

(Original Article)



Genotype-by-Environment Interaction and Stability Analysis of Seed Yield and its Components of Faba Bean Genotypes under Different Irrigation Systems

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Abstract

The present research aimed to evaluate and select faba bean stable genotypes with high productivity across diverse irrigation systems (i. e. surface, drip, and sprinkler irrigation systems). Twenty genotypes were grown in a randomized complete block design with three replicates at three different irrigation systems during two successive seasons of 2020/2021 and 2021/2022 representing six environments. The genotypes were evaluated for seed yield and its related traits. Two common methods used for multi-environment experiments, i.e., the additive main effects and multiplicative interaction (AMMI), and genotype plus genotype environment interaction (GGE) biplot. The ANOVA for AMMI model revealed highly significant differences among tested genotypes, investigated environments (irrigation systems), and genotype-by-environment interaction (GEI) for measured traits except threshing percentage that showed insignificant GEI. Moreover, partitioning the GEI by AMMI analysis revealed that the first two terms of AMMI (IPCA1 and IPCA2; Interaction Principal Components Axis term 1 to 2, respectively) were significant for all studied traits except threshing percentage, which IPCA2 was nonsignificant. Interestingly, the effect of environments (E) and GEI are more than four and three times the effect of genotypes (G) in seed yield trait, respectively. The GGE biplot analysis revealed negative correlations among each pair of environments in most cases, especially sprinkler irrigations (Spr-1 and Spr-2) showed long vectors from the origin. For seed yield, most of the high yielding genotypes were adapted to drip and surface irrigation environments which had mean performance above the average. Based on this, drip irrigation system comes first, then surface irrigation and last sprinkler irrigation. The genotypes G06, G08, G10, G13, G16, G18, and G20 could be considered as high yielding and stable genotypes across environments, G15 was the superior one but had great variability (unstable).

Keywords: GGE, AMMI, Irrigation environments, Stability, Faba bean (*Vicia faba L.*)

Introduction

Faba bean (*Vicia faba L.*), also known as fava and broad bean, is considered the first leguminous food crop in Egypt. It has been a mainstay of the Egyptian diet since the time of the pharaohs and is a strategic commodity for the

Egyptian citizen as a staple food because of the high nutritional value (Ouda and Zohry, 2017; Attia *et al.*, 2019). However, there is a gap between local faba bean production and consumption; therefore, Egypt is one of the most important importing countries for beans (Attia *et al.*, 2019). Hence, the percentage of self-sufficiency in faba beans declined from 97.9% in 2000 to 10.1% in 2020 (Abdelaal and Soliman, 2022). This huge reduction in self-sufficiency of faba bean may be due to that both area and production of faba bean crop decreased by a statistically significant annual rate in the same period (Kandil, 2022). Also, looking at the statistics of the FAO between 2018 and 2021, we find a decrease in the cultivated area from 34530 hectares (82181.4 feddans) to 26382 hectares (62789.16 feddans), and thus productivity decreased from 116435 tons to 105051 tons (FAOSTAT, 2023).

Most countries in the world suffer from the climate change and global warming, which affect the sources of fresh water, and lead to reduction in crop productivity. Egypt's climate is characterized by hot, dry summers and mild winters with relatively low, non-uniform, and unpredictable rainfall. (Morsy *et al.*, 2017). Therefore, the Egyptian state has paid great attention to the need to rationalize and optimal use of water in general and crop irrigation water in particular by following modern irrigation methods like drip and sprinkler irrigation in order to reduce the repercussions of climate change on Egypt. Zohry and Ouda, (2016) referred that water requirement for faba bean is expected to raise by 17 % in Upper Egypt and by 3 % in the Nile Delta in 2030.

Farmers use surface irrigation to irrigate their crops in old lands, which, when compared to modern irrigation systems such as sprinklers, drip, and improved irrigation systems, we find that surface irrigation has a very low field water use efficiency of about 50%. While at new-lands, sprinkler and drip irrigation regimes are practiced, using underground water and/or from the Nile (Amer *et al.*, 2017). Fayed *et al.*, (2018) mentioned that using modern irrigation systems provide an easy and cheap way to perform irrigation management strategies in Faba bean.

Plant breeders conduct multi-environment experiments with the aim of evaluating the genotypes for yield and its attributes under various environments especially under climate change and studying the genotype-by-environment interaction (GEI). The GEI refers to the ordering of genotypes across environments before recommending a specific genotype for a particular environment (Akter *et al.*, 2015; Lozada & Carter, 2020; Kindie *et al.*, 2022; Olanrewaju *et al.*, 2021; Sayed *et al.*, 2022). In faba bean “yield stability” is at least as important as yield itself as a breeding objective (Torres *et al.*, 2012). In plant breeding programs and agricultural research, modern multivariate statistical methods allow direct selection for greater stability. There are two common methods used for multi-environment experiments, i.e., genotype and genotype environment interaction (GGE) biplot and the additive main effects and multiplicative interaction (AMMI). Both biplot analyses are used for simple and easy graphical representation of evaluated genotypes under different

environments by two-way tables by using principal component analysis (PCA) (Alizadeh *et al.*, 2017; Oladosu *et al.*, 2017). Yan and Tinker, (2006) pointed out that the GGE confirms the understanding of both G, and GE interaction, which are the sources of variation related to genotype assessment. They must also be considered simultaneously to assess both the genotype and the environment. Therefore, the main objective of the present study was to evaluate the GEI using AMMI and GGE-biplot analyses for seed yield and its related traits of faba bean genotypes and detect stable faba bean genotypes under different irrigation systems.

