

Agronomic Performance and Yield Stability of Large Red Bean Genotypes Using AMMI Model in Midlands of Bale Zone, South-Eastern Ethiopia

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Abstract: In order to identify the agronomic performance and yield stability of the large red bean genotypes, sixteen large red bean genotypes were evaluated in the midlands of bale zone at Goro, Ginir and Dellomena for two consecutive years 2016 and 2017 main cropping season. The genotypes were arranged in randomized complete block design with four replications having plot size of 6.4m² (4 rows at 40cm spacing and 4m long). The analysis of variance revealed that highly significant variation for environment, genotypes and year X Location, whereas GEI (Genotypes by Environment interaction) showed significant variation for mean grain yield. Of the total sum squares of variation observed, 38.33% was accounted for environment followed by genotypes 11.53% and GEI 4.51%. The significant effect of GE interaction reflected on the differential response of genotypes in various environments and demonstrated that GE interaction had remarkable effect on genotypic performance in different environments. The application of AMMI model for partitioning the GE interaction effects showed that only the first two terms of AMMI were significant. In the AMMI analysis, out of the total GEI variation observed, the first AMMI explained 78.28% of the variation whereas 21.72% was accounted for the AMMI2. A combination of high grain yield potential, stability parameter of regression coefficient of unity and minimum deviation mean squares from regression identifies G4 as moderately stable genotype with high grain yield deserved to be promoted for possible release as commercial variety for the midlands of Bale zone and similar agro-ecologies.

Keywords: AMMI, Common Bean, GEI, Stability, Variation

1. Introduction

Common bean (*Phaseolus vulgaris* L.) is a major grain legume consumed worldwide for its edible seeds and pods. It is a highly polymorphic warm-season, herbaceous annual. There are 2 plant types: erect herbaceous bushes, up to 20-60 cm high; and twining, climbing vines up to 2-5 m long [1, 21]. It has a taproot with many adventitious roots. The stems of bushy types are rather slender, pubescent and many-branched. In twinning types, the stems are prostrate for most of their length and rise toward the end [6]. The leaves, borne on long green petioles, are green or purple in color and trifoliate. Leaflets are 6-15 cm long and 3-11 cm broad. The inflorescences are axillary or terminal, 15-35 cm long

racemes. The flowers are arranged in pairs or solitary along the rachis, white to purple and typically papilionaceous [1 22]. Once pollinated, each flower gives rise to one pod. Pods are slender, green, yellow, black or purple in color, sometimes striped. They can be cylindrical or flat, straight or curved, 1-1.5 cm wide and up to 20 cm in length [22]. The pods may contain 4 to 12 seeds. The seeds are 0.5-2 cm long, kidney-shaped and highly variable in color depending on the variety: white, red, green, tan, purple, gray or black. It was domesticated independently in two centers of diversity, giving rise to two gene groups: Mesoamerican and Andean [3]. Differences between these groups can be checked in the morphology of the plant, seed size and type of phaseolin (reserve protein), among others. Andean lines have larger

seed (100 seed weight above 30 grams) while Mesoamerican lines have smaller seed size (100 seed weight under 30 grams) [11]. When breeding new cultivars, the main obstacles is the presence of the genotype by environment interaction (G x E). For the cultivation of common bean, numerous studies have shown the presence of such interaction, mainly for grain yield. Thus, one should seek alternatives to mitigate and/or take advantage from the interaction effects, including the use of methods for analysis of stability and adaptability, which provide detailed information about the behavior of cultivars, such as predictability and responsiveness to environmental variation [6]. Among the methods for studying stability, genotype recommendation index takes the combining concepts of both adaptability and stability into a single parameter [2 and 18]. Another methodology used in stability studies is the AMMI method (Additive Main Effects and Multiplicative Interactions) which allows a more detailed analysis of the G x E interaction [24]. AMMI model is a popular extension of ANOVA for studying GE interaction [9]. This method extracts genotype and environment main effects and uses interaction principal components (IPCs) to explain patterns in the GE interaction or residual matrix, which provides a multiplicative model [20]. Therefore, the present study focused in identifying high yielding, stable large red bean genotypes for possible releases in the midlands of Bale zone, southeastern Ethiopia.

