

Additive Main Effect and Multiplicative Interaction Analysis for Grain Yield Stability in Faba Bean Genotypes (*Vicia faba* L.)

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ABSTRACT

Genotype-by-environment interactions (GEI) are an important tool for identifying and selecting optimal plant genotypes that ensure stable yields under diverse conditions. Assessing GEI is therefore crucial for understanding genetic variation and tailoring breeding strategies to specific agro-ecological regions. The aim of this study was to evaluate the quantitative impact of GEI on the grain yield and quality of faba bean (*Vicia faba* L.) genotypes in the Bale region (southern Ethiopia). Twelve genotypes were evaluated using a randomized complete block design with four replications across two locations (Sinana and Agarfa) over three consecutive cropping seasons (2018–2020). Analysis of variance revealed a significant effect ($P < 0.01$) of genotype, environment, and GEI on grain yield, indicating that the genotypes responded differently to varying environmental conditions. Environmental factors accounted for the largest share of grain yield variation (31.84%), followed by the effects of genotype (6.77%) and GEI (2.49%), demonstrating that environmental conditions significantly shaped the production performance of the tested genotypes. Grain yield ranged from 1.94 t ha⁻¹ at Agarfa in 2018 to 3.85 t ha⁻¹ at Sinana in 2019, with an overall mean of 2.61 t ha⁻¹. AMMI (Additive Main effects and Multiplicative Interaction) analysis revealed the presence of genotype-by-environment interaction (GEI), with the first two interaction axes accounting for 79.2% of the total sum of squares for the interaction. Through stability analysis based on the AMMI Stability Value (ASV) and the Genotype Stability Index (GSI), genotypes G4, G9, G5, and G8 were identified as stable across the various environment. The genotype G2 exhibited superior grain yield performance with moderate stability and surpassed the standard checks by 19.05%. Therefore, G2 was identified as a promising candidate genotype for further verification and possible release for commercial cultivation in Southeastern Ethiopia and similar agro-ecological zones.

Keywords: AMMI, Faba bean, Genotype, crops, Environment Interaction, and GSI.

1. Introduction

Faba bean (*Vicia faba* L.) is strategic cool-season pulse crop of global agronomic and nutritional importance, valued for its high seed protein content, essential amino acids, and contribution to sustainable agroecosystems [4, 14]. The crop plays a dual role in food security and soil fertility enhancement through biological nitrogen fixation, thereby improving system productivity in cereal-based cropping systems [7, 11, 16]. The global productivity remains relatively low and unstable, averaging about 2.0 t ha⁻¹, largely due to strong environmental variability and genotype × environment interaction [7, 25]. In Ethiopia, faba bean is the most important pulse crop and is widely cultivated in the highland agro-ecologies between 1800 and 3000 m a.s.l. The country is the largest producer in Africa and the second largest globally after China [7]. According to the Central Statistical Agency [6], the national average productivity is approximately 2.1 t ha⁻¹, which remains substantially below the yield potential of improved cultivars exceeding 5.0 t ha⁻¹ under optimal management conditions. This persistent yield gap is attributed to abiotic stresses (moisture fluctuation, frost), biotic constraints (diseases and pests), and limited deployment of stable, high-yielding genotypes adapted to diverse environments [1, 6, 19, 20, 22]. A major limitation in faba bean breeding is the prevalence of genotype × environment interaction (GEI), which causes inconsistent genotype

performance across environments and reduces selection efficiency [8, 18, 24]. Grain yield, being a complex quantitative trait, is highly influenced by both genetic and environmental factors, making multi-environment testing essential for reliable genotype evaluation [12]. Failure to account for GEI often leads to biased selection and poor varietal recommendation across target production environments. To effectively dissect GEI, several statistical approaches have been developed, among which the Additive Main Effects and Multiplicative Interaction (AMMI) model is widely recognized for its robustness and interpretability [9]. The AMMI model integrates ANOVA for additive effects and principal component analysis for multiplicative interaction effects, enabling precise identification of stable and high-performing genotypes across environments. Recent studies in Ethiopia have demonstrated the effectiveness of AMMI-based approaches in identifying adaptable faba bean genotypes under multi-environment conditions [23]. And the several varietal development efforts, limited information exists on the stability performance of faba bean genotypes across contrasting highland environments, particularly in Bale, Southeastern Ethiopia, where strong environmental heterogeneity is expected to intensify GEI effects. Therefore, evaluating genotype performance across multiple environments using robust stability models is essential for identifying broadly adapted and stable genotypes.