Martials and Methods

Plant material, experimental sites and design

Twenty faba bean genotypes were included in current study; the names of genotypes, pedigree and origin are presented in Table 1. These genotypes were evaluated for seed yield and its related traits under three distinct irrigation systems (surface, drip, and sprinkler irrigation) at the Experimental Farm, Faculty of agriculture, Assiut University (where the surface irrigation is used), and at Al-Wadi Al-Assiuty on the newly reclaimed site of the Experimental Station (where the drip and sprinkler irrigation are used), Al-Wadi Al-Assiuty Farm, Faculty of Agriculture, Assiut University (about 25 km Southeast of Assiut) during the two growing seasons of 2020/2021 and 2021/2022, representing six environments.

Table 1. The origin and pedigree of the studied faba bean genotypes

No.	Genotype	Origin	Pedigree
G1	Assiut 120		
G2	Assiut 121	These breeding lines provided by Prof Dr. E.A. Waly and Prof. Dr. S.A. Abdel-Aal ; Vegetable Crops Dept., Faculty of Agriculture, Assiut University (WAA).	These breeding lines derived from intercrossing of five parents <i>i.e.</i> , 1-Somaly, 2-Local Balady, 3- Kobrosy, 4- Long Equadore and 5- Bunyard's Exhibition (SLKLB).
G3	Assiut 136		
G4	Assiut Brown flower		
G5	Assiut 159		
G6	Assiut 142		
G7	Assiut 143		
G8	Assiut 115		
G9	Wadi 1		
G10	Misir 1	Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Egypt	(Giza3*123A/45/76)*(62/1570/66*Giza2)*(Romi*Habashi)
G11	Nubaria 1		(Single plant selection from Rena Blanka•)
G12	Sakha 3		Promising line 716/402/2001 derived from Giza716 (Giza 461*503/453/83)
G13	Giza 843		(85/2076/561 SKH *461*845/83)
G14	Giza 716		(416/842/83*503/453/83)
G15	Sahara	Desert Research Center, Egypt	Sahara derived from the registered seeds of Mariott 2 variety
G16	Assiut 12	(WAA)	(SLKLB)
G17	Dwarf	(FCRI), (ARC), Egypt	IG 12658/accession DOI # 10.18730/60V47) is a dwarf accession from Ethiopia
G18	Assiut 104		
G19	Assiut 167	(WAA)	(SLKLB)
G20	Assiut 10		

•: the genotype originated from Spain.

°: the genotypes originated from Sudan.

Each trial was laid down in randomized complete block design (RCBD) with three replicates. Each genotype in each replication was planted in one row (plot) of 4 m length by 0.6 m spacing between rows, with 0.1 m interplant spacing and two seeds per hill.

Irrigation systems applied

The total irrigated water for each system was used as 1500 m³ in equal amount of water across different irrigation times according to the irrigation system during the season. The number of irrigation times were four for surface irrigation and fifteen for both of drip and sprinkler systems during the sowing season, respectively.

Measured traits

Data for different agronomic traits on a plant or plot basis were collected. Number of branches per plant (NBP), number of pods per plant (NPP), pods yield per plot (PYPL; g), hundred seed weight (SI; g), seed yield per plot (SYPL; g), and thrashing percentage (THR; %).

Statistical analyses

The combination of three irrigation systems and two years was considered as six environments. The data of seed yield and related traits of the six environments have been subjected to the analysis of variance (ANOVA) for additive main effects and multiplicative Interaction (AMMI) model using GenStat software version no. 15.2 (Payne *et al.*, 2012). The combined analysis of AMMI model was conducted to determine the presence of the genotype-by-environments interaction (GEI), the significance of the first two principal component axes, the contribution of the genotype (G), environments (E), and GEI to the total sum of squares, and the residual effect.

The genotype-genotype-by-environment (GGE) biplot approach proposed by Yan and Tinker, (2006) was conducted using GenStat software to quantify GEI, grouping of mega-environments, describe testing environments, and select the genotypes based on stability and mean performance of a trait. The results of AMMI and GGE analyses are presented by analysis of variance and biplot graphs, respectively.

The phenotypic Pearson Correlation matrix analysis among measured traits in each trial (environment) was calculated by R-software (R Core Team, 2023).

Results and Discussions

Analysis of variance

The additive main effect (AM) and multiplicative interaction (MI); (AMMI) analysis of variance revealed highly significant differences among tested genotypes, investigated environments (irrigation systems), and genotype-by-environment interaction (GEI) for measured traits except THR that showed insignificant GE interaction (Table 2). In addition, the coefficient of variation (C.V.) ranged between 9.42% (SI) and 14.69% (NBP). THR (0.52) showed the

lowest value of the coefficient of determination (R^2), while NPP exhibited the greatest value (0.94). Teklay *et al.*, (2015) reported that the AMMI analysis revealed significant differences ($P < 0.01$) among faba bean genotypes, environment and GEI. Additionally, the environment gave higher sum of square for the response variable seed yield. Also, the results are in line with those obtained by (Haile and Kebede, 2021; Papastylianou *et al.*, 2021; Abou-Khater *et al.*, 2022).

Partitioning the GEI by AMMI analysis revealed that the first two components of AMMI (IPCA1 and IPCA2) were significant for all studied traits except THR, since the first principal component axis (IPCA1) was the only significant one. In addition, a high total contribution of both axes from the GEI's sum of squares was observed for all traits and ranged between 68.30% (NPP) and 80.93% (PYPL). The maximum contribution of the IPCA1 was recorded for NBP, followed by SI and explained 61.51% and 56.87% of the variation of GEI, respectively. Whereas, the maximum contribution of the IPCA2 was observed for NPP, followed by PYPL and explained 29.08% and 28.16% of the variation of GEI, respectively. Gauch *et al.*, (2008) reported that the IPCA1 and IPCA2 of the AMMI model are adequate and suitable for cross-validation of the trait variation explained by the interaction of genotype by environment (GEI).

