

Full Length Research Paper

Additive main effects and multiplicative interaction (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot analysis of large white bean (*Phaseolus vulgaris* L.) genotypes across environments in Ethiopia

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Undertaking a multi-environment trial prior to releasing a high yielding and stable varieties for a specific environment is a major step in plant breeding. Therefore, the objective of this work was to study the effect of Genotype × Environment Interaction (GEI) and evaluate the adaptability and stability of sixteen large white common bean genotypes. Additive main effects and multiplicative interaction (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot models were used. The experimental design was 4 × 4 triple lattice across environments. AMMI analysis of variance showed environments that explained the greater proportion (72.42%) of the total variation, followed by GEI (10.75%) and genotype (2.32%). This indicates the possibility of selecting stable genotypes. AMMI biplot analysis revealed that the first and second interaction axes captured 42.62 and 26.77% of the total variation due to GEI. GGE model showed that the nine environments used for the study belonged to two mega-environments. AMMI stability value (ASV), AMMI and GGE biplot identified one common genotype, G14 (SAA 2) that was the overall best in performance in relation to yield and stability. This suggests that for reliability and optimum result it is better to combine the result of two or more analytical tools for yield and stability in recommendation genotype for verification and release.

Key words: Biplot, genotype × environment interaction (GEI), grain yield, stability, additive main effects and multiplicative interaction (AMMI), AMMI stability value (ASV).

INTRODUCTION

The common bean (*Phaseolus vulgaris* L., $2n = 2x = 22$) is one of the main cash crop and cheap protein sources in most lowland and mid-altitude areas of Ethiopia.

Currently, common bean occupies 18.8% of the total area cultivated by pulses in Ethiopia, and contributes to 17.2% of the total pulse production in the country (CSA, 2017). It

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is cultivated primarily for dry seed and green pods (as snap beans). There are wide ranges of common bean types grown in Ethiopia including mottled, red, white and black varieties (Ali et al., 2006). The most commercial varieties are red and white color beans and these are becoming the most commonly grown types with increasing market demand (Ferris and Kaganzi, 2008). The white beans are grown for export to the canning industry and other types are mainly for households' food for national and regional markets (Yayis et al., 2011). Despite its importance, progress on large white bean genetic improvement is not well utilized. The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. However, attaining this goal is made more complicated by genotype and environment interaction (Gauch and Zobel, 1996).

Genotype × Environment Interaction (GEI), which is the differential response of cultivars to environmental changes, is an important factor determining the performance of cultivars (Crossa et al., 1990; Vargas et al., 1999). In order to exploit the existing variability and develop new high yielding cultivars, common bean improvement efforts under diverse environmental conditions are needed. The improved common bean genotypes are evaluated in multi-environment trial to test their performance across environments and to select the best genotypes in specific environments.

Different methods of statistical analysis are applied to understand GEI. The Analysis of Variance (ANOVA) is an additive model that describes the main effects effectively; it determines if GEI is a significant source of variation or not and estimates the proportion of contribution. It does not give an insight into the patterns of genotypes or environment that give rise to interaction (Samonte et al., 2005). Therefore, to see the details of interaction and their interpretation the combined data will be analyzed using additive main effects and multiplicative interaction (AMMI) and GGE models proposed by Gauch (1992) and Yan et al. (2000).

The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically (Mukherjee et al., 2013). The model separates the additive variance from the multiplicative variance and then applies Principal Component Analysis (PCA) to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern and the estimation accomplished using the least squares principle (Thillainathan and Fernandez, 2001). The GGE biplot analysis is another method which integrates the genotype and the GEI effect in the evaluation of cultivars (Yan et al., 2000). GGE biplot is done using singular value decomposition to break the data matrix into component matrices. Therefore, the objectives of this study were to assess the yield performance and stability of large white bean genotypes evaluated in a multi-

environmental condition and discovers high yielding and stable candidate varieties for possible release using AMMI and GGE models.

MATERIALS AND METHODS

Description of experimental sites

Field experiments were conducted at seven representative bean growing areas of Ethiopia in 2014-2016. The locations were namely Melkassa, Meiso, Pawe, Arsinegelle, Goffa, Jimma and Aletena. Each year and location was treated as a separate environment, making 9 test environments. Descriptions of the locations are presented in Table 1.

Experimental materials

The fifteen large white common bean genotypes used in the study were obtained from CIAT – Uganda and one nationally released variety "Batu" was used as a standard check (Table 2).

Experimental design and analysis

The experiment was laid down in a 4 × 4 triple lattice across location. Each plot consisted of six rows of 4 m long with 0.4 m spacing between rows and 0.1 m between plants. Two seeds per hill were used, within 10 days after emergence; seedlings were thinned to one per hill. Fertilizer was applied to each plot at the rate of 18 kg N and 46 kg P₂O₅ ha⁻¹ in the form of di-ammonium phosphate (DAP) at planting. Other agronomic practices were treated as non-experimental variables and applied uniformly to the entire experimental area. For data analysis, grain yield measured from the middle 4 rows of each plot was converted into kg ha⁻¹ at 12.5% grain moisture content. Separation of the additive main effect was done using Duncan's Multiple Range Test (DMRT).

