International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

IJBSM February 2025, 16(2): 01-11

Article AR5969

Research Article

Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2025.5969

Multi-environment Performance Evaluation and Stability Analysis of Large Seeded Faba Bean (*Vicia faba*) Genotypes in High Potential Areas

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ABSTRACT

The study was conducted during the main cropping seasons of 2016, 2017 and 2018 at Kulumsa, Bekoji, Asasa and Kofele in potential areas of South Eastern Ethiopia from June to November with the objective to assess the performance of faba bean genotypes for grain yield and yield stability. Twelve faba bean genotypes were evaluated using randomized complete block design with four replications under rain-fed condition. The combined analysis of variance revealed that grain yield of faba bean was significantly influenced by genotype (15.8%), environment (32.6%) and genotype by environment interaction (51.6%). The highest mean grain yield was obtained from G-12 (3692.3 kg ha^{-1}) and G-10 (3619.0 kg ha^{-1}) with an overall mean yield of 3403.9 kg ha^{-1} across nine environments while the lowest yield recorded from G-8. The first two principal components of AMMI biplot showed that PC 1 explained 47.8% and PC 2 accounted 19.6% of the genotype by environment interaction sum of squares. Some genotypes, such as G-12, G-10, G-1, G-7 and G-5 exhibited significantly higher yields than the average, while others had yields lower than the average. Genotypes G-10, G-6 and G-2 showed the highest stability consistently based on most stability parameters, AMMI and GGE biplot analysis. G-10 could be considered as ideal genotype due to its high yield and stability which was widely adaptable across environments. Finally, top ranked genotypes G-10, G-7 and G-5 were identified for both grain yield and seed weight.

KEYWORDS: Adaptability, AMMI, biplot, environment, GGE, interaction, potential, stability

***Citation* (VANCOUVER):** Yimam et al., Multi-environment Performance Evaluation and Stability Analysis of Large Seeded Faba Bean (*Vicia faba*) Genotypes in High Potential Areas. *International Journal of Bio-resource and Stress Management,* 2025; 16(2), 01-11. HTTPS://DOI.ORG/10.23910/1.2025.5969.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 04th December 2024 RECEIVED in revised form on 26th January 2025 ACCEPTED in final form on 08th February 2025 PUBLISHED on 10th February 2025

1. INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most important cool season grain legumes in the world. According to Anonymous (2021a) Ethiopia is the second faba bean producer in the world next to China. Ethiopia is also the first country in Africa in producing faba bean, followed by Egypt, Sudan, and Morocco. The total annual production of faba bean in the 2020 "Meher" production season in the country is estimated to be 10,706,36.538 t under 504,569.99 ha of total area coverage and average productivity of 2.122 t ha^{-1} (Anonymous, 2021b). The crop is mainly cultivated in mid-and high-altitude areas of the country, with an elevation ranging from 1800 to 3000 m above sea level. Faba bean has many versatile purposes in socioeconomic well-being of the agricultural societies of the country such as a source of food, animal feed and income generation (Bulti et al., 2019). Additionally, it provides foreign currency for the nation and serves as a good break crop for pests and for restoring soil fertility.

Despite its huge importance in the country, the national average yield of the crop is low as compared to its potential yield (Anonymous, 2021b) primarily due to low yielding potential of the indigenous cultivar, limited availability of source materials and improved stress tolerant varieties for biotic stress like disease (checolet spot (Mekuria and Ashenafi, 2018), rust, root rot and ascocayta blight (Kedir et al., 2024)), weeds(broad leaved and grass weed), Storage pest(adzuki bean beetle), and abiotic factors (soil acidity (Mesfin et al., 2020), water logging (Emebet et al., 2024) and frost etc.), instability of cultivars (Gebeyaw and Muluken, 2024), lodging (Kedir et al., 2024)., flower abortion, inaccessibility of improved varities with good quality seed supply (Meselu, 2019), poor adaptation and poor crop management. Thus, the primary objectives of faba bean breeding program is identification and selection of high yielding genotypes with wide adaptation, genotypes with large seed size and resistance to biotic and abiotic stress. However, seed yield in Faba bean, like other crops, is a complex trait (polygenic) which is as a result of many morphological and physiological traits which are in turn highly influenced by environment and genotype by environment interaction effects (Peyman, 2014). Due to this, selecting superior genotypes only on a single environment is ineffective (Carl et al., 2014).

Thus, multi-environment trials are essential in the selection cycle of variety development programs to identify superior and stable genotypes through estimating genotype by environment interaction (GEI) effect (Papastylianou et al., 2021). Genotype by environment interaction (GEI) refers to the inconsistent performance (differential response) of different genotypes for measured trait across different environmental conditions. Even though the existence of GEI challenges breeders for selection of superior and wide adaptable varieties, the study of genotype by environment interaction (GEI) is very important for crop improvements (Tekalign et al., 2019)and it is necessary to understand the pattern of GEI and performance stability across environments especially at the final stage of variety development (Alemu et al.,2023). There are advanced statistical tools such as Additive main effects and multiplicative interaction (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot models that will enable breeders for analyzing GEI and to visualize the phenotypic stability of genotypes over environments from multi-environmental trial data and to easily identify superior genotypes within a given environment (Yan et al., 2007). Therefore, the objectives of this study was to access the magnitude of genotype by environment interaction (GEI) and identify faba bean genotypes with a high and stable yield across potential production areas using AMMI and GGE model biplot analysis and some stability parameters.

