

## Research Article

# Genotype by Environment Interaction and Grain Yield Stability Analysis of Small Red Common Bean (*Phaseolus vulgaris* L.) Genotypes in the Southern Parts of Oromia Region, Ethiopia

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## Abstract

The selection of stable genotypes that interact less with the varying environment in which they are to be grown is required. This study was in order to identify stable small red common bean genotypes with high grain yield. The field experiments were conducted with 15 genotypes for two years from 2022 to 2023 at three locations in the midlands of Guji zone, Southern Oromia. The genotypes were laid out in randomized complete design with four replications in each environment. The analysis of variance using Additive Main effect and Multiplicative Interaction (AMMI) model revealed highly significant ( $P \leq 0.01$ ) variations among genotypes, environments, G x E interaction and Interaction Principal Component Analysis (IPCA1) but insignificant variations among the remaining IPCAs. The ASV, GSI and GGE-biplot are importantly confirmed stable genotypes across environments. Accordingly, genotypes G8(G-1569) and G11(G-1368) were identified for their high yielding and found stable performance, tolerant to major bean diseases and possess other important characteristics. Therefore, these two genotypes were identified as candidate varieties to be verified for final release.

**Keywords:** AMMI; Interactions effect; *Phaseolus vulgaris*; Stability

## Introduction

Common bean (*Phaseolus vulgaris* L.) is a diploid ( $2n=2x=22$ ) annual plant that belongs to the *Fabaceae* family in the genus *Phaseolus*, which has about 50 species globally and is joined by two other species (lima bean, *Phaseolus lunatus* and scarlet runner bean, *Phaseolus coccineus*) in Ethiopia. This crop is also called kidney bean, haricot bean, French bean and field bean. It is known by various names in Ethiopian languages, the commonest of which is "BOLOQE". A useful plant species or variety that has so many vernacular names usually an indicate importance, wide usage and popularity. Nutritionally, common bean contains high protein content and micronutrients (iron and folic acid, dietary fiber and complex carbohydrates) and it has been described as a pulse crop with high nutritional quality. For the low-income segment of the population, it plays a strategic role in alleviating malnutrition and for other health related functions.

Common bean was initially introduced from the New World (South and Central America) to Europe and Africa in the sixteenth century by returning Portuguese and Spanish explorers. Since that time, many different forms have been developed through selective breeding by local farmers. Furthermore, since the 1980s, efforts to improve farm-level productivity resulted in continuous introduction of new germplasm sources to African farming systems from different parts of the world through national bean-breeding programs. The existence of both the Andean and Mesoamerican gene pools in Africa is documented by various authors including Martin & Adams most

likely as a result of the original introductions and subsequent imports of novel germplasm to Africa. As a consequence of this, and given the secondary diversification within Africa, the continent has high diversity of landraces of *Phaseolus vulgaris* and Ethiopia is one among countries with high landrace diversity in this species.

Common bean is an important pulse crop in Guji zone, especially red beans are mostly preferred for local market and home consumption in the southern regions. However, lack of improved high yielder and resistant variety is one of the major production constraints contributing for low production and productivity of the crop in the zones. Since the National and Regional Bean Research Programs have been released several varieties. Hence a given variety has performed well for specific period of time and reduces its production potential after a while becoming susceptible to diseases. 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) [1,2]. Yan and Tinker, (2006) pointed out that the GGE confirms the understanding of both G, and GE interaction, which are the sources of variation related to

genotype assessment. They must also be considered simultaneously to assess both the genotype and the environment. Therefore, the main objective of 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

### Genetic Materials and Experimental Design

The genetic materials of the present investigation comprised 15 small red common bean genotypes along with two released varieties viz., SCR-26 and SER-119 as standard checks and local cultivar were evaluated at three locations for two years constituting six environments. The experiments were conducted for consecutive two years of 2022 and 2023 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<sup>-1</sup> 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 four rows were used as net plot for data collection including yield.

