$\mathcal{R}$esearch Article

AMMI Analysis for Green Pod Yield Stability of Snap Bean (*Phaseolus vulgaris* L.) Genotypes Evaluated in East Shewa Zone, Oromia, Ethiopia

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ABSTRACT

The experiment was conducted at Adami Tulu Agricultural Research Center (ATARC), Lume and Dugda Districts during the 2019 and 2020 main cropping seasons to identify adaptable and high yielder snap bean genotypes for East Shewa Zone and similar agro ecologies. Ten snap bean genotypes were used as planting material. The experiment was laid down in Randomized Complete Block Design (RCBD) with three replications. The AMMI model shows that the environment accounted for 40.93%, GXE 31.79%, and genotype 12.70% of the total variation. The high percentage of the environment indicates that the major factor influencing the yield performance of snap beans is the environment. The first two IPCAs are the most accurate model that could predict the genotype's stability and explained by IPCA-I (53.10%) and IPCA-II (21.1%) of GEI. This result revealed that there were differential yield performances among snap bean genotypes across testing environments due to the presence of GEI. According to stability parameters (ASV, and GGE Biplot) and mean yield results revealed that G-24 and G-12 genotypes are the most stable genotypes across test locations. Therefore, G-24 and G-12 were proposed as candidate genotypes for possible release.

KEYWORDS: Snap bean, Genotype by Environment Interaction, Stability, AMMI, GGE Biplot

INTRODUCTION

Snap bean (*Phaseolus vulgaris* L.), a herbaceous annual plant domesticated independently in ancient Mesoamerica and in the Andes, and now is grown worldwide for both dry seeds and as a green bean. Thousands of legume species exist but snap beans in any form are most eaten by human beings compared to any other legume (Broughton *et al.*, 2003). It is one of the most important legume vegetable crops and contributes a substantial amount of protein to the human diet. Nitrogen fixation and the subsequent internal supply of nitrogen (N) from their symbiosis with rhizobia make legume crops richer in protein on a dry weight basis than all other plants (Broughton *et al.*, 2003).

In Ethiopia, snap beans are economically one of the most important vegetable crops grown for both export and local markets. It is mostly grown in the Rift Valley region, especially for export. Snap beans production in Ethiopia has increased from time to time both for export and local markets. In addition to large commercial vegetable farms which produce snap beans for export, snap beans are increasingly popular for small-scale vegetable producers for local markets. Although the market demand both international and local is very high, the production is low due to the lack of improved variety that suits various environmental factors.

Evaluating crop performances across different environments generates importance in formations on their adaptation and stability (Crossa, 1990; Ceccarelli, 1996). The performance of any character is a combined result of the genotype (G) of the variety, the environment (E) and the interaction between genotype and environment (GE). GE interactions exist when the responses of two genotypes to different levels of environmental stress are not consistent. A better understanding of GE interactions and stability in crops was used as a decision tool, particularly at the final stage of the variety introduction process, to generate essential information on the pattern of adaptation in breeding lines, screen new varieties for release, and determine the recommendation domains for released varieties (Yan & Kang, 2003). Among several statistical models, the most used statistical analyses for GEI are: The additive main effects and multiplicative interaction (AMMI) model (Gauch, 2006) and the genotype main effect and the genotype x environment interaction effect (GGE).

The basic cause of differences among genotypes (varieties) in relation to production stabilities is the genotype x environment (GE) interaction, so the performance of the genotypes depends on the specific environmental conditions where they are grown (Ferreira *et al.*, 2006). Keeping this in view, the present research study was conducted with the objective to identify high yielding and stable snap bean genotypes in the study areas.

MATERIALS AND METHODS

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at ATARC, Lume and Dugda Districts. Ten snap bean genotypes were used as a planting material (Table 1). Plot sizes will be 2 m x 3 m (6 m²). Each plot had five rows with 0.1 m between plants within each row and 0.4 m between rows with a row length of 3 m. The distance between adjacent blocks was 1 m. NPS and Urea were applied at the rate of 142 and 79 kg/ha respectively and with a seed rate of 60 kg/ha. The two outer rows were considered border rows. Weeding and all other recommended agronomic practice was followed for all locations.