2. Materials and Methods

In order to identify stability of genotypes across the testing environments for grain yield, sixteen large red bean genotypes were evaluated for two consecutive years (2016-2017) at three midlands (Ginir, Goro and Dellomena) south eastern of bale zone, Ethiopia. At all locations randomized complete block design with four replications was used to evaluate the genotypes. Plot size used was 6.4m² (4 rows at 40cm spacing and 4m long). The two central rows were used for data collection. Combined analysis of variance LSD multiple range test were done using Cropstat9 software. The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by [5]. The stability parameters like regression coefficient (bi), deviation from regression were also calculated using Cropsta9 program. AMMI Stability Value (ASV) the distance from the coordinate point to the origin in a two dimensional of IPCA1 scores against IPCA2 scores was computed by the model suggested by [19].

Table 2. ANOVA for grain yield of 16 Large red bean genotypes.

Source of Variation	Degree freedom	Sum Squares	Mean Squares	% of total variation
YEAR (Y)	1	11.3988	11.3988**	9.13
Location (L)	2	47.8791	23.9396**	38.33
Replication	3	0.889754	0.296585	0.71
Genotype (G)	15	14.4049	0.960329**	11.53
Y X L	2	5.14002	2.57001**	4.11
L X G	30	5.63363	0.187788*	4.51
Y X L X G	45	5.11653	0.113701*	4.09
RESIDUAL	285	34.4391	0.120839	
TOTAL	383	124.902	0.326115	

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1score) \right]^2 + [IPCA2]^2}$$

Where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1 value by dividing the IPCA1 sum squares by the IPCA2 sum of squares

Genotype Selection Index (GSI) 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).

$$GSI_i = RASV_i + RY_i$$

Table 1. Lists of large red bean genotypes used in the study.

SN	Genotype Code	Genotype name
1	G1	DAB-525
2	G2	DAB-531
3	G3	DAB-538
4	G4	DAB-523
5	G5	DAB-498
6	G6	DAB-504
7	G7	DAB-491
8	G8	DAB-537
9	G9	DAB-488
10	G10	DAB-518
11	G11	DAB-496
12	G12	DAB-526
13	G13	DAB-507
14	G14	DAB-522
15	G15	Melkadima
16	G16	Red kidney

3. Result and Discussion

The combined analysis of variance revealed that highly significant variation for environment, genotypes, and year x location. GEI for grain yield was significant across the tested environment (Table 2). The pooled analysis detected significant differences ($p < 0.01$) for environments and genotypes, which confirm the variation between the studied environments and genetic variability between lines (Table 2). From the total variation observed 38.33% was accounted for the locations followed by genotypes (11.53%). This implies the environment was much more contributes for the mean grain yield variation observed among the tested genotypes than other main effects. Significant variation for genotypes by environment interaction has also reported by [14, 17]. Similarly significant variation for the environment, genotypes and their interaction in wheat under normal and drought stress condition was also reported by [16].

AMMI Analysis

The combined analysis of variance showed that there are highly significant differences for environment, genotype and their interactions; combined analysis of variance and AMMI analysis is shown in Table 3. These result showed that 70.50% of the total variation is attributed for environmental effect. The genotype and the GEI effects only contributed to 21.21% and 8.29% respectively. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing variation in the plant grain yields. The AMMI model demonstrated the presence of G x E interactions, and this has been partitioned among the first and second IPCA (Interaction Principal Components Axes). Of the total variation observed, AMMI1 explained 78.28% of the interaction sum of squares; AMMI2 captured 21.72% of the interaction sum of squares (Table 3). This indicates that the use of AMMI model fit the data well and justifies the use of AMMI2. According to [5 and 24] the first two interaction principal component axis best predictive model explains the interaction sum of squares. This made it possible to construct the biplot and calculate genotypes and environment effects [10, 12 and 23].

Table 3. Analysis of Variance for grain yield of large red common bean for the AMMI model.

Source of variation	D.F.	S.S.	M.S.F	%TSS
Genotypes	15	1.80062	0.120041	21.21
LOCATIONS	2	5.98489	2.99245	70.50
TREATMENT X SITES	30	0.704204	0.023474	8.29
AMMI COMPONENT 1	16	0.551273	0.034455	78.28
AMMI COMPONENT 2	14	0.15293	0.010924	21.72
Total	47	8.48971		

Mean of the genotypes over all environments ranged from 0.91 t/ha (G13) to 1.67 t/ha (G4) (Table 4). In relation to the

stability parameters mean grain yield, slope (bi) and deviation from regression, G4 showed maximum grain yield with bi close to unity and deviation from regression close to unity implying the genotype is more stable than others. Similar stability of rice genotypes for grain yield was also reported by [7] Furthermore, AMMI Stability Value (ASV), which is the distance from the coordinate point to the origin in a two dimensional scattergram of IPCA1 scores against IPCA2 score should also be seen to decide the stability of a genotypes [19]. Accordingly, G8, G7 and G12 though they had the lowest ASV, they gave mean grain yield lower than the check and it was below than the grand mean. On the other hand G11, G1 and G4 had lower ASV as well as higher mean grain yield than the check and gave grain yield above the grand mean and showed wide adaptation over the testing environments (Table 4).