2. MATERIALS AND METHODS

2.1. *Description of experimental site*

The study was conducted during the main("*Meher*") cropping seasons of 2016, 2017 and 2018 at Kulumsa, Bekoji, Asasa and Kofele in potential areas of South Eastern Ethiopia from June to November i.e for two growing seasons (2017 and 2018) at all locations and one growing season (2016) at one location (Kulumsa) under rain fed condition. Each year with each location combination was considered as a separate environment, making nine test environments. The testing sites were characterized by mid- and high-altitude agro- ecology (Table 1).

2.2. *Experimental materials and design*

Twelve advanced faba bean genotypes were evaluated under potential environments of South Eastern Ethiopia. The experiment was laid out in a randomized complete block design (RCBD) with four replications across environments, having a plot size of 6.4 m^2. Each plot consisted of four rows and 4 m long with a spacing of 0.4 m and 0.1 m between rows and plants, respectively. Two central rows were used for harvesting and each plot had net harvestable area of 3.2 m^2. All necessary agronomic packages were applied as per the recommended package for faba bean (Table 2).

2.3. *Data collected*

Days to 50% flowering (DF), days to 90% maturity (DM), thousand seed weight (TSW) (g) and grain yield (GY) (kg ha^{-1}) were collected on plot basis from the two central rows, whereas plant height (PH) (cm), number of pods

Table 1: Description of Experimental Site

Sl. No.	Env.	Year	Location	Altitude (m.a.s.l)	Rain Fall (mm)	Latitude	Longitude
1.	E1	2016	Kulumsa	2200	820	08001'10"N	39009'11"E
2.	E2	2017					
3.	E3	2018					
4.	E4	2017	Bekoji	2780	1020	07032'37"N	39015'21"E
5.	E5	2018					
6.	E6	2017	Asasa	2340	620	07007'09"N	39011'56"E
7.	E7	2018					
8.	E8	2017	Kofele	2660	1211	07004'28"N	38047'11"E
9.	E9	2018					

Source: Kulumsa Agricultural Research Center

Table 2: List of experimental materials used

Sl. No.	Genotype	Code	Status
1.	Gora	G-1	Released Variety
2.	EKLS/CSR 02017-3-4	G-2	Advanced Line
3.	EKLS/CSR 02014-2-4	G-3	Advanced Line
4.	EKLS/CSR 02010-4-3	G-4	Advanced Line
5.	EKLS/CSR 02023-2-1	G-5	Advanced Line
6.	EKLS/CSR 02012-2-3	G-6	Advanced Line
7.	EKLS/CSR 02022-2-1	G-7	Advanced Line
8.	EKLS/CSR 02028-1-1	G-8	Advanced Line
9.	EKLS/CSR 02019-2-1	G-9	Advanced Line
10.	EKLS/CSR 02019-2-4	G-10	Advanced Line
11.	EKLS/CSR 02013-2-3	G-11	Advanced Line
12.	Tumsa	G-12	Released Variety

plant^{-1} (PPL) (number) and number of seeds pod^{-1} (SPP) (number) were recorded on five random samples of plants selected from the central two rows of each plot. The mean value was used for analysis. Grain yield measured from the entire two rows of each plot was adjusted to 10% moisture level and converted to kg ha^{-1}. Responses of genotypes to disease reactions like chocolate spot, and rust were recorded at late pod setting based on 1–9 scoring methods.

2.4. Statistical analysis

2.4.1. Combined analysis of variance

All measured traits were subjected to combined analysis of variance using agricolae package in R software version 4.2.3 to assess the significance of genotype and environment. Homogeneity of variance was tested using Bartlett test. The following model for combined location were used for analysis to partition the total variation into components due to genotype (G), environment (E), and G×E interaction (GEI) effects

$$Yij=\mu+Gi+Ej+GEij+\beta(E)jk+\varepsilon ijk \;.......………………(1)$$

Where; Y_{ij} was the grain yield of the ith genotype in the jth environment, μ=the grand mean, G_1=the effect of the ith genotype, E_j=the effect of the jth environment, GE_{ij}=the interaction of the ith genotype with the jth environment, (E)=the effect of the kth replication in the jth environment, and ε_{ijk}=the error.

2.4.2. Additive main and multiplicative interaction (AMMI) analysis

The additive main effects and multiplicative interaction (AMMI) model analysis was performed to assess the effect of genotype (G), environment(E), and G×E interactions on grain yield by ANOVA and partition GEI in to interaction principal component axis (IPCA) through PCA using performs ammi() function in metan packages of R software. The following model was used for AMMI analysis (Gauch, 1992).

$$Y_{ij}+\mu+G_i+E_j+(\Sigma^n_{k=1}\lambda_k\alpha_{ik}\,\gamma_{jk})+\varepsilon_{ij} \;.................................... (2)$$

where Y_{ij}=the yield of the ith genotype in the jth environment; μ=is the grand mean; G_i and E_j were the genotype and environment deviations from the grand mean, respectively; λ_k= the eigenvalue of the PCA analysis axis k; α_{ik} and γ_{jk}=were the genotype and environment principal component scores for axis k; n was the number of principal components retained in the model, and e_{ij} was the error term.

Graphical AMMI Biplot Analysis was also employed for determining the yield stability (GEI) and performance of the tested genotypes across environments.

2.4.3. AMMI stability indices

AMMI Stability Value (ASV) was calculated numerically to measure genotype stability for each genotype and environment according to the relative contribution of IPCA1 to IPCA2 to the interaction Sum of Squares as follows (Purchase et al., 2000).