AMMI analysis uses ANOVA and PCA for estimating stability and GEI (Gauch, 1992). The AMMI model used for stability analysis is as follows:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{k=1}^n \lambda_n \gamma_{gn} \delta_{en} + \theta_{ge} + E_{ge}$$

Where: Y_{ge} = the mean yield of genotype g in environment e, μ = the grand mean, α_g = the deviation of the genotype mean from the grand mean, β_e = the deviation of the environment mean from the grand mean, λ_n = the singular value for the IPCA n, n = the number of PCA axis retained in the model, γ_{gn} = the PCA score of a genotype for PCA axis n, δ_{en} = the environmental PCA score for PCA axis n, θ_{ge} = the AMMI residual and E_{ge} = the residuals.

The AMMI stability value (ASV) as described by Purchase et al. (2000) was calculated as follows:

$$ASV = \sqrt{\left[\frac{SS\ IPCA1}{SS\ IPCA2} \times IPCA1\ Score \right]^2 + (IPCA2\ score)^2}$$

Where, ASV= AMMI stability value; SS= sum of square; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively.

Table 1. Description of the experimental sites.

Location	Soil type	Altitude (m.a.s.l)	Latitude	Longitude	Annual average		
					Min T (°C)	Max T (°C)	Rainfall (mm)
Alemtena	Andosols	1610	8° 18'N	38° 57'E	12.9	29.8	728
Arsinegelle	Nitosols	1890	7° 35'N	38° 65'E	13.8	23.3	807
Goffa	Acrisol	1284	6°19'N	36° 55'E	14.8	351	1020
Jimma	Eutric nitosols	1753	7°41'N	36° 48'E	11.5	26.2	1584
Melkassa	Andosols	1550	8°30'N	39° 21'E	14.0	33.0	763
Meiso	Vertisol	1332	9° 28'N	38° 08'E	14.9	28.2	787
Pawe	Nitosol	1120	11° 18'N	36° 32'E	15.9	33.0	1587

Where, m.a.s.l = meters above sea level, E=east, N=north, Min=minimum, Max=maximum, T=temperature, °c= degree centigrade, mm=millimeter

Table 2. Description of 16 large white bean genotypes used for a study.

Genotype name	Genotype code	Seed size and color
SAB 794	G1	Large white
SAA 15	G2	Large white
SAB 797	G3	Large white
SAA 8	G4	Large white
SAB 791	G5	Large white
SAA 10	G6	Large white
SAB 793	G7	Large white
SAA 7	G8	Large white
DAB 553	G9	Large white
SAA 1	G10	Large white
DAB 551	G11	Large white
SAA 18	G12	Large white
SAA 9	G13	Large white
SAA 2	G14	Large white
DAB 562	G15	Large white
Batu (check)	G16	Large white

GGE biplot analysis

Singular value decomposition (SVD) of the first two principal components was used to fit the GGE biplot model (Yan, 2002).

$$Y_{ij} - \mu - \beta_j = \xi_{i1}\eta_{j1} + \lambda_2\xi_{i2}\eta_{j2} + \varepsilon_{ij}$$

Where, Y_{ij} is the trait mean of genotype i in environment j , μ is the grand mean, β_j is the main effect of environment j , $\mu + \beta_j$ being the mean yield across all genotypes in environment j , λ_1 and λ_2 are the singular values (SV) for the first and second principal components (PC1 and PC2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively, η_{j1} and η_{j2} are

eigenvectors of j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j .

RESULTS AND DISCUSSION

AMMI analysis of variance for grain yield of the 16 large white common bean genotypes tested across 9 environments is presented in Table 3. The analysis showed that grain yield was significantly ($p \leq 0.01$) affected by environment, genotype and GEI. Of the total variance of grain yield, environment accounted for 72.42%, whereas genotype and GEI effects accounted

Table 3. AMMI analysis of variance for grain yield (kg ha^{-1}) of 16 large white common bean genotypes at 9 environments.

Source of variation	Degrees of freedom	Sum of Square	Mean square	F-values	Total Variation explained (%)	G × E explained (%)
Total	431	319095837	740362			
Treatments	143	272798936	1907685		85.49	
Genotypes	15	7408773	493918	4.67**	2.32	
Environments	8	231087201	28885900	29.34**	72.42	
Replications (E)	18	17722460	984581	9.30**	5.55	
Interactions	120	34302962	285858	2.70**	10.75	
IPCA 1	22	14618347	664470	6.28**		42.62
IPCA 2	20	9182739	459137	4.34**		26.77
IPCA 3	18	4556565	253142	2.39**		13.28
Pooled error	270	28574441	105831		8.95	

** Significant at 1% level of probability.

2.32 and 10.75% of the total variation, respectively (Table 3). The highly significant environmental effect and its high variance component could be attributed to the large difference between the test locations in altitude, daily temperature and a difference in both amount and distribution of rainfall. Previous reports on common bean in Ethiopia also indicated that environmental effects accounted for the largest part of the total variation (Firew, 2003; Asfaw et al., 2008; Zeleke et al., 2016).

