Environmentally Stable Large Red Common Bean (*Phaseolus vulgaris* L.) Genotypes for Production in Different Bean Growing Regions of Ethiopia

Abel Moges[1], Berhanu Amsalu Fenta[1,2], Dagmawit Tsegaye[1], Girum Kifle[1], Kidane Tumsa[1,] Behailu Tesfaye[1], Samir Hashim[1], Kassaye Negash[1], Megra Dugo[1], Yonas Moges[3], Genet Kebede[4], and Zeru Yimer[5]

[1] Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Center, P.O.Box 436, Adama, Ethiopia; [2]Mohammed VI Polytechnic University (UM6P), Collage of Agriculture & Environmental Science - African Sustainable Agriculture Research Institute (ASARI),Morocco [3] Haramaya University, Diredawa, Ethiopia; [4] Amhara Regional Agricultural Research Institute, Sirinka Agricultural Research Center, Woldiya, Ethiopia; [5] Ethiopian Institute of Agricultural Research, Pawe Agricultural Research Center, P.O.Box 25, Pawe, Ethiopia; Corresponding author, E-mail: abvan23@gmail.com

Abstract

This study examines the yield stability and adaptability of large red bean genotypes across various bean-growing regions in Ethiopia. Sixteen genotypes were tested in fourteen different environments over four years (2015-2018) using a triple lattice design. Grain yield data were analyzed using several methods: Additive Main Effect and Multiplicative Interaction (AMMI), Genotype Main Effects plus Genotype × Environment Interaction (GGE), AMMI Stability Value (ASV), and Yield Stability Index (YSI). The results showed that grain yields were significantly influenced by the environment (77.03%), genotype (3.18%), and their interaction (10.26%) ($P \leq 0.01$). GGE biplot analysis identified four mega-environments, with MS16 (MEISO in 2016) being the most discriminative and representative site. Genotypes G4, G14, G15, and G9 were the most stable and high-yielding according to GGE biplot, while G12, G13, and G8 were stable but low-yielding based on ASV analysis. YSI identified G15, G10, G13, G14, and G9 as high-yielding and stable. Overall, GGE biplot stability statistics and YSI highlighted G9 (DAB 544) and G14 (DAB 481) as superior genotypes, suitable for commercial cultivation in Ethiopia.

Keywords: Adaptability, AMMI, GGE, stability, yield stability index

Introduction

In Ethiopia, common beans (*Phaseolus vulgaris* L.) are vital for generating foreign exchange and serve as a key staple legume in the national agricultural system (Habte *et al*., 2021). Their high protein, iron (Fe), and zinc (Zn) content significantly enhance human health and well-being (Huertas *et al*., 2023; Stevens *et al*., 2013). Over 4.3 million smallholders cultivate common beans on more than 256,000 hectares, accounting for about 2 % of all land planted to grain crops during the main season 2019 (CSA, 2020). Despite its importance, common bean production and yield have not reached their full potential due to various limiting factors.

The common bean (*Phaseolus vulgaris* L) was domesticated independently in South America and Central America/Mexico, resulting in two distinct gene pools: the Andean and Mesoamerican (Debouck *et al*., 1993). Genetic and morphological studies across various agroecological zones have highlighted clear differences between these gene pools. Andean beans typically have larger seeds, whereas Mesoamerican beans are characterized by smaller seeds (Blair *et al*., 2009; Sicard *et al*., 2005). Today, both gene pools of *Phaseolus vulgaris* L. hold commercial value. Mesoamerican beans are primarily produced in North and Central America, while Andean beans are more common in parts of Africa, Europe, and South America (Cichy *et al*., 2015). The introduction of the common bean to Ethiopia is likely linked to Portuguese exploration in the 16th century (IRMU, 1985 in Kefyalew, 1990). Although Ethiopia mainly grows beans from the Mesoamerican gene pool (Abebe & Lema, 2019), detailed information on the proportions and distribution of the two gene pools is lacking. This is because official statistics only classify beans as 'small red' and 'small white, without considering other seed colors and sizes (CSA, 2020). Small bean cultivars have shown superior agronomic performance in Ethiopia, leading to their widespread cultivation due to their high yield potential, in contrast to the lower productivity of larger bean varieties.

