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Full Length Research Paper

Evaluation of Common bean (*Phaseolus vulgaris*) Genotypes for their Yield and Adaptability in Amhara Regional State, Ethiopia

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Abstract

Considering the lack of improved varieties as a major problem in common bean production in Amhara region, an experiment was conducted to select high yielder and stable genotype/s. The experiment was done in 2011 and 2012 at Sirinka, Kobo, Jari and Shewarobit. Ten genotypes including the check were evaluated in randomized complete block design. The analysis of variance showed that there is high significant interaction of genotype by location by year which can need further analysis using AMMI model. In the AMMI, the first two interaction principal component analysis accounted for 71.6% for the total interaction and MR 14000-2-10P and MR 14195-13-4P with yield 1.75 and 1.73 t ha^{-1}, have low IPCA scores and AMMI stability value. Thought, its IPCA scores and AMMI stability value are high, genotype MR 14152-43-2P ranked first in its seed yield (2.2 t ha^{-1},) in all environments except Shewarobit 2012. Overall, MR 14152-43-2P is found best genotype and can increase productivity and production in common bean growing areas of Amhara and it was released with vernacular name Fetene.

Key words: Common bean, Genotype, Interaction, Stability

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Introduction

Common bean (*Phaseolus vulgaris*) is considered as the main cash crop and protein source of farmers in many low lands and mid altitude of Ethiopia, consequently, it is known as "the poor man's meat" due to its high protein content, which compensates for the deficiency that could have occurred in a population with low income. The crop is grown by subsistence farmers either as a sole crop or intercropped with cereal and tree corps. It is well adapted to areas that receive an annual average rainfall ranging from 500-1500 mm with optimum temperature ranges of 16^{o}C-24^{o}C, and a frost free period. Usually high temperatures do not affect it if adequate soil water is present, although high night temperature will inhibit pollination (Katungi *et al.,* 2009). Variable nature of common bean production areas of Ethiopia in general and Amhara region in particular is a challenge to exploit the potential of the crop. Interaction effect of genotypes and environments complicate varietal recommendation and breeders have been tried to cope up doing by multi-environmental trials.

Multi-environment trials (METs) play an important role in selecting the best genotypes and for assessing a genotype's stability across environments before its commercial release (Kang, 1998). When the performance of genotypes is compared across sites, several genotypes attributes are considered, of which seed yield is one of the most important. Genotypes grown in MET trials interact differently to environmental changes and known as genotype by environment (GE) interaction. A significant GE interaction for quantitative traits such as seed yield can seriously limit progress in selection (Navabi *et al*., 2006). Information on the structure and nature of GE interaction is particularly useful to breeders because it can help determine if they need to develop varieties for all environments of interest or if they should develop specific varieties for specific target environments. A comprehensive description of GE interaction requires more sophisticated statistical methods than standard analysis of variance (ANOVA). A popular extension of ANOVA for studying GE interaction is the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992).

Different varieties of common beans grow in different parts of Ethiopia, white beans, grow in the central rift valley as cash crop, colored beans grow in the southern part of Ethiopia for local consumption and climbing beans grow in the North West (Metekel) and western Ethiopia (Wollega), climbing type of common bean are planted along fences and on the borders of maize fields (Menbere, 2017). However, red and white types are predominantly grown in the nation. Oromiya and the Southern Nation Nationality and peoples Region accounts about 74.8 percent of the total national production (CSA, 2017). The production share and area coverage of Common bean in Amhara region is 21.9 and 22 percent of the national, respectively. Both red and white bean cultivated by 256,494 and 219,160 smallholders on 41,688.2 and 39,546.9 hectare of land, respectively in the region. Currently, the average productivity of beans in Amhara region and in the nation is almost equal and it is 1.6 and 1.7 t ha^{-} for white and red bean respectively (CSA, 2017). A diversity study in farmers' varieties by Menbere (2017) reported about 1.1 t/ha^{-} in Amhara region which is highly deviant from the CSA report. However, the experience from experimental plots indicates that 2.0-3.2 t ha^{-1}. The major cause of this yield difference in the region is due to environmental (both location and seasonal) variation as well as the agronomic managements. However due to its early maturity and moderate drought tolerance characteristics than other crops can be exploited by farmers for risk aversion in drought prone lowland areas of the region

