

Identification of Stability and Adaptability of Small Red Bean Cultivars Using AMMI Analysis

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To cite this article:

Tadele Tadesse, Amanuel Tekalign, Behailu Mulugeta, Gashaw Sefera. Identification of Stability and Adaptability of Small Red Bean Cultivars Using AMMI Analysis. *Plant*. Vol. 5, No. 6, 2017, pp. 99-103. doi: 10.11648/j.plant.20170506.13

Received: October 24, 2017; **Accepted:** November 3, 2017; **Published:** December 7, 2017

Abstract: Genotype x location interaction effects are of special interest for breeding programs to identify adaptation targets, adaptive traits and test sites. In order to identify stability and adaptability of small red bean cultivars sixteen genotypes were evaluated at the mid altitude of bale zone southeastern Ethiopia during main season 2015 and 2016. The cultivars were arranged in a randomized complete block design with three replications at each site of Goro, Ginir and Dellomena. The combined analysis of variance for mean grain yield revealed significant variation for genotypes, environment and GE interaction. The analysis of variance for the AMMI (Additive Main effects and Multiplicative Interaction) revealed that significant variation for genotypes, environment and GE interaction. From this analysis 42.53% was explained by AMMI 1 followed by AMMI 2 (28.29%), AMMI 3 (19.76%) and AMMI 4 (7.10%) of the interaction sum of squares. Therefore, the first two AMMI components justified 70.82% of the GE interaction sum of squares. The stability parameters regression coefficient (bi), deviation from regression analysis and ASV identifies G7, G6, G11, G1 and G12 showed the least value for ASV indicating as these genotypes showed stable performance over the sites. However stable cultivar wouldn't necessarily gave the highest seed yield. Therefore based on Genotype Selection Index (GSI) which considers both the ASV and the mean yield, G8, G3, G6 and G7 were the most stable genotypes identified over the tested environments. Therefore, out of the tested genotypes, G8 and G3 were identified as stable cultivar to be selected for possible release during the coming cropping seasons.

Keywords: Stability, Adaptability, AMMI, ASV, GSI

1. Introduction

The common dry bean or *Phaseolus vulgaris* L., is the most important food legume for direct consumption in the world. Among major food crops, it has one of the highest levels of variation in growth habit, seed characteristics (size, shape, and color), maturity, and adaptation. It also has a tremendous variability (> 40,000 varieties). Germplasm collection in beans compares well with other important commodities on a worldwide basis. *Phaseolus vulgaris* is produced in a range of crop systems and environments in regions as diverse as Latin America, Africa, the Middle East, China, Europe, the United States, and Canada [20, 27]. Common bean is the most important crop for soil health due its excellent biological nitrogen fixation and food security crops for its source of starch, protein, dietary fiber, minerals and vitamins [4].

It is the most important grain legume in nearly all lowland and mid altitude areas of Ethiopia. It is produced primarily by smallholder farmers both for cash and consumption. In 2014, it was cultivated by 3.34 million smallholders on 340 thousand hectare of land which is about 20% of total farm land allocated for pulses [5]. It is also an important source of income for the farmers and an export commodity that generates foreign currency for the country. It ranks third as an export commodity in Ethiopia, contributing about 9.5% of total export value from agriculture. Its fastest ripening at the critical hunger period earlier than other crops made it an ideal food security crop. It is double or triple cropped per year enabling cultivation of free land and engaging relatively cheaper labor after the harvest or failure of main season crops. Its high protein content made it the poor man's meat securing more than 16.7 million people against hidden hunger. Despite its multifaceted importance, most small red

common bean varieties at production are more than 15 years old and low seed yielding at small holder's farm. Therefore, advanced small red common bean lines reported for their higher seed yield potential were introduced and evaluated at multiple locations.