### Data Collected

Data were collected based on plot and plant bases for days to flowering and days to maturity plant height(cm), lodging (%) diseases severity score (1-9 scale); yield related traits and yields like 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 [7] versions 9.3. AMMI biplots were analyzed using GEA-R version 2.0 [4]. 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 [8]:

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

where,  $Y_{ij}$  = the yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $\mu$  = the grand mean,  $G_i$  and  $E_j$  = the genotype and environment deviations from the grand mean respectively,  $\lambda_k$  = the eigen value for IPCA analysis axis  $k$ ,  $\alpha_{ik}$  and  $\gamma_{jk}$  = the genotype and environment principal component scores for axis  $k$ , the summation handles  $N$  number of principal components retained in the model,  $\theta_{ij}$  = the AMMI residual and  $\epsilon_{ij}$  = the error [9]. 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  $n^{\text{th}}$  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).

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

where,  $\frac{SS_{IPCA1}}{SS_{IPCA2}}$  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 [11]. 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 criterion (GSI<sub>i</sub>) 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 [11].

### 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 [12,13].

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

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

where;  $\bar{Y}_{ij}$  = the performance of genotype  $i$  in environment  $j$ ,  $\mu$  = the grand mean,  $\beta_j$  = the main effect of environment  $j$ ,  $k$  = the number

of principal components (PC);  $\lambda_k$  = singular value of the  $k^{th}$  PC; and  $\alpha_{jk}$  and  $\gamma_{jk}$  = the scores of  $i^{th}$  genotype and  $j^{th}$  environment, respectively for PC  $k$ ;  $\epsilon_{ij}$  = 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.

## Result and Discussions

### Analysis of Variance and Mean Performances

The result of combined analysis of variance showed highly significant differences for genotypes, environment and G x E interaction indicating the effect of environment in the G x E interaction, genetic variability and possibility of selection for stable genotypes. Mean comparison for the tested genotypes indicated that maximum grain yield was obtained from G8 (2.814 tons/ha), G11 (2.771 tons/ha) and G4 (2.739 tons/ha) whereas the least mean grain yield was obtained from G3 (1.936 tons/ha).

### Evaluation of Genotypes to Diseases

In terms of diseases reaction, the manifestation of common bacterial blight, angular leaf spot and bean leaf rust on plant parts were generally low for genotypes G8, G11 and G4, indicating (2 to 3 score), the possibility of tolerant to the diseases.

### Performance of Agronomic Traits

The genotypes revealed highly significant difference ( $p < 0.001$ ) for days to flowering, days to maturity, plant height, number of pods per plant, number of seeds and thousand seed weight across the tested environments except number of primary branches, which showed insignificant response.

**Table 1:** Combined ANOVA for grain yield of 15 genotypes tested across six environments over two years.

Source of variation	Degree of freedom	Sum of Square	Mean Square	SS(%)	P-value
Total	269	159.408			
Replication	2	3.1799	1.59		
Environments (E)	5	23.722	4.74**	14.88	<.001
Genotypes (G)	14	15.126	1.08 **	9.49	0.002
G x E Interaction	70	41.668	0.60*	26.14	0.040
Residual	178	75.713	0.43		
CV (%)	26.7				

**Table 2:** Mean grain yield (tons/ha) and reaction to diseases of small red common bean genotypes over locations and years.

