Yield Stability Analysis of Large-Seeded Common Bean Varieties in Major Bean Growing Areas of Ethiopia

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Abstract

Twenty large seeded common bean varieties released over two decades were evaluated at five locations in 2017 main cropping seasons in Ethiopia. The objective of the study was to determine the magnitude and pattern of G × E interaction and yield stability. The study was conducted using a randomized complete block design with three replications. G × E interaction and yield stability were estimated using AMMI and GGE stability methods. Pooled analysis of variance for grain yield showed significant differences at $p \leq 0.01$ among the main effects of genotypes and environments and at ($p \leq 0.01$) for G × E interaction effects. This indicated that either the genotypes differentially responded to the changes in the test environments or the test environments discriminated the genotypes or both. Environment effect accounted for 43.05% of the total yield variation; whereas, genotype and G × E interaction effects accounted for 26.27% and 30.67%, respectively. Environmental variation contributes a high percent to the total variability which indicates that differences among environments were the major reason for a different performance on grain yield. GEI variance was a little higher than a genetic variance. The first two principal components accounted for cumulative 71.67% interaction effects, which, indicated the majority of interaction effects were within two principal components. The AMM and GGE models identified genotypes G10, G1, G3, and G18 that display higher grain yield and stability. The five testing locations were grouped into two mega environments, namely; Arsi Negele, Haramaya, and Sirinka as one group with 'G13'and 'G14' as the best genotypes, and Alem Tena and Melkassa as the second group with G19 (DAB-107) as the best genotype. Hence, it can be recommended that a rigorous breeding effort is aimed at the development of enhanced populations and the release of stable and high yielding genotypes.

Keywords*: Phaseolus vulgaris* L., Grain yield, Stability, AMMI, GGE

Introduction

Common bean (*Phaseolus vulgaris* L.) is considered the main grain legume for human consumption and represents an essential source of proteins, carbohydrates, fibers, and trace minerals in several countries worldwide (Myers and Kmiecik, 2017). Common bean is one of the major pulses in Ethiopia. It is a basic food used daily in the Ethiopian diet and export crop. To meet this demand, common beans are grown throughout

the year under different cultivation systems. It holds the second-largest share of the area (306,186.59 ha) under pulse crops preceded by Faba bean in main season production. It also ranks second (520,979.3 tons) after Faba beans (9, 217, 61.5 tons) in total production in the 2017/18 cropping season (CSA, 2017). The average yield for the 2016/17 crop is approximately 1.4 t/ha and total production is 520,979.3 tons (CSA,2017), which is low as compared to some top producing countries in Africa like Tanzania (1,140,444 tons), Uganda (1,024,742 tons), and Kenya (846,000 tons).

The crop is well adapted to areas that receive average annual rainfall ranges from 500 – 1500 mm with an optimum temperature range of 16 – 24 °C, and with a frost-free period of 105 to 120 days. It performs best on deep, friable, and well-aerated soils with an optimum pH range of 6.0 to 6.8 (Kay, 1979). Areas within altitude ranges of 1200 – 2200 m.a.s.l are optimum altitude for common bean production (Acland, 1971; Cobley, 1976).

Although common bean is one of the most important crops in the country, productivity has been regarded as very low. This was due to the current farming systems being a result of the interaction of abiotic, biotic, and social factors, each of which causes a significant reduction of yield (Wortmann et al., 1998).

In Ethiopia, the common bean breeding program was initiated in 1972, at Melkassa Agricultural Research Centre (MARC) of the Ethiopian Institute of Agriculture Research (EIAR) with the objectives of improving grain yield, resistance to important common bean diseases, and development of improved crop management practices. The national bean improvement program has released fifty-eight improved common bean varieties until the year 2017 (MoA, 2017) that can meet local consumption and export market. Though improved common bean varieties have been released for general production under different recommendation areas or a wide range of environments. However, crop genotypes grown in different environments would frequently encounter significant fluctuations in yield performance and stability.

The concept of genotype by environment interaction for yield stability has been a concern for plant breeders. Common bean is cultivated in diverse environments. Studies on adaptability and yield stability of cultivars and lines have indicated the importance of the interaction between genotypes and environments (GEI). Robertson (1959); and Yang and Baker (1991) agreed that the genotype by environment interactions is usually perceived as uneven variations among genotypes from one environment to another. They also explained as the expression of different sets of genes from different environments and the response variation of the same set of genes to variable environments could be the factors accountable for the inconsistency issue. In addition,

significant differences among the test genotypes/ varieties, locations, and genotypes /variety by location interaction in grain yield have been extensively reviewed by different authorities (Barili et al. 2016, Singh et al., 2007, Ghaderi et al. 1984, Wondimu et al., 2011, and Keneni et al., 2011).

Stability analysis is used to identify greater stability and high yielding genotypes. There is an extensive set of techniques widely applied in stability analysis to provide further information on the real multivariate response of genotypes to environments. But the universal method that has been approved by everyone has not been yet introduced (Kaya et al., 2006). Among the multivariate analysis techniques, the additive main effects and multiplicative interaction (AMMI) model is the powerful method in assessing GEI and stability of genotypes from multi-environment trials and the genotype main effects and genotype by environment interaction effects (GGE) model. The results can be graphed in a useful biplot that shows both main and interaction effects for genotypes and environments. AMMI and GGE models are used frequently for statistical analyses in agricultural research (Gauch, 2006).

The Additive Main Effects and Multiplicative Interaction Model (AMMI) was found suitable to handle both the main effects and GEI in multilocational yield trials. The AMMI model combines regular analysis of variance for additive effects with principal component analysis for multiplicative structure within the interaction. AMMI biplot is considered to be an effective tool to diagnose GEI patterns graphically. The biplot displays the PCA scores plotted against each other provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on the similarity of performance across diverse environments. AMMI analysis is commonly being used in GE interaction data analysis in many crops to identify superior genotypes for specific or wide adaptation. In common bean crops (Carbonell et al. 2004; Ferreira et al., 2006) were used AMMI analysis to identify superior genotypes for specific or wide adaptation.

The GGE model (GGE biplot) was proposed by Yan et al. (2000), allowing visual examination of the relationships among the test environments, genotypes, and the genotype-by-environment interactions (GxE interaction). The GGE biplot displays the genotype main effect (G) and the genotype by environment interaction (GE) in two-way data. It is an effective tool for mega environment analysis ("which-won-where" pattern), whereby specific genotypes can be recommended to specific mega-environments, to identify the mean

performance and stability of genotype, and environmental evaluation.

Based on seed size, yield stability and performance of released varieties of common beans were not studied, and hence evaluation of high-yielding and well-adapted common bean varieties is required to use materials for further breeding purposes and revalidate the production domain. Therefore, the objective of this study was attempted to study the magnitude and pattern of genotype by environment interaction effects and performance stability of grain yield in 20 large seeded common bean varieties released in the period 1970 to 2017.