Several factors limit common bean production and productivity in Ethiopia. Climate variability, including temperature extremes, erratic rainfall, and increased disease and pest incidence, significantly affects common bean productivity and quality (Botero & Barnes, 2022; Diaz *et al*., 2018; Ntukamazina *et al*., 2017). These environmental challenges with poor agronomic practices, contribute to the persistently low national average yield of 1.7 tons per hectare (CSA, 2020), which falls significantly below the potential yield of over 3 tons per hectare achievable with most small bean cultivars (Amsalu *et al*., 2018). This gap is further pronounced for large bean genotypes. Due to a lack of high-yielding cultivars and various biotic and abiotic constraints for large beans, the average yield of this gene pool is expected to fall short of the national average of 1.7 tons per hectare. The interaction between genotypes and environmental factors is crucial in determining how beans respond to these challenges. Certain bean varieties may show better resilience or adaptability to specific environmental stresses. Therefore, developing high-yielding and stress-tolerant large bean cultivars is essential to improve productivity. The national research program has released only three large red bean varieties (Amsalu *et al*., 2018). These beans significantly underperform compared to their potential, mainly due to the lack of well-adapted cultivars and the negative impact of genotype-environment interactions (GEI).

Genotype by Environment Interaction (GEI) complicates the selection of superior varieties due to its interference with superior genotype selection and its negative impact on heritability (Ebdon & Gauch, 2002; Ramburan *et al*., 2011). Bean varieties exhibit different responses to environmental changes (Pereira *et al*., 2018), necessitating extensive multi-environment field trials to develop agronomically superior and stable new varieties. Conducting multi-location trials across diverse, representative environments helps identify ideal bean genotypes that perform well in target environments and have superior agronomic traits, potentially enhancing productivity (Castiano *et al*., 2023). Numerous studies on common beans have shown significant differences in grain yield and GEI (Firew *et al*., 2019; Mutari *et al*., 2022; Philipo *et al*., 2021). Therefore, screening various large red bean genotypes is crucial to identify high-yielding and stable varieties across different growing environments. This study aimed to evaluate the performance of different large red bean genotypes in various environments and identify those with superior yield stability across agroecologies for use in plant breeding programs focused on bean varietal development and release.

Table 2

Materials and Methods

Study materials and experimental design

Table 1 lists fourteen large red common bean genotypes received from the Alliance of Bioversity International and CIAT, along with two nationally released varieties, 'Melkadima' and 'ACOS Red,' used as checks in this study. The multi-environment trial was conducted across 14 different environments (combinations of locations and years) during the main cropping seasons from 2015 to 2018. That is i.e AT16=Alemtena_2016; AT17= Alemtena_2017; GF16=Goffa_2016; HU16=Haramaya_2016; KB16=Kobo_2016; MK16= Melkassa_2016; MK17=Melkassa_2017; MK18=Melkassa_2018; MS16=Meiso_2016; NA15=Negelle Arsi_2015; NA17=Negelle Arsi_2017; NA18=Negelle Arsi_2018; PW16=Pawe_2016; SK17=Sirinka_2017 (Figure 1). Information on test environments is given in Table 2.

Table 1 - Description of 16 large red bean genotypes evaluated in 14 environments during the 2015 – 2018 cropping season.

Geno_Code	Genotype	Pedigree
G1	DAB 497	BEAN5879/SAB679
G2	DAB 317	AS16334/AS16311
G3	DAB 482	BEAN5874/AS16309
G4	DAB 523	RMX8/AS16374
G5	DAB 512	ICA QUIMBAYA/AS16314
G6	DAB 513	BEAN5885/SAB686
G7	DAB 496	BEAN5886/ICA QUIMBAYA
G8	DAB 478	AS16321/SAB626
G9	DAB 544	BEAN5919/AS16309
G10	DAB 525	AS16334/AS16316
G11	DAB 545	AS16334/AS16311
G12	DAB 540	BEAN5919/AS16309
G13	DAB 532	AS16334/AS16311
G14	DAB 481	AS16321/SAB626
G15	Melkedima	G17661/BAT1297
G16	*ACOS red*	NA

The experiment utilized a 4 × 4 triple lattice design. Each experimental unit comprised 6 rows, each 4 meters long, with 40 cm spacing between rows and 10 cm between plants. All other management practices, including fertilization, followed the recommendations specific to each location. Data were collected from the middle 4 rows, and grain yields were measured per plot and converted to tons per hectare for statistical analysis.”