Regarding the proportional effect of each variant component over the total sum of squares, the contribution of genotypes, environments, and GEI to the total sum of squares (TSS) varied from low to high based on the measured trait. Since, the genotypes' contribution to TSS ranged between 6.87% (THR) and 48.64% (SI). The contribution of tested environments to the TSS varied from 8.84% (SI) to 43.83% (SYPL), while GEI's contributions ranged between 16.87% (NBP) and 37.81% (PYPL). Low contribution values of the genotypes to the TSS were observed for THR, PYPL, and SYPL indicate low differences among tested genotypes for these traits. In contrast, moderate and high contribution of the genotypes to the TSS in case of traits NBP, NPP, and SI refer to sufficient existing variation among genotypes. Furthermore, moderate to high contribution of environments to the TSS was observed for all traits except SI (8.84%), while GEI contributed with moderate percentages for all traits. Interestingly, the effect of environments (E) and GEI are more than four and three times the effect of genotypes (G) in SYPL, respectively. This magnitude has been observed for traits NPP, PYPL, and THR. If the GEI effect is greater than the effect of G, this maybe suggest the possible presence of the mega-environments (Jalata, 2011). In cowpea, Kindie *et al.*, (2022) found that most of the total sum of squares was attributed to the GEI and environmental effects indicated larger genotypic differences across environments which differed as well.

Looking at the residual effect, a large proportion of the variance was still left unexplained by the AMMI pooled model in the residual effect. Since, the AMMI revealed highly significant residual effects for NPP, PYPL, and SYPL. Similar results were obtained by Sayed *et al.*, (2021).

Table 2. AMMI analysis of variance, coefficient of variation (C.V.), coefficient of determination (R^2) and contribution percentage to the total sum of squares of seed yield and its related traits of 20 faba bean genotypes tested across 6 environments

Source	Df.	NBP	NPP	PYPL	SI	SYPL	THR
Genotypes	19	19.25**	334.50**	208155.00**	1964.10**	98306.00**	120.60*
Environments	5	66.41**	2118.70**	2532081.00**	1357.30**	1468035.00**	1302.20**
Env (Rep)	12	1.09	11.20	12925.00	69.70	12585.00	11.60
GEI	95	1.80**	74.10**	121869.00**	167.10**	63167.00**	88.30
IPCA1	23	4.58**	120.10**	265638.00**	392.50**	132868.00**	190.30**
IPCA2	21	1.50**	97.50**	155243.00**	133.00*	77280.00**	79.80
Residual	51	0.67	43.80**	43289.00**	79.50	25921.00**	45.90
Error	228	0.58	6.60	9952.00	69.80	6082.00	70.20
C.V.		14.69	12.52	10.83	9.42	11.36	11.46
R²		0.87	0.94	0.93	0.79	0.92	0.52
Contribution % to the SS of the GEI							
IPCA1 %		61.51	39.22	52.77	56.87	50.93	52.17
IPCA2 %		18.46	29.08	28.16	17.59	27.04	19.97
Total		79.96	68.30	80.93	74.46	77.97	72.14
Contribution % to TSS							
Genotypes		36.05	24.79	12.92	48.64	11.15	6.87
Environments		32.72	41.32	41.35	8.84	43.83	19.52
GEI		16.87	27.46	37.81	20.69	35.83	25.16

*, **: significant at 0.05 and 0.01 probability levels, respectively. Df: degrees of freedom, NBP: number of branches/plant, NPP: number of pods/plant, PYPL: pod yield/plot, SI: seed index (100-seed weight), SYPL: seed yield/plot, THR: thrashing percentage, GEI: genotype by environment interaction, IPCA1 and IPCA2: Interaction Principal Components Axis term 1 to 2, respectively. C.V.: coefficient of variation, R^2 : coefficient of determination.

Correlation among traits

The strength and magnitude of the correlation coefficients among studied traits differed from environment to another one as shown in Figure 1, A-F. Strong and positive correlation was observed between PYPL and SYPL in all environments. Moderate and positive correlation was noticed between NPP and SYPL under surface and drip irrigation systems (Sur-1, Sur-2, Drip-1, and Drip-2), while it was neglectable under sprinkler irrigation. Furthermore, SI showed negative correlations with other traits at all environments except at Drip-2, it was moderate and positive with SYPL. Papastylianou *et al.*, (2021) referred that seed yield trait was significantly and positively correlated to the number of pods per plant and the number of seeds per plant and non-significantly correlated to SI. Koç *et al.*, (2018) reported weak but positive correlation of the seed yield trait with branches number and pods number, and between them as well. Ibrahim and Ghareeb, (2020) estimated highly significant positive correlation between the number of branches/plant, number of pods/plant, number of seeds/plant and 100-seed weight, and they concluded that the strong correlation suggested that seed yield may be raised through selection for the more branches, pods, seeds, and seed index.

