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Analysis of Genotype by Environment Interaction and Grain Yield Stability for Small White Common Bean (Phaseolus vulgaris L.) Genotypes in Southern Oromia, Ethiopia

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Abstract

In multi-environment trial, considering both the stability and mean grain yield is vital. This study was conducted aimed to determine the magnitude of G x E interaction and detect stable high yielding and specifically performed genotypes for target environment(s). A total of 13 small white common bean genotypes including the standard checks were evaluated at seven locations during 2020/21 and 2021/22 main cropping season. The genotypes were arranged in Randomized Complete Block Design and replicated three times. Combined ANOVA, AMMI and GGE bi-plot models were used to analyze the data. Both AMMI and GGE biplot analyses identified that genotypes (Genotype#285) and (Genotype#111) were declared as widely adapted genotypes with likewise recorded higher grain yield of 2.618 tons/ha and 2.503 tons/ha, respectively. Both genotypes were superior to the standard checks with grain yield advantage of 27% and 22%, respectively and they were recommended as candidate varieties for further evaluation and eventual release.

Keywords: AMMI; Genetic-environment interactions; Stability; Phaseolus vulgaris

Introduction

Common bean (*Phaseolus vulgaris* L.) is an annual pulse crop with considerable variation in growth habit, vegetative characters, flower color and the size, shape and color of the pods and seeds (Onwueme and Sinha, 1991). The crop is rich in protein (22%), is a source of mineral especially iron and Zinc in the diet, and has an advantage of improving soil fertility. 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 (GE) interaction. The GE interaction refers to the ordering of genotypes across environments before recommending a specific genotype for a particular environment [2,17,18,20,22].

Common bean is highly preferred by Ethiopian farmers because of its fast-maturing characteristics that enable households to get cash income required to purchase other food and household needs when other crops have not yet matured (Legesse *et al.*, 2006). It is also an important food and cash crop in Guji zone. Similarly, it contributed 39.49% for household consumption, 13.33% for seeds, 44.1% for sale, 0.58% for animal feed and 2.05% for other uses in the studied zone (CSA, 2018). Beans of small white market class seed had limited varietal option which are highly demanded by the canning industry and needed for export market. Bore Agricultural Research Center of

Pulse Research Program focuses on strengthening bean acquiring/introducing of germplasm (advanced lines) from National Bean Research Program and conducting different performance trials and releasing varieties. Since the National and Regional Bean Research Programs have been released several varieties. Hence, the performance evaluation of those genotypes before release were done in limited areas. Even if, a given varieties has performed well for specific period of time and reduces its production potential after a while becoming susceptible to diseases due to different factors. Therefore, to tackle this problem this breeding activity was initiated to develop varieties that revealed stable high yielding and resistance/tolerant to diseases for the mid-lowlands of Guji zones and similar agro-ecologies

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) [3,19]. Yan and Tinker, (2006) pointed out that the GGE confirms the understanding of both G, and GE interaction, which are the sources

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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 this study was to evaluate the GE interaction using AMMI and GGE-biplot analyses for grain yield and its related traits and detect stable small white common bean genotypes fitting for optimum environments of Guji zones as well as similar agro-ecologies in Ethiopia.

Materials and Methods

Plant Materials and Field Management

The genetic materials of the present investigation comprised 13 small white common bean genotypes along with 2 released varieties *viz*., Awash mitin and Awash-2 that were used as standard checks were evaluated at four locations for two years constituting seven environments. The experiments were conducted for consecutive two years of 2020/21 and 2021/22 main cropping seasons from April to July at potential common bean producing areas of Guji zones. Randomized Complete Block Design (RCBD) with three replications was used across all locations. Each genotypes were sown in 6 rows; 3m length with 40cm inter-row spacing and 10cm between plants. Fertilizer rates of 121 NPS Kg ha^{-1} was applied at planting time. All pertinent management practices were carried out at all sites following standard recommendation. Harvesting was done by hand. The central two rows were used as net plot for data collection including yield.