Table 2 - Description of the 9 locations used for the evaluation of 16 large red bean genotypes in Ethiopia

		Geographical position		Altitude (m.a.s.l)	Average rainfall (mm)	Temperature (°C)	
Location	Growing season	Latitude	Longitude			Min	Max
Alemtena	2016 - 2017	8^{0}18’N	38^{0}57’E	1610	728	12.9	29.8
Negelle Arsi	2015 & 2017 - 2018	7^{0}35’N	38^{0}65’E	1890	807	13.8	23.3
Melkassa	2016 - 2018	8^{o}30’N	39^{o}21’E	1550	763	14	33
Sirinka	2017	11^{0}08’N	39^{0}28’E	1880	876	13.6	27.3
Pawe	2016	11°19'N	36°24'E	1120	1587	16	32
Meiso	2016	9028' N	38^{0}08’E	1332	787	14.9	28.2
Goffa	2016	7^{0}15’N	37^{0}04’E	1750	964	14.4	25.9
Haramaya	2016	9^{0}26’N	42^{0}03’E	1980	790	3.5	25
Kobo	2016	12^{0}08’N	39^{0}18’E	1450	673	13	34

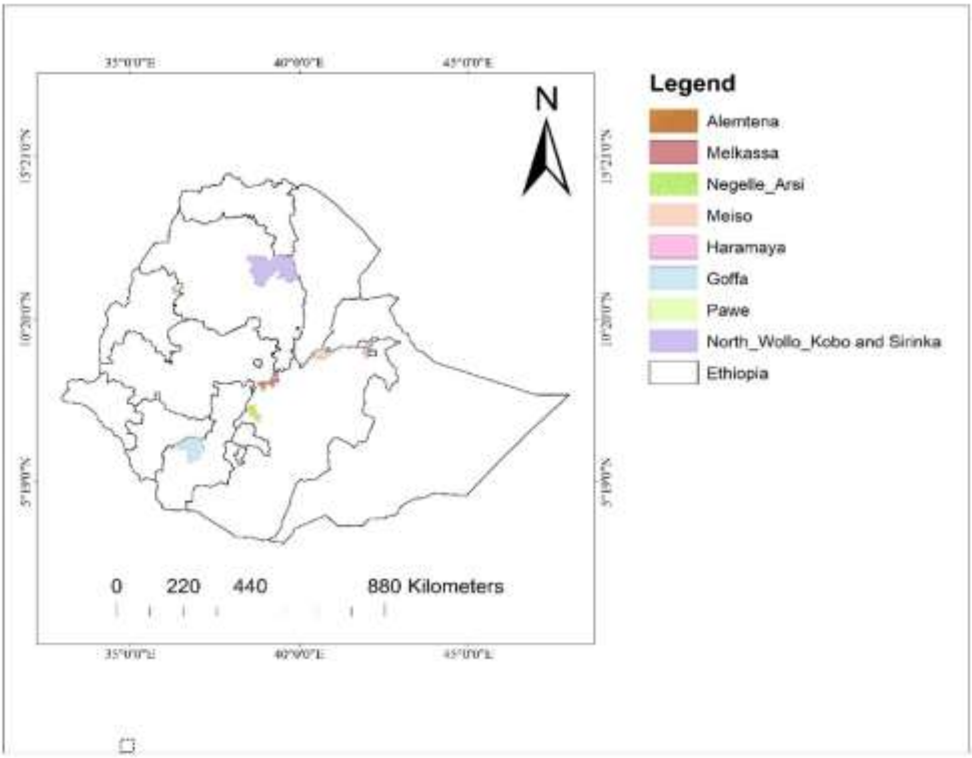

Figure 1. Map of Ethiopia showing the field experimental sites

Statistical analysis

The grain yield data were subjected to a combined analysis of variance and the G × E interaction was estimated using the AMMI model (Zobel *et al* ., 1988). Analysis of variance is used to partition variance into three components: how much genotypes differ on average, how much environments contribute to the differences, and how much a genotype's performance depends on the specific environment in GEI. Subsequently, a multiplication effect analysis further dissects them into independent components called interaction principal component axes (IPCAs), which can be evaluated for significance through ANOVA. The Genstat 18 edition (VSN International Ltd., 2014) software was used for combined analysis of variance and AMMI analysis.

GGE biplots summarize genotype and genotype-environment interaction effects on yield data using singular value decomposition (Yan, 2002; Yan *et al*., 2000). The study employed a GGE biplot to rank yield and stability genotypes. Also, vector length and cosine value of the angle between the location and the average location were used to measure location discrimination and representativeness. The GGE biplot analysis produced graphs that identified winning genotypes in specific environments, revealing whether distinct mega-environments (groups of similar environments) were present (Yan, 2001; Yan & Rajcan, 2002). The CIMMYT's GEA-R software was used for GGE biplot analysis.

The yield stability of common bean genotypes was assessed using the AMMI Stability Value (ASV) described by Purchase *et al.* (2000). This approach allowed the quantification and ranking of genotypes based on their performance consistency across varied environments.

$$ASV = \sqrt{\left[\frac{SSIPC1}{SSIPC2}(IPC1)\right]^2 + (IPC2)^2}$$

Where *SSIPC1* is the interaction principal component one sum of the square, *SSIPC2* is the interaction principal component two sum of the square, *IPC1* and *IPC2* are interaction principal components 1 and 2 respectively.

