Exploring Genotype by Environment Interactions and Stability of Medium-Seeded Faba Bean (Vicia faba L.) Genotypes in High-Potential Environments: Utilizing AMMI, GGE Biplot and BLUP Models

providing food and feed to small-holder farming communities and providing foreign exchange and income for farmers.

same goal. From a statistical point of view, these models are vastly di erent. e AMMI analysis retains most of the GEI pattern in the rst interaction principal component axis (IPCA) resulting from the singular value decomposition (SVD) of the nonadditive e ects matrix, while most of the random error is retained in the last IPCAs. e BLUP initially estimates the e ects of the ANOVA model and then attributes weights to these e ects; it could thus be considered a shrinkage estimator (Piepho 1994). is method estimates the mean yield of genotypes in mixed models with high e ciency. On the other hand, GGE biplot analysis is a bene cial graphical tool since it o ers visual pictures and a clear summary of the main data and outcomes (Yan, W., 2015). e AMMI model is o en used together with the GGE biplot graphical model to identify MEs as well as winning genotypes in each ME. e unique feature of the GGE biplot is that, based on the plots, it can be decided which genotype has the highest potential in which environment. ese models are frequently used alone in the evaluation of METs. Some studies were successful in estimating genotypic values in MET using BLUP (Olivoto et al., 2017; Nardino et al., 2016), while others were successful in modeling GEI patterns using AMMI (Bocianowski et al., 2019; Veenstra et al., 2019). Combining the graphical tools of AMMI, GGE biplot, and the predictive accuracy of BLUP is very important in exploring GEI. us, this study aims to assess the genotype x environment interaction, apply the stability parameters, identify environments that are more suitable for faba bean growing, and identify varieties with a high and stable yield [3].

e experiment was conducted during the main cropping season (Meher) of 2018 and 2019 for two consecutive growing seasons at four locations, namely Kulumsa, Bekoji, Asasa, and Kofele experimental stations of the Kulumsa Agricultural Research Center in south-eastern Ethiopia. e testing sites are located in di erent districts of the Oromia Regional States of Ethiopia, which are characterized by mid- and high-altitude agroecology. e dominant crops grown within the experimental areas are wheat, barley, faba bean, and root crops like potatoes (Table 1) [4].

Fourteen faba bean (Vacia faba L) genotypes obtained from Holeta Agricultural Research Center were evaluated under potential environments. e experiment was laid out in a randomized complete block design (RCBD) with four replications. Each genotype was planted on a plot size of 6.4 m^2, with 4 rows at 40 cm spacing between rows and 4 m length at all the testing sites. e central two rows were seed kg/ha and fertilizer followed uniformly for all plots throughout the experiment and location, as per the recommendation for faba bean (Table 2).

Table 1: Descriptions Geographical Descriptions of the Experimental Environments.

S/No	Environment	Year	Location	Altitude (m.a.s.l.)	Rainfall (mm)	Geographical position	
						Latitude	Longitude
1.	E1	2018	Kulumsa	2200	820	08001’10”N	39009’11”E
2.	E2	2019					
3.	E3	2018	Bekoji	2780	1020	07032’37”N	39015’21”E
4.	E4	2019					
5.	E5	2018	Asasa	2340	620	07007’09”N	39011’56”E
6.	E6	2019					
7.	E7	2018	Kofele	2660	1211	07004’28”N	38047’11”E
8.	E8	2019					
Source: Kulumsa Agricultural Research Center							

Table 2: Lists of genotypes used in the study.

Entry No	Genotype	Origin	Seed source
1.	Degaga	Released from Introduction	HARC
2.	Cool-12	Collection	HARC
3.	Cool-0030	Collection	HARC
4.	Cool-0025	Collection	HARC
5.	Cool-0011	Collection	HARC
6.	Cool-0002	Collection	HARC
7.	Cool-0018	Collection	HARC
Entry No	Genotype	Origin	Seed source
1.	Cool-0035	Collection	HARC
2.			
3.			
4.			
5.			
6.			
9.	Cool-0034	Collection	HARC
10.	Cool-0003	Collection	HARC
11.	Cool-0031	Collection	HARC
12.	Cool-0024	Collection	HARC
13.	Dosha	Released from collections	HARC
14.	Numan	Released from Hybridization	KARC

Data on grain yield, agronomic conditions, and disease reactions were collected from each plot. Days to owering (DF) and days to physiological maturity (DM) were taken when each plot reached 50% of ower initiation and 90% of the pod attained physiological maturity, respectively. e days were calculated starting from the date of sowing. Plant height (cm) was taken at full maturity from ve randomly selected plants in the central two rows, measured from the ground level to the top of the plant. e mean value is recorded as plant height per plot for analysis. Responses of genotypes to disease reactions like chocolate spot, ascochyta blight, and rust were recorded at late pod setting based on 1 9 scoring methods. Grain yield was measured on clean, dried seed, and plot yields were adjusted to 10% moisture level and converted to kilograms per hectare. ousand seed weights (TSW) (gm) were counted and weighted. Data on the number of pods per plant and seeds per pod were also collected based on ve plant bases and averaged for data analysis [5].