Material and Methods

Experimental Design

Cultivars were evaluated at the experimental stations of Melkassa, Arisi Negele, Alem Tena, Haramaya, and Sirinka during the main season of 2017. Soil physiochemical analyses and other characteristics related to the assessment sites are shown in Table 1.

Table 1. Description of locations used for the study

Location	Soil type	Altitude (m.a.s.l)	Latitude	Longitude	Annual average		Rainfall (mm)	Sowing date
					Min (°c)	Max (°c)		
Alem Tena	Andosols	1610	$8^0$18'N	$38^0$57'E	12.9	29.8	728	19th July 2017
Aris Negele	Nitosols	1890	7^0 35'N	$38^0$65'E	11.1	25.2	876	14th July 2017
Haramaya	Fluvisol	1980	9^0 26'N	$42^0$03'E	12.3	24.3	790	24th July, 2017
Melkassa	Andosols	1550	8^o 30'N	39^o 21'E	16	28.8	763	13th July, 2017
Sirinka	Eutricvertiol	1880	$11^0$08'N	$39^0$28'E	15.3	28.3	806	1st August 2017

Where, m.a.s.l = meters above sea level
Source: Melkassa Agricultural Research Centers and National Meteorology Agency

Plant Material

Twenty Ethiopian large seeded common bean varieties released from 1970 to 2017 were evaluated (Table 2). These varieties represent a large part of the genetic variability that exists among large seeded common bean cultivars grown during the approximately 20 years of history of large seeded common bean breeding in Ethiopia. Seed samples were obtained from MARC, Haramaya universities, and South Agricultural Research Institute (SARI). Information about the cultivars is available in supplementary Table 2. The experiments were arranged in a randomized complete block design with three replications. The experimental plots consisted of four 4-m rows, spaced 0.4 m apart, with 10cm between seeds. Fertilizer was applied to each plot at the rate of 18 kg N and 46 kg P_2O_5 ha^{-1} in the form of Di-ammonium phosphate (DAP) at planting. Hand weeding was used to control weeds during the growing period. No pesticide or fungicide was used for the control of insects or diseases. The trials were conducted under rain-fed conditions. The central two rows were used for data

collection. For data analysis, grain yield measured from a net plot size of 3.2 m^2 was converted into kg ha^{-1} at 12.5 % standard grain moisture content.

Table 2. Description of large-seeded common bean varieties used in the study.

S.N	Official/local Name	Variety Name	Year of release	Breeder/Maintainer
G1	ICS-15541	Gobe Rasha-1	1998/99	MARC/EIAR
G2	AFR-772	Ibado	2003	ARARC/SRARI
G3	RAB-484	Melkadima	2006	MARC/EIAR
G4	Cranscope	Cranscope	2007	MARC/EIAR
G5	ACOS Red	Montcalm	2007	MARC/EIAR
G6	Batu	Batu	2008	MARC/EIAR
G7	SUG131	Deme	2008	MARC/EIAR
G8	AFR-716	Loko	2009	BARC/OARI
G9	GLP-2	GLP-2	2011	MARC/EIAR
G10	ECAB 0247	Babile	2012	HU
G11	ECAB0060	Fedis	2012	HU
G12	ECAB0203	Hirna	2012	HU
G13	K-132	Hundane	2012	HU
G14	ECAB-0056	Morka	2012	MARC/EIAR
G15	RXR-10	Tininke	2012	HU
G16	AFR-702-1	Ramada	2013	HwRC/SARI
G17	SAB 736	Ado	2015	MARC/EIAR
G18	SAB 632	Tafach	2015	MARC/EIAR
G19		DAB-107	2017	MARC/EIAR
G20	Bifort large seeded-5	Gorossa	2017	MARC/EIAR

Where BARC = Bako Agricultural Research Centre, HU = Haramaya University, EIAR = Ethiopian Institute of Agricultural Research, MARC = Melkassa Agricultural Research Centre, SRARI = South Regional Agricultural Research Institute,

Data Analysis

The grain yield data was used to analyses of variance using SAS (statistical analysis system) version 9.2 (SAS, 2009) and analysis of variance for each location, combined analysis of variance over locations. AMMI and GGE biplot analyses were computed using the GenStat 18th edition software program2016. Simple inspection of the residual plot was used to examine if there is an issue on the heterogeneity of variances or homogeneity of error variances of the locations was tested using Bartlett test (Bartlett, 1947 in Steel and Torrie, 1980). The combined analyses of the trials (across locations) were done to determine differences between genotypes across locations and also to determine whether there was a significant difference among environments and GEI. The combined analysis was performed using a mixed model, for each character across location (Location, block, as random, was genotype considered fixed variable (McIntosh, 1983). Mean separation was carried out using Tukey at a 5% probability level of significance.

Stability analysis

Additive Main effects and Multiplicative Interaction (AMMI) model

AMMI analysis: - Following testing of the significance of the GxE mean square means over three replications for grain yield of genotype i at location j was subjected to Additive Main Effects and Multiplicative Interaction (AMMI) stability analysis using SAS (Hussien et al., 2000). The AMMI model is

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_i$$

Where: Y_{ij} = is the yield of ith genotype in the jth environment

μ = the grand mean

g_i and e_j= are the genotype and environment deviations from the grand mean, respectively;

λ_k= the singular value of the principal component (PC) axis k; these are usually known as Interaction Principal Component Axes (IPCA). There are (Min (G, E))-1 PC axes. If number of environments is less than number of genotypes then we have a total E-1 PC axis.

$\gamma_{ik} and\ \delta_{jk}$= are the genotype and environment principal components scores for axis k;

n = is the number of statistically significant principal components in the AMMI model

ε_i= is the residual term consisting statistically non-significant PC axes. If we have E IPCA, then εi has E-n components.

The degrees of freedom (df) for the IPCA were calculated based on the following Method (Zobel et al., 1988).

df = G +E -1-2n

Where: G = the number of genotypes. E = the number of environments. n = the nth axis of IPCA

Identification of stable and high yielding Genotypes

The identification of stable and high yielding common bean genotypes was done based on AMMI Stability Value (ASV) and Genotype Selection Index (GSI).

AMMIs Stability Value (ASV)

After testing the significance of the GEI mean square for yield and AMMI stability analysis AMMI stability value (ASV) for each genotype was calculated using the following formula.

$$\text{ASV} = \sqrt{\left[\frac{SS\ IPCA1}{SS\ IPCA2} \times IPCA1\ Score\right]^2 + (IPCA2\ score)^2}$$ (Purchase et al. 2000)

Where, ASV= AMMI stability value; SS= sum of square; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively. Genotypes with lower values of ASV were considered to be stable.