The amount of variance contributed by GEI was 4 times larger than that contributed by genotype main effect. This result indicated that there was a noticeable GEI effect present in large white common bean multi-environment data, leading a substantial difference in genotypic responses across the test environments. The genotypes average grain yield across environments ranged from the lowest $1546.4 \text{ kg ha}^{-1}$ for G12 to the highest $2035.1 \text{ kg ha}^{-1}$ for G14 (Table 4). Genotypes give differential yield ranking across environments revealed that GEI effect was a crossover type (Matus-Cadiz et al., 2003; Kaya et al., 2006). The averaged environmental grain yield across genotypes ranged from the lowest 647.5 kg ha^{-1} at ME14 to the highest at $2910.5 \text{ kg ha}^{-1}$ at JM16 (Table 4).

AMMI biplot analysis

The application of AMMI model for partitioning the GEI (Table 3) reveals the first three terms were significant and explained 82.67% of the GEI. In the study, the first and second multiplicative axis terms explained 42.62 and 26.77% of GEI sum of squares (SS), respectively. The adequacy of the multiplicative terms containing the real structure of GEI was inspected by estimating the amount of noise present in the interaction from the pooled error and comparing it with the sum of squares retained in the consecutive AMMI models (Voltas et al., 2002). Accordingly, the interaction contained about $120 \times 105831 = 12699720$ noise SS (27.02%), and $120 \times$

$285858 = 34302960$ pattern SS (72.98%). This last percentage was larger than that retained by the first two multiplicative terms that together accounted for 69.39% of GEI SS. Moreover, the first two terms had SS greater than that of genotypes and were highly significant ($p < 0.01$). Hence, the AMMI with two interaction principal component axes was the best predictive model, which is in harmony with Zobel et al. (1988) and Annicchiarico (2002). Further AMMI axes captured mostly noise and therefore did not help to predict validation of observation.

In the AMMI1 biplot (Figure 1), the abscissa represents the main effects and its ordinate represents IPC1 scores. The horizontal dotted line showed the interaction PC1 score of zero and the vertical dotted lines indicated the mean of genotype effect. It thus provides a means of simultaneously visualizing both mean performance and stability of genotypes. Genotypes with IPC1 scores close to zero expressed general adaptation whereas the larger scores depict more specific adaptation to environments with IPC1 scores of the same sign (Ebdon and Gauch, 2002). Accordingly, genotypes G14 and G13 with mean yields greater than the overall mean and low IPC1 scores had a combination of high yield and stability performance. Check variety G16, G1, G2, G4 and G5 were similar to G14 and G13 in the main effect but tend to contribute more to GEI. Genotype G14 (SAA 2) was superior to the check variety G16 (Batu) with respect to yield and stability performance. MK16 and PW14 relatively were most stable environments than others for growing of widely and specifically adapted large white bean genotypes due to low interaction effect. JM16 and AN15 exhibited high grain yield performance with farthest IPCA values from zero. Therefore, they were highly interactive environments and suitable for specifically adapted genotypes.

According to AMMI2 biplot (Figure 2), the distance from biplot origin are indicative of the amount of interaction that was exhibited by genotypes over environments or vice versa. As genotypes located near the biplot origin

Table 4. Mean grain yield (kg ha⁻¹) of 16 large white common bean genotypes evaluated over 9 environments.