$ASV=\sqrt{[(\text{IPCA1 sum squares}/\text{IPCA2 sum squares})(\text{IPCA1score})]^2+[\text{IPCA2score}]^2}$ ……........……………..(3)

Where: IPCA1=interaction principal component axis 1; IPCA2=interaction principal component, axis 2.

The genotype performance and stability across environments were also measured by yield stability index (YSI), which was the sum of rank of AMMI stability value and rank of mean grain yield.

$YSI=rASV+rGY$ .... (4)

Where: YSI= yield stability index, rASV=rank AMMI stability value, rGY=rank mean grain yield

2.4.4. GGE biplot model

The GGE biplot model was used to display genotype main effects (G) and genotype×environment effects (GE) from a two-way data table in a biplot as suggested by Yan, et al. (2000). The first component of the GGE biplot (PC1) represented the genotype main effect (G) while the second component (PC2) indicated the proportion explained by genotype-environment interaction (GEI). Singular value decomposition (SVD) of the first two principal components was employed to fit the GGE biplot model and to generate this biplot we used the “gge” function in the R software metan package

$Yij=\mu+\beta j+\lambda 1\xi i1\eta j1+2\eta j2+\varepsilon ij$ …..………………………..(5)

where, Y_{ij} was the trait mean for genotype i in environment j, μ was the grand mean, β_j was the main effect of environment j, $\mu+\beta_j$ was the mean yield across all genotypes in environment j, λ_1 and λ_2 were the singular values (SV) for the first and second principal components (PC_1 and PC_2), respectively, ξ_{i1} and ξ_{i2} were eigenvectors of genotype i for PC1 and PC_2, respectively, $\eta\ j_1$ and η_{j2} were eigenvectors of environment j for PC_1 and PC_2, respectively, ε_{ij} was the residual associated with genotype i in environment j. In GGE biplot analysis, scores of PC_1 were plotted against PC_2.

3. RESULTS AND DISCUSSION

3.1. Combined analysis of variance

The result of combined analysis of variance revealed that the studied traits were exhibited from significant to highly significant difference among faba bean genotypes due to mean square of genotype and genotype by environment interaction except days to 90% maturity, plant height, number of pods plant^{-1} and number of seeds plant^{-1} due to mean square of genotype by environment interaction, which were non-significant (Table 3). There was the presence of substantial genotypic variation among advanced faba bean lines especially for thousand seed weight and disease parameter (severity of checolet spot and rust disease) relative to other traits. In parallel to this finding, significant differences were reported for days to flowering and grain yield (Dereje et al., 2019; Mesfin et al., 2020; Tamene, 2015) for one or more of sources variations. The significance nature of genotype by environment interaction on the studied characters suggested the differential performance of faba bean genotypes with respect to these traits across environment. All traits were highly significant ($p<0.01$) due to mean square of environment, indicated the variation of testing environments that leads the presence of large environmental influence on the phenotypic expression of these traits. Similar finding was observed by Gebyaw and Tesfahun (2020).

3.3. Genotype performance for grain yield and thousand seed weight

The analysis of combined mean performance across nine environments indicated that the highest grain yield was

Table 3: Mean square of combined ANOVA for nine traits of 12 faba bean genotypes conducted at nine environments

Source of variation	Df	DF	DM	PH	Mean square					
					PPL	SPP	TSW	GY	CHS	Rust
Environment	8	1255.2^{***}	19583^{***}	9444.9^{***}	459.0^{***}	0.42^{***}	89171.0^{***}	3000236^{***}	33.0^{***}	44.0^{***}
Replication (Environment)	27	3.0	9.2	166.7	14.7	0.17	3851.0	888073.4	1.1	0.9
Genotype	11	25.8^{***}	5.5^{*}	244.8^{**}	7.5	0.18^{*}	16187.9^{***}	1058116^{*}	1.1^{***}	1.5^{***}
Genotype× Environment	88	3.3^{***}	3.0	77.5	12.7	0.12	12261.4^{***}	431155.1^{*}	0.3	0.4*
Residuals	297	1.4	3.1	85.9	12.2	0.09	4391.3	461093.2	0.4	0.3
CV (%)		2.2	1.3	7.3	22.5	10.4	8	19.9	16.2	14.9
Mean		55.3	141.9	126.4	15.5	2.9	828.3	3403.9	3.7	3.7

DF: Days to 50% flowering, DM: Days to 90% maturity, PH: Plant height, PPL: Pods plant^{-1}, SPP: Seeds pod^{-1}, TSW: Thousand seed weight, Gy: Grain yield, CHS: Checolet spot, df: Degree of freedom recorded from genotype G-12 (3692.3 kg ha^{-1}) and G-10 (3619.0 kg ha^{-1}) followed by G-1 (3536.9 kg ha^{-1}), G-7 (3535.8 kg ha^{-1}) and G-5 (3470.8 kg ha^{-1}) with an overall mean grain yield of 3403.9 kg ha^{-1} (Table 4). Whereas, relatively the low yield was obtained from G-8. The environmental mean exhibited that relatively the highest yield were obtained in E-4 (Bekoji, 2017), E-1 (Kulumsa, 2016) and E-5(Bekoji, 2018) in the present result with the current studied faba bean genotypes. Some superior genotypes such as G-10, G-1, G-7, G-12 and G-5 showed less fluctuation (relatively adaptable) across different environments (Table 4 and Figure 1). The thousand seed weight of faba bean genotypes across environments ranged from 798.9 g for G-4 to 862.2 g for G-7 with an overall grand mean of 828.3 g (Table 4).