Genotype Selection Index (GSI)

Mohammadi and Amri, (2008) suggested that the most stable genotypes would not necessarily have the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index. For the simultaneous selection of yield and stability, a new approach known as genotype selection index (GSI) was recommended by Farshadfar (2008). GSI was calculated by the following formula:

$$GSI = RASV + RY$$

Where RASV is the rank of a genotype by its AMMI stability value and RY is the rank of a genotype by mean grain yield. The lowest ASV is given rank of 1 and the highest mean grain yield is given rank of 1. GSI incorporate both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and high stability.

GGE model

In order to have a clear insight into the interaction and the general pattern of adaptation of varieties, GGE biplot of varieties and environments was performed. The GGE model (GGE biplot) was proposed by Yan et al., (2000), allowing genotype by environment interaction (GEI) of multiple environmental trail data to be visually examined.

The model for a GGE biplot (Yan, 2002) based on singular value decomposition (SVD) of the first two principal components is:

P = G + GEI + E or P – E = G + GEI

The observed phenotypic value (P) consists of variances of the environment (E), the genotype (G) and the genotype and environment interaction (GEI).

The above formula was in terms of variance components, when presented as effects which have the unit of originally measured values, they become.

$$y_{ij} = \mu + \alpha_i + \beta_j + \emptyset_{ij}$$

$$y_{ij} - \mu - \beta_j = \alpha_i + \emptyset_{ij}$$

Where; yij= the expected yield of genotype i in environment j

μ = the grand mean of all observation

αj= the main effect of genotype i

βj= the main effect of genotype j

Øij= the interaction between genotype i and environment j

Instead of trying to separate G and GEI, GGE biplot keeps G and GEI together and partition this mixture GGE into two multiplicative terms.

$$y_{ij} - \mu - \beta_j = g_{i1}e_{i1} + g_{i2}e_{2i}\alpha_j + \emptyset_{ij} + \varepsilon_{ij}$$

Where g1i and e1j are called the primary scores of genotype i and environment j, respectively; g2i and e2j are the secondary scores for genotype i and environment j, $\emptyset_{ij}$ is the residue not explained by the primary and secondary effect. Actually, a GGE biplot is constructed by plotting gi1 against gi2 and e1i against e2j in a single scatter plot. The most common way to implement the above formula is by subjecting the GGE data to singular value decomposition (SVD) as shown below;

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

Where λ1 and λ2 are the singular values of the first and second largest principal components, PC1 and PC2, respectively; ξ1 and ξ2 are the eigenvectors of genotype i for PC1 and PC2, respectively, and η1 and η2 are the eigenvectors of environment j for PC1 and PC2.

Result and Discussion

Results of single location analysis of variance for grain yield traits for large-seeded common bean genotypes tested at five locations in the 2017 cropping season are presented in Table 3. ANOVA of data at individual locations revealed a significant difference (P< 0.01) among the genotypes in grain yield traits at all locations. There was a large genotypic variance in the 20 large-seeded genotypes included in this study.

Table 3. Single location analysis of variance for grain yield in large-seeded common bean genotypes measures in five locations in 2017 cropping season

Source of variation	DF	Mean Square				
		Alem Tena	Arsi Negele	Haramaya	Melkassa	Sirinka
Rep	2	5167712***	9288613***	2124632***	1019339.5**	1165126.7**
Genotype	19	386141.5***	866159.6***	507687.8***	654257.4***	358619.3**
Error	38	88676.54	167356.8	135956.9	139605	145901.4
CV		14.41	12.93	15.19	15.97	14.89

*, **, *** = Significant at p<0.05; p<0.01; p<0.001 respectively; Degrees of freedom (DF); replication (Rep); Coefficient of variance (CV)

Combined analysis of variance revealed significant differences (P<0.01) among environments, genotype, and genotype x environment interaction for grain yield (Table 4). The results showed that the genotypes have different performance in the testing environments and the environment have a different impact on the genotype yield performances. A significant GEI is common in experiments of this nature and it refers to the modification of genetic factors by environmental factors and the role of genetic factors in determining the performance of genotypes in different

environments. The current result was in agreement with the finding of Kebere *et al*., (2006), and Barili *et al.*, (2016) reported the presence of the significant effect of genotype, environments, and their interaction on common bean grain yield.

Table 4. Combined analysis of variances of yield for 20 large-seeded genotypes grown at five locations during the 2017 cropping seasons

Source of variation	DF	MS
Gen	19	1279164.3**
Env	4	9956847**
Rep(Env)	10	3753084.4**
GEI	76	373425.31**
Residue	190	135499.3
CV%		14.6

** = Significant at 1% probability, DF = degrees of freedom, CV % = coefficient of variance and MS = mean square

Mean performance of genotypes across locations for grain yield

Grain yields at Alem Tena ranged from 1326 kg ha^{-1} for Deme released in 2008 to 2737.8 kg ha^{-1} for DAB-107 released in 2017. At Arsi Negele, this range was from 2038 kg ha^{-1} for Montcalm released in 2007 to 3991.6 kg ha^{-1} for Babile released in 2012. The mean yield ranges from 3205 kg ha^{-1} for Ado released in 2015 to 3205 kg ha^{-1} for Hirna released in 2012 at Haramaya. Similarly, the mean grain yield attained at Melkassa, ranged from 1311.3 for Tinike released in 2012 to 3014.4 kg ha^{-1} DAB-107 released in 2017. At Sirinka, this range was from 1579.2 kg ha^{-1} for Montcalm released in 2007 to 3113.7 kg ha^{-1} for Babile released in 2012.

In grain yield, frequent changes in rank orders were observed among the performances of the genotypes across the environments. For instance, genotype DAB-107 exhibited the highest grain yield of 3113.7 kg ha^{-1} at Sirinka, 3014.4 kg ha^{-1} at Melkassa, and 2737.8 kg ha^{-1} at Alem Tena while at Aris Negele and Haramaya it ranked 13^{th} and 10^{th}, respectively. These results showed differences in grain yield performance among the tested genotypes in different environments. Likewise, Kassaye (2006), Yayis, *et al*, (2011) indicated differential responses in yield among different common bean genotypes.

The average grain yield of genotypes released after 2012 that showed maximum values includes 2737.8 (DAB-107), 3991.6 (Babile), 3205 (Hirina), 3014.4 (DAB-107), and 3113.7(DAB-107), at Alem Tena, Aris Negele, Haramaya, Melkassa, and Sirinka respectively. The minimum grain yield of 1326 (Deme) released in 2008, 2038 (Montcalm) released in 2007, 1623.7 (Ado) released in 2015, 1311.3 (Tinike) released in 2012 and 1579.2 (Montcalm) released in 2007 was achieved at Alem Tena, Aris Negele, Haramaya, Melkassa, and

Sirinka accordingly. Generally, the mean of individual genotypes in each location showed that there was a gradual increase in grain yield however; the increment was not in association with a year of release or age of the genotypes.