The wide occurrence of genotype x environment interaction (GEI) is the basic cause of difference between genotypes in their yield stability, or in other words: ranking of the genotype depends on the particular environmental conditions where it is grown. Numerous stability parameters have been developed to investigate GEI [14]. Among them Additive main effects and multiplicative interaction (AMMI) analysis [12] is particularly effective for depicting adaptive responses [1, 7]. Parametric stability statistics obtained by linear regression models [9, 11, 23] are mathematically simple and biologically interpretable; however, few researchers use statistical measures of yield stability in their breeding programs. To maintain improved agricultural productivity, the development of varieties with high yielding potential is the ultimate goal of plant breeders in a crop improvement program. In the recent years of haricot bean breeding in Ethiopia, special focuses have been paid to develop varieties with improved grain yield, good seed color and size as well as, resistant to major diseases. In addition to high yielding potential, a successfully developed new cultivar should have a stable performance and broad adaptation over a wide range of environments. However, frequent variation experienced both from season to season and from place to place within a shorter distance is among the most important features of the Ethiopian environmental conditions [10]. The objectives of this study were therefore to identify the most stable bean lines across the studied environments.

2. Materials and Methods

2.1. Testing Sites

In order to see the stability and adaptability of small red bean cultivars 16 genotypes including the checks (Table 1) were evaluated in the mid-altitude of bale zone, southeastern Ethiopia at three locations, Goro, Ginnir, and dellomena during bona 2015 and 2016 cropping season.

2.2. Experimental Design Statistical Analysis

The genotypes were arranged using randomized complete block design with four replications with plot size of 6.4m² (4 rows at 0.4m spacing of 4m row length). Combined analysis of variance using balanced ANOVA (Analysis of Variance) was computed using Cropstat program. AMMI analysis was performed using the model suggested by [8].

The ASV is the distance from the coordinate point to the origin in a two dimensional of IPCA1 score against IPCA2 scores in the AMMI model [21]. This weight is calculated for each genotypes and environment according to the relative contribution of IPCA1 to IPCA2 to the interaction SS as follows,

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

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. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller IPCA score indicate a more stable genotype across environment.

Genotype Selection Index (GSI): 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

$$GSI_i = RY_i + RASV_i$$

Table 1. Lists of genotypes used in the trial along with their genotypic code.

Genotype code	Genotype name
G1	ECAB-0295
G2	ECAB-0287
G3	SELIAN-97
G4	ECAB-020203
G5	SIMAMA
G6	SER-119
G7	ECAB-0281
G8	RBC-592
G9	ECAB-0236
G10	SER-118
G11	ECAB-0242
G12	625-BRB-183
G13	ECAB-0224
G14	MELKA DAME
G15	NASIR
G16	OMO-95

3. Result and Discussions

The combined analysis for the mean grain yield showed that genotypes (G), locations (L), years (Y), genotype x location (GL), genotypes x year (GY), location by year (LY), and genotypes x location x year (GLY) effects were highly significant ($p < 0.01$) (Table 2). This indicated the diversity of locations and years and presence of substantial genetic differences among the lines for seed yield performance. Similar findings were reported by [2, 18, 24] for common bean varieties performance and their growing environments in Ethiopia. The significant GL, GY, LY, and GLY were also indicated that the relative performance of genotypes at different locations and years was not similar.

Table 2. Combined mean grain yield of Small red bean genotypes tested over three locations (Goro, Ginnir and Dellomena) during meher 2015 to 2016.

Source of variation	DF	Sum of squares	Mean squares
Year (Y)	1	12.0496	12.0496**
Location (L)	2	31.9999	16.0**
Replication	3	0.844609	0.281536**
Genotype (G)	15	8.92123	0.594749**
Y X L	2	10.0307	5.01533**
Y X G	15	3.22062	0.214708**
L X G	30	8.1449	0.271497**
Y X L X G	30	8.34951	0.278317**
RESIDUAL	285	55.8643	0.196015
Total	383	139.425	0.364035

AMMI analysis: Genotype, location and genotype by environment interaction were assessed by the additive main effect and multiplicative interaction (AMMI) model (Table 3). The analysis of variance of AMMI model for grain yield showed significant effect for genotypes, environment, and GE interaction. These result showed that 65.05% of the total sum of square was attributed to environment effects, only 10.77 and 24.17% to genotype and GE interaction effects, respectively. The effect of environment was responsible for the largest part of the variation, tailed by genotype and genotype by environment interaction. The same result was

reported by [19, 22, 25] and. The GX E sum of squares was 2.24 times larger than for genotypes, which determined substantial differences in genotypic response across environment.