Accordingly, this study was conducted to assess genotype × environment interaction and grain yield stability of faba bean genotypes using the AMMI model under the highland agro-ecological conditions of Bale, Southeastern Ethiopia.

2. Materials and Methods

Nine faba bean genotypes, as well as two standard and local check varieties, were evaluated under rainy conditions during three consecutive active growing seasons (2018–2020) in Sinana and Agarfa in the Bale Highlands of southeastern Ethiopia. The tests were conducted on Vertisol clay soil. The Sinana Agricultural Research Institute (07°07'10.837" N, 040°13'32.933" E; elevation 2400 m) is located 463 km southeast of Addis Ababa and 33 km southeast of Robe. The experiments used a fully reinforced block design (RCBD) with four replicates. Each experimental plot consisted of four rows, each 4 m long with 40 cm spacing between rows, resulting in a total length of 6.4 m and a net length of 3.2 m. Seeds were sown at a rate of 100 kg ha⁻¹, and NPS fertilizer was applied as a base fertilizer at a rate of 100 kg ha⁻¹ at planting, following the recommended tillage practices. Other weed control practices were applied uniformly in all experimental plots. Yield data were analyzed separately for each plot using CropStat software (version 7.2) prior to cross-plot analysis.

Stability analysis: The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by [5] as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^h \lambda_n \alpha_{ni} \cdot Y_{nj} + R_{ij} \text{ where,}$$

Y_{ij} represents the performance of genotype i in environment j; μ is the grand mean; g_i is the mean of genotype i minus the grand mean; e_j is the mean of environment j minus the grand mean; λ_n is the eigenvalue of the axis in the principal component analysis (PCA); α_{ni} and Y_{nj} are the principal component scores for PCA axes n, corresponding to genotype i and environment j; and R_{ij} represents the residual values. Genotype-environment interaction biplots were generated for 12 faba bean genotypes evaluated across 6 environments. Regression analysis of cultivar yield against mean environmental yield was performed using CropStat 7.2 software. The ASV (AMMI Stability Value) index represents the distance from the origin to the point on a two-dimensional plot where IPCA1 values are plotted against IPCA2 values from the AMMI model; the analysis was conducted using the method proposed in [18].

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1_{score}) \right]^2 + [IPCA2]^2}$$

Where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$

The weight assigned to the IPCA1 value is determined by dividing the sum of squares of IPCA1 by the sum of squares of IPCA2. Genotypes with higher IPCA scores—whether positive or negative—tend to be more adapted to specific conditions. Conversely, genotypes with IPCA scores close to zero can be considered more robust, as they demonstrate consistent performance across various environmental conditions.

Genotype Selection Index (GSI): The selection probability for each genotype is calculated for both seed and single-cross scenarios, using the method developed in [9].

$$GSI_i = RY_i + RASV_i$$

Table 1: Genotype code and the name of 12 faba bean genotypes

Genotype Code	Genotypes	Source of genotypes	Genotype Code	Genotypes	Source of genotypes
G1	EH010012-1	Holeta ARC	G8	EH010008-5	Holeta ARC
G2	EH010028-1	Holeta ARC	G9	EH09028-6	Holeta ARC
G3	EH010016-1	Holeta ARC	G10	Mosisa	Sinana ARC
G4	EH010051-1	Holeta ARC	G11	Alloshe	Sinana ARC
G5	EH010012-2	Holeta ARC	G12	Local	Sinana ARC
G6	EH010049-5	Holeta ARC			
G7	EH010028-4	Holeta ARC			

HARC= Holeta Agricultural Research Center, SARC=Sinana Agricultural Research Center.