Code	Genotypes	Test Locations						Overall means	Yield Advan tage(%)	Diseases severity (1-9 scale)		
		2022			2023					CBB	ALS	Anthr acnose
		Adola-woyu	Kiltu-sorsa	Dugda-goromsa	Adola-woyu	Kiltu-sorsa	Dugda-goromsa					
G1	G-941	2.029	2.396	2.025a-c	3.010ab	2.352b-d	1.654cd	2.211ac		3	3	2
G2	G-1318	2.150	2.317	2.117a-c	3.359ab	2.967a-c	2.337a-d	2.541ab		3	5	2
G3	G-819	2.138	2.500	1.467c	2.266d	2.192b-d	1.154d	1.936d		3	5	3
G4	G-609	2.371	2.808	2.742a	2.969a-c	2.540a-d	3.004a	2.739a	11.39	3	3	2
G5	G-973	2.479	2.200	2.008a-c	2.854a-c	3.194a-c	1.971b-d	2.434ab		4	5	3
G6	G-847	1.775	2.554	2.029a-c	2.859a-c	2.248b-d	2.337a-d	2.301ab		3	4	2
G7	G-1389	2.221	2.233	2.429ab	2.812a-c	4.017a	1.996b-d	2.618a		3	3	2
G8	G-1569	2.321	2.500	2.300ab	3.758ab	3.274a-c	2.729ab	2.814a	14.44	2	3	1
G9	G-1348	2.229	2.625	2.396ab	2.833a-c	1.761cd	2.462a-c	2.384ab		4	4	3
G10	G-1068	2.163	2.454	2.038a-c	3.417ab	20.36b-d	2.237a-d	2.391ab		3	4	2
G11	G-1368	2.121	2.367	2.192a-c	3.961a	3.646ab	2.438a-c	2.771a	12.69	3	4	2
G12	G-1359	2.525	2.575	2.488ab	2.470bc	3.131a-c	2.837ab	2.621a		3	3	2
	SCR-26	1.946	2.404	2.383ab	2.349cd	2.448a-d	1.754cd	2.247ac		4	5	2
	SER-119	2.567	2.829	1.829bc	3.656ab	2.028b-d	1.646cd	2.459ab		3	4	2
	Local Cultivar	2.317	2.633	2.108a-c	2.411bc	1.150d	2.167bc	2.198cd		4	5	3
	Mean	2.223	2.493	2.170	2.999	2.599	2.182	2.444		3	4	2
	LSD (5%)	0.678	0.956	0.7376	1.3495	1.4314	1.5965	1.1705				
	CV (%)	18.2	22.9	20.3	26.9	22.9	23.8	26.7				

### Bean Seed Appearance Characteristics

Seed shape, brilliance and seed weight were considered to determine commercial value for marketing beans. The candidate varieties (G8 and G11) had kidney shape, brilliant red seeded and had good thousand seed weight of (291.4g and 277.7g), respectively.

### Additive Main Effect and Multiplicative Interaction (AMMI)

The AMMI ANOVA for grain yield revealed highly significant ( $P < 0.001$ ) differences for genotype and environment and significant difference ( $P < 0.05$ ) for interaction effects. Environment captured 14.88% of the total variation, whereas genotype and G x E interaction contributed 9.49% and 26.14%, respectively. A large total variation due to G x E interaction indicated the performance of genotypes were different at different testing environments, the GxE interaction was crossover type. This study suggests the possible presence of different mega-environments with different winner genotypes [18]. Similar result on soybean in Ethiopia was revealed by Atnaf et al. (2013). Existence of significant and large G x E interaction on other crops in Ethiopia and other African countries has been revealed [14-17]. The significant G x E interaction effect was decomposed into PCA.

### AMMI Stability Value (ASV)

In ASV, the genotypes with least ASV score are the most stable where as those which have highest ASV are considered as unstable [10]. However, stability needs to be considered in combination with yield [11]. Accordingly, genotype (G8 and G11) was considered as the most stable across all environments. In contrast, local cultivar, SCR-26 and G7 have large ASV and these genotypes are unstable.

### Genotype Selection Index (GSI)

Genotype selection index was utilized to further identify stable genotypes with better yield performance. In this regard, genotypes G8, G11 and G4 were considered as the two most stable genotypes with high grain yield.