The mean average grain yield of the genotypes across the environments ranged from the lowest to the highest grain yield (1875 – 2875 kg ha^{-1}). The highest means grain yield value is obtained 2872 kg ha^{-1} on the recently released (2017) large-seeded genotype DAB-107 followed by Hirina released in 2012 with mean 2802 kg ha^{-1}, whereas the lowest mean grain yield value of 1875 kg ha^{-1} was obtained on Montcalm genotype released in 2007 (Table 5). The difference between the highest yielder 'DAB-107' genotype and the lowest yielder Montcalm genotype was 997 kg ha^{-1} in grain yield.

The average environmental grain yield across genotypes ranged from the lowest of 2066.8 kg ha^{-1} at Alem Tena to the highest of 3164.6 kg ha^{-1} at, Aris Negele with a grand mean of 2512.89 kg ha^{-1} (Table 5). The overall yield performance of Alem Tena and Melkassa was lower than that of Aris Negele, Haramaya, and Sirinka. Mainly due to higher temperature and lower total rainfall that might shorten the growth period at Melkassa and Alem Tena, gave rise to lower yields (Table 5 and Table 1). The present study indicated that genotypes responded differently to the different environments in terms of grain yield. Different authors support this finding. Perreira *et al.*, (2010), Fikre *et al.*, (2011), and Faria *et al.*, (2013) indicated that bean genotypes can have a different response and relate highly to environmental change.

Stability analysis based on Additive Main effects and Multiplicative Interaction (AMMI) model

AMMI analysis of variance for grain yield of tested large-seeded genotypes across environments showed that genotypes, environment, and the GEI were highly significant (Table 6). According to Table 6, the main effects of genotype and environment accounted for 26.27 % and 43.05%, respectively and GEI accounted for 30.67% of the total sum of squares for grain yield. This indicated that the environments were diverse and caused the greatest variation in grain yield.

The major component of environmental variability was rainfall, with annual rainfall ranging between 728 mm (Alem Tena) and 876 mm (Arsi Negele) (Table 5) and it is common in Ethiopia; the higher the altitude the higher the rainfall. This study clearly showed that the environments were distinct, and the genotypes responded differently to the different environments in terms of grain yield. The GEI sum of squares was larger than that of genotypes, which complicates the selection of superior and adaptable genotypes. Similar results were reported in common beans by Asfaw (2011), Correa, *et al.*, (2016).

Table 5. Mean grain yield in kg ha^{-1} of 20 large-seeded common bean genotypes tested at five locations during the 2017 cropping season

	Yield					
Genotypes	**AT**	**AN**	**HU**	**MK**	**SK**	**Mean**
Gobe Rasha-1	2406.1^{ab}	3302.3^{abcd}	2321.3^{abc}	2652.5^{ab}	2928.4^{a}	2722
Ibado	2250.6^{abc}	3625.3^{ab}	2308.5^{abc}	2973.1^{a}	2586.3^{ab}	2749
Melka Dima	2388.6^{ab}	3351.6^{abc}	2457.4^{abc}	2109.3^{abc}	2410.5^{ab}	2544
Cranscope	2527.3^{a}b	3256.8^{abcd}	1901.3^{bc}	1716.3^{bc}	2405.6^{ab}	2361
Montcalm	2076.5^{abcd}	2038^{d}	1723.2^{bc}	1955.8^{abc}	1579.2^{b}	1875
Deme	1326^{d}	3217^{abcd}	2104.2^{abc}	1913.8^{abc}	2601.8^{ab}	2233
Batu	1680.8^{bcd}	2656.9^{bcd}	2679.3^{abc}	1704^{bc}	2595.3^{ab}	2263
Loko	2419.8^{ab}	3625.3^{ab}	2781.2^{ab}	2152.3^{abc}	2526.2^{ab}	2701
GLP-2	2086.9^{abcd}	2874.9^{abcd}	3070.4^{a}	2681.5^{ab}	2540.5^{ab}	2651
Morka	1984.3^{abcd}	3190^{abcd}	2649.5^{abc}	2855.3^{ab}	2720.7^{ab}	2680
Tininke	1963.7^{abcd}	2238.1^{cd}	2237.8^{abc}	1311.3^{c}	2467.6^{ab}	2044
Fedis	1760.9^{bcd}	3662.9^{ab}	2334.2^{abc}	2500.5^{ab}	2893.3^{a}	2630
Babile	1995.4^{abcd}	3991.6^{a}	2617.3^{abc}	2518.6^{ab}	2844.9^{a}	2794
Hirna	1840.8^{abcd}	3701.8^{ab}	3205^{a}	2228^{abc}	3032.7^{a}	2802
Ramada	1449.5^{bcd}	3562.4^{ab}	2613.5^{abc}	2179.5^{abc}	2533.8^{ab}	2468
Ado	1811^{bcd}	2239.2^{cd}	1623.7^{c}	2466.7^{abc}	1959.5^{ab}	2020
Tafach	2183.1^{abcd}	2863.1^{abcd}	2084.9^{abc}	2479.1^{ab}	2522.4^{ab}	2427
Hundane	2098.9^{abcd}	3324.7^{abc}	2833.8^{ab}	2405.7^{abc}	2555.2^{ab}	2644
DAB-107	2737.8^{a}	3015.8^{abcd}	2477.5^{abc}	3014.4^{a}	3113.7^{a}	2872
Gorossa	2348.9^{abc}	3554.2^{ab}	2526.2^{abc}	2974.9^{a}	2500.4^{ab}	2781
Mean	2066.8	3164.6	2427.5	2339.6	2565.9	2512.9
CV%	14.4	12.9	15.2	16.0	14.9	14.6

AT: Alem Tena; AN Aris Negele; HU: Haramaya; Mk: Melkassa; SK: Sirinka; CV: coefficient of variation; Means in a column followed by similar letters are not significantly different at the 0.05 probability level based on Tukey HDS; bold values are highest yields in each test environment.

Table 6. Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for grain yield (kg/ha) of large-seeded genotypes across environments

Source of variation	DF	SS	MS	TSS Explained %
ENV	4	39827388	9956847.00***	43.05113
GEN	19	24304122	1279164.33***	26.27137
GEI	76	28380323	373425.30***	30.67751
PC1	22	12852083	584185.59***	45.28519
PC2	20	7487645	374382.25***	26.38323
PC3	18	5361280	297848.89***	18.89084
PC4	16	2679315	167457.19***	9.44075
Residuals	190	25744870	135499	

*, **, and *** implies significance at p<0.05, p<0.01 and p<0.001, respectively; DF = degree of freedom; SS = sum square; MS= mean square; TSS= total sum square; ENV= environment; GEN= genotype; GEI =genotype by environment interaction and PC = principal component

AMMI stability value (ASV) and Genotype selection index (GSI)

Table 7 indicates the different stability parameters that can determine the stability of a given genotype across the tested environment. Accordingly, the AMMI stability value and Genotype selection index should be simultaneously seen before deciding on the stability of a genotype.