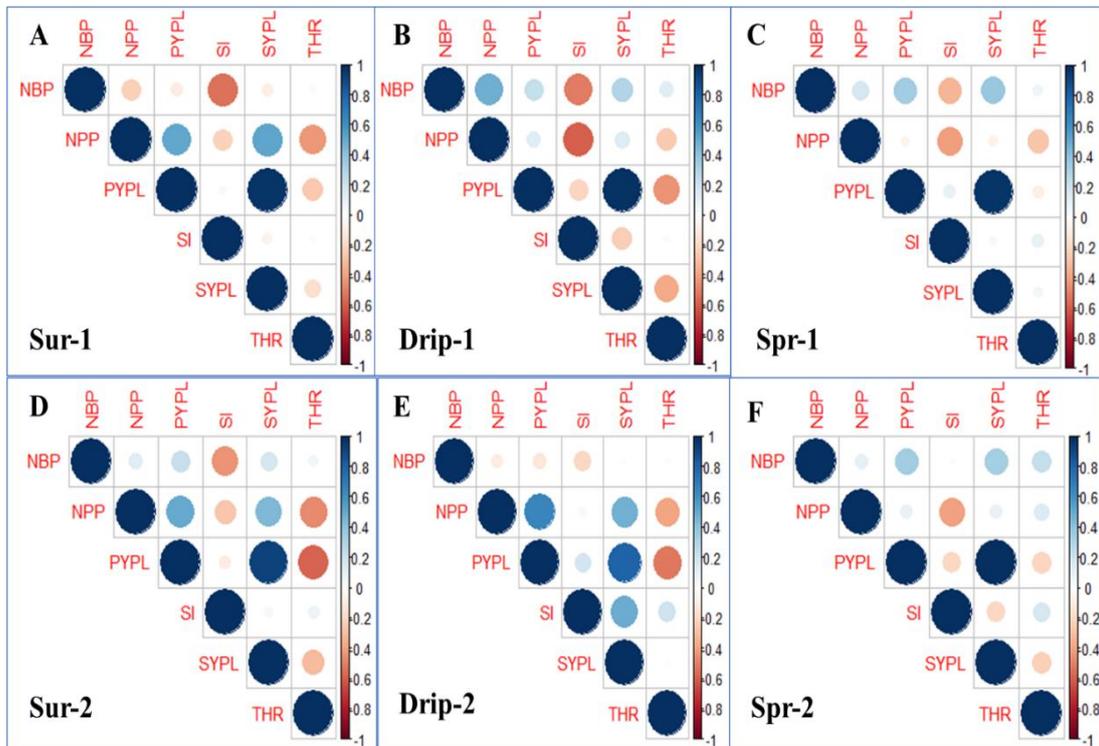


Figure 1. Correlation matrix among studied traits at each environment (irrigation systems). A), B), and C) Surface, Drip, and Sprinkler irrigations at first season, respectively. D), E), and F) Surface, Drip, and Sprinkler irrigations at second season, respectively.

GGE Biplot Analysis

In the GGE biplot (Figures 2-7; A), the genotypes and environments are represented in the same plot with tester vectors connecting the environments with the origin. The calculated angle between the vectors of any two environments provides information about the correlation coefficient between them (Yan and Tinker, 2006; Koç *et al.*, 2018; Papastylianou *et al.*, 2021). Also, the discriminating ability of each environment can be measured by the length of its vector; the longer the environment vector, the more the discriminating and description ability of the environment (Yan and Tinker, 2006; Abou-Khater *et al.*, 2022). Additionally, the polygon view of GGE biplot analysis provides information about the “which-won-where modality”, which helps to visualize the interaction of GE, mega-environments, and specific adaptation (Yan and Tinker, 2006) as presented in Figures 2-7; B. Moreover, the genotypes that are existing on the vertices of the polygon performed either the best (good performance) or the poorest (bad performance) in one or more environments. In order to compare the mean performance and stability of the genotypes over all environments, the average-environment coordination (AEC) view resultant of the GGE biplot analysis is used to rank the genotypes based on mean trait from highest to lowest across all environments. The AEC ordinate classifies and groups the tested genotypes with below-average means to those with above-average means. Furthermore, genotypic stability is very critical for the tested genotype besides its

seed yield mean. A shorter projection (dropping) to the AEC ordinate (regardless of the direction), represents a less tendency of the GEI of the genotype, which means more stability across all environments and vice versa (Yan and Tinker, 2006; Beksisa, 2021).

Based on the previous information, the GGE biplot analysis of NBP explained 91.87% of the total variability, and revealed that the first two principal components (PC1 and PC2) explained 85.30% and 6.57%, respectively (Figure 2.A). Because of the acute angle between each two environments, high positive correlations were observed. This result reflects that this trait did not affect by environments (irrigation systems), because the contribution of GEI effect is less than of G and E effects. This result has been confirmed by the polygon view of GEI, which presented one mega-environment (Figure 2.B). Sur-1, Spr-2 and Drip-2 are the most correlated environments. The genotypes G10, G11, G12, G13, G14, and G15 performed well under all irrigation systems (Figure 2.B). However, the genotypes G11 and G15 had short projection, that means they are the most stable and had highest NBP. Whereas, G14 had high NBP over environments, but unstable genotype because of its long projection. In addition, G11 and G15 are adapted to Sur-1, Drip-2, and Spr-2, G10, G13, and G17 are adapted to Drip-1, while G12 and G14 are adapted to Spr-1.

For NPP, the first two PCs explained 79.65% of the total variation of the GGE model (PC1 = 60.50% and PC2 = 19.15%). The six environments showed a positive correlation between each two of them, but less than observed in the case of NBP (Figure 3.A). The GGE biplot analysis revealed two mega-environments. The first mega-environment contained Spr-1, Spr-2, and Drip-1, and included the adapted genotypes G15, G16, and G17 to these environments. While the second one contained Drip-2, Sur-1, and Sur-2 and the adapted genotypes G06, G08, and G10 (Figure 3.B). The highest genotypes in NPP across environments were G17, G16, and G08, but they showed moderate stability. Whereas the genotypes G10 and G06 exhibited stability across environments (Figure 3.C).