Statistical Analysis

AMMI model

AMMI is used for analyzing GEI to identify patterns of interaction and reduce background noise. It combines conventional ANOVA with principal component analysis. Provide more reliable estimates of genotype performance than the mean across sites. To identify target breeding environments and to choose representative testing sites in those environments. To select genotypes with good adaptation in targeted breeding environments (Angela *et al.*, 2015).

$$Y_{ij} = \mu + g_i + e_j + \sum_{1}^{N} \lambda_K Y_{ik} \delta_{jk} + \varepsilon_{ij}$$

Where Y_{ij} is the grain yield of the ith genotype in the jth environment, μ is the grand mean, g_i and e_j are the genotype and environment deviation from the grand mean, respectively, Λ_k is the eigenvalue of the principal component analysis (PCA) axis , Y_{ik} and δ_{jk} are the genotype and environment principal component scores for axis k, N is the number of principal components retained in the model, and ε_{ij} is the residual term.

GGE biplot

GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.*, 2000) was used to visually analyze the METs data.

This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the source of variation in GEI analysis of METs data (Yan, 2001). The GGE biplot shows the first two principal components derived from subjecting environment centered yield data (yield variation due to GGE) to singular value decomposition (Yan *et al.*, 2000).

AMMI Stability Value (ASV)

ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the GxE interaction sum of squares, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{[SS_{IPCA1} \div SS_{IPCA2})(IPCA1 score)]^2 + (IPCA2 score)^2}$$

Where, SS_{IPCA1}/SS_{IPCA2} is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments (Purchase, 1997).

Genotype Selection Index (GSI)

Stability is not the only parameter for selection as most stable genotypes would not necessarily give the best yield performance. Therefore, based on the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value RASVi), the genotype selection index (GSI) was calculated for each genotype as:

$$GSIi = RASVi + RYi$$

A genotype with the least GSI is considered as the most stable (Farshadfar, 2008). Analysis of the variance was carried out using statistical analysis system (SAS) version 9.2 software (SAS, 2008). Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE biplot analysis was performed using Gen Stat 15th edition statistical package VSN International (2012).

RESULTS AND DISCUSSION

Additive Main Effect and Multiple Interaction (AMMI) Model

The AMMI model ANOVA for green pod yield is shown in Table 2. The analysis revealed the presence of highly significant (P< 0.01) differences among snap bean genotypes for pod yield performance. The environmental effect explained 40.93% of the G+E+GE variation. GEI and Genotype also accounted for 31.79% and 12.70% of the total variation, respectively. As discussed above, the high percentage of environmental variation indicates that the major factor influencing the yield performance of sap beans is the environment. A high percent of variation due to the environment was also reported by Seyni *et al.* 2017 on sesame, Temesgen *et al.* 2015 and Tadele *et al.* 2017, on faba bean and Dagnachew *et al.* 2014 on Triticale. Environmental pod yields (averaged across genotypes) ranged from 64.7 qun/ha at Dugda in 2019/20 to 122.3 qun/ha at

ATARC in 2020/21 with a grand mean of 93.0 qun/ha. Genotypes pod yield (averagedacross environments) ranged from the lowest of G19 78.21 qun/ha to the highest of 110.55 qun/ha for G24.

As the G x E interaction was significant, further calculation of genotype stability is possible. In the AMMI ANOVA, the GEI was further partitioned using PCA. The result of ANOVA showed that the first two IPCA were highly significant at (P<0.01) implying the inclusion of the first two interaction PCA axes in the model. A significant percentage of GEI was explained by IPCA1 (53.10%) followed by IPCA2 (21.25%). This result revealed that there were differential yield performances among snap bean genotypes across testing environments due to the presence of GEI. The presence of GEI could complicate the selection process of superior genotypes and might reduce the selection efficiency in a breeding program according to Gauch (2006).