Genotype	Environments									Mean
	MK14	ME14	PW14	AN15	GF16	JM16	MK16	PW16	AT14	
SAB 794	2659.4 ^a	389.2 ^e	1733.0 ^{de}	1923.6 ^{cde}	853.7 ^{abcd}	3783.8 ^a	2622.2 ^{ab}	1064.2 ^b	1415.8 ^d	1827.2 ^{cdef}
SAA 15	2649.4 ^a	790.0 ^{abc}	2240.4 ^{bcd}	1858.7 ^{cdef}	1042.9 ^a	3149.6 ^{abc}	2427.3 ^{ab}	1213.3 ^b	1440.6 ^{cd}	1868.0 ^{abcd}
SAB 797	2157.9 ^{ab}	390.8 ^e	1815.9 ^{cde}	1314.6 ^{fgh}	782.2 ^{bcde}	3281.7 ^{ab}	2264.9 ^{ab}	1378.6 ^{ab}	1557.8 ^{abcd}	1660.5 ^{fgh}
SAA 8	2308.8 ^{ab}	399.5 ^e	1622.6 ^e	2840.8 ^a	927.5 ^{abc}	3020.0 ^{abc}	2497.7 ^{ab}	1305.6 ^{ab}	1753.4 ^{abcd}	1852.9 ^{bcde}
SAB 791	1881.6 ^b	807.6 ^{ab}	2057.5 ^{bcde}	2652.4 ^{ab}	582.3 ^e	3300.4 ^{ab}	2599.4 ^{ab}	1150.8 ^b	1897.6 ^{abc}	1881.1 ^{abc}
SAA 10	2619.8 ^a	806.8 ^{ab}	1998.2 ^{cde}	1741.3 ^{cdef}	718.7 ^{cde}	2953.0 ^{bc}	2162.3 ^{ab}	911.6 ^b	1385.8 ^d	1699.7 ^{defgh}
SAB 793	1888.4 ^b	675.6 ^{bcde}	1978.3 ^{cde}	2122.1 ^{bcd}	639.0 ^{de}	2450.0 ^{cd}	2653.8 ^{ab}	921.0 ^b	1913.5 ^{ab}	1693.5 ^{efgh}
SAA 7	2271.9 ^{ab}	736.2 ^{abcd}	2099.8 ^{bcde}	1959.1 ^{cde}	666.1 ^{de}	2365.8 ^{cd}	2361.4 ^{ab}	1275.1 ^{ab}	2005.8 ^a	1749.0 ^{cdefg}
DAB 553	2580.5 ^a	488.5 ^{cde}	1693.8 ^e	1107.6 ^{gh}	988.7 ^{ab}	2838.4 ^{bcd}	2447.4 ^{ab}	1109.7 ^b	1501.5 ^{bcd}	1639.6 ^{gh}
SAA 1	2449.2 ^{ab}	817.4 ^{ab}	2505.5 ^{ab}	1633.8 ^{cdefg}	780.2 ^{bcde}	2665.1 ^{bcd}	2384.9 ^{ab}	1301.4 ^{ab}	969.7 ^e	1723.0 ^{cdefg}
DAB 551	2426.2 ^{ab}	580.0 ^{bcde}	2036.1 ^{bcde}	1443.3 ^{efgh}	912.8 ^{abc}	2387.5 ^{cd}	2348.6 ^{ab}	1307.1 ^{ab}	1600.6 ^{abcd}	1671.3 ^{fgh}
SAA 18	2166.4 ^{ab}	471.2 ^{de}	1887.8 ^{cde}	931.3 ^h	860.2 ^{abcd}	3053.5 ^{abc}	2011.4 ^{ab}	949.6 ^b	1586.1 ^{abcd}	<u>1546.4^h</u>
SAA 9	2625.1 ^a	709.1 ^{babcd}	1998.1 ^{cde}	2042.5 ^{cde}	1026.6 ^a	3287.1 ^{ab}	2773.8 ^{ab}	957.8 ^b	1481.2 ^{bcd}	1877.9 ^{abc}
SAA 2	2384.9 ^{ab}	995.7 ^a	2252.6 ^{bc}	2193.8 ^{bc}	727.9 ^{cde}	3324.3 ^{ab}	3073.8 ^a	1718.6 ^a	1644.1 ^{abcd}	<u>2035.1^a</u>
DAB 562	2341.5 ^{ab}	436.3 ^{de}	2010.2 ^{bcde}	1539.0 ^{defg}	751.1 ^{cde}	2539.5 ^{bcd}	2218.7 ^{ab}	1149.8 ^b	1759.2 ^{abcd}	1638.4 ^{gh}
Batu(ch)	2403.3 ^{ab}	865.7 ^{ab}	2906.5 ^a	2775.5 ^a	755.1 ^{cde}	2168.8 ^d	3043.7 ^a	1280.5 ^{ab}	1551.1 ^{abcd}	1972.3 ^{ab}
Mean	2363.4^b	<u>647.5^h</u>	2052.3^c	1880.0^d	813.4^g	<u>2910.5^a</u>	2493.2^b	1187.2^f	1591.5^e	
CV%	12.98	24.7	12.6	16.7	14.42	13.78	19.79	20.24	14.78	

Abbreviations: ME14 = Meiso 2014; AN15 = Arsinegelle 2015; GF16 = Goffa 2016; JM16 = Jimma 2016; AT14 = Alemtena 2016; MK14 = Melkassa 2014; MK16 = Melkassa 2016; PW14 = Pawe 2014; PW16 = Pawe 2016. Means followed by similar letters are not significantly different at the 0.05 probability level based on DMRT; underline values are highest and lowest means of genotypes yield across location and highest and lowest means of environmental grain yield across genotypes

are less responsive than the vertex genotypes indicating general adaptability to all growing environments (Voltas et al., 2002). Based on these, G14, G2, G6 and G13 relatively scattered close to the origin expressed genotypes have minimal interaction and more adapted to all growing environments. G4, G5, G16 and G1 scattered away from the origin in the biplot indicating that these genotypes were more sensitive to environmental effects. The biplot showed JM16, AN15 and PW14 with longer vectors which indicated very interactive and discriminated the difference among genotypes

more than other environments with shorter vectors.

