

Adaptability Evaluation of Common Bean (*Phaseolus vulgaris* L.) Genotypes at Western Ethiopia

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Abstract

Fifteen common bean genotypes were tested at four environments with two management regimes of lime treated and lime untreated on acidic soils. The experiment was laid out in split plot design with three replications during 2016/17 cropping season. The combined analysis of variance over environments showed significant differences among Environments, Genotypes, Genotype x Environment interaction (GEI), Management, Genotype by Management interaction (G x M) and Genotype by Environment by Management interaction (G x E x M) on seed yield. Analysis of variance for seed yield from AMMI model indicated that contribution of the IPCA 1 and IPCA 2 accounted for 53.37% and 25.04% respectively for lime treated soils while 72.89% and 18.30% respectively for lime untreated soils of the observed variation due to GEI. The result indicated environment was contributed much to the observed variations suggested the need to test common bean genotypes at diverse environments. Two genotypes, ALB 212 (1.65 t/ha) and BFS 39 (1.63 t/ha) had first and second highest yield, identified as responsive to both environments but more to favorable environments suggested the need to further test to develop as varieties. It could be possible to recommend genotypes ALB 179, ALB 207, ALB 209, BFS 35, BFS 39 and ALB 212 to be tested as National Variety trial for all environments with both management measures as they have wider adaptability.

Keywords: AMMI; Common bean; GIE and split plot

Introduction

Common bean (*Phaseolus vulgaris* L), locally known as 'Boleqe' also known as dry bean and haricot bean, is a very important legume crop grown worldwide and it is one of the most important and widely cultivated species of *Phaseolus* in Ethiopia. It is grown predominantly under small holder producers as an important food crop and source of cash. It is one of the fast expanding legume crops that provide an essential part of the daily diet and foreign export earnings for the country [1]. Common bean is the Ethiopia's most important grain legume for direct human consumption with 513,725 tons of dry beans harvested from 323,318 ha in Ethiopia [2]. It is cultivated primarily for dry seeds, green pods (as snap beans) and green-shelled seed. There are wide ranges of common bean types grown in Ethiopia including mottled, red, white and black varieties [3]. The most commercial varieties are pure red and pure white color beans and these are becoming the most commonly grown types with increasing market demand [4].

Common bean production is heterogeneous in terms of ecology, cropping system and yield [5]. Common bean is grown predominantly in low land area (300-1100 m) mainly in the rift valley and some mid highland areas (1400-2000 m) of the country. Common bean produced in the rift valley is mainly white pea beans that are preferred for export markets [6]. Beans offer a low-cost alternative to beef and milk because bean seed is rich in protein, iron, fibers, and complex carbohydrates [7]. Ethiopian farmers grow beans for two major consumption uses namely: canning and cooking types. The white navy beans are grown for export canning industry and other types are mainly for households' food for national and regional markets.

In Ethiopia, dry beans are grown by small scale famers. They are major source of proteins in the lowlands where they are consumed as Nifro, Shirowat, soup and samosa. They are important export crop especially navy beans from the Central Rift Valley region and some parts of east and west highlands. In addition, beans are important crop in farming systems. They are intercropped with sorghum, maize, enset, coffee and chat.

Acid soil infertility is a major limitation to crop production on highly weathered and leached soils in both tropical and temperate regions of the world [8]. Soil acidity may be partitioned into exchangeable (chiefly monomeric Al) and non-exchangeable (titratable or pH-dependent acidity) components based on extraction with a neutral salt solution such as 1 M KCl [9]. Common bean is considered to be relatively more sensitive to Al toxicity compared to other crops [10]. Generally, common bean is less adapted to acid soil environments and improving Al resistance of common bean to reduce the dependence of small-scale farmers on lime and nutrient inputs is a major challenge [11]. However, efforts to develop adapted genotypes indicate that there are genotypic differences in Al resistance in the bean germplasm [11]. Reportedly, common bean genotypes showed considerable variability for soil acidity tolerance among the bred lines and improved genotypes [12]. Soil acidity has become a serious threat to crop production in most highlands of Ethiopia in general and in the western part of the country in particular. Currently, it is estimated that about 40% of the total arable land of Ethiopia is affected by soil acidity [13]. So, with this problem encountering the production and productivity of crops in western Ethiopia, this research was conducted to estimate magnitude of genotype, environment and genotype x environment interaction for seed yield of common bean in western Ethiopia, and to test adaptability of common bean genotypes both on lime treated soil and lime untreated acidic soils of western Ethiopia.

Materials and Methods

Experimental sites

The experiment was conducted during the 2016 main cropping season at four locations representing acid affected areas of western

Ethiopia where the crop is widely grown. The locations were Nedjo, Mandi, Bambasi and Assosa which are found along the main road side from Addis Ababa to Assosa with a distance of 490, 565, 616 and 661 km from Addis Ababa, respectively. The descriptions of the locations indicated in Table 1.