Evaluation of Genotypes Based on GGE biplot model

The estimation of yield and stability of genotype was done by using the average coordinates of the environment (AEC) methods (Yan, 2001; Yan & Hunt, 2001). The average environment is defined by the average values of PC1 and PC2 for all environments, and it is presented with a circle. The average ordinate environment (AOE) defines by the line which

is perpendicular to the AEA (average environment axis) line and pass through the origin.

This line divides the genotypes into those with higher yields than average and those with lower yields than average. By projecting the genotypes on the AEA axis, the genotypes are ranked by yield; where the yield increases in the direction of the arrow. In this case, the highest pod yield had genotypes G-24, G-12 and G-26 but the lowers had G-10, G-19 and C1 (Figure 1). The stability of the genotypes depends on their distance from the AE abscissa. Genotypes closer to or around the center of the concentric circle indicated these genotypes are more stable than others. Therefore, the greatest stability in the high yielding group had genotypes G-24, G-12 and G-26. The genotype ranking is shown on the graph of the genotype so-called "ideal" genotype (Figure 1). An ideal genotype is defined as one that is the highest yielding across test environments and it is completely stable in performance which ranks the highest in all test environments; such genotypes, in this case, were G-24 and G-12.

Genotypes by Environment Interaction (GGE) Bi-plot Analysis

GGE biplot is an essential tool for addressing the mega environmental issues, by showing which cultivar won in which environments, and it was effective for visualizing mega-environment identification (Yan et al., 2000). Polygon views the GGE biplot showing the mega-environments and their respective highest yielding genotypes (Figure 2), and explicitly displays the "which-won-where pattern" as a concise summary of the GEI pattern derived from multi-environment yield trial data set for the three locations. The polygon dictated that G-24, G-12, C3 G-19 and C1 were vertex genotypes, whereas the remaining genotypes lie inside the polygon. The winning genotypes for each sector are those placed at the vertex. Therefore, G24 is the winner at both ATARC and Dugda locations, similarly G-12 genotype winning at the Lume environment. G-19, G-10 and C1 had below the pod grain yield less than the grand mean (Figure 2). G-24 is more stable than the other
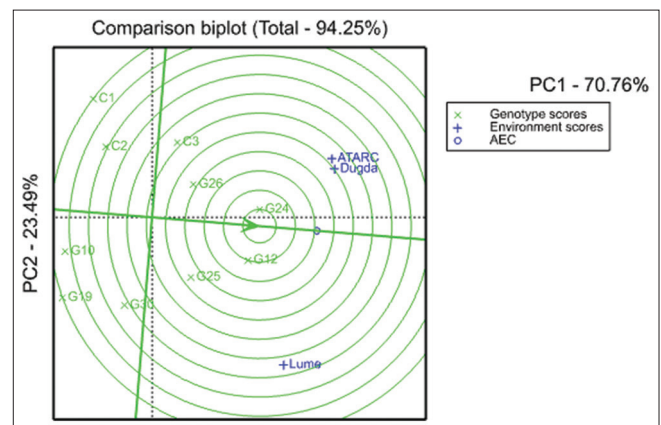
Table 1: List and description of snap bean genotypes were used in the experiment

No	Codes	Genotypes	Source
1	G10	HAV 130	CIAT
2	G12	Tarrot	CIAT
3	G19	HAB 404	CIAT
4	G24	Oxinel	CIAT
5	G25	LOIRET BLAC PETITE GRAIN	CIAT
6	G26	LOIRET BLAC GROSSE GRAIN	CIAT
7	G30	HAV134	CIAT
8	C1	Contender	MARC
9	C2	BC 44	MARC
10	C3	Plati	MARC

CIAT = International Center for Tropical Agriculture,
MARC = Melkassa Agricultural Research Center

Table 2: Additive main effect and multiplicative interaction analysis of variance (AMMI) for grain yield of 10 snap bean genotypes

Source of Variation	Df	Sum Sq	Mean Sq	Pr(>f)	G*E explained (%)
Total	179	172274.5	962.4274		
ENV	5	70518.3	14103.66	0.0001	40.93
REP (ENV)	12	4559.6	379.9667	0.35	2.64
GEN	9	21879.3	2431.033	0.001	12.70
ENV*GEN	45	54781.9	1217.376	0.001	31.79
IPCA 1	13	7851.85	603.98	0.001	53.10
IPCA 2	11	3101.4	281.94	0.041	21.25
Residual	108	20535.4	190.1426		

DF = Degree of freedom, ENV = Environment,
REP = Replication, GEN = Genotype, S.S = Sum of square,
M.S = Mean of square, IPCA = Interaction principal component axis,
** = highly significance difference, Ex. SS% = Explained sum of square.