AMMI stability value (ASV)

The AMMI model does not make provision for a quantitative stability measure. Such a measure is crucial in order to quantify and rank genotypes according to their trait stability. In the ASV method, genotypes with least ASV score are the most stable (Purchase et al., 2000). Accordingly, G14, G13, G8 and G15 were most stable

genotypes and G 12, G 16 and G 7 were unstable (Table 5). The ASV parameter has been used as an auxiliary criterion to define more stable genotypes in common bean (Tadele et al., 2018) and other crops such as wheat (Farshadfar et al., 2011).

GGE biplot analysis

Mega environment of trial environment

The PC1 and PC2 score of GGE biplot were used

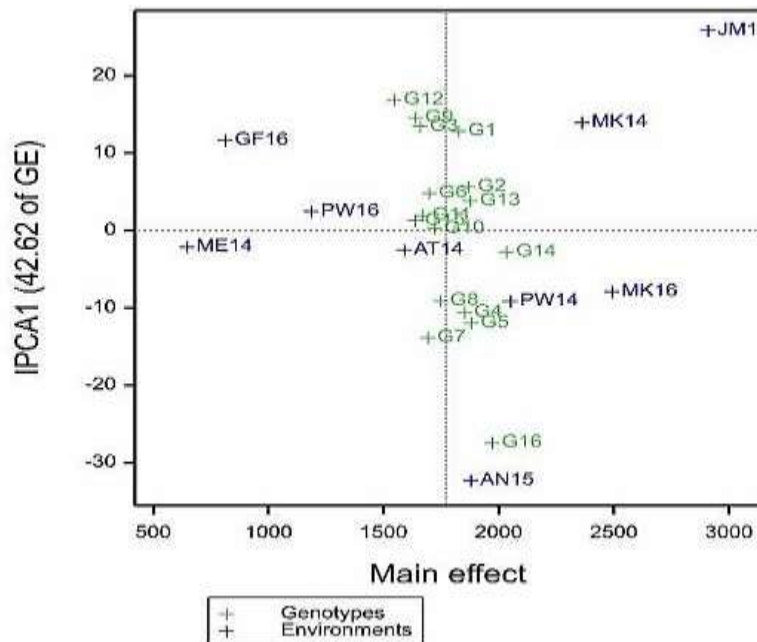


Figure 1. AMMI1 biplot showing the mean (main effect) vs. stability (IPCA1) view of both genotype and environment on grain yield.

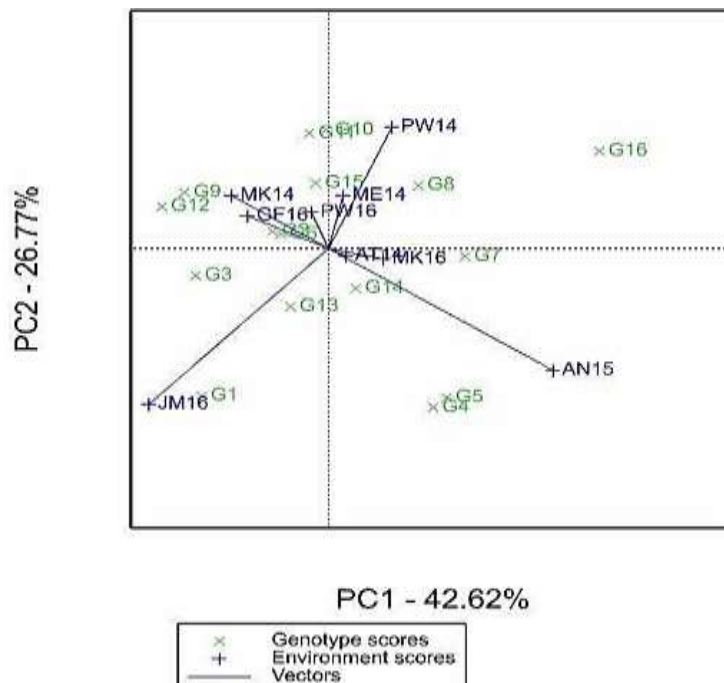


Figure 2. AMMI2 biplot of the first interaction principal component axis (IPCA1) vs. the second principal component axis (IPCA2) for grain yield.

to estimate the patterns of environments as shown in Figure 3. Environment PC1 and PC2 scores had positive and negative scores indicating that there was a difference in ranking for yield performance among genotypes across

environments leading to a crossover GEI. Visualization of the which-won-where pattern of Multi-environment Trial (MET) data is important for studying the possible existence of different mega environments in a region

Table 5. Performance and stability of 16 large white common bean genotypes based on mean grain yield (kg/ha), IPCA1, IPCA2 scores and AMMI stability value (ASV).