Location	Altitude (m.a.s.l.)	Temp./min and max (°C)	Rain fall Average (mm)	Soil type	Global position	
					Latitude	Longitude
Nedjo	1735	12 and 26	1386	Inceptisols	9°3'N	35°45'E
Mandi	1601	15 and 31	1674	Inceptisols	9°47'N	35°06'E
Bambasi	1425	21 and 35	1433	Entisols(Fluvisols)	9°75'N	34°73'E
Assosa	1553	17 and 32	1275	Nitisols	10°02'N	34°34'E

Table 1: Description of the study sites. Source: Benishangul Gumuz Regional State Meteorological Office.

Experimental materials and design

Fifteen common bean genotypes (Table 2), which had been selected based on their background on adaptability to low soil fertility and acid soil were obtained from Melkassa Agricultural Research Center (MARC), Lowland Pulse Research program and were evaluated at the selected sites. The selected genotypes were assumed to be variable in their tolerance to soil acidity as sensitive, tolerant and mildly tolerant.

Triple Super Phosphate (46% P₂O₅), Urea and ground lime (85% calcium carbonate) with fineness of 25% were used as sources of Phosphorus, Nitrogen and as liming materials, respectively. The experiment was conducted by using both lime treated and untreated soils by using split plot design with three replications at the four locations by assigning liming as a main plot and genotypes as sub-plots. The size of the experimental plot was 9.6 m² with 6 rows 4 of meters long and the net plot size was 4 rows × 0.4 m × 4 m=6.4 m². The spacing was 0.4 m and 0.1 m between rows and plants, respectively. The spacing between replications and blocks were 1.5 m and 1 m respectively.

S. No	Genotype	Background information	Source
1	ALB 212	Acid soil tolerant segregating population	CIAT
2	ALB 133	Acid soil tolerant segregating population	CIAT
3	ALB 163	Acid soil tolerant segregating population	CIAT
4	ALB 204	Acid soil tolerant segregating population	CIAT
5	ALB 25	Acid soil tolerant segregating population	CIAT
6	ALB 149	Acid soil tolerant segregating population	CIAT
7	ALB 179	Acid soil tolerant segregating population	CIAT
8	ALB 209	Acid soil tolerant segregating population	CIAT
9	ALB 207	Acid soil tolerant segregating population	CIAT
10	BFS 320	Low soil fertility tolerant segregating population	CIAT
11	BFS 35	Low soil fertility tolerant segregating population	CIAT

12	BFS 24	Low soil fertility tolerant segregating population	CIAT
13	BFS 39	Low soil fertility tolerant segregating population	CIAT
14	ROBA	Released variety (Check)	CIAT
15	NASIR	Released variety (Check)	CIAT

Table 2: Common bean genotypes used for the experiment.

Pre-planting composite soil sample from the experimental site was collected in a zigzag pattern from the depth of 0-30 cm before planting. Uniform volumes of soil were taken at each sub-sample by vertical insertion of an auger. The samples were air dried, ground using a pestle and a mortar and allowed to pass through a 2 mm sieve to remove the coarser materials. Working samples were obtained from each submitted samples and analyzed for organic carbon, total N, soil pH, available phosphorus, cation exchange capacity (CEC) and textural analysis using standard laboratory procedures.

Data Collection

Agronomic, phenological and morphological traits of each genotype under all management measures across all locations were collected following *Phaseolus vulgaris* L. descriptors [14]. The data were collected for Days to flowering, days to maturity, Plant height, number of nodule, seed yield, biological yield, harvest index, pod per plant and seed per pod.

Data Analysis

SAS and different statistical software packages were used to analyze the data. Analysis of variance for each location, combined analysis of variance over locations and AMMI analysis were computed using the Genstat statistical software.

Results and Discussion

Analysis of variance for each environment revealed the presence of highly significant ($P \leq 0.01$) difference in seed yield among common bean genotypes tested at Assosa, Bambasi, Mandi and Nedjo

(Supplementary Table). This indicated the presence of performance variation among the tested genotypes for yield, which is supported by the earlier works of Negash, Kefelegn and Rezene et al. [6,15,16], who noticed a large variation in yield performance among different bean genotypes. The combined analysis of variance (Table 3) for seed yield showed significant different ($P \leq 0.01$) among all main factors as well as all their interactions (Supplementary Table). This indicated that the environments had different impact on the yield performance of the genotypes while the genotypes had different performance in the testing environments so that they showed rank difference. In line with this finding, Kang et al. showed that corn genotypes had responded differently across environment [17].