Data Collected

Data were collected based on plot and plant bases for phenological parameters such as: days to flowering and days to maturity growth: plant height(cm), lodging (%); diseases reaction: diseases severity score (1-9 scale); yield related traits and yields: number of pods per plant, number of seeds per pod, 1000 seed weight (g) and seed yield (kg/plot) and converted into per hectare unit. The data's were managed and analyzed for the evaluated parameters and recommended the candidate varieties.

Statistical Analysis

The homogeneity of error variance was tested using the F-max test method of Hartley (1950) prior to pooled analysis over locations. Different statistical software packages were used to analyze the data. The analysis of variance for each location and combined analysis of variance over locations were computed using the SAS program (SAS institute, 2011) versions 9.3. AMMI biplots were analyzed using GEA-R version 2.0 [5]. GenStat 18th edition (2012) was used to draw GGE biplots.

AMMI Analysis

The common bean managed data were subjected to combined analysis of variance and AMMI analysis, which is a combination of analysis of variance and multiplication effect analysis. Briefly, analysis of variance was used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and G × E deviations from the grand mean. Subsequently, multiplication effect analysis was used to partition G × E deviations into different Interaction Principal Component Axes (IPCA), which were tested for statistical significance through ANOVA. To determine the G × E interaction for yield parameters, AMMI and GGE bi-plot analyses were performed. The following AMMI model was used [10]:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{N} \lambda_k \alpha_{ik}\gamma_{jk} + \theta_{ij} + \varepsilon_{ij}$$

where, Y_{ij} = the yield of the ith genotype in the jth environment, μ = the grand mean, G_i and E_j = the genotype and environment deviations from the grand mean respectively, λ_k = the eigen value for IPCA analysis axis k, α_{ik} and γ_{jk} = the genotype and environment principal component scores for axis k, the summation handles N number of principal components retained in the model, θ_{ij} = the AMMI residual and ε_{ij} = the error [27]. The Degrees of Freedom (DF) for the IPCA axes were calculated according to Zobel *et al*. (1988) with the following formula.

DF = G + E − 1 − 2n where, G = the number of genotypes E = the number of environments n = the nth axis of IPCA.

In order to show a clear insight of the interaction and the general pattern of adaptation of varieties, a biplot of varieties and environments (Kempton, 1984) were done. In the biplots the first IPCA was used as the ordinate (Y-axis) and the main effects (mean of the genotype and environment) represent abscissa (X-axis). Similarly, the IPCA1 as abscissa and IPCA2 as ordinate was used to further explore stability.

AMMI Stability Value

AMMI stability value was calculated in the excel spread sheet using the formula developed by Purchase *et al.* (1997).

$$ASV = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1\ Score)\right]^2 + [IPCA2\ Score]^2}$$

where, $\frac{SSIPCA1}{SSIPCA2}$ is the weight given to the IPCA value by dividing the IPCA1 sum of squares by the IPCA2 sum of square.

Genotype Selection Index

Genotype selection index was also calculated by the formula suggested by [8]. Here it is calculated by taking the rank of mean grain yield of genotypes (RY$_i$) across environments and rank of AMMI Stability Value (RASV$_i$) a selection index GSI was calculated for each genotype which incorporate both mean grain yield and stability index in a single criteria (GSI$_i$) as:

$$GSI_i = RASV_i + RY_i$$

where, RASV is the rank value of genotypes for AMMI stability value and RY is the rank value of genotypes for grain yield. A genotype with the least GSI is considered as the most stable [8].

GGE Biplot Analysis

The most recent method, GGE biplot model, provides breeders a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments [6,24].