Five genotypes namely G-7, G-10, G-11, G-5 and G-2 gave large thousand seed weight (seed size) over the best reference genotype (G-12). Four faba bean genotypes were also recorded with higher test weight over the grand mean. The evaluated faba bean genotypes were exhibited moderate resistance for both checolet spot and rust disease.

3.3. *AMMI analysis*

The AMMI analysis of variance showed that grain yield was significantly influenced by main effect i.e. genotype and environment and interaction between genotype and environment (Table 5). This implied the differences of testing environments and presence of considerable genetic variation among the lines for grain yield performance. The performance of faba bean genotypes was also varied from one environment to other environment. In the current study, the largest effects of genotype by environment interaction (51.6%) followed by environment (32.6%) and then by genotype main effects (15.8%) were observed from out of explained treatment variation (Table 5). Genotype by environment interaction exerted more than three times larger effect than genotype main effect to the observed phenotype. This made significantly complicated selection of superior and wide adaptable elite genotypes across environment. Thus, it was important simultaneously to

Table 4: Mean performance of 12 large seeded Faba bean genotypes across nine environments for grain yield and other desirable traits

Genotype	Mean grain yield (GY) (kg ha^{-1})									GY	TSW	CHS	Rust
	E1	E2	E3	E4	E5	E6	E7	E8	E9				
G-1	3778	3400.3	3099.5	4018	3282.5	3188.3	3666.5	3433	3966	3536.9	810.1	3.6	3.6
G-2	3556.8	3243.8	3245	4097.8	3830.3	2868.8	3128.8	2788.3	3574	3370.4	828.2	3.6	3.6
G-3	4042.5	2717.8	2965.8	3873.8	3592.8	2770.5	3306.3	3087	3251.3	3289.7	803.1	3.9	4.1
G-4	3628.3	3630.5	3032	3261	3150	3421.8	3358	3224.8	2611.8	3257.6	798.9	3.7	3.9
G-5	4199.5	3605.8	3375.8	3435.3	2802.3	3112	3722.8	3227.5	3756.3	3470.8	836.4	3.8	3.7
G-6	3745.3	3483.8	3071	3879.3	3433.8	3075.5	3503	2959.5	3209.3	3373.4	818.1	3.7	3.7
G-7	3701.8	3010.8	3555	3662.8	3433.5	3643.5	3700.5	3135.3	3978.8	3535.8	862.2	3.8	3.5
G-8	2545.3	3115.0	3193.8	3750	3745.3	2806.8	2867	3100	2842.5	3107.3	815.4	3.9	3.9
G-9	3150.3	3225.5	2858.8	4117	3362.5	3116.5	2860.8	2928.3	3521.5	3237.9	826.3	3.7	4.0
G-10	3585.5	4030.0	3587.3	4265.8	3403.3	3265	3669.8	3287	3477.3	3619.0	860.7	3.5	3.7
G-11	2801.3	3102.0	3133	4519.8	3778	3560	3246.5	3065.8	3000.5	3356.3	852.4	3.4	3.4
G-12	3370	3928.5	3214.8	4720.8	4022.5	3521.3	3260	3326.5	3866.8	3692.3	827.7	3.4	3.5
EM	3508.7	3374.5	3194.3	3966.8	3486.4	3195.8	3357.5	3130.2	3421.3	3403.9	828.3	3.7	3.7
CV (%)	19.8	23.6	13.4	17.2	13.3	13.8	14.7	20	24	19.9	8	16.2	14.9

E1: Kulumsa 2016; E2: Kulumsa 2017; E3:Kulumsa 2018; E4: Bekoji 2017; E5: Bekoji 2018; E6: Asasa 2017; E7: Asasa 2018; E8:Kofele 2017; E9: Kofele 2018

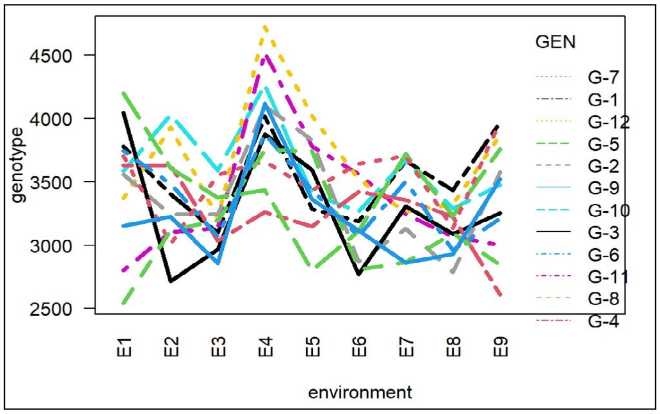

Figure 1: Line map showing genotype by environment interaction (GEI) plot for grain yield

Table 5: AMMI analysis table for grain yield (GY) of 12 faba bean genotypes

Source	Df	Sum square	Mean square	Treatment variation explained (%)	G*E explained (%)
Treatment	107	73582819.8	687689.9047		
ENV	8	24001888.6	3000236.07^{**}	32.6	
REP (ENV)	27	23977982.4	888073.42		
GEN	11	11639280.4	1058116.4^{*}	15.8	
GEN: ENV	88	37941650.8	431155.12^{*}	51.6	
PC1	18	18141768.1	1007876^{*}		47.8
PC2	16	7422909.8	463931.86^{*}		19.6
PC3	14	4352127.3	310866.24		11.5
PC4	12	3649609.7	304134.14		9.6
PC5	10	2038885.1	203888.51		5.4
PC6	8	1083907.6	135488.45		2.9
PC7	6	1032334.6	172055.77		2.7
PC8	4	220108.8	55027.19		0.6
Residuals	297	136944692.9	461093.24		
Total	519	272447145.9	524946.33		