Purchase *et al*. (2000) proposed a new method for a quantitative stability measure named AMMI stability value (ASV). The ASV, which is the distance from the coordinate point to the origin in a two-dimensional scatter gram of PC1 scores against PC2 score, should also be seen to decide the stability of a genotype. In the ASV method, the genotype with the least ASV score is the most stable whereas those with the highest ASV are considered unstable. ASV discriminated genotypes Melka Dima, Morka, GLP-2, and Hundane respectively the most stable, and Montcalm, Hirna and SAB 736 were unstable (Table 16). However, Mohammadi and Amri, (2008) suggested that the most stable genotypes would not necessarily give the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index.

For a simultaneous selection of yield and stability, Farshadfar (2008) recommended a new approach known as the genotype selection index (GSI). GSI was calculated by adding the rank of AMMI stability value (RASV) and the rank of mean grain yield of genotypes (RY) across environments. This parameter's least value is considered the most stable with a high grain yield genotype. Based on the genotype selection index, the most desirable genotype for selection of both stability and high grain yield was Morka (G10) followed by GLP-2 (G9), Gobe Rasha-1(G1), Gorossa (G18), and Melka Dima (G3). While, genotypes Montcalm (G5), SAB 736 (G16), and Tininke (G11) were unstable among tested genotypes, in addition, this study found out that Morka, GLP-2, and Gobe Rasha-1, Gorossa, and Melka Dima genotypes have the highest mean performance and stable (used for wide adaptation). However, Montcalm, SAB 736, and Tininke had the lowest mean performance and were unstable. These results are similar to the results, observed in the AMMI2 biplot in this study. Hagos and Fetien (2011) and Ezatollah et al. (2011) studied the effect of GEI using AMMI in corn genotypes, using different stability parameters. As result, they presented GSI as the best approach, due to identified genotypes that have both high mean yield and stable yield performance across different environments. Genotypes G19, G14, and G13 had high mean grain yield among tested genotypes but were placed far from the biplot origin suggesting that they were not stable (Table 7). However, G14 and G13 genotypes appeared to be specifically adapted to the environment Arsi Negele, Haramaya, and Sirinka. G19 specifically adapted to Alem Tena and Melkassa (Figure 2).

Table 7. Mean grain yield, ASV, GSI values, and ranks of large-seeded size common bean genotypes in five environments 2017.

Genotypes Code	Genotypes Name	Mean yield	RYi	IPCA1	IPCA2	ASVi	RASVi	GSIi	RGSIi
G1	Gobe Rasha-1	2722	6	5.315	-2.771	9.534	6	12	2
G2	Ibado	2749	5	3.77	-14.611	15.98	10	15	8
G3	Melka Dima	2543	12	0.355	4.393	4.435	1	13	5
G4	Cranscope	2361	15	3.747	6.173	8.915	5	20	11
G5	Montcalm	1875	20	18.831	4.909	32.693	20	40	20
G6	Deme	2233	17	-12.485	-4.674	21.934	14	31	17
G7	Batu	2263	16	-7.142	15.067	19.424	12	28	15
G8	Loko	2701	7	-4.879	5.601	10.074	7	14	6
G9	GLP-2	2651	9	2.345	5.582	6.882	3	12	2
G10	Morka	2680	8	1.221	-5.83	6.195	2	10	1
G11	Tininke	2044	18	1.702	22.502	22.691	15	33	18
G12	Fedis	2630	11	-9.145	-10.403	18.831	11	22	13
G13	Babile	2794	3	-11.581	-8.712	21.703	13	16	9
G14	Hirna	2802	2	-17.975	5.618	31.361	19	21	12
G15	Ramada	2468	13	-15.875	-5.499	27.797	17	30	16
G16	SAB 736	2020	19	16.912	-7.339	29.942	18	37	19
G17	SAB 632	2427	14	9.15	-2.292	15.871	9	23	14
G18	Hundane	2644	10	-3.771	2.468	6.928	4	14	6
G19	DAB-107	2872	1	14.798	0.499	25.404	16	17	10
G20	Gorossa	2781	4	4.709	-10.682	13.395	8	12	2

RYi=rank in yield, IPCA1, 2= interaction principal component axis 1 and 2, ASVi= AMMI stability value, RASVi= rank of AMMI stability value, GSIi= genotype selection index, RGSIi=Rank genotype selection index

AMMI Biplots

Analysis of the AMMI model Table 7 showed that the first principal component (PC1) accounted for 45.29% and the second principal component (PC2) accounted for 26.38% interaction sum of squares. The other interaction effects were explained by the remaining principal components. The first two principal components accounted for cumulative 71.67% interaction effects, which, indicated the majority of interaction effects were within two principal components. In agreement with this, Tadesse *et al.* (2017) reported the first two axes (71.2%) explained a high percentage of the sum square of the GEI and the highest part of the pattern of the GEI will be captured. Furthermore, Zobel *et al*. (1988) showed that AMMI with PCA1 and PCA2 is usually selected and more appropriate to clarify the GEI and relationship of genotypes and environments.

AMMI2 biplot was generated using genotypic and environmental scores of the first two AMMI multiplicative components to cross-validate the interaction pattern of the 20 large-seeded common bean genotypes within five environments (Figure 1). In the AMMI2 biplot, environments with low IPCA1 and IPCA2 scores that are placed close to the origin have a high contribution to the stability of genotypes and low contribution to GE interaction. Furthermore, when IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the

genotypes score to the center of the biplot (fig. 1), the more stable they are. In this study, AMMI2 biplots indicated genotypes G10 (Morka), G1 (Gobe Rasha-1), G3 (Melka Dima), G9 (GLP-2), and G18 (Hundana) were demonstrated low interactive action over environments. This revealed that these genotypes demonstrated lower fluctuations to the changes in the growing environment. Whereas G11(Tininke), G5(Montcalm)), G14 (Hirna), and G16 (SAB 736) were located far away from the origin indicating their large contribution to the total GEI variance are considered as unstable genotypes.