3. Result and Discussion

3.1. The Analysis of Variance

A combined analysis of seed variation across locations and years revealed significant differences ($P < 0.01$) regarding genotype and environment (Table 2). Similar results for beans have been reported in [10, 21, 23]. Based on the sum of squares (SS) for seeds, environmental factors contributed 31.84% to the variation, followed by genotype (6.77%) and the interaction (2.49%). This indicates that environmental factors played a significant role in the variation in seed yield among the genotypes studied. Environmental factors determine genotype expression, and the selection of resistant genotypes constitutes an important breeding strategy.

Table 2: ANOVA for combined mean grain yield of Fababean genotypes over locations and years

Source of Variation	Degree freedom	Sum Squares	Mean Squares	%Of the variation
YEAR (Y)	2	23.59	11.79**	
Location (L)	1	78.89	78.89**	31.84
Replication	3	2.798	0.932	
Genotype (G)	11	16.78	1.52**	6.77
Y X L	2	22.65	11.32**	
G X L	11	6.18	0.562**	2.49
Y X L X G	44	30.72	0.698**	
RESIDUAL	213	66.12	0.310	
TOTAL	287	247.76	0.863	

The highest average maize yield was recorded for genotype EH010028-1 (3.51 t ha⁻¹), followed by EH010049-5 (2.78 t ha⁻¹), the reference variety Alloshe (2.73 t ha⁻¹), and EH01010-10 (2.6 t ha⁻¹). Under the environmental conditions analyzed, the average grain yield ranged from 1.94 t ha⁻¹ in Agarfa (2018) to 3.85 t ha⁻¹ in Sinana (2019); this indicates significant variation in genotype performance depending on the environment. The final average wheat yield, considering all locations and years, was 2.61 t ha⁻¹ (Table 3), representing the average productivity level under the agroecological conditions studied.

Table 3: Mean grain yield (t/ha) of faba bean genotypes x site over three years, 2018-2020

Genotype	Environment (Year x Location) t/ha						TRT MEANS
	SN2018	Ag2018	SN2019	Ag2019	SN2020	Ag2020	
EH010028-1	3.30	2.99	4.18	2.86	3.46	2.7	3.51(1)
EH010049-5	2.44	1.88	4.05	2.57	3.56	2.17	2.78(2)
Alloshe	2.85	1.94	3.51	2.35	3.23	2.48	2.73(3)
EH010016-1	2.46	1.64	4.25	1.95	3.31	2.55	2.67(4)
EH010012-2	2.44	1.97	4.42	1.73	3.01	2.49	2.68(5)
EH010012-1	2.6	1.77	4.29	1.43	2.88	2.8	2.63(6)
Mosisa	2.25	1.37	4.01	2.1	3.41	2.28	2.57(7)
EH010008-5	2.56	2.08	3.51	1.89	2.68	2.14	2.48(8)
EH010028-4	2.13	1.86	3.6	2.33	3.06	1.63	2.44(9)
EH09028-6	3.09	2.68	2.98	1.37	1.82	2.42	2.40(10)
Local	2.25	1.29	3.38	2.02	3.11	2.05	2.35(11)
EH010051-1	2.01	1.86	4.05	1.59	2.63	1.84	2.36(12)
Mean	2.53	1.94	3.85	2.02	3.01	2.3	2.61

3.2. AMMI Analysis

Table 5 presents the estimated mean score, the interaction principal component axis (IPCA), the AMMI stability value (ASV), the genotype selection index (GSI), and the corresponding rankings for the two phage strains evaluated across the six environments. The AMMI analysis partitioned the genotype × environment interaction (GEI) sum of squares into four interaction principal component axes; of these, only the first two IPCA axes were statistically and biologically significant (Table 4). The first interaction principal component axis (IPCA1) explains 53.3% of the total GEI, while IPCA2 accounts for an additional 25.9%. The two axes accounted for 79.2% of the interaction variance, suggesting that the first two multivariate components explained a substantial portion of the differential genotypic responses to the environment.