Source of variation	DF	MS
Environment	3	12851470**
Replication	8	188898
Management	1	1732959**
Residual	2	12924
Genotype	14	321241**
Management x Genotype	14	78048**
Residual	56	18687

Management x Environment	3	804686**
Genotype x Environment	42	111906**
Genotype x Environment x Management	42	44268**
Residual	112	48005.5

Table 3: Combined ANOVA of yield for fifteen common bean genotypes. *=significant difference ($p \leq 0.05$) and **=highly significant difference ($p < 0.01$). Management=Lime treated and Lime Untreated; Environment=Location.

Mean performance of genotypes for grain yield

The first three genotypes with highest mean grain yield were ALB 179 (1.10 ton/ha), ALB 207 (1.03 ton/ha) and ALB 212 (1.02 ton/ha) on lime treated soil while genotypes BFS 35 (0.89 ton/ha) followed by BFS 39 and ALB 179 both (0.84 ton/ha) on lime-untreated soil. Roba variety was the lowest mean grain yielder on both lime treated (0.5 ton/ha) and lime untreated soil (0.46 ton/ha). This implies that all the tested genotypes have better adaptation than one of the standard checks (Roba) both on lime treated and lime untreated soils while most of the tested genotypes performed poorer than the other standard check (Nasir) on both soil management regimes (Table 4).

Entry	Genotypes	Testing Environment									
		Assosa		Bambasi		Mandi		Nedjo		GM	
		LT	LUT	LT	LUT	LT	LUT	LT	LUT	LT	LUT
1	ALB 212	0.51 ^{abcd}	0.17 ^d	1.65 ^a	1.30 ^{bcd}	1.38 ^b	1.01 ^{efghi}	0.39 ^{ab}	0.47 ^{ab}	1.02 ^{ab}	0.70 ^{defg}
2	ALB 133	0.47 ^{abcd}	0.66 ^{abcd}	1.12 ^{cd}	1.10 ^{cde}	0.98 ^{efghi}	0.52 ^{mn}	0.34 ^b	0.37 ^b	0.73 ^{cdefg}	0.66 ^{defgh}
3	ALB 163	0.97 ^{ab}	0.63 ^{abcd}	1.01 ^{cde}	0.95 ^{def}	1.10 ^{cdefg}	0.65 ^{lmn}	0.19 ^b	0.20 ^b	0.82 ^{bcdef}	0.60 ^{fgh}
4	ALB 204	0.44 ^{abcd}	0.28 ^{bcd}	1.32 ^{abc}	1.33 ^{abc}	1.09 ^{cdefg}	0.81 ^{hijkl}	0.37 ^b	0.48 ^{ab}	0.83 ^{bcdef}	0.70 ^{defg}
5	ALB 25	0.71 ^{abcd}	0.47 ^{abcd}	1.15 ^{cd}	1.06 ^{cde}	1.20 ^{bcde}	0.66 ^{klmn}	0.25 ^b	0.22 ^b	0.83 ^{bcdef}	0.60 ^{fgh}
6	ALB 149	0.63 ^{abcd}	0.61 ^{abcd}	1.31 ^{bcd}	1.18 ^{bcd}	1.12 ^{cdef}	0.81 ^{hijkl}	0.32 ^b	0.36 ^b	0.84 ^{bcdef}	0.74 ^{cdef}
7	ALB 179	0.89 ^{abc}	0.41 ^{abcd}	1.53 ^{ab}	1.35 ^{abc}	1.42 ^{ab}	1.04 ^{defgh}	0.56 ^{ab}	0.55 ^{ab}	1.10 ^a	0.84 ^{bcdef}
8	ALB 209	0.36 ^{abcd}	0.45 ^{abcd}	1.08 ^{cde}	1.17 ^{cd}	1.27 ^{bcd}	0.98 ^{efghi}	0.46 ^{ab}	0.74 ^a	0.86 ^{bcd}	0.76 ^{cdef}
9	ALB 207	0.65 ^{abcd}	0.55 ^{abcd}	1.34 ^{abc}	1.28 ^{bcd}	1.42 ^{ab}	0.85 ^{ghijkl}	0.40 ^{ab}	0.73 ^a	1.03 ^{ab}	0.77 ^{cdef}
10	BFS 320	0.53 ^{abcd}	0.65 ^{abcd}	1.12 ^{cd}	1.20 ^{bcd}	0.98 ^{efghi}	0.72 ^{klm}	0.20 ^b	0.51 ^{ab}	0.71 ^{cdefg}	0.77 ^{cdef}
11	BFS 35	0.33 ^{abcd}	0.44 ^{abcd}	1.21 ^{bcd}	1.26 ^{bcd}	1.39 ^{ab}	1.12 ^{cdef}	0.46 ^{ab}	0.73 ^a	0.85 ^{bcde}	0.89 ^{abcd}
12	BFS 24	0.50 ^{abcd}	0.38 ^{abcd}	1.30 ^{bcd}	1.13 ^{cd}	1.30 ^{bc}	0.7 ^{klm}	0.20 ^b	0.28 ^b	0.82 ^{bcdef}	0.62 ^{efgh}
13	BFS 39	0.54 ^{abcd}	0.68 ^{abcd}	1.10 ^{cde}	1.28 ^{bcd}	1.63 ^a	0.91 ^{fghijk}	0.32 ^b	0.50 ^{ab}	0.90 ^{abcd}	0.84 ^{bcdef}
14	Roba	0.38 ^{abcd}	0.22 ^{ab}	0.66 ^f	0.77 ^{ef}	0.76 ^{ijklm}	0.5 ⁿ	0.21 ^b	0.34 ^b	0.50 ^{gh}	0.46 ^h
15	Nasir	1.01 ^a	0.37 ^{abcd}	1.04 ^{cde}	1.25 ^{bcd}	1.30 ^{bc}	0.94 ^{efghij}	0.42 ^{ab}	0.47 ^{ab}	0.94 ^{abc}	0.76 ^{cdef}
	EM	0.59	0.46	1.2	1.17	1.22	0.81	0.34	0.46	0.85	0.71