Genotype	Mean yield	Yield rank	IPCA1	IPCA2	ASV	ASV rank
SAB 794	1827.2 ^{cdef}	7	12.84648	-17.4192	13.48026	7
SAA 15	1868.0 ^{abcd}	5	5.65917	2.01629	9.692995	6
SAB 797	1660.5 ^{fgh}	13	13.4516	-3.20938	27.35149	13
SAA 8	1852.9 ^{bcde}	6	-10.585	-18.7757	20.38855	11
SAB 791	1881.1 ^{abc}	3	-11.9597	-17.6203	20.18803	10
SAA 10	1699.7 ^{defgh}	10	4.83298	1.69072	8.344297	5
SAB 793	1693.5 ^{efgh}	11	-13.8308	-0.93001	53.3451	16
SAA 7	1749.0 ^{cdefg}	8	-9.08284	7.45041	6.713061	3
DAB 553	1639.6 ^{gh}	14	14.57859	6.62643	22.6164	12
SAA 1	1723.0 ^{cdefg}	9	0.28519	13.97456	13.97462	9
DAB 551	1671.3 ^{fgh}	12	1.96159	13.59659	13.61699	8
SAA 18	1546.4 ^h	16	16.87828	4.96994	31.49859	14
SAA 9	1877.9 ^{abc}	4	3.84634	-6.86665	6.234089	2
SAA 2	2035.1 ^a	1	-2.76676	-4.70369	5.160177	1
DAB 562	1638.4 ^{gh}	15	1.30246	7.7078	7.726373	4
Batu(ch)	1972.3 ^{ab}	2	-27.4176	11.49213	40.75994	15

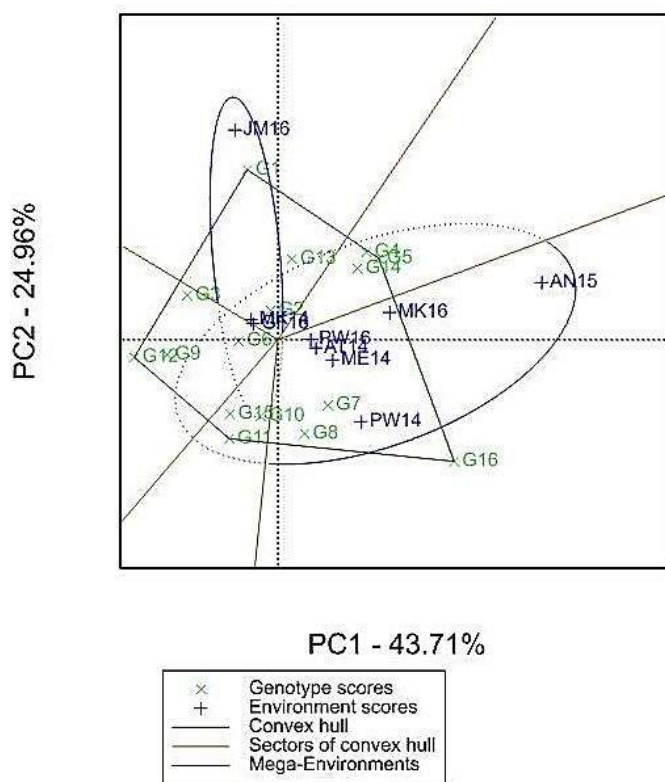


Figure 3. GGE biplot identification of winning genotypes and their related mega-environments.

(Gauch and Zobel, 1997; Yan et al., 2001). The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin, such that all

other genotypes are contained in the polygon. Genotypes located at the vertices of the polygon performed either the best or the poorest in one or more locations since

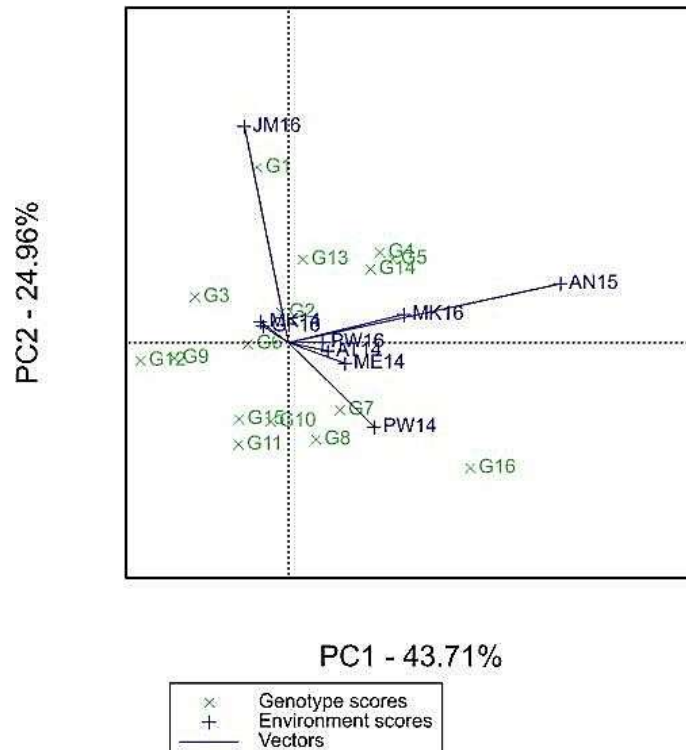


Figure 4. GGE biplot based on environment-focused scaling for environments.

they had the longest distance from the origin of biplot.