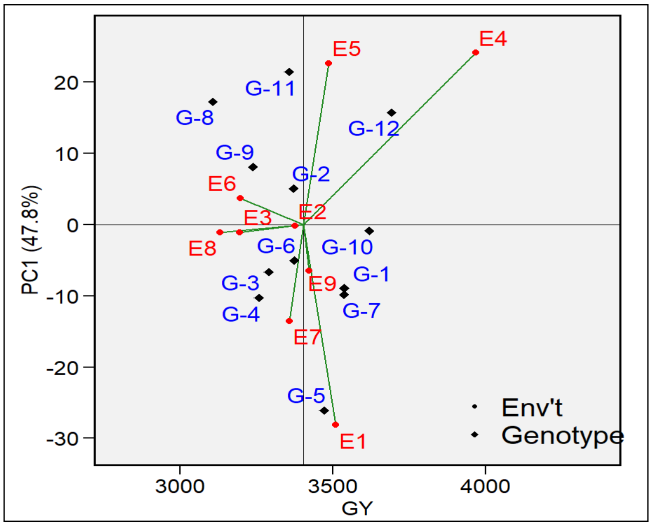

Figure 2: AMMI 1 biplot for grain yield of 12 faba bean genotypes genotypes under nine environmental condition

consider both higher mean grain yield performance (main effects) and genotype stability (genotype by environment interaction effect) for selecting best performance and wide adaptable lines among the large seeded faba bean genotypes evaluated. The genotype by environment interaction (GEI) partitioned in to eight interaction principal component axis (IPCA) through AMMI model analysis (Table 6). However, only two IPCA (IPCA1 and IPCA2) were statistically significant at $p<0.05$. Hence, the AMMI model and the AMMI 2 biplot analysis revealed that PC1 and PC2 explained 47.8% and 19.6% of the total variation in seed yield due to GEI, respectively and accumulating 67.4% together in the first two interaction principal component axis (Table 5 ad Figure 3).

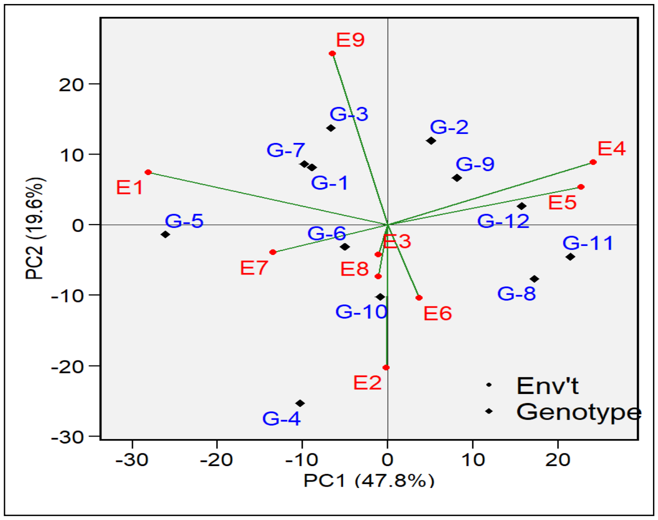

Figure 3: AMMI 2 biplot for grain yield of 12 faba bean under nine environmental condition

3.4. *Joint regression and AMMI stability indices*

There were many statistical stability measures developed to identify stable genotypes across environment. Out of this, regression coefficients (*bi*), and deviation from regression (s^2di) and AMMI stability index (ASV) and yield stability index (YSI) were the most commonly used parameters as joint regression and AMMI stability indices in genotype by environment interaction study, respectively. In the present study, the genotypes were categorized in to three groups based on their regression coefficients (*bi*), G-10, G-6 and G-1 with regression coefficients (*bi*) approaches unity (*bi*=1), which were widely adaptable across environments (Table 6). Five genotypes (G-12, G-2, G-11, G-9 and G-3) were positively responded in favorable (high yielding) environments (*bi*>1). While the remaining four genotypes (G-4, G-5, G-7 and G-8) were adapted to poor (low yielding) environment (*bi*<1).

According to Purchase et al. (2000) lower ASV value indicated the more stable genotypes whereas genotypes with high ASV value were more unstable. Based on this fact, G-10, G-6, G-2 and G-1 were distinguished as the most stable genotypes, indicating the lowest AMMI stability value and yield stability index (Table 6). Whereas, G-5, G-11 and G-8 displayed high AMMI stability value and yield stability index, implying they were the most unstable genotypes. There was no single genotype that exhibited superior yield performance at all environments (Table 7).

3.5. Graphical AMMI biplot analysis

The AMMI1 biplot was a widely recognized component and commonly used techniques in genotype by environment interaction and stability analysis to visualize graphically

Table 6: Combined genotypic mean yield; first interaction principal component axis (IPCA1); AMMI stability value (ASV); yield stability index (YSI); regression coefficients; and deviation from regression

Genotype	Mean GY	IPCA1	ASV	YSI	rASV	rGY	bi	s^2di
G-1	3536.89	-8.90	23.24	9	6	3	0.95	0.56
G-2	3370.36	5.09	17.27	10	3	7	1.55	0.37
G-3	3289.72	-6.67	21.35	14	5	9	1.36	1.02
G-4	3257.56	-10.28	35.66	18	8	10	0.05	0.98
G-5	3470.78	-26.09	63.77	17	12	5	0.30	1.60
G-6	3373.36	-5.02	12.66	8	2	6	1.11	0.23
G-7	3535.75	-9.81	25.50	11	7	4	0.36	0.82
G-8	3107.28	17.27	42.88	22	10	12	0.82	1.27
G-9	3237.89	8.12	20.94	15	4	11	1.42	0.34
G-10	3618.97	-0.89	10.42	3	1	2	0.99	0.50
G-11	3356.31	21.44	52.59	19	11	8	1.44	1.46
G-12	3692.33	15.75	38.59	10	9	1	1.65	0.71