### GGE bi-plot Analysis

#### 'Which-Won-Where' Patterns of Genotypes

The GGE biplot displays the Genotypic main effect (G) and

**Table 3:** Combined mean of agronomic traits of small red common bean genotypes during 2022 to 2023 cropping season.

Genotypes	Days to		Plant height (cm)	Number of primary branches	Number of pods per plant	Number of seeds per pod	1000 seed weight (g)
	Flowering (days)	Maturity (days)					
G1	44.67ab	96.39a-d	89.80bc	1.597	14.46a-c	5.169ab	264.1c-e
G2	40.67e	92.67d	81.54cd	1.269	15.77a-c	4.939b-d	263.8c-e
G3	45.67a	98.83ab	73.78d	1.296	11.81c	4.987a-d	254.5e
G4	44.89ab	100.11ab	98.46b	1.617	17.46ab	5.489a	261.8de
G5	42.67a-c	96.45a-d	92.75bc	1.342	14.28a-c	4.788b-d	268.2c-e
G6	45.67a	99.95ab	70.31d	1.426	14.46a-c	5.133a-c	262.9c-e
G7	45.33ab	97.83a-c	69.63d	1.399	15.09a-c	4.528d	263.7c-e
G8	41.89a-d	95.61b-d	78.47cd	1.324	15.08a-c	4.571c-d	291.4ab
G9	44.44ab	99.17ab	69.56d	1.407	13.57a-c	4.909b-d	304.5a
G10	41.11a-e	93.45cd	80.51cd	1.351	17.94a	807b-d	264.8c-e
G11	45.78a	99.56ab	70.59d	1.316	12.50c	5.109a-c	277.7b-d
G12	45.11ab	98.22a-c	78.46cd	1.501	14.83a-c	4.728b-d	284.5a-c
SCR-26	42.22a-d	96.17a-d	81.89cd	1.232	13.32bc	4.877b-d	297.6ab
SER-119	44.11a-c	96.34a-d	67.27d	1.342	13.54a-c	5.096a-c	299.3a
Local Cultivar	45.66a	101.17a	112.17a	1.287	15.09a-c	5.087a-c	261.1de
MEANS	43.85	97.46	81.01	1.38	14.61	4.95	274.9
LSD (5%)	3.988	7.311	22.923	0.450	6.472	0.811	32.650
CV (%)	9.7	6.6	14.9	28.6	18.9	14.4	10.4

genotype by Environment (G x E) interaction of a genotype by environment data set [3]. The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 34.21% and 26.53% of GGE sum of squares, respectively (Figure 1). The genotypes located at the vertex of the polygon performed either best-performance or poorest (bad performance) in the Mega-Environments (MGE). Genotypes G4, G8, G12 and G11 were the vertex (winning genotypes) in the sector where environments located in the MGE sector. The biplot analysis presented three mega-environments.