In the which-won-where view of the GGE biplot (Figure 3) based on the data in Table 4, the nine environments fell in two sectors with different winning genotypes. Sector 1 (Mega environment-1) consists of ME14, AN15, AT14, MK16, PW14 and PW16, or there are six environments that have good yielding capacity for genotypes G7, G8 and G16. The mega-environment-2 represents JM16, GF16 and MK14 are environments that are suitable for genotypes G2 and G13.

Relationship among test environments

To visualize the relationship between environments, lines are drawn to connect test environments to the biplot origin known as environment vectors. The cosine of the angle between the vectors of two environments is used to approximate the correlation between them (Yan, 2002). Based on the angle of environment vectors, the nine environments are separated into two groups (Figure 4). Group one includes MK16, PW16, AN15, ME14, PW14 and AT14 shows an angle less than 90° , which means these environments, are positively correlated. Group two involves JM16, MK14 and GF16, and the presence of obtuse angle from group one environments, they correlate negatively. The presence of close association among test environments suggests that the same

information about genotypes could be obtained from few test locations, and hence by dropping one or two environments from each group can reduce cost of multi-location replicated trials (Tukamuhabwa et al., 2012).

Performance and stability of the genotypes

The yield and stability of genotypes were evaluated by using so-called average environment coordinates (AEC) method (Yan 2001, 2002). In this method, the average principal components will be used in all environments and it is presented with a circle, as shown in (Figure 5). The average ordinate environment (AOE) defined by the line which is perpendicular to the average environment axis (AEA) line and pass through the origin. This line divides the genotypes into those with a higher yield than average and into those lower than average (Naheif et al., 2013). Thus, G4, G5, G14 and G16 had the highest mean yield and G12 and G9 were the lowest. The non-arrowed line is AEC; it points to greater variability (poorer stability) in either direction. Thus, G1 and G16 were highly unstable genotypes, whereas G4, G5 and G14 were highly stable.

Ranking genotypes relative to ideal genotypes

The ideal genotype should have the highest mean

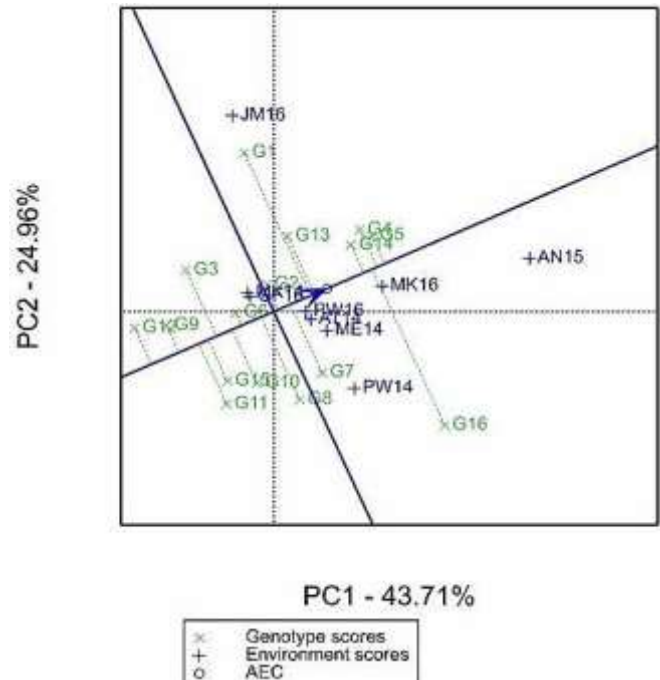


Figure 5. GGE biplot based on environment-focused scaling for mean performance and stability of the genotypes

