agreed with (Koç et al., 2018, Sharifi, 2015).

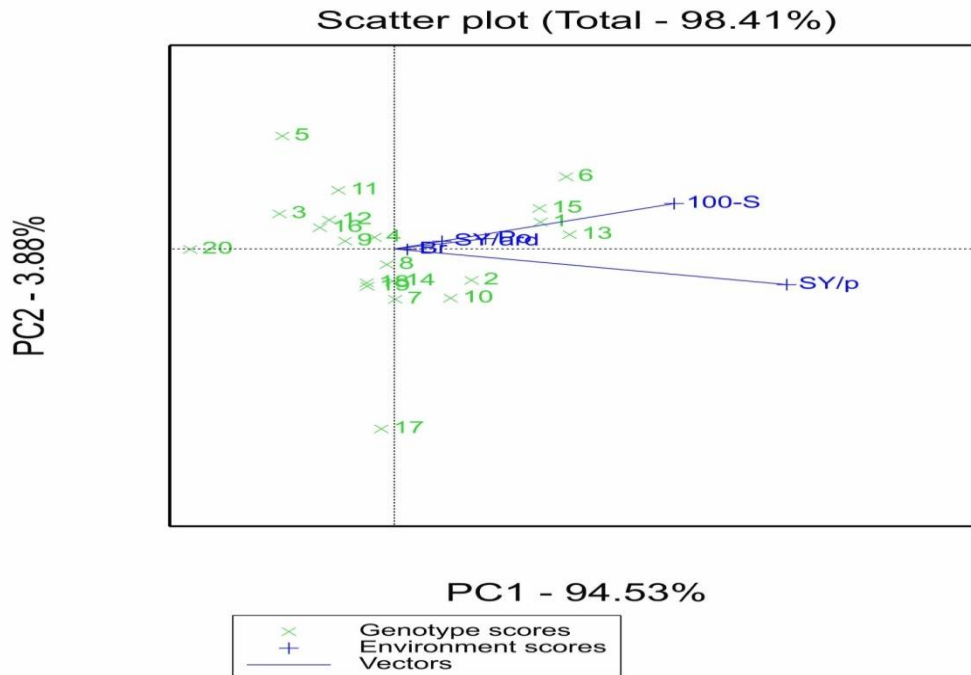


Figure 4. GT biplot for 20 genotypes of faba bean.

4. CONCLUSION

In this study, (GGE) model pattern analysis was used to determine stable faba genotypes for seed yield to examine genotype and environment performance and to conceive the relationships between environment and genotypes. Results revealed that the genotype's mean performance (PC1) and approximate GGE interaction effect (PC2) explained together 83.57% of the total variation. High essential variations were found between genotypes and their interaction with the environment. Genotypes G 6 (2199/318/2016), G 13 (2238/254/2018), G 15 (2143/633/2015), and G 1 (Giza 843) were the best ones for all traits in all locations. All these genotypes are promising and could be recommended for advanced evaluation to release the best.

Conflicts of Interest: The authors declare no conflicts of interest

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الملخص العربي

سلوك بعض التركيب الوراثية من الفول البلدي باستخدام تحليل GGE

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قسم بحوث المحاصيل البقولية - معهد المحاصيل الحقلية - مركز البحوث الزراعية - مصر

أجريت الدراسة الحالية في ثلاثة مواقع بمحطات البحوث الزراعية بكلاً من سخا وسدس والمطاعنة - مركز البحوث الزراعية خلال موسمين متتاليين ٢٠٢٠/٢٠٢١ و ٢٠٢١/٢٠٢٢. وتم استخدام ثماني عشر سلالة مبشرة من الفول البلدي مشتقة من أحد عشر هجين بالإضافة إلى صنفين تجاريين للمقارنة هما: الجيزة ٨٤٣ و سخا ١. تم استخدام تحليل GGE لتحديد التركيب الوراثية الأعلى محصولاً والأكثر ثباتاً. لفحص التركيب الوراثي والأداء البيئي وتصور العلاقات بين البيئة والتركيب الوراثية. أظهرت النتائج وجود فروق معنوية عالية بين التركيب الوراثية والمواقع مما يشير إلى تباين وراثي واسع لهذه الصفات في هذه المواد الوراثية. أظهر متوسط أداء التركيب الوراثية أن التركيب الوراثية G6، G13، G15 و G1 كانت الأعلى إنتاجية. كما أوضحت النتائج أن متوسط أداء التركيب الوراثية PC1 (٧٣,٨٦%) و تأثير تفاعل بين البيئة والتركيب الوراثية PC2 (٩,٧١%) اوضحوا معاً ٨٣,٥٧% من التباين الكلي. بشكل عام كانت التركيب الوراثية G6، G13، G15 و G1 هي الأكثر ثباتاً والأعلى محصولاً في جميع المواقع والتي تستحق مستويات أعلى من التقييم وتسجيل أفضلها كصنف جديد.