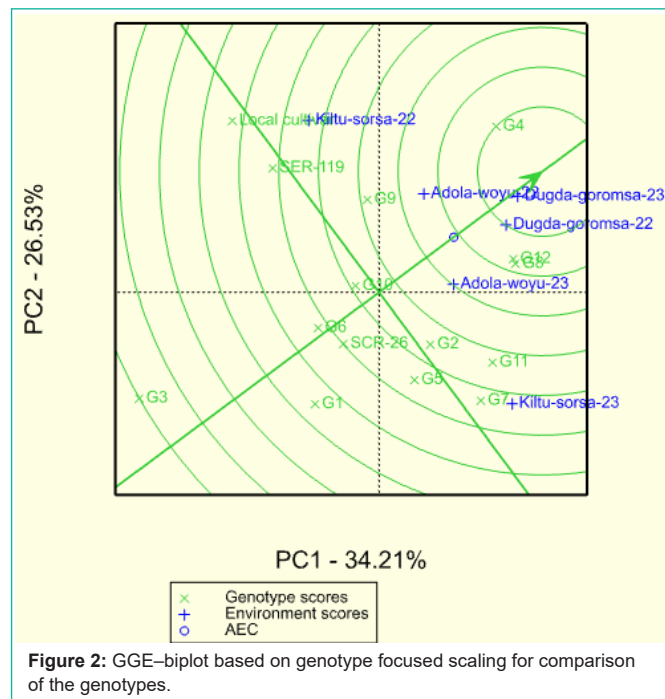
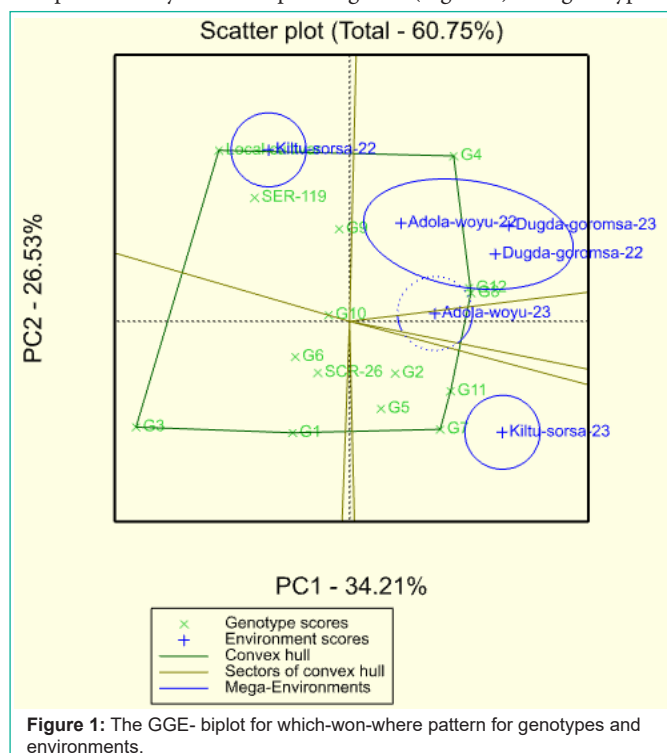
**Evaluation of Genotypes Relative to Ideal Genotype**

The GGE bi-plot analysis for grain yield of faba bean varieties based on genotype-focused scaling comparison is presented in Figure 1. 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 1). If a genotype is

located closer to the ideal genotype, it becomes more desirable than other genotypes which are located far away from the ideal genotype. Thus, starting from the middle of concentric circle pointed with arrow concentric circles were drawn to help visualize the distance between genotypes and the ideal genotype [3]. Because the units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype focused scaling (Figure 2). The ideal genotype can be used as a benchmark for selection. Genotype G4, which fell into the centre of concentric circles, was the ideal genotype in terms of higher yielding ability and stable. But the genotype was not selected because of unable to uniform seed color and haven't good morphological character (semi-climb). In addition, G8, G12 and G11 were located on the next consecutive concentric circle, they were regarded as desirable genotypes. G8 and G11 can be recommended for wider production Genotypes those very distant from the first concentric circle;(G3) was undesirable.

**Mean Performance and Stability of Genotypes**

A genotype which has shorter absolute length of projection in



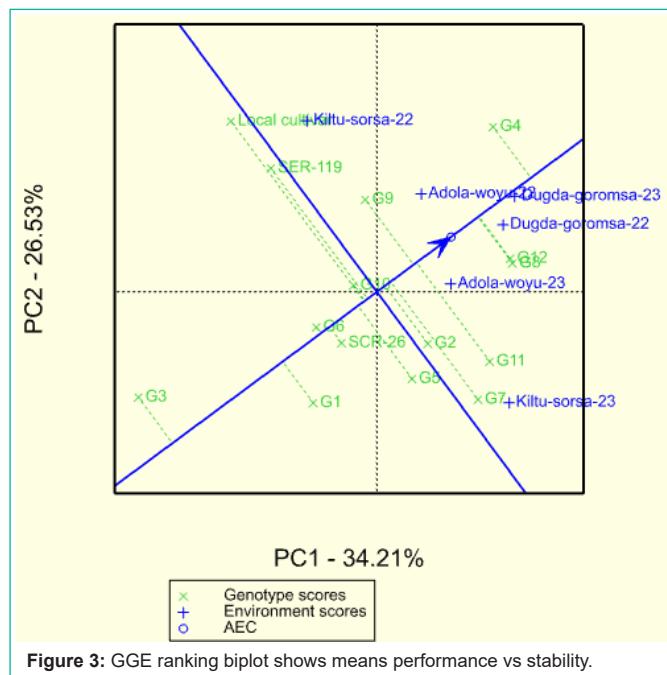


Figure 3: GGE ranking biplot shows means performance vs stability.