The development of new varieties involve selection of varieties with desired characteristics such as high yield, tolerance or resistance to biotic and abiotic stresses and the stability of these traits in target environments. Inconsistent genotypic response to environmental factors such as temperature, soil moisture, soil type or fertility level from location to location and year to year are a function of genotype x environment interactions. Yield stability of a genotype across a range of production environments is very important for varietal recommendation. The genotype must have intrinsic genetic potential for superior performance under ideal growing conditions, and must also produce acceptable yield under less favorable environments.

Therefore, the objectives of this study are to evaluate ten bean genotypes for their seed yield and stability across the different bean growing environments of Amhara regional state using AMMI Analysis.

Material and Methods

Ten common bean genotypes were evaluated for their grain yield and adaptability at different growing environments of the Amhara Regional State during 2011 and 2012 cropping season. The genotypes were obtained from MARC and detail of the genotype is indicated in Table 1.The experiments were conducted at four different research stations of Amhara Agricultural Research Center at Sirinka, Kobo, Jari and Shewarobit, which vary with their geographical and agro-ecological characteristic as indicated in Table 2.

Table 1: Some morphological detail of the genotypes

Sr.no	Genotypes	Seed color	Growth type
1	MN 13935-25-1P	Red	Determinate –bush type
2	MR 14000-2-10P	Creamy	Indeterminate
3	MR 14198-13-1P	Shining red	Determinate
4	MR 14215-9-2P	Red	Determinate
5	MR 14266-52-2P	Red	Determinate
6	MR 14152-43-2P	Shining red	Determinate - Bush type
7	MR 14195-13-4P	Creamy	Indeterminate -bush type
8	MR 13937-27-3p	Creamy	determinate -bush type
9	MR 13937-27-4P	Creamy	Determinate-bush type
10	Melkie	Creamy	Indeterminate -prostrate

Table 2: Geographic and agro-ecological characteristics of testing locations

Locations	Altitude (m.a.s.l.)	Temp./min and max	Rain fall average (mm)	Soil type	Global position	
					Latitude	Longitude
Sirinka	1850	13.6-27.3$^{o}_{c}$	876	Eutric vertisol	11^{o} 08’	39^{o}28’
Kobo	1470	15.8-29.1$^{o}_{c}$	637	Eutric fluvisol	12^{o}8’21”	39^{o}18’21”
Jari	1680	NA	NA	Vertisol	11^{o}21’	39^{o}38’
Shewarobit	1200	13.1-32.5 $^{o}_{c}$	928	NA	10^{o}06’	39^{o}53’

Source: *Sirinka and Debre birehan Agricultural Research Centers for Altitude, rain fall and soil type; Wikipedia for global position. NA=non-available*

The experiments were carried out in a randomized complete block design (RCBD) with three replications in all environments. The experimental plot area was 6.4m^{2}and consists of four rows of 4 m length each. A row-to-row and plant-to-plant distance was kept at 40 cm and 10 cm, respectively at all environments. Weeds were controlled by hand-weeding two or three times as required. No fertilizer was applied and neither herbicides nor insecticides were used in any trials as there was no need for them. Data on seed yield were taken from the middle two rows of each plot.

Combined analysis of variance over locations and AMMI analysis for yield data were computed using Genstat 18th edition software after variance homogeneity test using Bartlett's test. 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 genotypes and environment) represent abscissa (X-axis). Similarly, the IPCA1 as abscissa and IPCA2 as ordinate were used to further explore stability. AMMI stability value is also calculated using the following formula to support exploring stability.

$$ASV = \sqrt{\left[\frac{SSIPCA1score}{SSIPCA2score}\ x\, IPCA1score\right]^2 + (IPCA1score)^2}$$

Result and Discussion

The combined analysis for the mean seed yield showed that genotypes (G), locations (L), genotype x location (GL), location x year (LY), and genotypes x location x year (GLY) effects were highly significant ($p<0.01$) (Table 3). The result showed that all the testing sites have different productivity as well as the productivity of the genotypes is immensely different. The Significant effect of LG and GLY interaction showed that the response of genotypes to changes in the locations or environments was under genetic control. These interactions showed the presence of rank variation of the genotypes across the environments. Similar results were reported by Asfaw *et al*. (2008); Mekbib (2003) and Tamene and Tadesse (2014) for common bean varieties performance and their growing environments at, Bako, Alemaya, Melkasa, Awassa, Ziway, Pawe, Ambo, Areka, Kulumsa, Assasa, Dhera.