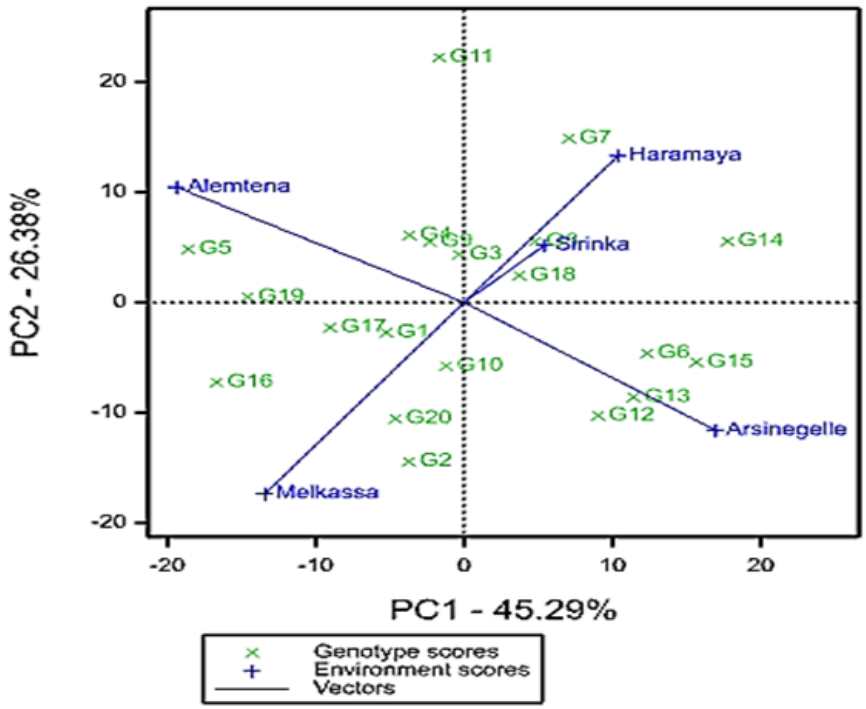

Figure 1. AMMI biplot with the first two components from data on 20 large seeded genotypes across five environments in Ethiopia. The shortening (codes) of genotypes is as given in Table 7.

Genotype and genotype by environment interaction effects (GGE) model

In this study, the GGE biplot will be interpreted using two principal components that explained 74.44% of yield variations. In agreement with Sousa *et al.* (2015) who evaluated twenty-seven early-cycle soybean genotypes; the GGE biplot model were presented greater efficiency by retaining most of the variation in the first two main components (61.46%).

Determining the best genotype in an environment (Which-won-where)

Which-won-where graph is constructed first by joining the farthest genotypes forming a polygon.

Subsequently, perpendicular lines are drawn from the origin of the biplot to each side of the polygon, separating the biplot into several sectors with one genotype at the vertex of the polygon. These lines are referred to as equality lines (Yan 2001). Genotypes at the vertices of the polygon are either the best or poorest in one or more environments.

In the current study, at the vertices of the polygon there are seven divisions with genotypes 'G19' (DAB-107), 'G13'(Babile), 'G14 (Hirna), 'G7' (Batu), 'G11 (Tininke)', 'G5' (Montcalm) and 'G16' (SAB 736) as the corner or vertex genotypes (fig 2). Based on this analysis, the testing locations were partitioned into two mega-environments. mega-environment one was represented by Alem Tena and Melkassa with G19 (DAB-107) the winning genotype and mega-environment two consisted of Arsi Negele, Haramaya, and Sirinka with 'G13' (Babile) and 'G14'(Hirna) as the winning genotypes. While, G5', 'G7', 'G11,' and 'G16' (released in 2007, 2008, 2012, and 2013 respectively) were not the best in any of the environments since no environments fell into sectors with these cultivars. Correa et al. (2016) used this model when evaluating the common bean genotypes that exhibit high grain yield and stability across multiple environments.

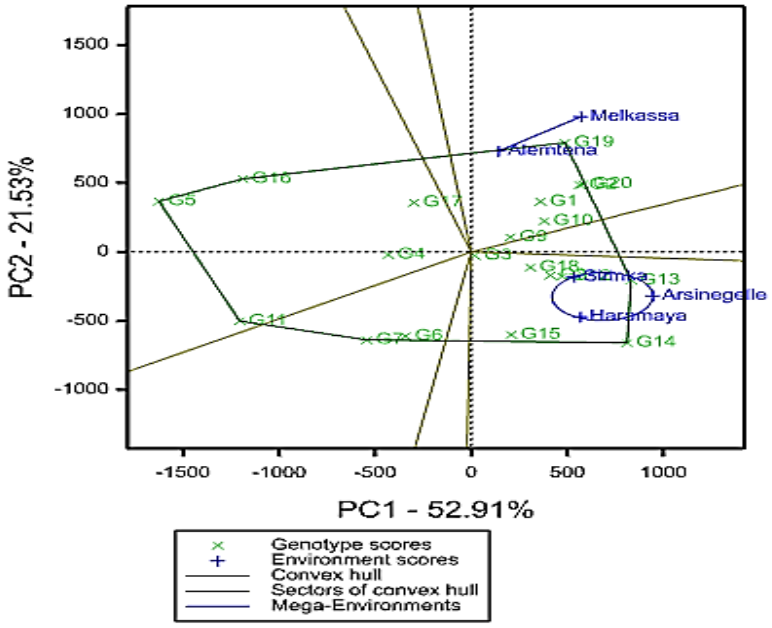

Figure 2. The which-won-where view of the GGE biplot for 20 large seeded genotypes data growing in 5 environments. The shortening (codes) of genotypes is as given in Table 7

Comparison of the Genotypes with the Ideal Genotype

The ideal genotype is defined as one that has the highest performance in all environments and is stable. Genotype-focused scaling generates a ranking of the cultivars in terms of both mean performance and stability. GGE biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype is presented in Fig 3. Yan and Rajcan, (2002) suggested that an ideal genotype should have the highest mean performance and be consistently stable in all environments and it is graphically defined by having the longest vector length without GEI and represented by an arrow in the center of the concentric circles. Hence, genotypes located closer to the ideal genotype are more desirable than others are. In line with this, Morka (G10) was more stable than others were and G1, G3, and G18 were greater than the other genotypes (Figure 3).

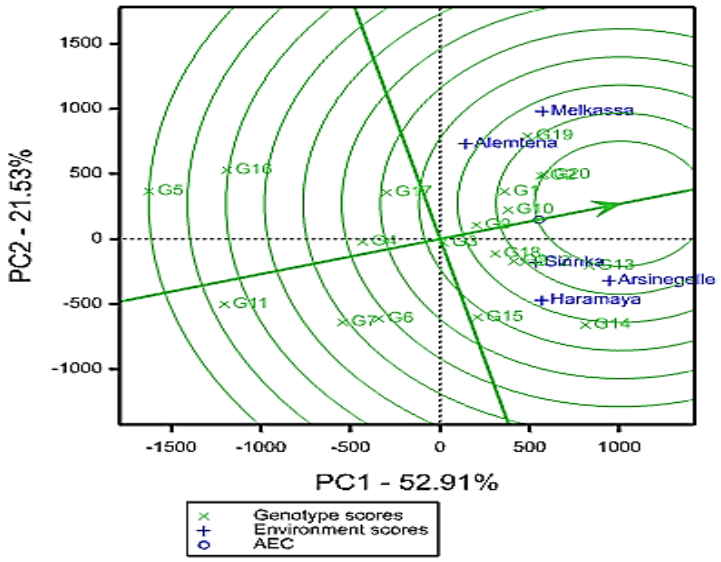

Figure 3. GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype for 20 large seeded common beans. The shortening (codes) of genotypes is as given in Table 7.