For PYPL, the scatter biplot explained 75.47% of the total variance observed, of which 42.23% was explained by PC1, while the PC2 explained 33.24% (Figure 4.A). Negative correlation was observed between Sur-1 and each of Spr-1 and Spr-2, and between Drip-1 and Sur-1. Two mega-environments were obtained by GGE biplot analysis. The first one contained Spr-1, Spr-2, Drip-1, and Sur-2, while the second one contained Sur-1 and Drip-2. G06, G08 and G15 are performed and adapted well at Drip-1, the G10, G19, and G20 are adapted to Drip-2 and Sur-2, the G13, G17 and G18 are adapted to Sur-1, while the other genotypes were adapted to Spr-1 and Spr-2 (Figure 4.B). In addition, G15 had the highest PYPL amongst all genotypes, but considered unstable genotype because of its greater variability. The genotypes G06, G08, G10, and G20 were superior in PYPL and showed good stability across environments (Figure 4.C).

The GGE biplot analysis revealed 88.31% of the total variance observed for SI, since PC1 and PC2 explained 74.35% and 13.96%, respectively (Figure 5.A).

Positive correlations among each pair of environments were obtained by GGE biplot analysis, however, the environment Spr-1 is far from other environments. This result emphasizes the low contribution of E to the TSS. Two mega-environments were obtained by GGE biplot analysis, the first one contained Sur-1, Sur-2, Drip-1, Drip-2, and Spr-2, while the second one contained only the Spr-1 (Figure 5.B). Most of the genotypes were adapted to all environments except Spr-1, which had only one adapted genotype, which is G19. In addition, all genotypes exhibited good stability across all environments except G19, which was unstable because of its greater variability (Figure 5.C). The genotypes G02, G03, G05, and G08 recorded highest SI across all environments.

For SYPL, the GGE biplot analysis explained 74.28% of the total variation, and revealed that the first two principal components (PC1 and PC2) explained 39.17% and 35.12%, respectively (Figure 6.A). The same scenario has been observed in SYPL as noticed for PYPL, and this may be due to the positive correlation between them. Since, negative correlation was observed between Sur-1 and each of Spr-1 and Spr-2, and between Drip-1 and Sur-1 (Figure 6.A). Two mega-environments were obtained by GGE biplot analysis. The first one contained Spr-1, Spr-2, Drip-1, and Sur-2, while the second one contained Sur-1 and Drip-2. The genotype G15 was performed and adapted well at Drip-1, the genotypes G08 and G10 are adapted to Sur-2, the genotypes G13, G17, G18 and G20 are adapted to Sur-1, while the other genotypes were adapted to Drip-2, Spr-1 and Spr-2 (Figure 6.B). In addition, G15 had the highest SYPL amongst all genotypes, but considered unstable genotype because of its greater variability. However, the genotypes G08, G10, G13, G18, and G20 were superior in SYPL and showed good stability across environments (Figure 6.C). Based on mean seed yield, Haile and Kebede, (2021) used GGE biplot analysis to identify high yield and stable faba bean genotypes across seven locations, and found that the genotype G12 was the winning genotypes in all environments. They identified also two mega-environments through GGE biplot technique. Similar results were obtained by Hailemariam and Tesfaye, (2019) in Soybean; Gurmu *et al.*, (2012); Ibrahim and Ghareeb, (2020); Maga, (2021); Papastylianou *et al.*, (2021); Olanrewaju *et al.*, (2021); Abou-Khater *et al.*, (2022) in Faba bean; Beksisa, 2021 in Arabica Coffee.

For THR, the GGE biplot analysis revealed 69.47% of the total variance, since PC1 and PC2 explained 52.01% and 17.47%, respectively (Figure 7.A). Sur-2 correlated positively with each of Sur-1, Drip-1, Drip-2, and Sur-1. While Spr-2 correlated negatively with all environments except Spr-1. The GGE biplot analysis revealed two mega-environments, the first one contained the surface and drip irrigation systems, while the second one contained the sprinkler irrigation system. Most of the genotypes were adapted to surface and drip irrigation systems, while the genotypes G08, G15, G16, G19, and G20 were adapted to sprinkler irrigation environments (Figure 7.B). In addition, the genotype G14 ranked the first in relation to THR percentage but showed moderate stability (Figure 7.C). The genotypes G05, G08, G11, and G12 had high THR and short

projection to the AEC ordinate and considered stable genotypes across environments.

In conclusion, twenty faba bean genotypes were evaluated under surface, drip, and sprinkler irrigation systems over two years, that representing six environments. The current study aimed at selecting the highest yielding and stable faba bean genotypes across tested environments and identifying the genotypes that adapt to specific irrigation system. Not only to select the superior genotypes, but also to rationalize the use of water, especially under drip and sprinkler irrigation systems at newly reclaimed soils. To achieve this goal, the AMMI and GGE biplot analyses were applied. Highly significant differences were obtained for genotypes, environments, and GEI in all investigated traits, i. e., NBP, NPP, PYPL, SI, SYPL, and THR. In addition, the first two IPCA were highly significant for the majority of studied traits, and the residual effect was highly significant for NPP, PYPL, and SYPL. High contribution percentages were observed for E, and GEI in NPP, PYPL, SYPL and THR, which exceeded the contribution of G effect, indicating the variability among environments. The GGE biplot analysis revealed negative correlations among each pair of environments in most cases, especially sprinkler irrigations (Spr-1 and Spr-2) showed long vectors from the origin. For SYPL, most of the high yielding genotypes were adapted to drip and surface irrigation environments which had mean performance above the average. Based on this, drip irrigation system comes first, then surface irrigation and last sprinkler irrigation. The genotypes G06, G08, G10, G13, G16, G18, and G20 could be considered as high yielding and stable genotypes across environments, G15 was the superior one but had great variability (unstable). Interestingly, some of the high yielding (in SYPL) and stable genotypes, were superior in one or more traits of yield components. The better performance of many genotypes under the surface and drip irrigation systems may be attributed to the availability and increase of moisture in the stages of vegetative growth and reproduction of the faba bean, which increases the process of photosynthesis and thus the accumulation of nutrients, which leads to an increase in yield and its components (Awadalla *et al.*, 2018).