Table 3: combined ANOVA of yield for ten common bean genotypes over eight environments

Source of variation	DF	Sum squares	Mean sum squares	Variance ratio	Fissure probability
L(location)	3	21.43856	7.14619	9.69	0.01
Y(year)	1	0.00098	0.00098	0	0.983
L.Y	3	9.33367	3.11122	31.92	<.001
G(Genotype)	9	40.9593	4.55103	58.05	<.001
L.G	27	5.65411	0.20941	2.67	<.001
Y.G	9	1.0192	0.11324	1.44	0.174
L.Y.G	27	5.49799	0.20363	2.6	<.001
Residual	144	11.28956	0.0784		
Total	239	104.3612			

DF-degree of freedom

Genotype, location and genotype by environment interaction were assessed by the additive main effect and multiplicative interaction (AMMI) model (Table 4). The AMMI analysis for grain yield showed significant effect for genotypes, environment, and GE interaction; and they contributed 39.2, 29.5 and 11.7 of the total sum of square, respectively. Thus, only about 50.9% of the variation was relevant for identifying highest yielding genotypes in different environments as only G and GE interaction affect the ranking. This result disagrees with the report by Nigussie (2012); Kaya *et al*., (2002) where they showed largest contribution was attributed to the total sum of squares by environment. Experimental location, seasonal variation and their interaction effects are the probable reason for the disagreement. Variation due to G is larger than due to GE, but GE interaction is significant at P = 0.01 which is agreed with the finding of Admassu *et al*. (2008) on maize. The GE interaction was partitioned into seven interaction principal component analysis (IPCA). The first interaction principal component analysis accounted 48.1% while the second accounted 23.5% and the third 13.5%. The other four interaction component analyses have no significant share to GE interaction. The first two interaction principal component analysis accounted for 71.6% of the GE sum of squares and according to Zobel *et al*. (1988) they are enough to explain the nature of interaction. This helps to draw AMMI 2 biplot using the first two IPCA.

Table 4: AMMI analysis of variance for yield across the testing environments

Source of Variation	**SS**	**MS**	**% cont. to total**	**% cont. to interaction**
Total	104.36	0.44		
Genotypes	40.96	4.55**	39.2	
Environments	30.77	4.40**	29.5	
Interactions	12.17	0.19**	11.7	
IPCA 1	5.85	0.39**		48.1
IPCA 2	2.86	0.22**		23.5
IPCA 3	1.64	0.15*		13.5
Error	11.29	0.08		

DF-degree of freedom, SS-sum of squares, MS-mean sum of squares, VR-variance ratio

Genotypes with least AMMI stability value (ASV) and IPCA scores or have smallest distance from the origin are considered as the most stable, where as those which have highest ASV and IPCA scores are considered as unstable (Purchase, 1997). Accordingly, genotypes MR14195-13-4P and MR14000-2-10P are most stable considering IPCA 1 while MR14000-2-10P, MN13935-25-1P and MR14198-13-1P are the most stable considering IPCA 2. The ASV was also lower for MR14000-2-10P, MR13937-27-4P and MR14198-13-1P. Mean seed yield, IPCA scores and ASV of the 9 bean genotype and the standard check are presented in table 5. MR14000-2-10P has smallest distance from the origin and yields 1.75t ha^{-1} which is little greater than 1.74 t ha^{-1} the regional average productivity (CSA, 2017). MR14152-43-2P is the highest yielder and it yields 2.2t ha^{-1} with high IPCA scores and ASV.