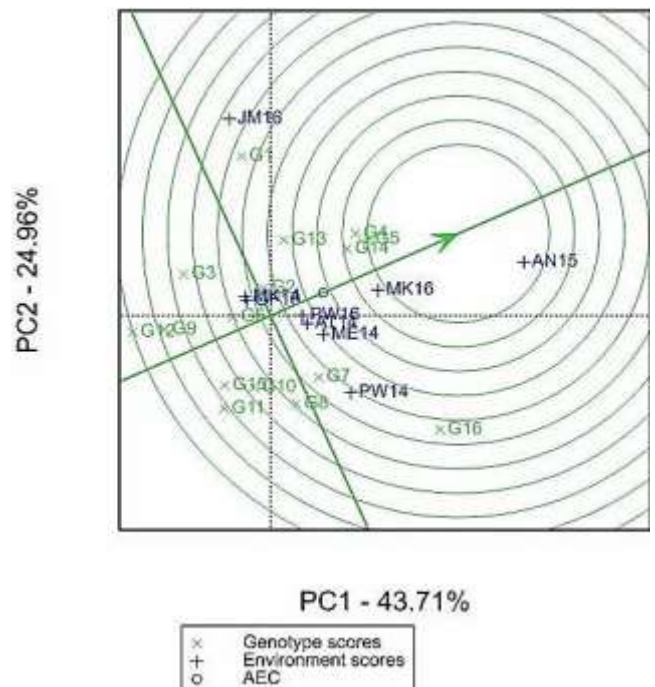


Figure 6. GGE biplot based on genotype-focused comparison of the genotype with ideal genotype.

performance and be absolutely stable (Yan and Kang, 2003), which represented by the small circle an arrow pointing to it (Figure 6). Such an ideal genotype is defined by having the greatest vector length of the high

yielding genotype and with zero GEI. Concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype; a genotype is more desirable if it is located closer to the ideal genotype

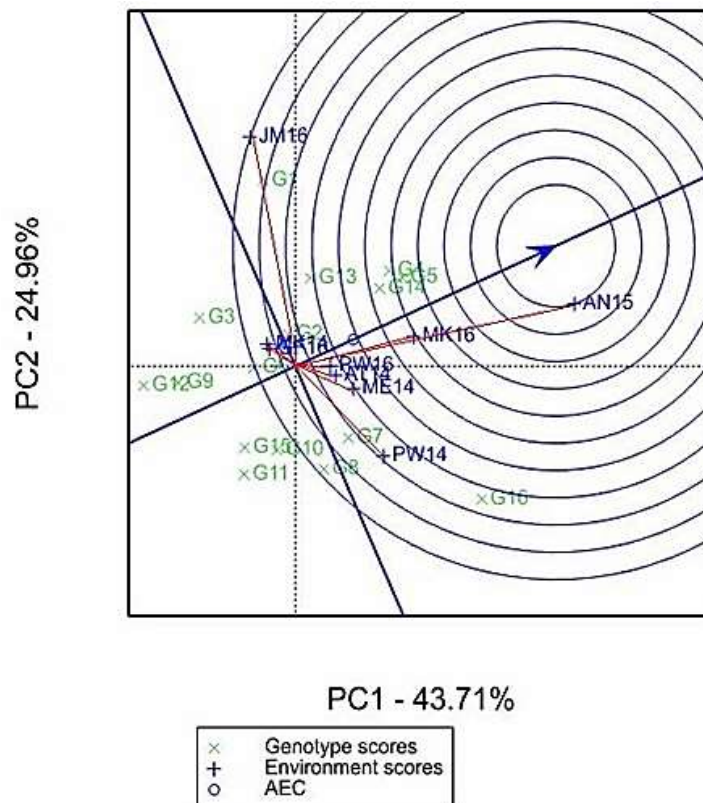


Figure 7. GGE biplot based on environment focused scaling for comparison of the environment with ideal environment.

(Mitrovic et al., 2012), so genotype G5 which fell into the center concentric circles was ideal in terms of high yielding ability and stability. In addition, G4 and G14, located on the next consecutive concentric circle, may be regarded as desirable genotypes.

Discriminating ability and representativeness

The concentric circle on the biplot help to visualize the length of environment vectors, which is proportional to the standard deviation within the respective environments (Yan and Tinker, 2006) (Figure 7). Therefore, among the nine environments AN15 and JM14 were most discriminating (informative) and GF16, MK14, PW16 and AT14 are least discriminating. The average environment (represented by the small circle at the end of the arrow) has the average coordinates of all the environments, and AEA is the line that passes through the average environment and the biplot origin (Yan and Tinker, 2006). A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, AN15 is the most representative whereas JM16, GF16 and MK14 are least representative. Test environments that are both discriminating and representative (e.g., AN15) are good test environment for selecting generally

adapted genotypes.

Conclusion

Genotype \times Environment Interaction (GEI) has been an important and challenging issue for plant breeders to select superior and adaptable cultivars for growing environments. Both yield and stability should be considered simultaneously to reduce the effect of GEI and to make a selection of genotypes more precise. The present study indicated that the large white common bean yield was liable to significant fluctuation with changes in the growing environments followed by the GEI and genotypic effect. AMMI analysis revealed that the high yielding genotypes SAA 2 and SAA 9 were top ranked in most environments and found the most stable across environments. According to GGE biplot, genotypes SAA 8, SAB 791 and SAA 2 were exhibited high yield and stable performance. By both models best performing genotype SAA 2 selected as stable genotype. Generally, the current study clearly demonstrates that the application of AMMI and GGE biplot facilitated the visual comparison and identification of superior and stable genotype, thereby supporting decisions of large white bean genotype recommended for the bean growing areas

of Ethiopia.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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