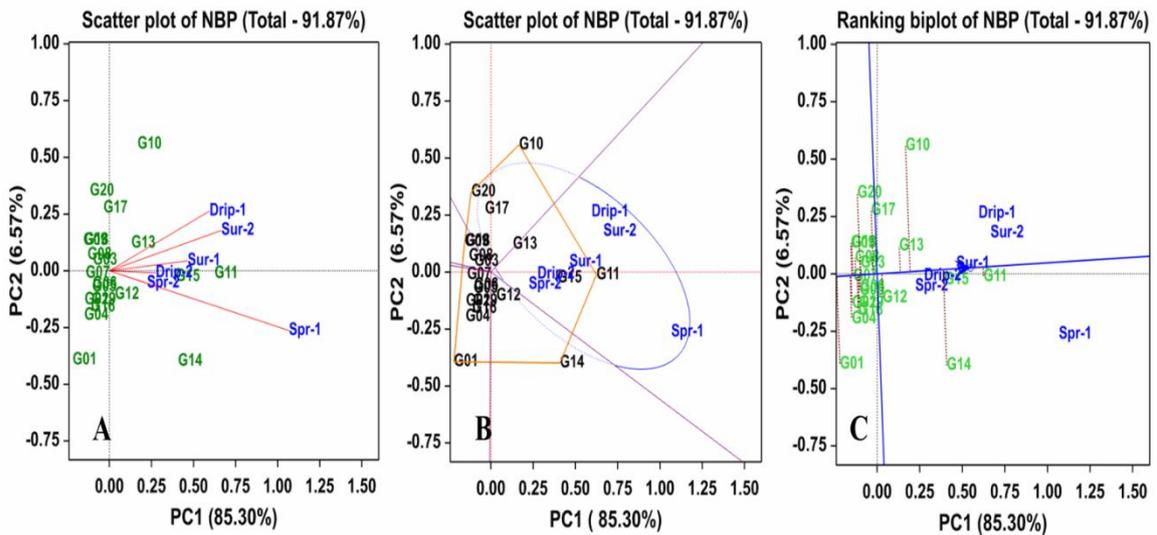


Figure 2. Analysis of GGE-Biplot for number of branches/plant (NBP) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

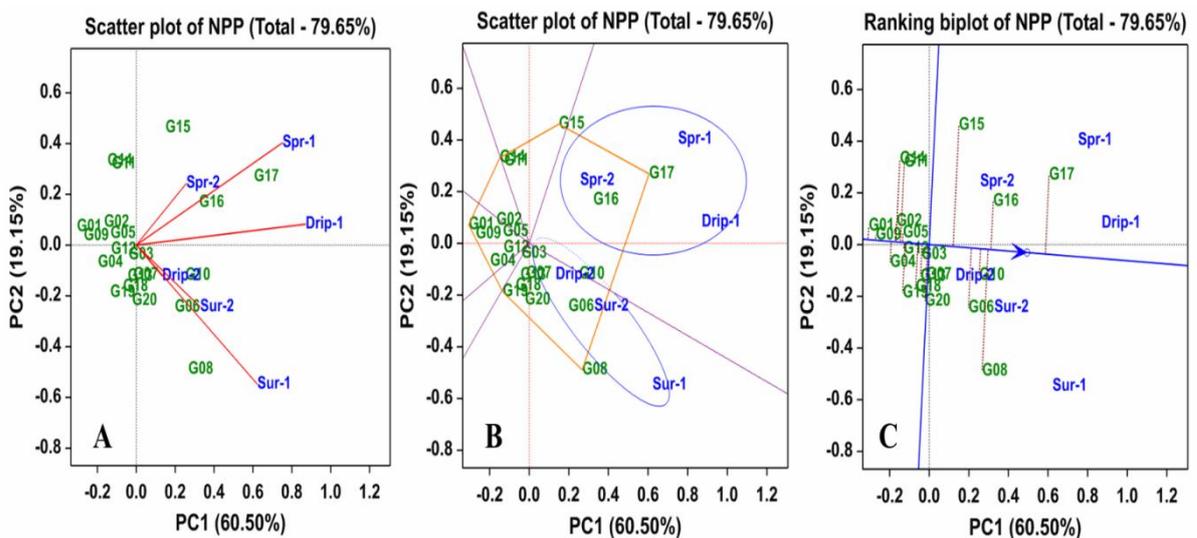


Figure 3. Analysis of GGE-Biplot for number of pods/plant (NPP) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