Table 5: Mean seed yield, IPCA scores and ASV for common bean genotypes across environments

Sr.no	Genotype	Mean	IPCA1	IPCA2	IPCA3	ASV
1	MN 13935-25-1P	1.812	-0.3447	0.04619	0.02468	0.495491
2	MR 14000-2-10P	1.753	-0.04285	0.04119	0.14593	0.073875
3	MR 14198-13-1P	1.504	-0.24941	-0.07852	-0.50244	0.365488
4	MR 14215-9-2P	1.842	-0.37705	0.32294	-0.2875	0.628882
5	MR 14266-52-2P	1.622	-0.23191	0.24638	0.4825	0.41336
6	MR 14152-43-2P	2.201	-0.32573	-0.75825	0.07243	0.890095
7	MR 14195-13-4P	1.733	0.03816	0.3970	0.14249	0.400739
8	MR 13937-27-3p	1.597	0.59393	-0.22636	0.19288	0.879653
9	MR 13937-27-4P	1.324	0.22842	-0.08827	0.02229	0.338621
10	Melkie	0.544	0.71114	0.0977	-0.29327	1.022459

IPCA1, 2, 3-Interaction Principal Component Analysis, ASV-AMMI Stability Value

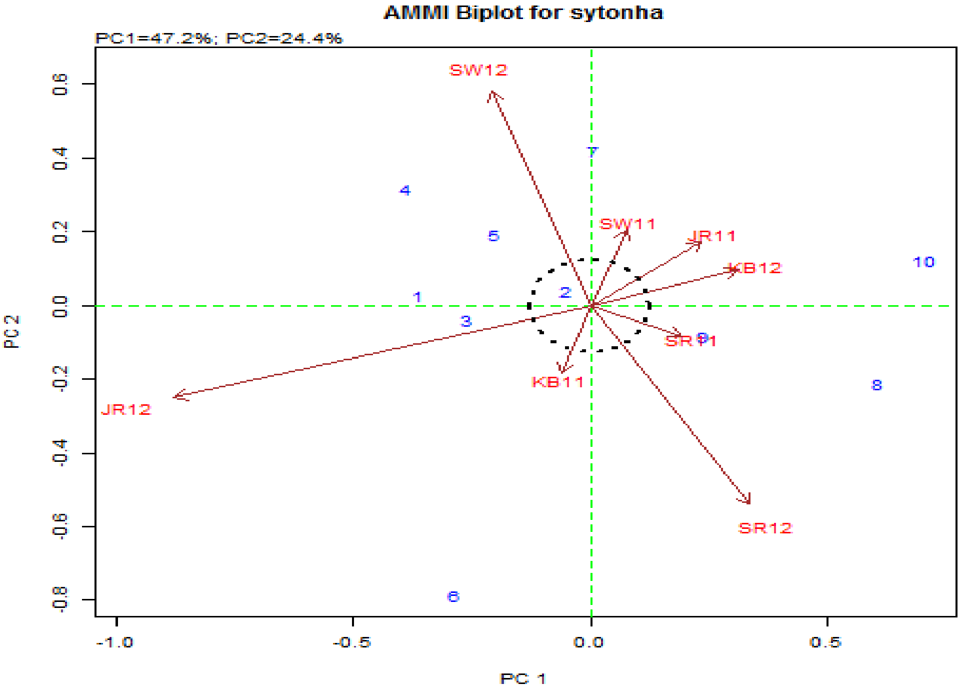
First four AMMI selections per environment are presented in table 6. MR14152-43-2P was found the best genotype for all of the testing location and similar areas. It ranks first in all environments except at Shewarobit in 2012. The minimum and maximum yielding environments were Kobo 2012 and Jari 2012, and their yield was 0.796 and 2.092 t ha^{-1}, respectively. Jari 2012 and Kobo 2012 followed by Sirinka 2012 have highest IPCA 1 score while Shewarobit 2012 followed by Sirinka 2012 has highest IPCA 2 score; hence those environments have highest contribution to GE interaction. This result showed that the year variation brought high variability in the location responses to the genotypes which can be proven by the significant interaction of year and location mentioned in the analysis of variance. All locations have high contribution to the interaction effect in 2012 than 2011.