The GE interaction was partitioned into four parts of interaction principal component analysis (IPCA). AMMI 1 accounted for 42.53%, the second AMMI accounted for 28.29%, the third 19.76% and the fourth 7.10% respectively. The first two AMMI accounted for 70.82% of the GE sum of squares. This made as the construction of the biplot and genotype and environment effects [13, 16, 28].

Table 3. Analysis of Variance for the AMMI model for small red bean grain yield (t/ha) of the genotypes across environments.

Source of Variation	D.F.	S.S.	M.S.	%TSS
Genotypes (G)	15	2.23833	0.149222**	10.77
Locations (L)	5	13.5158	2.70316**	65.05
G X L	75	5.02163	0.066955**	24.17
AMMI COMPONENT 1	19	2.13592	0.112417**	42.53
AMMI COMPONENT 2	17	1.42043	0.083555**	28.29
AMMI COMPONENT 3	15	0.992167	0.066145**	19.76
AMMI COMPONENT 4	13	0.356746	0.027442**	7.10
GXE RESIDUAL	11	0.116365		2.32
TOTAL	95	20.7767		

Stability performance

The stability parameters i.e. regression coefficient (bi), deviation from regression (S^2_{di}), IPCA scores, AMMI Stability Value (ASV) and Genotype Selection Index (GSI) for the grain yield of the genotypes are presented in Table 4.

According to the result for of the stability parameters, regression of coefficient (bi), G5 (1.035), G8 (1.04), G11 (1.065) and G13 (1.085) showed a value close to unity implying these genotypes are stable over the environments. Furthermore, the deviation from regression for G8 (0.02), G6

(0.01), and G7 (0.01) were the lowest compared to others. The ASV was also lower for G7, G6, G11, G1, G12 and G2. But when we see the mean performance of the genotypes for those which showed lowest ASV it is lower than the mean grain yield. When genotypes were seen against GSI, which explained both the mean grain yield and the ASV, G6, G8, G3, and G7 are the one with the lowest value with high grain yield. Therefore, based on the stability parameters and their higher grain yield G8, G3 and G6 were the most stable genotypes across the studied environments.

Table 4. Mean grain yield, regression coefficient, deviation from regression, IPCA scores ASV and GSI for small red bean genotypes across environments.

Genotypes Code	MEAN	Slop (bi)	MS-DEV (s^2_{di})	IPCA1	IPCA2	IPCA3	IPCA4	ASV	GSI
G1	1.83	0.876	0.05	0.15	-0.19	-0.32	0.20	0.31	12
G2	1.81	0.712	0.06	0.18	-0.26	-0.37	0.24	0.39	15
G3	2.04	0.763	0.06	-0.18	0.35	0.19	0.31	0.46	12
G4	1.86	0.866	0.05	-0.24	-0.12	-0.28	-0.18	0.41	15
G5	2.01	1.035	0.07	-0.19	0.38	0.06	-0.24	0.49	15
G6	2.01	0.939	0.01	-0.16	0.04	0.04	0.02	0.27	6
G7	1.78	0.918	0.01	-0.10	0.04	0.11	0.12	0.17	12
G8	2.04	1.04	0.02	0.20	-0.28	0.16	-0.33	0.43	10
G9	1.81	0.66	0.07	-0.38	-0.26	-0.26	0.03	0.67	23
G10	1.88	1.172	0.06	-0.19	-0.26	0.33	-0.25	0.40	12
G11	1.87	1.065	0.08	-0.01	-0.28	0.46	0.07	0.28	9
G12	1.73	0.898	0.03	-0.14	-0.30	-0.04	0.05	0.38	18
G13	1.64	1.085	0.08	0.12	0.41	-0.30	-0.20	0.45	25
G14	1.71	0.778	0.09	-0.31	0.46	-0.06	0.01	0.68	29
G15	1.76	1.133	0.08	0.35	0.14	0.33	0.26	0.59	25
G16	1.45	1.544	0.23	0.88	0.11	-0.07	-0.13	1.44	32