e analysis of variance of each location and combined data over location were performed using a mixed linear model to assess the di erences among genotypes as per Gomez and Gomez (1984). R so ware version 4.4.0 with the packages agricolae and metan were used. Homogeneity of variance was tested and a combined analysis of variance was done using the Mixed Linear Model procedure to partition the total variation into components due to genotype (G), environment (E), and G × E interaction e ects. e following individual and combined RCBD models were used for analysis.

where; Y_{ij} is the grain yield of the i^{th} genotype in the j^{th} environment, μ = the grand mean, E_j = the e ect of the i^{th} genotype, $'_F$ = the e ect of the j^{th} location, $)'_{EF}$ = the interaction of the i^{th} genotype with the j^{th} location, $Ú()_{FG}$ = the e ect of the k^{th} replication in the j^{th} location, and $Ý_{EFG}$ = the error.

e Additive main e ects and multiplicative interaction (AMMI) model was performed for grain yield and thousand seed weight of 14 faba bean genotypes using performs ammi() function in the metan packages of R so ware. erefore, the estimate of the response variable for the i^{th} genotype in the j^{th} environment (U_{EF}) using the AMMI model, is given as follows (Gauch, 1992).

where Y_{ij} = is the yield of the i^{th} genotype in the j^{th} environment; μ = is the grand mean; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; λ_k = is the eigenvalue of the PCA analysis axis k; and l_{ik} and j_{jk} = are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model, and d_{ij} is the error term.

AMMI Stability Value (ASV) which is the distance from the coordinate point to the origin in a two-dimensional of IPCA1 score against IPCA2 scores in the AMMI model was calculated using the formula dev6.2 Tw T*p9929oy(e11.[Purchal Tw T*pko,al T4 5.247 190.3943 15SV) whis,t 7.213uT*pkoc:r1s.,j)T0S0 the ee f

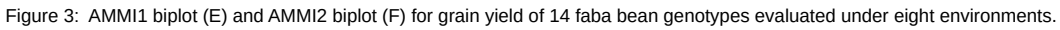

Figure 3: AMMI1 biplot (E) and AMMI2 biplot (F) for grain yield of 14 faba bean genotypes evaluated under eight environments.

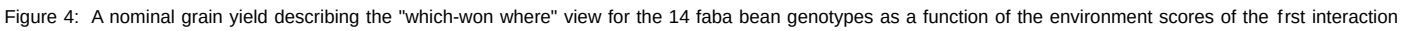

Figure 4: A nominal grain yield describing the "which-won where" view for the 14 faba bean genotypes as a function of the environment scores of the first interaction principal component axis (IPCA1) (G) and Line map showing the grain yield variation of 14 faba bean genotypes across 8 environments (H).

Figure 5: Polygon view of biplot 3 (Which-Won-Where) for TSW (I) and GYLD (J) of 14 faba bean genotypes under 8 environments.

average environment in their genotype di erentiation capabilities. In contrast, E8 and E4 had the largest angle from the average environment for TSW and E1 and E8 for GYLD, suggesting greater variability in terms of genotypes performance (Figure 6) [11].

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e application of gge-biplot analysis enabled the determination of optimal and most desirable genotype from a set of genotypes. ideal genotype is consistently located within the middle region and

Figure 6: Discriminativeness versus representativeness of GGE biplot for TSW (K) and GYLD (L) of 14 faba bean genotypes under 8 environments.

Figure 7: Ranking genotypes based on PC1 and PC2 of TSW (M Pattern) and GYLD (N pattern) showing G × E interactions of the 14 faba bean genotypes under 4 locations and two seasons (8 environments).

Figure 8: Best linear unbiased prediction (BLUP) for 14 faba bean genotypes evaluated under 8 environments for TSW on the left (a) and GYLD on the right side (b).

in close proximity to the peak of the arrow within the circular band. Accordingly, from this study for TSW, it was noted that variety Numan was located within the inner circle and considered to be optimal. For GYLD, Dosha and Numan variety exhibited closeness to the inner circle. In contrast, Cool-0011 exhibited the greatest distance from the arrowhead in the plot for both TSW and GYLD (Figure 7) [12].

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Overall performance of genotypes presented as BLUP values indicated that Dosha, Cool-0030 and Numan varieties were ranked the highest for TSW. whereas, for GYLD, Numan, Dosha, Cool-0018, Cool-0030, Cool-0024, Cool-0035, Cool-0031, and Cool-0034 scored above average with better yield stability across environments. Conversely, Cool-0011 performed poorly in both TSW, and GYLD (Figure 8).

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Stability analysis was done using AMMI, and GGE biplot for the TSW and GYLD traits. Accordingly, the variability explained by the AMMI model for TSW was 85%, and GGE biplot was 95.9%. for GYLD, the variability explained by the AMMI model was 52.3% and GGE biplot was 73.38% (Figure 9) [13].

level for TSW, indicating that interactions a ecting TSW are primarily captured by these two principal components. e AMMI model analysis revealed that PC1 and PC2 together accounted for 85.3% of the total variation in thousand seed weight (TSW).

References

1. Bocianowski J, Niemann J, Nowosad K (2019)