Table 6: first four AMMI selections per environment

Environment	Mean	IPCA1	IPCA2	1	2	3	4
KB12	0.796	0.3564	0.1114	G6	G7	G8	G4
SR12	1.691	0.342	-0.5939	G6	G8	G2	G1
JR11	1.794	0.2667	0.1584	G6	G7	G4	G2
SR11	1.424	0.2368	-0.1286	G6	G8	G2	G1
SW11	1.695	0.0784	0.2371	G6	G4	G7	G1
KB11	1 .469	-0.0914	-0.1781	G6	G1	G4	G2
SW12	1.787	-0.2042	0.64618	G4	G7	G1	G5
JR12	2.092	-0.9847	-0.2525	G6	G1	G4	G5

G1-MN13935-25-1P, G2-MR14000-2-10P, G4-MR14215-9-2P, G5-MR14266-52-2P, G6-MR14152-43-2P, G7-MR14195-13-4P, G8-MR13937-27-3P; KB11, 12-Kobo 2011, 2012; SR11, 12-Sirinka 2011, 2012; JR 11, 12-Jari 2011, 2012; SW 11, 12-Shewarobit 2011, 2012

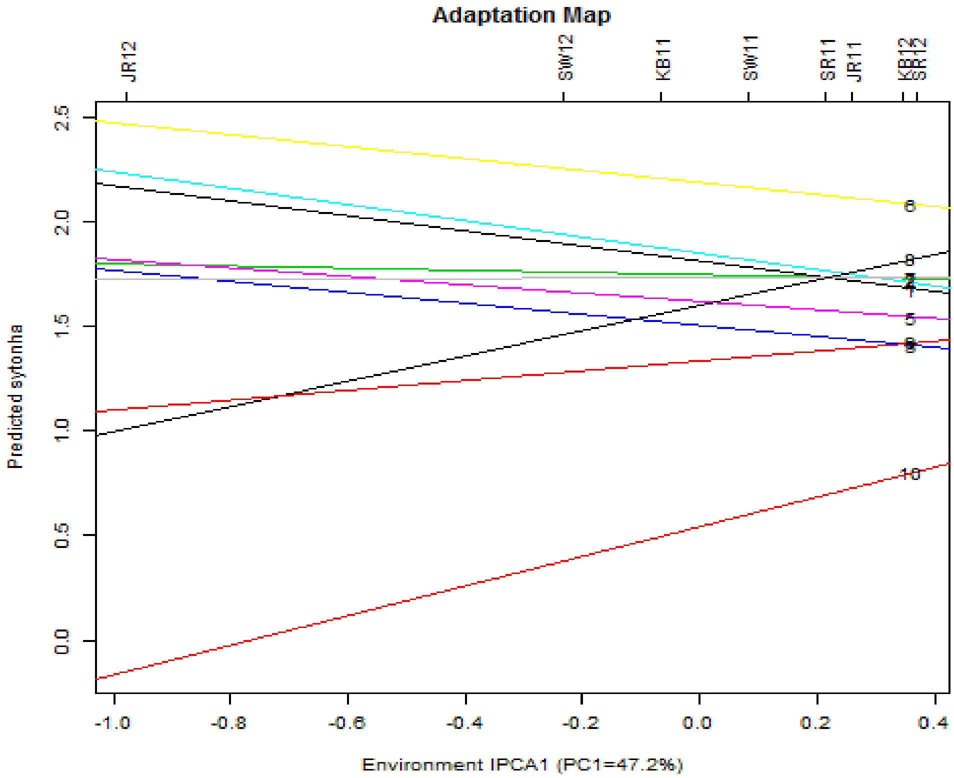
Though, the first three principal component axes of the interaction were significant for the model, the prediction assessment indicated that AMMI 2 with only two interaction principal component axes was the best predictive model (Zobel *et al*., 1988). Thus, the interaction of 10 genotypes with eight environments was best predicted by the first two principal components of varieties and environments. Genotypes and environments with similar signs of their IPCA scores interaction positively. In the AMMI 2 biplot, genotypes which occur close to each other will have similar yielding performance across all testing environments, while those genotypes which are far apart differ in mean seed yield or show a different pattern of response across the environments. Accordingly, genotype MR14215-9-2P and MR14266-52-2P which occur close to each other in the AMMI 2 biplot Figure (1) had similar yielding potential to all environments. Moreover, in the AMMI 2 biplot, genotypes which occur nearer to the origin were less sensitive to environmental changes where as those genotypes which occur distant from the origin are sensitive to environmental change and have large interaction. Hence, genotype MR14152-43-2P, MR13937-27-3P and Melkie were distant from the origin and have considerably contribution to the GE interaction variance considered to be unstable. Whereas genotype MR14000-2-10P, MR14198-13-1P and MR13937-27-4P were plotted relatively close to the origin indicating their minimum contribution to the total GEI variance and are considered as stable varieties. When looking at the environments it is clear that there was a good variation among the testing environments. Sirinka 2012, Jari 2012 and Shewarobit 2012 were plotted far from the origin indicating that these environments contribute higher amount of variation to the total GE interaction. On the other hand Shewarobit 2011, Jari 2011, Sirinka 2011, Kobo 2011 and 2012 were plotted relatively close to the origin indicating lower contribution to the GE interaction variance. This indicates that they have less discriminating power than the other environments. When we look the year influence on the locations, it is clearly observed that 2012 cropping season has high influence on the locations to respond to the interaction.