IPCA1: interaction principal component axis 1; ASV: AMMI stability value; YSI: Yield stability index; rASV: Rank AMMI stability value; rGY: Rank mean grain yield; bi: Regression coefficient; s^2di: Deviation from regression coefficient

Table 7: Environmental mean; interaction principal component axis (IPCA1 and IPCA2) and four top ranking genotypes in each environment

Environment	Mean	IPCA1	IPCA2	1	2	3	4
E1	3508.69	-28.12	7.47	G-5	G-3	G-1	G-6
E2	3374.46	-0.21	-20.25	G-10	G-12	G-4	G-5
E3	3194.29	-1.09	-4.25	G-10	G-7	G-5	G-2
E4	3966.75	24.15	8.93	G-12	G-11	G-10	G-9
E5	3486.38	22.67	5.37	G-12	G-2	G-11	G-8
E6	3195.81	3.73	-10.37	G-7	G-11	G-12	G-4
E7	3357.48	-13.52	-3.93	G-5	G-7	G-10	G-1
E8	3130.23	-1.09	-7.33	G-1	G-12	G-10	G-5
E9	3421.31	-6.52	24.35	G-7	G-1	G-12	G-5

IPCA1: Interaction principal component axis 1; IPCA2: Interaction principal component axis 2; E1: Kulumsa 2016; E2: Kulumsa 2017; E3: Kulumsa 2018; E4: Bekoji 2017; E5: Bekoji 2018; E6: Asasa 2017; E7: Asasa 2018; E8: Kofele 2017; E9: Kofele 2018

the mean performance of main effect(genotype and environment) and genotype by environment interaction (stability of genotypes) (Zobel et al., 1988). The AMMI 1 biplot was illustrated in figure 2. The AMMI1 biplot showed that genotypes and environments located on the right side of the mid-point were relatively high yielder than genotypes and environments positioned on the left side. When IPCA1 scores alone considered with positive or negative signs genotypes with large IPCA scores have high interactions (unstable) and genotypes with small IPCA1 scores close to zero have small interactions and were stable (Zobel et al., 1988). Based on this, G-10 and G-6 recorded low IPCA1 compared to other genotypes and positioned near to the biplot as illustrated on AMMI1 (Table 6 and figure 2). Thus, these genotypes were stable.

AMMI 2 biplot is one of AMMI biplot component commonly used to identify widely and specifically adapted lines (stability of genotypes) as well as to differentiate the impact of environmental contribution for genotype by environment interaction considering the first two interaction principal component axis (IPCA). According to Asfaw et al. (2009) the distance from the center of the bi-plot were indicative of the amount of interactions (degree of stability) that was exhibited by the genotype over environments or environments over genotypes. E-9 (Kofele, 2018), E-4 (Bekoji, 2017), E-1 (Kulumsa, 2016); E-5 (Bekoji, 2018) and E-2 (Kulumsa, 2017) showed significant contribution for genotype by environment interaction effect due to their large distance from the biplot origin and high IPCA value in IPCA1 and/or IPCA2 (Figure 3 and Table 7). Conversely, E-3 (Kulumsa, 2018) and E-8 (Kofele, 2017) had less contribution on genotype by environment interaction due to short distance from the biplot and low IPCA value in the present study (Figure 3 and Table 7). G-6 and G-10 were located near to the biplot origin that revealed low contribution for interactions and which were stable over the environments. Whereas G-4 was positioned far apart from the biplot origin that exhibited high contribution for interaction which were the most unstable compared to other genotypes.

3.6. GGE biplot analysis

3.6.1. The which won where view of GGE biplot

The which won where pattern in the polygon view of GGE biplot was commonly indicating the presence of different mega environments in the testing target environments (Yan and Tinker, 2006). Thus, it was used for identifying best performing lines for each testing environment or a group of mega environments. In the present study, figure 4 presents a polygon view of twelve large seeded faba bean genotypes tested in nine environments. The GGE biplot analysis demonstrated that PC1 and PC2 together explained 65.52% of the variation for grain yield. 58.14% of the total G×E interaction was explained together by PC1 and PC2 in previous study (Gebeyaw and Gizachew, 2021). A polygon was created by connecting the marker genotypes which were located far from the origin and all other genotypes contained within polygon. The vertex genotypes were positioned at the peak of the polygon including G-5, G-4, G-8, G-11 and G-12 (figure 4). These vertex genotypes were performed either higher or lower in one or more environments due to longest distance from the biplot origin. To each side of the polygon the perpendicular lines or extended lines starting from the origin were drawn and divide the biplot into five sectors. The environments fall in to three of them. This pattern indicates that the target environment may divide into three different mega environments.