SEM	90.36	104	78.3	104	126.5
CV (%)	21	15.2	13.3	24.4	15.5

Table 4: Mean value of yield (t/ha) of fifteen common bean genotypes at individual environment with different management measures.

The AMMI analysis of variance for seed yield showed the significant (P<0.01) effect of Environments, Genotypes, Genotype x Environment interaction (GEI), Management, Genotype by Management interaction (G x M) and Genotype by Environment by Management interaction (G x E x M). The main effects of environment and genotype accounted for 56.83% and 8.39%, respectively while G x E interaction accounted for 10.02% of the total variation in G x E data for bean seed yield on lime treated soils.

Similarly, on lime untreated acid soil, environment and genotype accounted for 64.12% and 7.86%, respectively while G x E interaction

accounted for 8.71% of the total variation in G x E. From this result, the large sum of squares for environments in both soil management regimes indicated that the environments were diverse, with large differences among environmental means causing most of the variation in seed yield. This result also indicated that those environments have a great influence on common bean production in bean growing areas of western Ethiopia. Different researchers reported the significant influence of environment in different crops performance so far. Mekbib in bean [18], Yan et al. in soybean [19] and Kan et al. in chick pea [20] are few of the authors.

Source	DF	MS		Total Variation Explained (%)		G x E Explained (%)		Cumulative	
		LT	LUT	LT	LUT	LT	LUT	LT	LUT
Total	179	234098	149034						
Treatments	59	534377**	364860**	75.24	80.69				
Genotypes	14	251186**	149770**	8.39	7.86				
Environments	3	7937765**	5702045**	56.83	64.12				
Block	8	515421**	101106*	9.84	3.03				
Interactions	42	99961**	55330ns	10.02	8.71				
IPCA 1	16	140046**	105869**			53.37	72.89	53.37	72.89
IPCA 2	14	75101*	30378*			25.04	18.3	78.42	91.19
Residuals	12	75517ns	17054ns						
Error	112	55821	38764						

Table 5: AMMI analysis of variance for yield (t/ha) across the testing environments. DF=Degree of freedom, MS=Mean square, LT=Lime treated, LUT=Lime untreated, ns=non-significant, * and **=significant at p<0.05 and p<0.01 respectively, IPCA 1 and IPCA 2=Interaction principal component axis one and two respectively.

The AMMI model further partitioned the genotype by environment interaction sum of square in to interaction principal component axes (IPCA) and residual term. The mean squares of the first two IPCAs were significant and all together contributed 78.42% and 91.19% of the total sum of squares of GEI for both lime treated and lime untreated soils respectively. The IPCA 1 and IPCA 2 accounted for 53.37% and 25.04% respectively for lime treated soils while 72.89% and 18.30% respectively for lime untreated soils of the observed variation due to GEI (Table 5). The first two principal component axis of the interaction were significant for the model for both soil management regimes and the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model [21,22].

Conclusion

AMMI analysis was used to identify the adaptability of the genotypes across four testing sites of acid affected areas of western

Ethiopia from one-year data. Based on this the genotypes with wider adaptation for all testing sites as well as specific adaptation to specific environment were identified. Genotypes ALB 212 (1.65 t/ha) and BFS 39 (1.63 t/ha) had first and second highest seed yield, identified as responsive to favorable environments (lime treated soil) suggested the need to further test to develop as varieties. Accordingly, even though their yielding performance varies across both soil management regimes it could be possible to recommend genotypes ALB 179, ALB 207, ALB 209, BFS 35, BFS 39 and ALB 212 to be tested as National Variety trial for all environments with both management measures as they have wider adaptability. But in order to get better and reliable result, it is better if the trial will be repeated for more years so that the performance of the genotypes across environment and lime application could clearly be identified.

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