To analysis stability and identify superior genotype across environment, GGE bi-plot analysis were conducted. GGE biplot best identifies G x E interaction pattern of data and clearly shows which variety performs best in which environment. The GGE biplot model of *t* principal components is given as follows:

$$\overline{Y}ij - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik}\gamma_{jk} + \varepsilon_{ij}$$

where; $\overline{Y}ij$ = the performance of genotype i in environment j, μ = the grand mean, β_j = the main effect of environment j, k = the number of Principal Components (PC); λ_k = singular value of the kth PC; and α_{ik} and γ_{jk} = the scores of ith genotype and jth environment, respectively for PC $_k$; ε_{ij} = the residual associated with genotype i in the environment j. Usually only the first two PCs are used especially if they account for the major portion of the G x E interaction.

Table 1: Combined ANOVA for grain yield of 13 genotypes tested across 7 locations.

Source of Variation	Degree of Freedom	Sum of Square	Mean Square	SS (%)	P-value
Total	272	166.1590	0.611		
Blocks (Envts)	14	16.2100	1.158**		
Environment (E)	6	56.7027	9.4504**	34.12	<.001
Genotype (G)	12	14.8156	1.2346**	8.92	<.001
GxE Interaction	72	26.9104	0.3738*	16.20	0.015
Residual	180	67.3969	0.3744		
CV (%)			27.4		

Table 2: Analysis of variance for grain yield using AMMI model.

Source	DF	SS	MS	Total variation explained To SS (%)	GxE explained (%)	GxE cumulative (%)	P- value
Genotypes (G)	12	14.82	1.235**	8.92			<0.001
Environments (E)	6	56.70	9.450**	34.12			<0.001
Blocks (Envts)	14	16.21	1.158**	9.76			<0.001
Interactions	72	26.91	0.374*	16.20			0.0151
IPCA 1	17	12.30	0.723**		45.71		0.0029
IPCA 2	15	6.05	0.403ns		22.48	68.19	0.1983
Residuals	40	8.57	0.214				0.9087
Total	272	166.16	0.611				
Error	168	51.52	0.307				
CV (%)			27.4				

*,**: Significant at 0.05 and 0.01 probability levels, respectively; DF: Degrees of Freedom, SS: Sum of Square, MS: Means of Square, C.V: Coefficient of Variation, R^2: Coefficient of Determination

Results and Discussion

Analysis of Variance and Mean Performances

The result of pooled analysis of variance revealed that highly significant differences (p<0.001) for days to flowering, days to phenological maturity, plant height, number of seeds, hundred seed weight and grain yields while non-significant was recorded for number of primary branches and number of pods. The highest combined mean performance of grain yield was recorded for the genotypes genotype#285 (2.618 tons ha^{-1}) followed genotype#111 (2.503 tons ha^{-1}) whereas the lowest mean was obtained from the genotype#288 (1.787 tons ha^{-1}). In addition, the manifestation of diseases on plant parts was generally low indicating the possibility of moderately resistant to common bean diseases such as common bean blight, angular leaf spot and anthracnose (Table 3).

Additive Main Effect and Multiplicative Interaction (AMMI)

The additive main effect and multiplicative interaction (AMMI) analysis of variance revealed highly significant effects (p<0.01) among tested genotypes, investigated environments and genotype-by-environment (G x E) interaction for grain yield (Table 2). The ANOVA using the AMMI model the contribution of genotype, environment and G x E interaction about 8.92%, 34.12% and 16.20% respectively, to the total variation observed in common bean yield (Table 2). This agrees with the findings of previous studies, [1,12,21]. The environment gave higher sum of square for the response variable grain yield. Likewise, Yan and Kang (2003) in which environment showed predominant effect on varietal performance. Partitioning the G x E interaction by AMMI analysis showed that the first Principal Component Axis (IPCA1) was the only significant one; the first IPCA explained 45.71% and the second IPCA additionally explained

Table 3: Mean grain yield and reaction to diseases of small white common bean genotypes over locations and year.