G1-MN13935-25-1P, G2-MR14000-2-10P, G3-MR14198-13-1P, G4-MR14215-9-2P, G5-MR14266-52-2P, G6-MR14152-43-2P, G7-MR14195-13-4P, G8-MR13937-27-3P, G9-MR13937-27-4P and G10-Melkie

Figure 1: AMMI 2 biplot of IPCA 1 vs. IPCA 2 using seed yield data

The lines in figure 2 resulted from the projection of the predicted yield of each genotype versus the environmental IPCA 1 scores. The slope of the lines reflects the adaptation patterns of the genotypes across environments (Gauch and Zobel, 1997). The result shows that these interactions led to different rankings of the genotypes across environments. MR13937-27-3P and Melkie (with sharp slopes) were found to have unstable yield; they exhibited the lowest yields in environments with a large negative IPCA 1 and the highest yields in environments with large positive IPCA 1 scores. MN13935-25-1P, MR14215-9-2P and MR14152-43-2P are better in all testing environments than the other genotypes. They showed high yield in environments with large negative IPCA 1 and their yield goes declining in environments with a large positive IPCA 1. MR14152-43-2P showed a good combination of yield and its consistence yielding in all the testing environments. MR14000-2-10P and MR14295-13-4P with better yield performance across the testing environments were found near to zero slop and hence they are stable genotypes. These results show that the genotypes contrasted in adaptation, yield performance and stability.



G1-MN13935-25-1P, G2-MR14000-2-10P, G3-MR14198-13-1P, G4-MR14215-9-2P, G5-MR14266-52-2P, G6-MR14152-43-2P, G7-MR14195-13-4P, G8-MR13937-27-3P, G9-MR13937-27-4P and G10-Melkie

Figure 2: Adaptation map showing the predicted mean yields of 10 common bean genotypes over eight environments

Conclusion

The significant interaction of genotypes, location and year was observed in the analysis of Variance of ten genotypes evaluated across two years and four locations. Based on IPCAs and AMMI Stability value, genotype MR 14000-2-10P and MR 14195-13-4p are the most stable compared to the other genotypes. MR14000 -2-10p and MR 14195-13- 4p yields 1.75 and 1.73t ha-, respectively which are almost equal to the national average of 1.7t ha-. Based on the adaptation map, MR 14000-2-10p and MR 14195-13-4p showed consistent performance across the environments. Genotype MR14152-43-2p was found the highest yielder genotype and yields 2.2t ha-. It was ranked first in all environments except Shewarobit 2012. However, it had high IPCA scores as well as AMM stability value and located far from AMM 2 biplot. Reponses of locations for the genotypes are higher affected by year and have showed high IPCA score in 2012 than in 2011. Higher yield was observed for most of the genotypes with negative IPCA scores in the adaptation map. Genotypes MR 14152-43-2p showed consistent yield performance in all testing environment as observed in the adaptation map and it was released with vernacular name 'Fetene'.

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Conflict of Interests

Authors have not declared any conflict of interests.

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