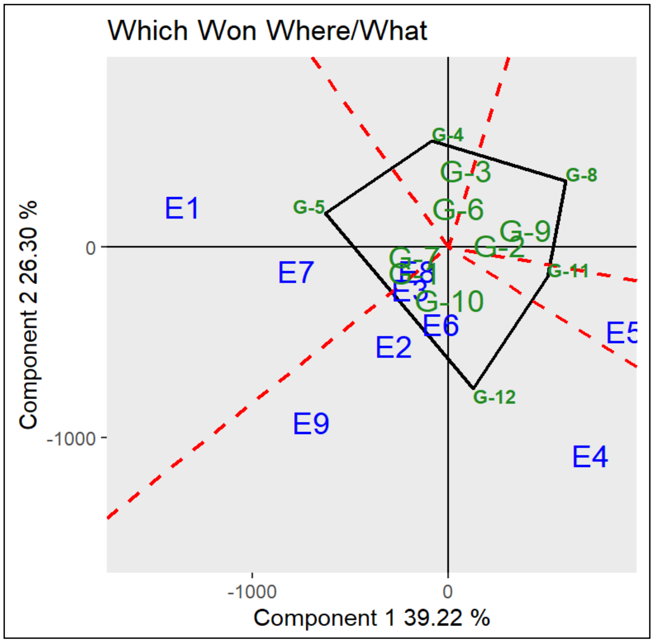

Figure 4: Which won where view of GGE biplot in 12 faba bean genotypes evaluated in nine environment using column metric preserving SVP and tester centered G+GE with no scaling

The vertex genotype was the winning genotype for an environment or set of environments contained in the sector. For example, the best performing genotype was G-5 at sector mega^{-1} environments one (E-1, E-7, E-3, E-8). G-12 at sector mega^{-1} environments two (E-4, E-2, E-6, E-9), and G-11 at sector mega^{-1} environment three (E-5) were the wining genotypes. The environments found in a sector were also suitable for the genotypes located in the sector contained within the polygon and they were less responsive in relation to the interaction with the environments within the sector since they have smaller vectors. The vertex genotype such as G-4 and G-8 in a sector where no environment was present was considered to be a poor performer in all environments (figure 4). The distance from the center of the bi-plot was indicative of the amount of interactions (degree of stability) that was exhibited by the genotype over environments or environments over genotypes (Asfaw et al., 2009). The genotypes that were located near the biplot origin such as G-2, G-6 and G-10 had exhibited less responsive to the changing environments and they were the most stable genotypes across environments.

3.6.2. Mean vs. stability view of GGE biplot

Visualization of the mean versus stability pattern of GGE biplot was helpful for easily comparing genotypes based on their mean and stability across environments. Figure 5 presents the ranking of 12 large seeded faba bean genotypes based on their mean yield and stability performance using GGE biplot analysis. The mean yield and stability of genotypes was estimated using the average environment coordinates (AEC) methods (Yan, 2001, 2002). Average environment coordinate (AEC) was a single arrowed lines passing through the small circle and the biplot origin indicated higher mean yield when genotypes positioned with AEC arrow pointing towards. The stability of genotype was determined from the projection as a vertical line from the AEC abscissa. A short projection from the AEC abscissa suggests stable genotypes across environment. Thus, the genotypes were ranked based on their mean yield and stability performance in this study. Genotype G-10 with high mean yield and most stability performance could be considered ideal or optimal genotype. Genotypes G-1 and G-7 showed relatively high yield and moderate stability and could be considered as desirable genotypes. Highest yield and low stability was observed on G-12. Genotype G-5 also recorded relatively high yield but unstable. Whereas, genotype G-8 was scored low yield and low stability. Genotypes G-2 and G-6 showed relative stability next to G-10.

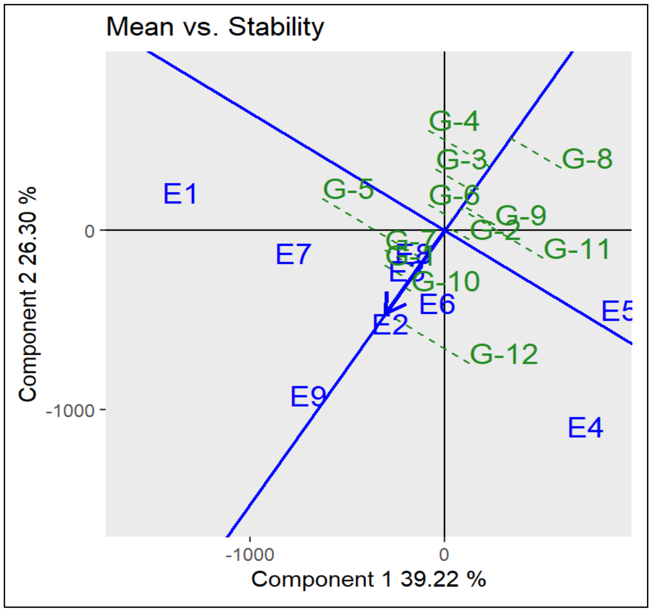

Figure 5: Genotypes mean yield performance and stability view of GGE biplot across nine environments

3.6.3. Ranking genotypes based on ideal genotype

Ideal genotype was defined as the genotype that had the highest mean yield with absolutely stable in all environments and represented by the small circle with an arrow pointing to it. Based on figure 6 genotype G-10 is showed closeness to the center of the concentric circle implies that the genotype was high yielder and most stable and could be considered as ideal. The genotypes were ranked based on their distance from the ideal genotype. The genotypes placed closer to the ideal genotype were more desirable than others. Hence, G-1 and G-7 were more desirable than others since they outperform next to G-10 from the set of testing materials. Conversely, G-8 and G-4 were located far from the center of concentric circle and exhibited longest distance from the arrow head thus, they were least desirable genotypes (Figure 7).