However, since stability in itself should not be the only parameter for selection, as the most stable genotype wouldn't necessarily gives the best yield performance [15], hence, simultaneous consideration of grain yield and ASV in single non-parametric index is needed or the Genotype Selection Index should be used to determine the stability of the genotypes by evaluating their mean grain yield and ASV..

Genotype Selection Index (GSI), when the rank of mean grain yield of genotypes across environments and rank of AMMI stability value considered to identify the tested genotypes in relation to stability, G11 and G4 had the lowest GSI values compared to the other genotypes and showed stable performance over the testing sites. However, the mean grain yield of G11 was equal to the check used in the study. Therefore, G4 was the stable and high yielder genotypes across the testing environments.

Table 4. Mean yield First and second IPCA and various yield-stability statistics investigated in large red common bean.

Genotype code	MEAN	Rank	SLOPE (bi)	MS-DEV	IPCA1	IPCA2	ASV	Rank	GSI
G1	1.38	6	0.927	0.23	-0.05	-0.01	0.19	5	11
G2	1.01	14	1.01	0.03	-0.01	-0.26	0.26	8	22
G3	1.38	5	1.31	0.45	0.22	-0.05	0.79	11	16
G4	1.63	1	0.97	0.02	0.45	0.02	0.20	6	7
G5	1.43	4	0.618	0.01	-0.26	0.16	0.96	13	17
G6	1.23	10	0.549	0.02	-0.33	-0.18	1.21	14	24
G7	1.17	12	0.95	0.35	-0.04	-0.04	0.14	3	15
G8	1.11	13	1.004	1.02	0.00	-0.04	0.04	1	14
G9	1.31	8	1.066	0.89	0.05	0.08	0.21	7	15
G10	1.38	7	1.313	0.03	0.21	-0.29	0.80	12	19
G11	1.48	2	0.976	0.67	-0.02	0.04	0.07	2	4
G12	1.2	11	1.055	0.78	0.04	0.07	0.17	4	15
G13	0.91	16	1.434	0.05	0.33	0.32	1.23	15	31
G14	1.27	9	0.904	0.01	-0.08	-0.12	0.30	9	18
G15	1.48	2	0.497	0.01	-0.35	0.18	1.27	16	18
G16	0.98	15	0.757	0.92	-0.17	0.11	0.61	10	25

Biplots: A graphical representation of grain yield showed in AMMI biplot, the relationship between the first interaction principal component axis (AMMI component 1) and mean of cultivars and locations [13], Cultivars and locations on the

same equivalent line, obtain similar yields and a cultivar or location on the right-hand side of the midpoint of this axis gave higher yields than those on the left-hand side [24]. The Interaction Principal Component Axes (IPCA) scores of a

genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA scores are to zero, the more stable the genotypes are across their testing environments. Basically, these biplots belong to two types: AMMI 1 and AMMI 2 [4]. In AMMI 1, the genotype and environment means are plotted on the abscissa, and the IPCA scores for the same genotypes and environments, on the ordinate. For interpretation of the AMMI 1 biplot, the magnitude and signal of the scores of the IPCA1 are observed; scores close to zero are characteristic of genotypes and environments, which contribute little to the interaction,

that is, they are stable.

Accordingly G4, G11, G15, G5, G3, G1, G10 and G9 found in the right hand side of the graph meaning they gave mean grain yield higher than the grand mean. From the three environments Goro site had grain yield above the grand mean of the tested genotypes, G1, G3, G4, G10, and G11 were more adapted to Goro site. Genotypes found near the vertex of the biplot were considered as more stable to the testing sites. G7, G12, G14 and G9 were found in this stable category. The rest genotypes were more suited for the other two sites Ginir and Dellomena.