Figure 1: GGE biplot based on genotypes focused scaling for comparison for their pod yield potential and stability.
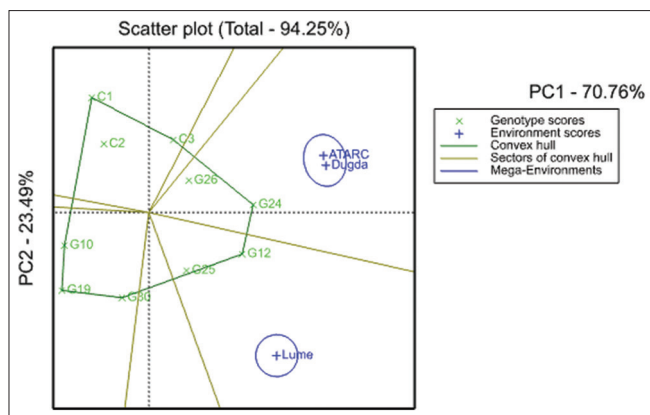
Figure 2: The GGE biplot to show which genotypes performed best in which environment.

Table 3: Mean grain yield of 10 Snap bean genotypes, AMMI stability values and genotypic selection index

Genotype	Mean	RYi	IPCA1	IPCA2	ASV	ASVi	GSIi
C1	83.88	8	1.95062	-0.67139	6.099963	6	14
C2	85.71	7	0.96937	0.24661	3.023064	3	10
C3	97.35	5	2.04333	0.90802	6.415645	7	13
G10	78.68	9	-2.14106	2.53147	7.120046	8	17
G12	108.49	2	0.27906	1.55846	1.783573	1	3
G19	78.21	10	-3.12314	0.06337	9.707527	10	20
G24	110.55	1	0.92867	0.34149	2.906615	2	3
G25	99.29	4	-0.71569	-2.32922	3.220819	4	8
G26	99.91	3	1.40029	-1.08079	4.484555	5	8
G30	88.34	6	-2.34145	-1.56802	7.444681	9	15

RYi = Rank of grain yield, IPCA = Interaction principal component axis, ASV = AMMI Stability value, ASVi = Rank of AMMI Stability value

genotypes since they it is found near to the origin and has general adaptability.

AMMI Stability Value (ASV): The importance of the AMMI model is the reduction of noises if the principal component did not cover much of the GE sum of squares (Gauch, 1992; Gauch & Zobel, 1996). It is the distance from zero in two dimensional scatter of the IPCA1 score against IPCA2 scores. Since the IPCA1 score contributes more to the GEI sum of the square, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GEI sum of square. According to the stability parameter, a genotype with the least ASV score is the most stable (Gauch, 1992; Gauch & Zobel, 1996). The genotypes such as G12, G24, C2 and G25 genotypes had the least ASV value and were the most stable respectively (Table 3). The high interaction of genotypes with the environment was confirmed by high ASV value and difference in ranking order, suggesting unstable yield across the environment. The most unstable genotypes were G19, G30 and G10 (Table 3).

CONCLUSION

The genotype, environment main effects and genotype x environment interaction effect were significant on Snap bean

genotypes. AMMI model shows the variation was largely due to environmental variation. The high percentage of environmental variation indicates that the major factor influencing the yield performance of snap bean genotypes is the environment. G-24 and G-12 were plotted to the ideal genotypes considered as desirable genotypes based on the GGE biplot graph and stable genotypes while G-19 and G-30 were far from the ideal genotypes considered as most unstable genotypes with poor performance across locations. G-24 and G-12 genotypes had the least AMMI stability and genotypic selection index value and were widely adaptable and stable high yielding genotypes.

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