A graphic representation of grain yield showed in AMMI biplot it was generated using the genotypic and environmental score of the first two IPCA (Figure 1). Most of the genotypes showed negative interaction with environment B, E and F. on the other hand, G1, G2, G10, G11 and G12 showed positive interaction with environment B, E and F. Genotypes 5, G13 and G14 were more specifically adapted to

environment A whereas G15 and G16 were more adapted to environment D. G1 G2 and G11 were more adapted to environment B. Similarly G9, G10 and G12 were more adapted to environment E. the other genotypes which found around the origin (with the lowest vector from the origin), i.e G6, G7, G8 and G3 were the most stable once across the studied environments.

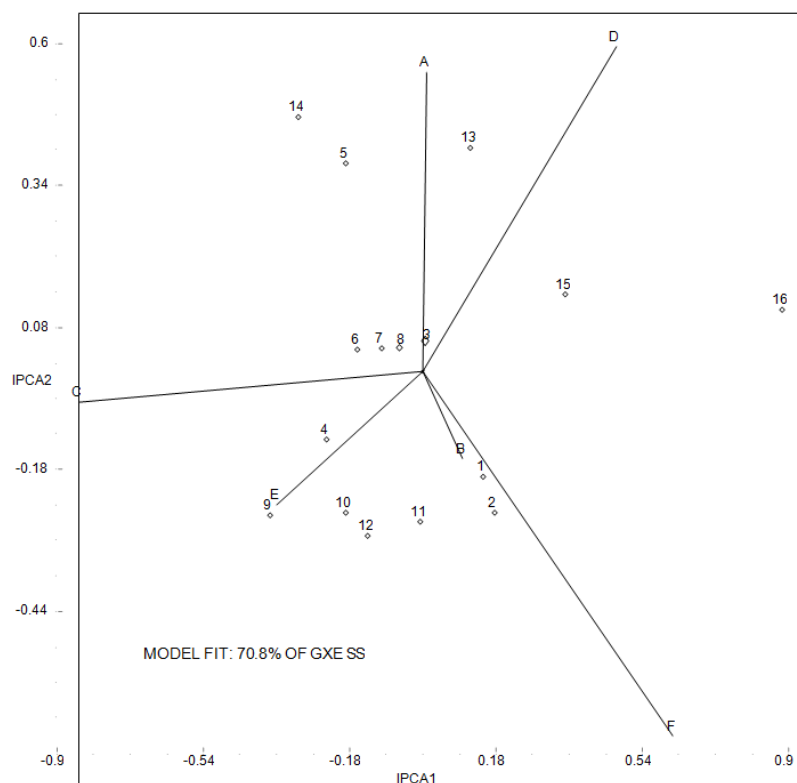


Figure 1. Biplot analysis of GE interaction based on AMM2 model for the first two interactions principal component scores.

4. Conclusion

Genotypes evaluation must be conducted in multiple locations for a number of years to fully sample the target environment [6]. Genotype in the presence of unpredictable GE interaction is a major problem in plant breeding [3]. To select for superior genotypes, it seems that there is no easier way other than to test widely [26] and select for both average yield and stability [15, 17]. According to the results based on mean of grain yield, coefficient of regression, deviation from regression, ASV and GSI genotype 8 and G3 are the genotype with well adaptability in all the studied environments and therefore selected for the possible release in the coming cropping season.

Acknowledgements

Oromia Agricultural Research Institute for the financial support, Sinana Agricultural Research Center for providing all necessary facilities and Pulse and Oil Crops Research Case team staffs for trial management and data collection well acknowledge.

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