The large proportion of GEI variation explained by IPCA1 and IPCA2 demonstrates the effectiveness of the AMMI model in describing the interaction structure and elucidating patterns of genotype adaptation across environments. According to the predictive assessment of the AMMI model, the first two interaction principal components are generally sufficient to capture the systematic portion of GEI, whereas higher-order IPCAs predominantly represent residual noise and non-predictive variation [8-9]. The AMMI model incorporating the first two significant IPCAs provides a robust and parsimonious framework for evaluating genotype stability and adaptation.

The magnitude of GEI explained by the first two IPCAs in the present study is comparable with previous reports in faba bean. Earlier studies documented that IPCA1 accounted for approximately 63.35–77.0% of the total interaction variation [3, 21], while [13] reported that the first two IPCAs collectively explained 60.1% of the GEI sum of squares. The relatively high cumulative contribution (79.2%) observed in the current investigation suggests that the AMMI model efficiently captured the underlying interaction patterns, thereby enhancing the reliability of genotype evaluation and the identification of stable and high-yielding genotypes across diverse environments.

Table 4: Analysis of Variance of AMMI model for grain yield of faba bean genotypes

Source of variation	Df	SS	MS	%Variance Explained	% Cumulative
Environment (E)	5	125.14	25.03		
Replication/E	18	17.41	0.97		
Genotype (G)	11	16.79	1.53		
GxE	55	36.91	0.67		
AMMI 1	15	19.68	1.31**	53.3	
AMMI 2	13	9.56	0.74**	25.9	79.2
AMMI 3	11	3.61	0.33	9.8	89
AMMI 4	9	3.33	0.37	2	98
Residuals	198	51.52	0.26		

** Significant difference at ($P \leq 0.01$), Df= degree of freedom, SS= sum of square, MS= mean squares

3.3 Stability Analysis

According to [17], the Interaction Principal Component Axis (IPCA) scores generated from the AMMI analysis provide valuable information regarding the stability and adaptability of genotypes across environments. Genotypes with larger absolute IPCA scores exhibit stronger interactions with the environment and are therefore considered specifically adapted to particular environments. Conversely, genotypes with IPCA scores closer to zero are characterized by greater stability and wider adaptation across the tested environments [8, 9]. Based on the IPCA1 scores, genotypes G1 (EH010012-1) and G4 (EH010049-5) exhibited the smallest absolute values and were therefore identified as the most stable genotypes, followed by G5 (Table 5). Previous studies have similarly indicated that genotypes with IPCA scores approaching zero in absolute magnitude tend to exhibit greater phenotypic stability and broader environmental adaptation [2]. When stability was assessed using IPCA2 scores, genotype G2 (EH010028-1) was identified as the most stable, followed by G10 (Mosisa).

The observed differences in genotype rankings between IPCA1 and IPCA2 indicate that each interaction principal component captures distinct portions of the genotype $\times$ environment interaction (GEI) pattern and therefore provides different information regarding genotype adaptation and stability. To overcome the limitations associated with interpreting individual IPCAs separately, the AMMI Stability Value (ASV) was calculated. The ASV integrates the contributions of both IPCA1 and IPCA2 into a single stability statistic, thereby providing a more comprehensive assessment of genotype stability. As reported by [17], ASV offers a balanced measure of stability by simultaneously accounting for the relative importance of the first two interaction principal component axes, facilitating more reliable genotype comparisons across environments.