Comparison of the Environment with the Ideal Environment

Rank environments with reference to the ideal environment. The ideal environment is defined as the most discriminating and representative. It generates a ranking of the test environments in terms of both criteria. An ideal environment should have a greater power of discrimination in terms of genotype main effects with high PC1 score and the most representative of all of the other

environments, which is zero PC2, scores (Yang *et al*., 2009). In the same way as the ideal genotype, the ideal environment is only an estimate and serves as a reference for the choice of site for multi-environment testing. Figure 4 defines an ideal test environment, which is the center of the concentric circles. This is a point on the AEA in the positive direction (most representative), with a distance to the biplot origin equal to the longest vector of all environments (most informative).

In the current study, Aris Negele is closest to this point, therefore, the greatest capacity for discriminating between genotypes, and favored the selection of superior genotypes, whereas Alem Tena was poorest for selecting cultivars adapted to the whole region. Recently, GGE biplots have been used in common bean (Asfaw *et al*. 2008), (Zeleke *et al*. 2016), (Correa *et al*. 2016) used to investigate the adaptability and phenotypic stability of different genotypes from different locations.

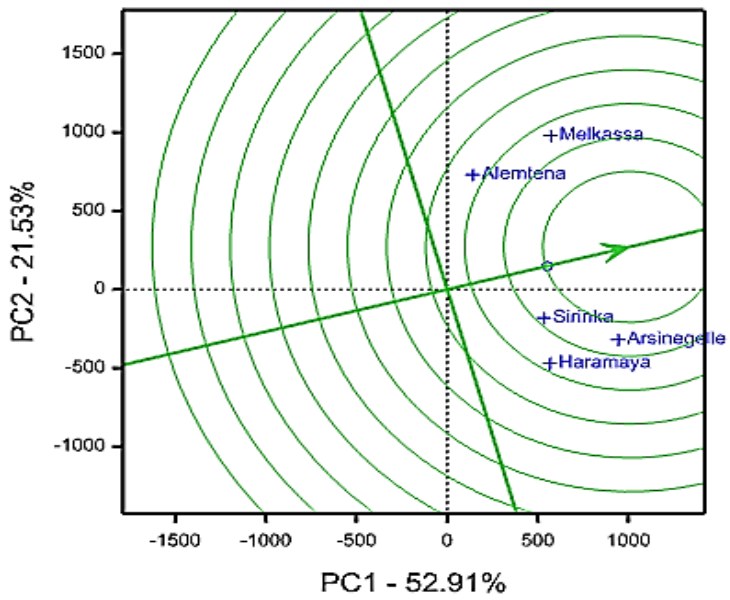

Figure 4. GGE-biplot based on environment-focused scaling for comparison the environments with the ideal environment for 20 large seeded genotypes data growing in 5 environments.

Conclusion and Recommendation

This study determined genotype by environment interaction effect, stability of genotypes, and representativeness and discriminating ability of environments of grain yield in large seeded common bean released varieties grown in Ethiopia. Whenever varieties are released for small-scale

and commercial production, information on genotype by environment interaction and stability indicates their general and/or specific adaptations need- to be available to the users. The study has clearly and with ease confirmed that large seeded common bean grain yield was highly affected by environmental variation followed by genotype by environment interaction and genotypic effect contributing the least.

In this study, AMMI and GGE models were used to identify the most stable and high yielding genotypes among the released large-seeded genotypes in Ethiopia. As a result, both models identified genotypes G10, G1, G3, and G18 display higher grain yield and stability among tested genotypes in this study. Except for G10, the remaining best performed and stable genotype genotypes were released for specific adaptations however this has a look discovered that G1, G3, and G18 genotypes may be directed as wide adaptation genotypes in the county. Genotypes 'G13'and 'G14' were exhibited average stability in location Arsi Negele, Haramaya, and Sirinka however these genotypes were released for east and west Hararghe. On the other hand, high yielding genotype G19 (DAB-107) specific adaptations on Alem Tena and Melkassa.

In addition, the environment Aris Negele preferred for the selection of superior genotypes for large-seeded common bean genotypes than the other testing locations. GGE biplot reveals that the five testing locations were grouped into two mega environments. Even though, the result is from one-year data at five locations. As a result, to conduct the over location trials effectively with limited resources, discriminative locations encompassing representative locations may be included, rather than extending the trials extensively over related locations.

References

Acland, J.D. 1971.East African Crops. *Longman Group Limited. London*.: 20-25.

Asfaw, A., T. Assefa., B. Amsalu., K. Negash., F. Alemayehu., F. Grum., Y. Rezene., C. Finensa., M. Atnaf., and C. Daba. 2008. Adaptation and Yield Stability of small Red Bean Elite Lines in Ethiopia. Int. J. of Plant Breed and Genet. 2(2): 51-63.

Asfaw, A (2011) Breeding for drought tolerance by integrative design: the case of common bean (*Phaseolus vulgaris* L.) in Ethiopia. Ph.D. thesis, Wageningen University, The Netherlands, 187pp.

Barili1 L.D., Vale N.M., Moura L.M., Paula R.G., Silva F.F.andCarneiro J.E.S. 2016. Genetic progress resulting from forty-three years of breeding of the carioca common bean in Brazil Genet. *Mol. Res*, 15 (3): 1-8.

Carbonell, S.A.M.; Azevedo Filho, J.A.; Dias, L.A.S.; Gonçalves, C.; Antonio, C.B. M L.K 2004 common bean cultivars and lines interaction with environments Sci. Agric. (Piracicaba, Braz.), v.61, n.2, p.169-177, Mar./Apr. 2004

Cobley, L.S. 1976.*An introduction to the Botany of Tropical crops.2nd ed*. Long man group limited. London. Correlation of morphological and quality traits with mineral element contents in Yunnan rice. Rice Sci., 12 (2): 101-106.

Correa AM, Teodoro PE, Gonçalves MC, Barroso LMA, .2016. Selection of common bean (*Phaseolus vulgaris* L.) genotypes using a genotype plus genotype x environment interaction biplot. Genet. Mol. Res. 15: gmr.15038427.

CSA (Central Statistical Agency).2017/18. Ethiopian Agricultural Sample survey, 2017/2018. Report on area and production of major crops. Statistical bulletin, volume v. Addis Ababa, Ethiopia.