Genotypes	Grain yield (tons ha^{-1})							Overall means	(%) Yield advantages	Diseases severity (1-9 scale)		
	2021				2022					CBB	ALS	Anthrac nose
	Adola-woyu	Kiltu-sorsa	Gobicha	Wodera	Adola-woyu	Kiltu-sorsa	Gobicha					
G-66	1.323a-c	1.604	2.417	2.062	2.307	2.872	1.875	2.066c-f		2	3	2
G-111	1.35a-c	2.431	2.306	2.632	2.568	3.253	2.944	2.503ab	22.34	2	3	2
G-238	1.865a	2.583	2.042	1.896	1.901	3.021	2.559	2.267a-e		4	5	3
G-241	0.990bc	1.951	1.750	2.396	2.724	2.726	2.677	2.173b-e		5	4	3
G-283	1.646a-c	1.812	1.750	2.618	2.365	2.892	2.902	2.284a-e		4	3	3
G-285	1.906a	2.806	2.528	2.319	2.245	3.465	3.056	2.618a	27.96	3	3	2
G-177	1.333a-c	1.208	1.625	2.014	2.344	2.844	2.138	1.929ef		5	4	2
G-288	0.885c	1.333	2.194	2.049	1.615	1.948	2.484	1.787f		4	5	2
G317	1.812ab	2.701	2.292	1.833	1.885	3.531	2.794	2.407a-d		4	2	3
G-331	2.083a	2.486	2.361	1.889	2.010	3.559	2.578	2.424a-c		4	4	2
G-341	1.677a-c	1.778	1.972	2.319	2.125	3.934	3.075	2.412a-d		4	3	3
Awash-2	1.354a-c	2.049	1.778	2.653	1.823	2.219	2.653	2.075c-f		5	3	2
Awash mitin	0.938c	1.257	1.944	2.222	2.146	2.938	2.878	2.046d-f		5	3	2
Mean	1.477	2.000	2.074	2.223	2.158	3.015	2.663	2.230		4	3	2
P-value	0.032	0.255	0.094	0.608	0.593	0.173	0.473	0.492				
LSD (5%)	0.735	1.407	0.632	0.929	0.980	1.281	1.019	0.986		0.577	0.545	0.620
CV (%)	29.5	21.8	18.1	24.8	27.0	25.2	22.7	27.4		23.4	18.9	17.3

22.48%, the first two IPCA totally 68.19% of the G x E interaction variation. Haynes et al. (1998); Yan and Kang (2003) reported that if the percentage of the first two principal components would explain more than 50% of the total variation, the biplot would be a good alternative to study the genotype by environment interaction.

Additive Main Effect and Multiplicative Interaction (AMMI 2) Bi-plot Analysis

The AMMI 2 bi-plot analysis was conducted by plotting IPCA 1 scores against IPCA 2 scores for genotypes and environments (Figure 1). The performance of a genotype in the environment is considered better than the average performance in that environment if the angle between its vector and the environment is less than 90^0 (acute angle); near average if the angle is 90^0 (right angle) and below average if the angle is greater than 90^0 (obtuse angle) [6]. The AMMI 2 bi-plot analyses of grain yield of the 13 genotypes evaluated in seven locations are shown in Figure 1. Genotypes G-111, G-66 and G-285 had broad adaptability across the environments as they were located closer to the center of the bi-plot. Genotypes Awash-2, G-317, G-288, G-177, G-331 and G-341 are placed furthest from the point of origin, showing specific adaptation to the environments within their proximity on the bi-plot. Moreover, genotypes G-285, G-238 and G-317 had above-average yields and were located on the acute angle of PC1. Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments on the same side. Kiltu-sorsa and Wodera locations were considered highly discriminating and had similar discriminating ability of the site since they had longer vectors.
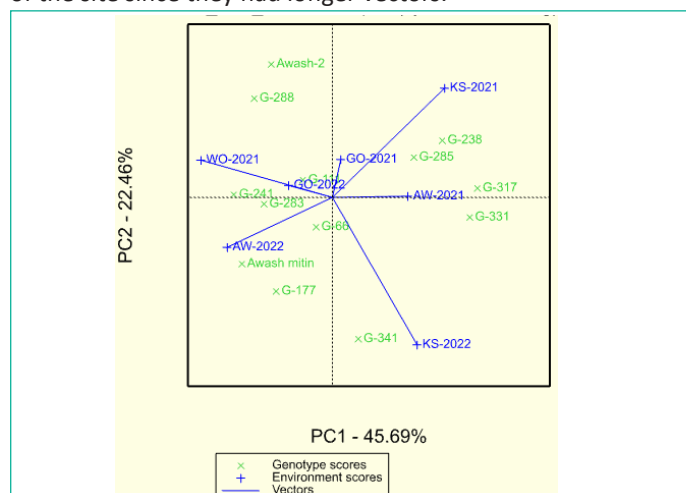