3.3.1 AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

The AMMI model does not inherently provide a single quantitative index for stability; therefore, additional stability parameters are required to quantify and rank genotypes based on their yield stability across environments. In this context, the AMMI Stability Value (ASV) serves as a useful metric, where genotypes with lower ASV scores or minimal distance from the origin in the AMMI biplot are considered more stable, whereas those with higher ASV values are regarded as less stable and more responsive to environmental variation [17, 18]. As indicated in Table 5, ASV analysis identified G4, G9, G5, and G8 as the most stable genotypes. Genotypes G7, G2, G3, and G6, which exhibited intermediate ASV values, were classified as moderately stable. However, since yield stability alone does not necessarily correspond to high productivity, the Genotype Selection Index (GSI), which integrates both mean grain yield and stability rank, was employed to facilitate simultaneous selection for performance and stability. Lower GSI values indicate superior genotypes combining high yield and greater stability. Based on GSI rankings, the genotype EH010028-1 was identified as the most desirable, exhibiting a favorable combination of high grain yield and moderate stability (Table 5).

Table 5: Mean grain yield, and Stability parameters for 12 Faba bean genotypes

Code	Genotypes	Mean	Rank Yi	Slope (bi)	MS-DEV (S^2di)	IPCA1	IPCA2	ASV	Rank ASV	GSI
G1	EH010012-1	2.63	6	1.316	0.15	-0.052	-0.718	0.73	9	15
G2	EH010028-1	3.25	1	0.962	0.04	-0.207	0.004	0.68	7	8
G3	EH010016-1	2.70	4	1.301	0.04	0.301	-0.315	0.70	8	12
G4	EH010051-1	2.34	12	1.296	0.07	0.062	-0.245	0.28	1	13
G5	EH010012-2	2.68	5	1.223	0.10	0.077	-0.487	0.51	3	8
G6	EH010049-5	2.78	2	1.150	0.12	0.402	0.297	0.88	10	12
G7	EH010028-4	2.44	9	0.870	0.17	0.223	0.489	0.67	6	15
G8	EH010008-5	2.48	8	0.833	0.03	-0.267	0.127	0.56	4	12
G9	EH09028-6	2.40	10	0.309	0.49	-1.196	0.019	2.46	2	12
G10	Mosisa	2.58	7	1.310	0.09	0.493	-0.009	1.02	11	18
G11	Alloshe	2.73	3	0.884	0.12	-0.493	0.314	1.06	12	15
G12	Local	2.35	11	0.846	0.16	0.283	0.230	0.63	5	16

1.1. AMMI Biplot

The AMMI1 biplot, constructed using the first interaction principal component axis (IPCA1) against mean grain yield, illustrated the main effects of genotypes and environments as well as their interaction patterns. Genotypes and environments positioned on the right side of the vertical axis passing through the origin exhibited mean grain yields above the grand mean (2.61 t ha^{-1}) (Table 4). Accordingly, genotypes G1, G2, G3, G5, G6, and G11, as well as environments SN2 and SN3, were identified as high-yielding, exceeding the final mean performance. In contrast, the remaining genotypes and environments were located on the left side of the origin, indicating yield performance below the grand mean (Figure 1).

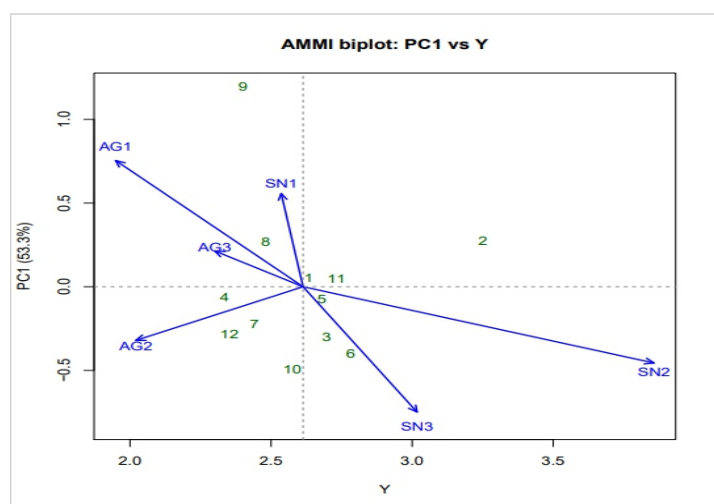


Figure 1: Bi-plot interaction based on AMMI 1 and the mean grain yield.