Table 4: Analysis of variance for grain yield using AMMI model.

Source of variation	Df	SS	MS	% Explained			P-value
				Total variation	G x E	G x E cumulative	
Total	269	159.41	0.593				
Blocks	12	17.52	1.460				0.0784
Environments (Env'ts)	5	23.72	4.744**	14.88			<0.001
Genotypes (G)	14	15.13	1.080**	9.49			0.0022
G x E	70	41.67	0.595*	26.14			0.0360
Interaction	18	22.63	1.257**		54.31	78.55	<0.001
IPCA1	16	10.10	0.631		24.24		0.1031
IPCA2	36	8.94	0.248		21.45		0.9676
Residuals	168	70.50	0.420				

\*, \*\*: 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<sup>2</sup>: coefficient of determination

either of the two directions of AEC ordinate (located closer to AEC), represents a less tendency of G x E interaction, which means it is the most stable genotype across all environments. The mean performance and stability of these genotypes showed G4, G8, G12 and G11 were high yielding and stable genotypes.

Table 5: The grain yield, AMMI Stability Value (ASV), Genotype Selection Index (GSI) and Principal Component Axis (IPCA).

Genotypes	Yield (tons ha <sup>-1</sup> )	Rank	IPCA1 Score	IPCA2 Score	ASV	Rank	GSI	Rank	Overall Rank
G1	2.211	13	-0.02763	-0.19352	0.20318	1	14	6	6
G2	2.541	6	-0.58938	-0.44239	1.39269	13	19	9	9
G3	1.936	15	-0.30034	-0.20755	0.70422	8	23	11	11
G4	2.739	3	0.23570	0.40860	0.66772	7	10	3	3
G5	2.434	8	-0.41234	0.03969	0.92474	10	18	8	8
G6	2.301	11	0.15365	0.05572	0.34875	3	14	6	6
G7	2.618	5	-0.79075	0.25338	1.78978	14	19	9	9
G8	2.814	1	0.08635	-0.14988	0.24474	2	3	1	1
G9	2.384	10	0.50612	0.18781	1.14946	11	21	10	10
G10	2.391	9	0.25597	-0.30538	0.64976	6	15	7	7
G11	2.771	2	-0.24611	-0.14748	0.57081	5	7	2	2
G12	2.621	4	-0.22059	0.64969	0.81632	9	13	5	5
SCR-26	2.247	12	0.40403	-0.73181	1.16407	12	24	12	11
SER-119	2.459	7	0.03370	0.39795	0.40505	4	11	4	4
Local cultivar	2.198	14	0.91162	0.18516	2.05095	15	29	13	12

### Conclusion and Recommendation

In multi-environment trial, considering both the stability and mean grain yield is vital. The genotype-environment interaction reduces association between phenotypic and genotypic values and leads bias in the estimates of gene effect and combining ability for various characters sensitive to environmental fluctuation. Such traits are less amenable to selection. Both yield and stability of performance should be considered simultaneously to reduce the effect of GE interaction and to make selection of genotypes more precise and refined. The ASV, GSI and GGE-biplot are importantly confirmed stable genotypes across environments. Accordingly, genotype G8 and G11 showed the best performances and their adaptation to a wide range of environments. Therefore, genotypes G8(G-1569) and G11(G-1368) were identified for their high yielding and found stable performance, tolerant to major bean diseases and possess other characters were recommended for further VVT evaluation and possible release.

### Author Statements

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