Figure 1: AMMI 2 biplot for IPCA 1 against IPCA 2 scores for 13 genotypes and seven environments.
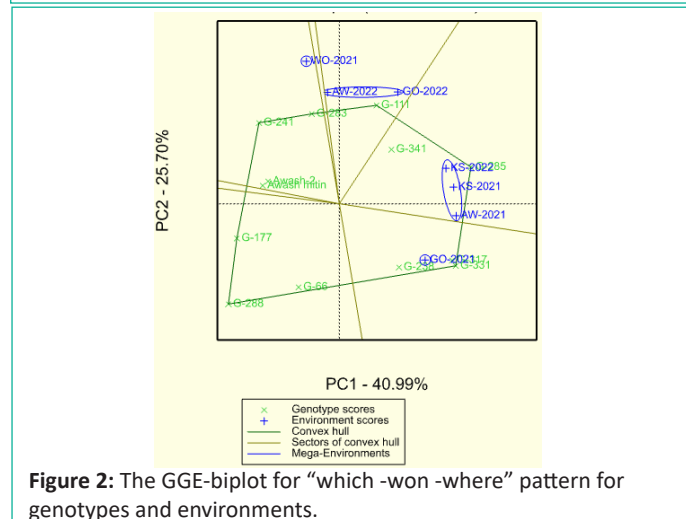

Figure 2: The GGE-biplot for "which -won -where" pattern for genotypes and environments.

AMMI Stability Value (ASV)

AMMI stability values revealed variations in yield stability among the 13 genotypes (Table 5). In the ASV method, a genotype with high pooled mean, small IPCA1score and the least ASV score is the most stable. Accordingly, G-66 and G-111 was the only genotype that was highly stable, with ASV value of 0.2045 and 0.2873, respectively. However, G-66 showed lower yield performance. Therefore, stable with higher yield genotypes can be promoted for further evaluation and for wider production. G-317, G-331 and G-238 were among the least stable genotypes; other genotypes had showed intermediate stability.

The AMMI model does not make provision for a quantitative stability measure. Such a measure is essential in order to quantify and rank genotypes according to their yield stability. In fact, ASV is the distance from zero in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributed more to G × E interaction sum of square, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total G × E interaction sum of squares.

Genotype Selection Index (GSI)

Genotype Selection Index (GSI) was utilized to further identify stable genotypes with better yield performance. Generally, genotypes G-111 and G-285 were considered as the two stable genotypes with high grain yield.

GGE Biplot Stability Analysis

GGE biplot was the best way to visualize the interaction patterns between genotypes and environments to effectively interpret a biplot [24]. In this study, the 'which won where' feature of the biplot identified the winning genotypes. The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 40.99% and 25.70% of GGE sum of squares, respectively (Figure 3).