AMMI Biplot II

The AMMI2 biplot, based on the first two interaction principal component axes (IPCA1 and IPCA2), was used to provide a more robust visualization of genotype $\times$ environment interaction (GEI) and to better characterize patterns of stability and adaptation (Figure 2). The inclusion of IPCA2, in addition to IPCA1, allows a more complete partitioning of GEI effects, thereby improving the resolution of genotype and environment relationships. In the biplot, genotypes located near the origin exhibited minimal interaction effects and were therefore considered broadly stable across environments. In contrast, genotypes and environments positioned farther from the origin, indicated by longer vector lengths, contributed more strongly to GEI and were either unstable or specifically adapted to particular environments. Based on this criterion, genotypes G8, G11, G4, and G12 showed relatively stable performance across testing environments. Importantly, genotype G2 combined high mean grain yield with moderate interaction effects, indicating superior adaptability and agronomic desirability. Among the environments, SN1 (2018), AG3 (2020), and AG1 (2018) were located closer to the origin, indicating low interaction effects and relatively consistent performance across genotypes. These environments were therefore less discriminating but more stable in their expression of genotype performance, the AMMI2 biplot effectively distinguished stable genotypes from those exhibiting specific adaptation, while also highlighting environments with differing levels of discriminating ability.

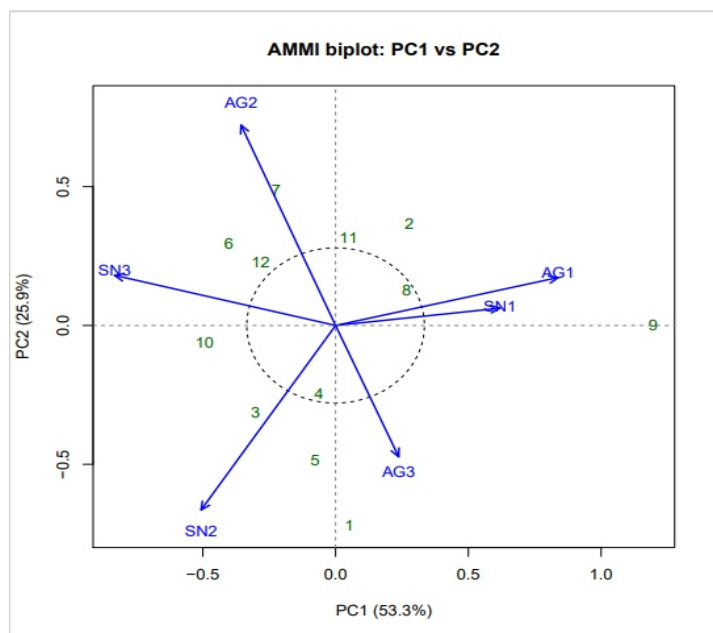


Figure 2: Interaction bi-plots for the AMMI 2

CONCLUSION

Analysis of variance (ANOVA) revealed highly significant effects ($P < 0.01$) for genotype (G), environment (E), and the genotype-by-environment interaction (GEI) on all observed traits; this indicates the presence of genetic variation, significant genotypic effects, and differential genotypic responses across the test sites. These results confirm that genotypic performance is not consistent across different environments, necessitating the use of a stability analysis approach. The AMMI (Additive Main Effects and Multiplicative Interaction) model accounts for GEI as a significant factor, allowing for a clearer interpretation of genotypic variation and stability. The model proved useful for identifying genotypes combining high yield potential with stable performance across environments. Among the evaluated entries, genotype G2 recorded the highest mean grain yield, exhibiting a 19.05% yield advantage over the standard checks. G2 demonstrated moderate stability across environments, indicating relatively low sensitivity to environmental fluctuations while maintaining superior productivity. Based on its high mean performance and acceptable stability parameters, G2 is identified as a promising candidate genotype. It is recommended for further multi-environment testing in advanced yield trials prior to potential release, and shows strong potential for commercial cultivation in Southeastern Ethiopia and agro-ecologically similar regions.

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CONFLICT OF INTEREST

The authors declare that they have no conflict of interests.

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