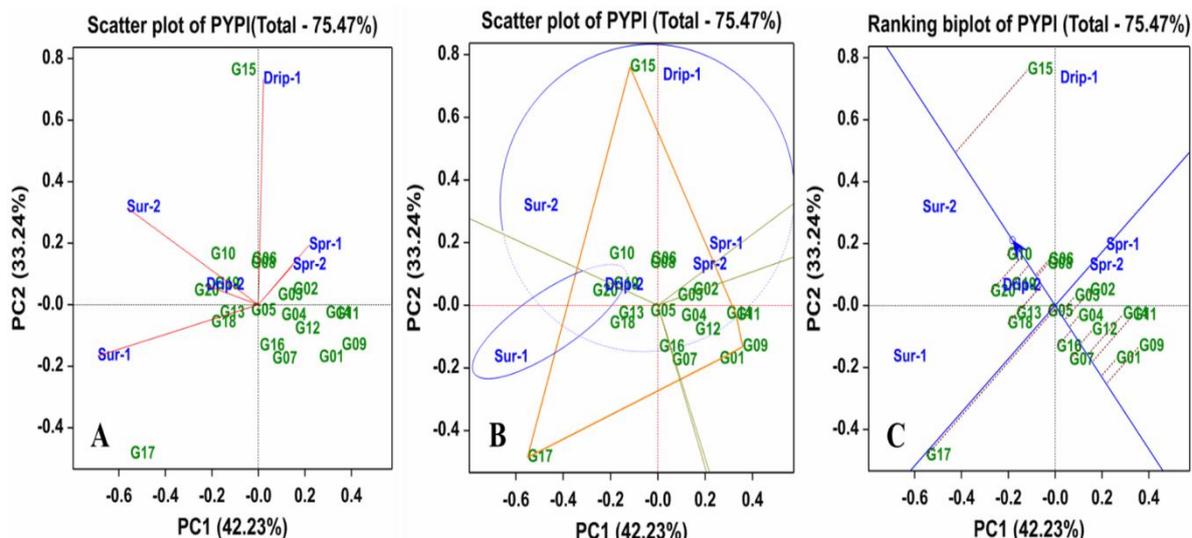


Figure 4. Analysis of GGE-Biplot for pod yield/plot (PYPL) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

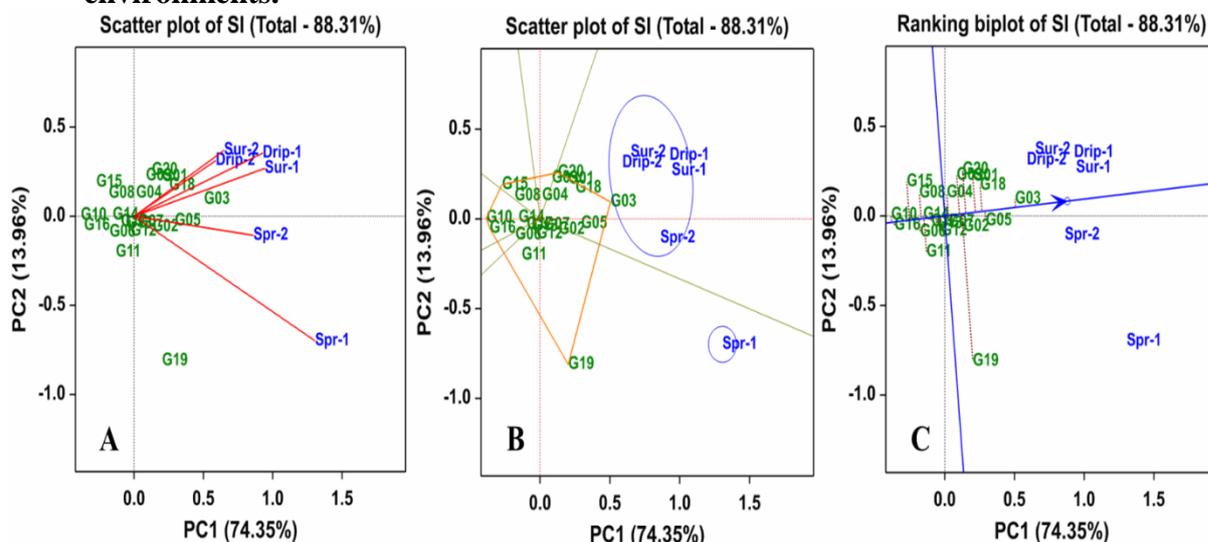


Figure 5. Analysis of GGE-Biplot for seed index (SI) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

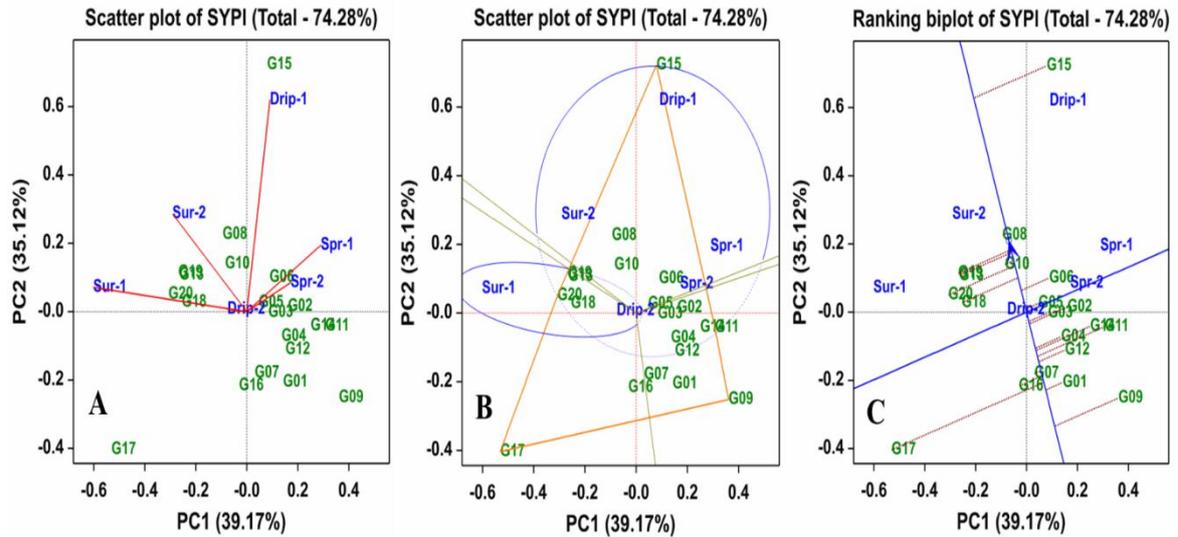


Figure 6. Analysis of GGE-Biplot for seed yield/plot (SYPL) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