Mega-Environments Analysis

The polygon view of a GGE biplot clearly displays the which-won-where pattern, and hence it arranged the genotypes in such a way that some of them were on the vertices while the rest were inside the polygon. The genotype located at the vertex of the sector was considered the best-performing genotype in the Mega-Environments (MGE). Genotypes G-285, G-111, G-317 and G-241 were the vertex (winning genotypes) in the sector where environments located in the MGE sector.

Another interesting feature of the GGE biplot is the identification of mega-environments. In the bi-plot, different MGEs were grouped into sectors. Environments within the same MGE were assumed to have a similar effect on genotype performance and were considered a homogeneous group. Similarly, genotypes within the same MGE were assumed to have a similar response to the environments located in the MGE sector.

In genotype focusing scaled comparison of GGE biplot, a genotype located nearest to the central concentric circles is both high grain yielding and most stable. The GGE bi-plot analysis for grain yield of faba bean genotypes based on genotype-focused scaling comparison is presented in Figure 3. An ideal genotype is defined as the genotype having the greatest PC1 score (high mean performance) and with zero G x E interaction, as represented by an arrow pointing to it (Figure 3). Figure 3 depicts that genotype G-285, which fell in the first concentric

Table 4: Combined mean performances for agronomic traits over locations and year.

| Genotypes	Days to		Plant height (cm)	Number of primary branches	Number of pods per plant	Number of seeds per pod	Thousand seed weight (g)
	Flowering (days)	Maturity (days)					
G-66	39.95[a-c]	90.95 [ab]	66.19[bc]	1.27	19.51	4.41[d]	166.5 [bc]
G-111	38.10[c]	88.71[d]	65.60[bc]	1.24	18.66	4.92[a-d]	163.7 [c]
G-238	38.86[bc]	89.34 [cd]	61.62[cd]	1.20	19.38	5.23[ab]	173.3 [bc]
G-241	40.14[a-c]	90.10 [bc]	72.55[ab]	1.12	16.13	4.89[b-d]	180.3 [ab]
G-283	38.05[c]	88.14 [d]	70.92[b]	1.16	16.31	5.11[a-c]	177.1 [a-c]
G-285	38.57[bc]	90.86 [ab]	79.79[a]	1.16	16.34	5.46[a]	176.3 [a-c]
G-177	38.48[bc]	88.62 [d]	65.53[bc]	1.15	15.90	4.88[b-d]	168.6 [bc]
G-288	40.90[ab]	91.86 [a]	71.57[b]	1.15	14.27	5.01[a-c]	188.1 [a]
G-317	39.81[a-c]	89.81 [b-d]	51.54[e]	1.21	18.32	4.62[cd]	187.7 [a]
G-331	38.90[bc]	89.52 [d]	67.55[bc]	1.19	19.11	4.93[a-d]	174.3 [bc]
G-341	39.14[a-c]	88.51[d]	64.99[b-d]	1.15	18.67	4.79[b-d]	163.5 [c]
Awash-2	38.95[a-c]	89.86 [b-d]	57.35[de]	1.24	15.04	4.72[b-d]	172.0 [bc]
Awash mitin	41.48[a]	91.05 [ab]	69.04[bc]	1.31	15.84	4.82[b-d]	167.9 [bc]
MEANS	39.33	89.80	66.48	1.20	17.19	4.91	173.8
LSD(5%)	2.202	2.392	7.398	0.174	3.779	0.479	25.98
CV(%)	9.2	4.4	18.3	23.9	16.2	16.1	24.6
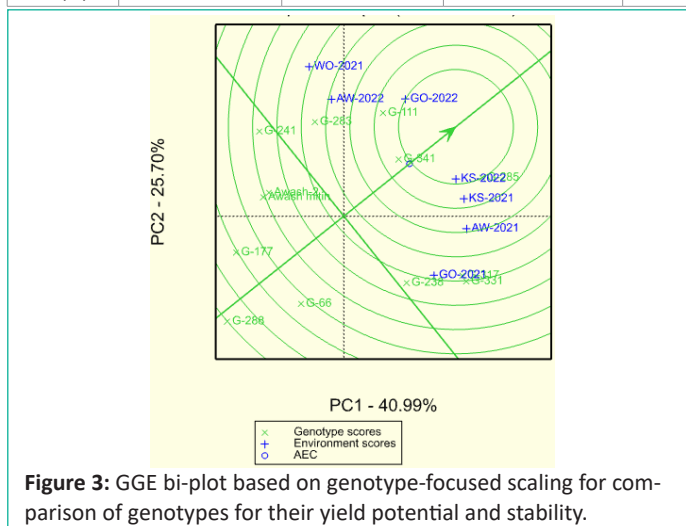
Figure 3: GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability.