Ezatollah Farshadfar, Nasrin Mahmodi, Anita Yaghotipoor 2011 AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.) Australian Journal of crop science AJCS 5(13):1837-1844 (2011)

Faria .LC , Melo P.G.S, Pereira H.S, Peloso M.J, Bras A.J.B , Moreira J.A.A, Carvalho H.W.L, Melo L.C 2013 Genetic progress during 22 years of improvement of carioca-type common bean in *Brazil filed crops research* 142(2013) pp 68-74 Elsevier

Farshadfar E (2008) Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. Pak J Biol Sci 11(14): 1791-1796

Ferreira D.F., Demetrio C.G.B., Manly B.F.J., Machado A.A., and Vencovsky R., 2006. Statistical model in agriculture: Biometrical methods for evaluating phenotypic stability in plant breeding. Cerne Lavras 12(4): 373-388.

Fikre A., Negwo T., Kuo Y., Lambein F., and Ahmed S. 2011. Climatic, edaphic, and altitudinal factors affecting yield and toxicity of Lathyrus sativus grown at five locations in Ethiopia. Food and Chemical Toxicology 49 (2011) 623–630

Gauch H.G. 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46:1488–1500.

Genstat Release 18th edition (PC/Windows 7) Copyright. 2016. VSN International Ltd. germplasm. In: Fatokun CA, Tarawali SA, Singh BB, Kormawa PM, Tamo M (eds) Challenges

Ghaderi, A.; G. L. Hosfield; M. W. Adams and M. A. Uebersax, 1984.Variability in culinary quality, component interrelationships, and breeding implications in navy and pinto beans. *Journal of American Society of Horticultural Sciences,*109 (1): 85-90.

Gomez, K. and Gomez A. 1984. *Statistical Procedure for Agricultural Research.2nd ed*. International Rice Research Institute. John Wiley and Sons Inc.680p.

Hagos Tadesse and Fetien Abay. 2011. Additive Main Effects and Multiplicative Interactions Analysis of Yield Performance of Sesame Genotypes across Environments in Northern Ethiopia. Journal of the Drylands 4(1): 259-266.

Hussein, M.A., A. Bjornstad and A.H. Aastveit, 2000. Sag x estab, A SAS Program for Computing Genotype x Environment Stability Statistics. *Agronomy Journal* 92:454–459. *J.* 80: 388-393.

Kassaye Negash., 2006. Studies on Genetic divergence in common bean (*Phaseolus vulgaris* L.) introductions of Ethiopia. An MSc Thesis Presented to the School of Graduate Studies of Addis Abeba University, 11p, and 46p.

Kay D. E. 1979. Food Legumes: Crop and Product Digest, No. 3. London: Tropical Products Institute. 435pp

Kaya Y, Aksura M, Taner S (2006) CGE-Biplot analysis of multi-environment yield trials in bread wheat. Bahari Dağdaş International Agricultural Research Institute, Turk J Agric For. 30: 325-337.

Kebere B., Ketema B., and Prapa S.2006. Genetic gain in grain yield potential and associated agronomic traits in haricot bean (Phaseolus vulgaris L.). Kasetsart Journal *(Natural Science)*, 40: 835-847.

Keneni, G., Bekele, E., Imtiaz, M., Getu, E., Dagne, K., and Assefa, F., 2011 Breeding chickpea (*Cicer arietnum* [Fabaceae]) for better seed quality inadvertently increased susceptibility to

adzuki bean beetle (*Callosobruchus Chinensis* [Coleoptera: Bruchidae]). Int J *Trop Insect Sci.* 31(4): 249-261.

McIntosh, M.S. 1983. Analysis of combined experiments. *Agron. J.*, 75:153-155.

MoA. (Ministry of Agriculture) 2017, Animal and Plant Health Regulatory Directorate. Crop Genotype Register Issue No. 17, June 2017, Addis Ababa, Ethiopia

Mohammadi R and Amri A (2008) Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. E*uphytica* 159: 419–432

Perreira H.S., Melo L.C., Faria L.C., Diaz J.L., Peloso M.J., and Wendland A., 2010. Environmental stratification in Parana and Santa Catarina to Evaluate Common Bean Genotypes. Crop Breeding and Applied Biotechnology 10: 132-139.

Purchase, J.L., H. Hatting, and Cs.Vandeventer. 2000. Genotype by environments interaction of wheat in South Africa: stability analysis of yield performance. South Africa Journal of plant science, vol.17, Pp, 101-107.

Robertson, G. E., 1959. The sampling variance of the genetic correlation coefficient. Biometrics 15: 469-485

SAS (Statistical Analysis System) Software, 2009. Version 9.2.inc.Carry, North Carolina, USA.

Singh SP, Terán H, Lema M, Webster DM, 2007. Seventy-five years of breeding dry bean of the western USA. Crop Sci. 47: 981-989.

Souza MA, Morais OP, Herán REC, Cargnin A and Pimentel AJB (2007) Progresso genético do melhoramento de arroz de terras altas no período de 1950 a 2001. Pesquisa Agropecuária Brasileira 42: 371-376

Steel, R. and J. Torrie. 1990. Principles and procedures of statistics a biometrical approach. 2nd ed. Mc Graw-Hill, Inc, pp. 471-472.

Wortmann C. S, Kirkby R.A., Eledu C.A., and Allen D. J. 1998.*Atlas of common bean production in Africa*. Cali Colombia: CIAT publication 297:133

Yan W., Hunt L.A., Sheng Q., and Sclavnica Z., 2000. Cultivar Evaluation and Mega environmental investigation based on GGE biplot. *Crop Science 40:597-605*.

Yan, W. 2002. Singular-value partitioning in biplot analysis of multi-environment trial data. Agron. J. 94: 990-996

Yan, W. and I. Rajan. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science. 42: 11-20.

Yang R.C., Baker R.J. (1991) Genotype-environment interactions in two wheat crosses. *Crop Science 31:83-87.*

Yang RC, Crossa J, Cornelius PL and Burgueño J (2009). Biplot analysis of genotype x environment interaction: proceed with caution. Crop Sci. 49: 1564-1576. http://dx.doi.org/10.2135/cropsci2008.11.0665

Yayis Rezene, Setegn Gebeyehu and Habitamu Zeleke, 2011. Genetic variability for drought resistance in small red seeded common bean genotypes. *African Crop Science Journal 19(4):303 – 311*

Zeleke A., A. Berhanu., T. Kidane., N. Kassaye and F. Asnake. 2016. Seed Yield Stability and Genotype x Environment Interaction of Common Bean (*Phaseolus vulgaris* L.) Lines in Ethiopia. International J. of Plant Breed. And *Crop Sci.*, 3(2): 135-144.

Zobel, R.W., M.J. Wright, and H.G. Gauch Jr. 1988. Statistical analysis of a yield trial. *Agron.*