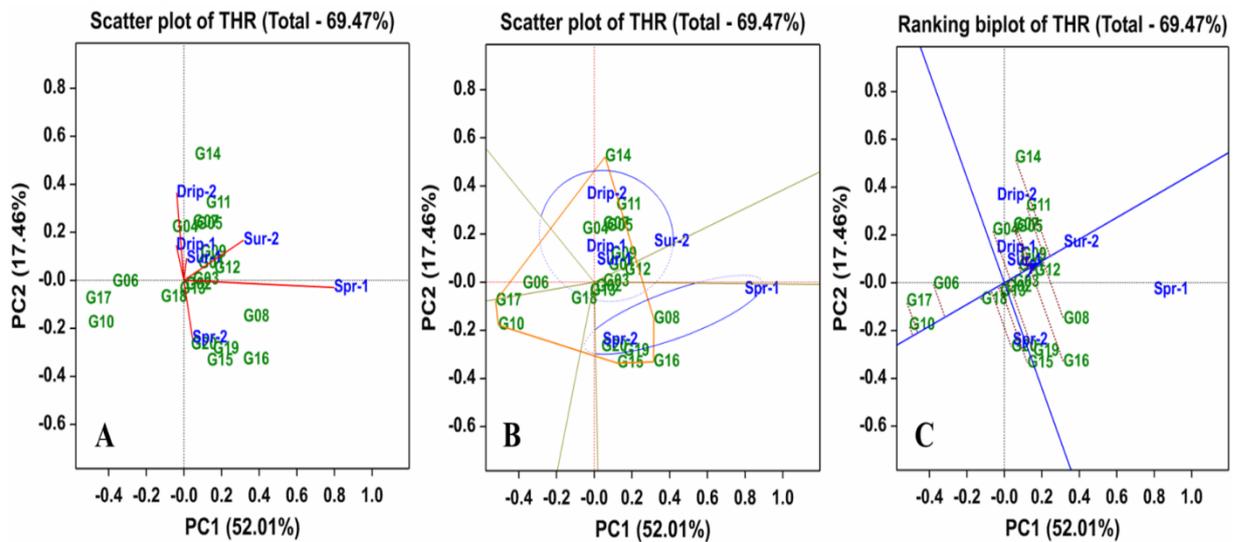


Figure 7. Analysis of GGE-Biplot for thrashing percentage (THR) of the 20 faba bean genotypes tested under six environments. A) Scatter plot shows the relationships among test environments, B) Polygon view of GEI shows “which-won-where” pattern across environments, and C) Ranking biplot shows the mean performance and stability of the genotype across all environments.

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التفاعل الوراثي-البيئي وتحليل الثبات لمحصول البذور ومكوناته لتراكيب وراثية من الفول البلدي تحت نظم ري مختلفة

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الملخص

تهدف هذه الدراسة الى تقييم وانتخاب تراكيب وراثية من الفول البلدي ذات انتاجية عالية وثابتة تحت نظم ري مختلفة وهي (الري السطحي، الري بالتنقيط والري بالرش). تمت زراعة عشرين تركيب وراثي في تصميم قطاعات كاملة العشوائية بثلاثة مكررات في ثلاثة أنظمة ري مختلفة خلال موسمين متتاليين (2021/2020) و (2022/2021) ممثلة ست بيئات. تم تقييم التراكيب الوراثية لصفة محصول البذور ومكوناته. تم استخدام تحليلي التأثير الرئيسي المضيف والتفاعل المضاعف (AMMI) وتحليل الشكل البياني ثنائي الاتجاه للتركيب الوراثي والتفاعل الوراثي البيئي (GGE-biplot). أشار تحليل الـ AMMI إلى وجود فروق معنوية جداً بين التراكيب الوراثية، والبيئات (أنظمة الري) والتفاعل الوراثي البيئي GEI لكل الصفات المدروسة ما عدا صفة نسبة التفريط والتي أعطت GEI غير معنوي. إضافة إلى ذلك، عند تجزئة التفاعل الوراثي البيئي، أشار التحليل إلى أن المكونين الرئيسيين الأولين IPCA1، IPCA2 كانا معنويين لكل الصفات ما عدا صفة نسبة التفريط كان الـ IPCA2 غير معنوي. كما أظهر التحليل أن تأثير البيئة والتفاعل الوراثي البيئي كان أكبر من تأثير التراكيب الوراثية بثلاث وأربع أضعاف على التوالي. كما أعطى تحليل GGE biplot ارتباط سلبى بين البيئات في معظم الحالات، خاصة تحت الري بالرش. بالنسبة لمحصول البذور، فإن معظم التراكيب الوراثية عالية المحصول كانت متأقلمة للري بالتنقيط والري السطحي والتي أظهرت متوسط أداء أعلى من المتوسط. بناءً على ذلك، جاء الري بالتنقيط أولاً ثم الري السطحي ثم أخيراً الري بالرش من ناحية متوسط المحصول. وكانت التراكيب الوراثية G06، G08، G10، G13، G16، G18، G20 عالية المحصول وثابتة عبر البيئات. بينما التركيب الوراثي G15 كان أعلى التراكيب الوراثية محصولاً إلا أنه كان غير ثابت.