circle, was the ideal genotype in terms of higher yielding ability and stable. Genotypes G-111 and G-341 were located closer to the ideal genotype, it becomes more desirable.

Genotype Yield and Stability Performance

The Average-Environment Axis (AEA) or Average-Tester-Axis (ATA) is the line that passes through the average environment and the biplot origin [25]. The average environment coordinates (AEC X-axis) or the performance line passes through the biplot origin with an arrow indicating the positive end of the axis (Figure 4). The AEC Y-axis or the stability axis passes through the plot origin with double arrow head and is perpendicular to the AEC X-axis. The mean performance and stability of these 13 genotypes in 7 locations showed genotypes G-285 and G-111 were high yielding and stable genotype.

Environment Discriminating Ability and Representativeness

Ideal test environment should be highly discriminative of the genotypes and representative of the mega-environment [23]. The positive correlation existing between the genotypes and environments indicated that these genotypes possessed a specific adaptation. However, when test environment markers fall close to the bi-plot origin because of their short vectors, it means that all genotypes performed similarly in those environments. This provides little or no information about the genotype differences, since the genotypes show broad adaptability.
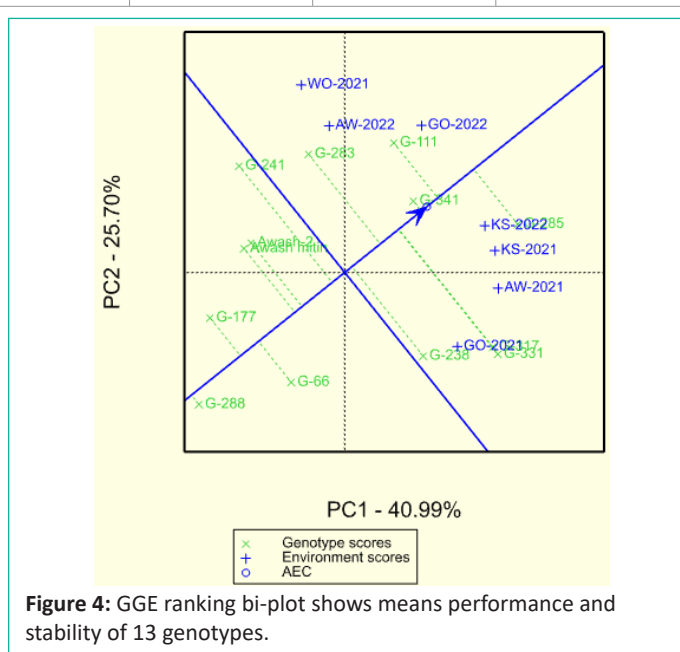