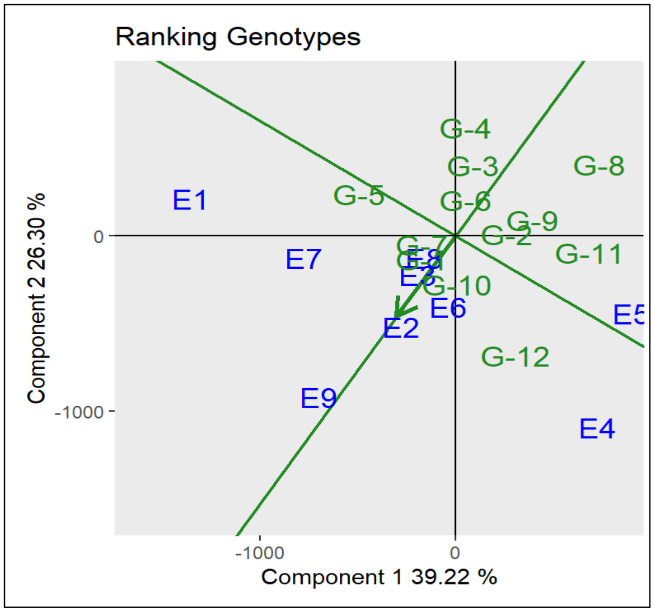

Figure 6: GGE biplot view genotype ranking relative to ideal genotype

The performance of genotypes was presented as best linear unbiased prediction (BLUP) values in figure 8 for grain yield and thousand seed weight. Genotypes G-12, G-10, G-1, G-7 and G-5 were the highest yield performing across environments (figure 8). While, for thousand seed weight (TSW), genotypes G-7, G-10, G-11 and G-5 were recorded above average (figure 9). However, G-8 and G-4 were showed relatively low performance for grain yield and thousand seed weight, respectively across environments.

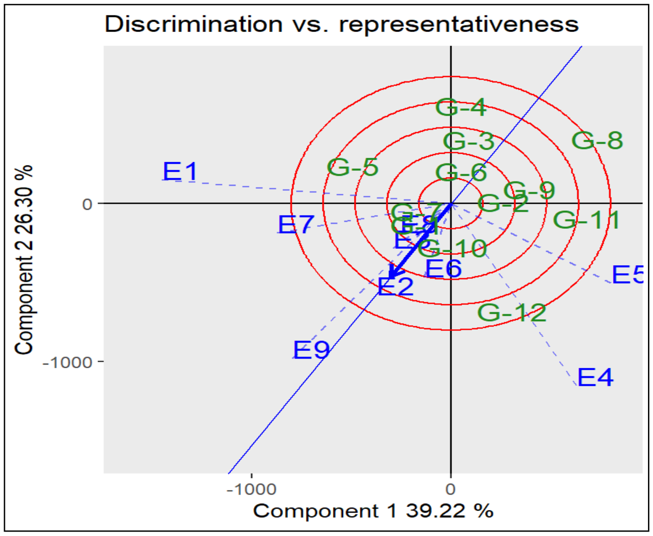

Figure 7: The discriminating and representativeness view of GGE biplot

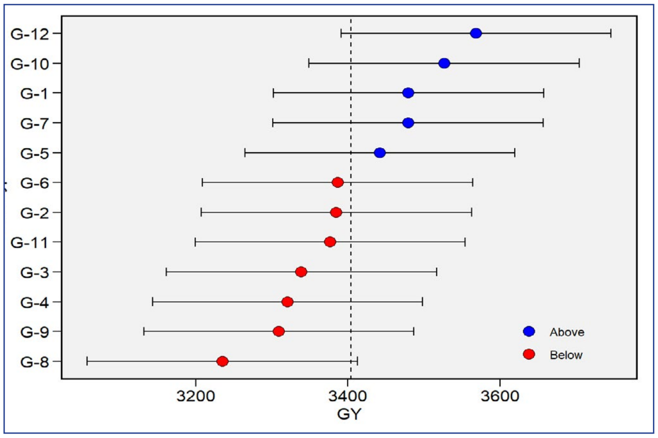

Figure 8: Best linear unbiased prediction (BLUP) for 12 faba bean genotypes evaluated under nine environments for grain yield (GY)

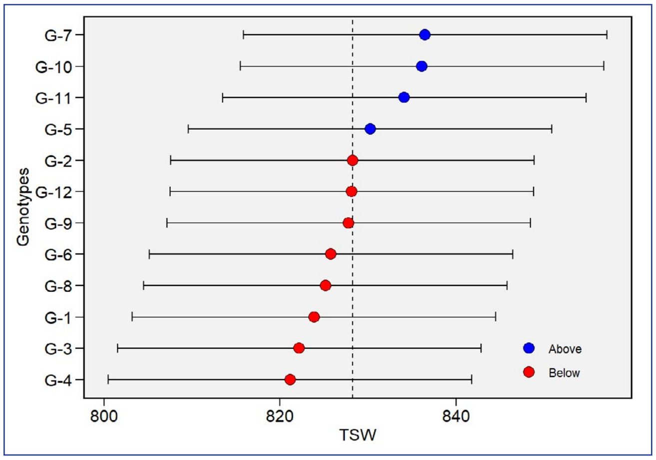

Figure 9: Best linear unbiased prediction (BLUP) for 12 faba bean genotypes evaluated under nine environments for thousand seed weight (TSW)

4. CONCLUSION

The grain yield performance of faba bean genotypes was significantly influenced by environment and interaction. The magnitude of interaction effect was more than three times higher than the genotype effect. AMMI and GGE biplot analysis had comparable significance for identification of the best performing and most stable genotypes. G-10 was the best performing, most stable and ideal genotype across environments. Great emphasis should be given for G-10, G-7 and G-5 for grain yield and seed size improvement in the future.

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