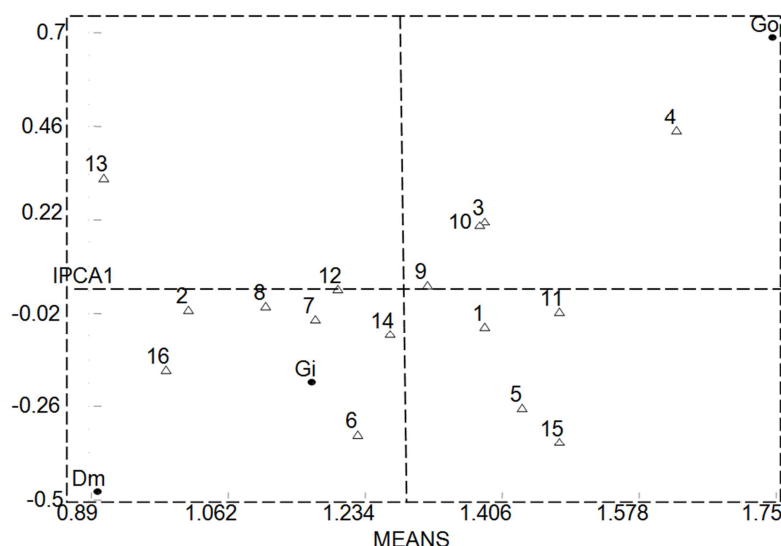


Figure 1. Biplot analysis of GEI based on AMMI 1 model for the PCA 1 scores and grain yield.

Regarding the other biplot, Figure 2, where IPCA 1 were plotted against IPCA 2 scores, Genotypes G1, G7, G8, G11 G12 and G9 were found very close to the origin implies these genotypes were more stable than the rest of the genotypes and contributes less to the GEI variation. On the other hand G3 and G4 were found slightly far from the origin and considered as moderately stable genotypes. The rest

genotypes which were found at very far distance away from the origin considered as unstable genotypes and contribute more to the GEI variation observed for grain yield. The results obtained by Figure 2 were in consistence with other stability parameters used to identify the stability of the tested genotypes.

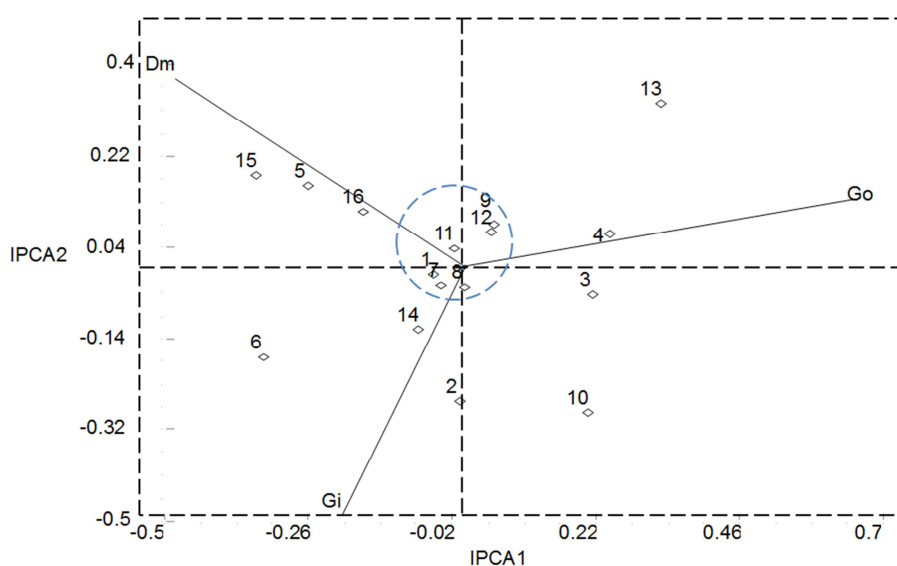


Figure 2. Biplot analysis of GEI based on AMMI 2 model for the first two IPCA scores.

4. Conclusion

The analysis of variance of the 16 genotypes in 6 six environments showed that genotype (G), location (L), crop-year (Y) and their interaction were significant ($P < 0.01$) for grain yield. The AMMI model was very effective for studying GEI interaction. The first bilinear AMMI model terms accounted for 78.28% of the GEI. Regarding to the different stability parameters used to identify the stability of genotypes like slop (bi), deviation from regression, ASV and GSI Genotypes G1, G7, G8, G12, G9 and G11 were found to be more stable than the other tested genotypes but showed mean grain yield lower than the check. However, G4 had high mean grain yield and showed moderate stability across the tested environments. Therefore, G4 was selected as candidate variety to be verified in the coming bona/main cropping season across the testing sites.

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