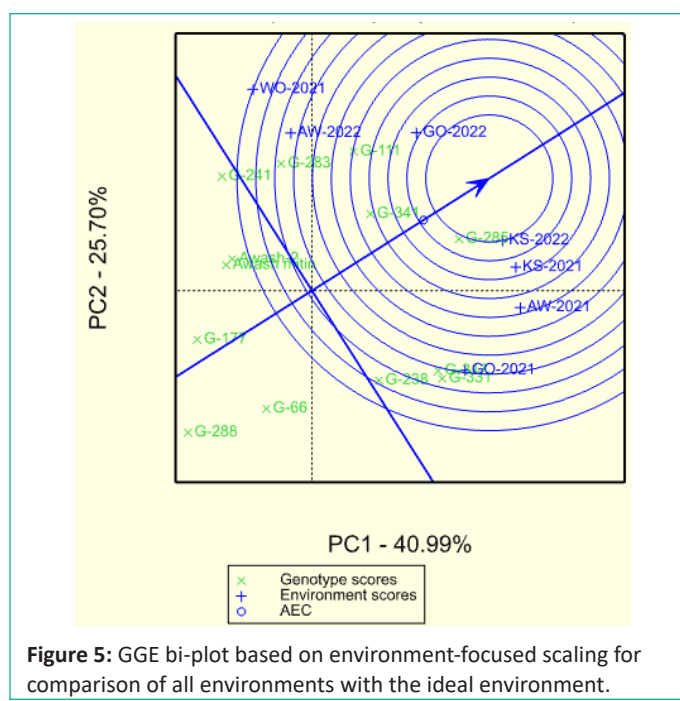**Figure 4:** GGE ranking bi-plot shows means performance and stability of 13 genotypes.

Figure 5: GGE bi-plot based on environment-focused scaling for comparison of all environments with the ideal environment.

Table 5: The grain yield, AMMI stability value (ASV), Genotype selection index (GSI)and principal component axis (IPCA).

Genotypes	Yield tons ha^{-1}	Rank	IPCA1 score	IPCA2 Score	ASV	Rank	GSI	Rank	Overall Rank
G-66	2.066	11	0.07517	-0.13587	0.2045	1	12	4	4
G-111	2.503	2	0.13579	0.07963	0.2873	2	4	1	1
G-238	2.267	7	-0.50434	0.26118	1.0581	11	18	7	7
G-241	2.173	8	0.45310	0.01255	0.9213	19	27	10	10
G-283	2.284	6	0.31403	-0.03035	0.6392	3	9	3	3
G-285	2.618	1	-0.37369	0.18370	0.7816	6	7	2	2
G-177	1.929	12	0.25841	-0.43121	0.6797	4	16	6	6
G-288	1.787	13	0.35928	0.45425	0.8602	8	21	9	9
G-317	2.407	5	-0.66559	0.04180	1.3538	13	18	7	7
G-331	2.424	3	-0.63056	-0.09153	1.2852	12	15	5	5
G-341	2.412	4	-0.11854	-0.64993	0.6932	5	9	3	3
Awash-2	2.075	9	0.28121	0.61121	0.8369	7	16	6	6
Awash mitin	2.046	10	0.41573	-0.30543	0.8987	9	19	8	8

In this case, breeders find it difficult to select high yielding and more stable genotypes. This study showed that Kiltu-sorsa had a high discriminating ability and representativeness for genotype evaluation.

Conclusion and Recommendation

Genotype by environment interaction and stability measuring trials helps to identify genotypes with both high performance and high stability. The study concluded the existence of a considerable degree of genotype by environment interaction for grain yield stability in small white common bean genotypes when tested under midland to low-altitudes of Southern Oromia in Guji zones. The G × E analysis enables identification of genotypes with narrow adaptation, which can significantly improve crop productivity in specific regions. Stable and high yielding genotypes were identified and selected based on their relative response to a respective locations.

As a result, two genotypes showed 27.96% and 22.34% grain yield advantage over the standard check, tolerant/resistant to major common bean diseases, revealed stable performances and also possessed other desirable agronomic characteristics. Considering simultaneously yield and stability, genotypes (G#285) and (G#111) were identified as the high yielding and suggesting their adaptation to a wide range of environments and recommended to be included in variety verification trial for eventual varietal release to the set of tested environments and similar agro-ecologies in Ethiopia.

Author Statements

Acknowledgements

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