The yield Stability Index (YSI) of each common bean genotype in terms of yield was calculated based on the rank of the ith genotype across environments based on AMMI Stability Value (RASVj) and rank of the ith genotype based on mean yield across environments (RYi) (Adjebeng-Danquah *et al.*, 2017; Bose *et al.*, 2014) as

$$YSI = RASVi + RYi$$

Results and Discussion

GEI interaction and genotypic mean performance

The combined analysis of variance revealed significant variability in grain yield, with highly significant differences ($p < 0.001$) observed across environments, genotypes, and their interaction (Table 3). This variability highlights the influence of genes, environment, and their interaction on grain yield in common bean seeds, presenting a prime opportunity for selection efforts. Consistent with previous studies by Philipo *et al.* (2021), Ligarreto–Moreno and Pimentel–Ladino (2022), and Castiano *et al.* (2023), this study observed significant variation attributable to the main effects of genotype (G), environment (E), and their interaction on common bean grain yield. The environment was the major contributor to this variation, accounting for 77.03% of the total variance, suggesting the significant influence of diverse environmental factors on grain yield. Environmental factors such as soil type, temperature, rainfall patterns, and sunlight exposure are major contributors to crop grain yield (Adams *et al.*, 1999). For instance, certain common bean genotypes may perform exceptionally well in moderate temperatures and consistent rainfall, while others may thrive in higher temperatures and less rainfall (Suárez *et al.*, 2020). This indicates a high sensitivity of common bean grain yield to environmental conditions, with the environment playing a dominant role in determining overall performance. This study findings, which highlight the significant impact of environmental effects on variation, are consistent with previous GEI studies on common bean (Firew *et al.*, 2019; Mekbib, 2003), faba bean (Tolessa T, 2015), and wheat (Roostaeia *et al.*, 2014). Consequently, breeding efforts aiming to develop common bean varieties must carefully consider environmental variability to ensure stable performance across diverse growing regions.

Although genotype effects contributed to grain yield, their impact was relatively minor (3.18%), indicating moderate inherent differences among the genotypes evaluated. The most notable discovery, however, was the significant Genotype by Environment Interaction (GEI), which accounted for 10.26% of the variance. This finding reveals that genotypes exhibit varying performances across different environments, underscoring the complex relationship between genetic makeup and environmental conditions. Remarkably, the GEI effect was nearly three times greater than the genotype effect, highlighting the importance of environment-specific performance in selecting superior genotypes. These results emphasize the need to consider both high mean grain yield and adaptability to diverse environments during the selection process. Relying solely on average performance across various environments may obscure genotypes that excel in specific conditions (Pour-Aboughadareh *et al.*, 2022). Therefore, incorporating stability measures alongside mean yield is essential for identifying superior and broadly adaptable genotypes that consistently perform well across different environmental contexts.

Table 4 presents the average grain yield performance of 16 genotypes across 14 environments. The environmental impact was substantial, with average yields ranging from 764.2 kg ha^{-1} in SK17 to a maximum of 3336 kg ha^{-1} in NA17 with a mean of 2053.9 kg ha^{-1}. For grain yield, the best environments were NA17 and MK17 with 3336 kg ha^{-1} and 3158.1 kg ha^{-1}, respectively which showed a significant difference to the other environments. Among the studied environments GF16, HU16, and SK17 exhibited yield of below 1 ton ha^{-1}. Variation in productivity across diverse environments is driven by the complex interaction of climate, cultivar-specific responses, and non-linear relationships (Delerce *et al.*, 2016). The findings underscore the significant influence of environmental factors on grain yield, with considerable variation observed across different locations and years

Table 3 - AMMI analysis of variance for grain yield (kg ha^{-1}) of 16 large red common bean genotypes at 14 environments.

Source of variation	Degrees of freedom	Sum of Square	Mean square	Total Variation explained (%)	G × E explained (%)
Total	671	663270713	988481		
Treatments	223	600061883	2690860		
Genotypes	15	21061531	1404102***	3.18	
Environments	13	510937570	39302890***	77.03	
Block	28	13830111	493933***	2.09	
Interactions	195	68062782	349040***	10.26	
IPCA 1	27	26543442	983090***		39
IPCA 2	25	14151992	566080***		20.79
IPCA 3	23	6750567	293503***		9.92
IPCA 4	21	5498642	261840**		8.08
IPCA 5	19	4319288	227331*		6.35
Error	420	49378718	117568	7.44	

Table 4 - Mean grain yield (kg ha^{-1}) of the sixteen large red bean genotypes across 14 environments during (2015-2018) main cropping season

Genotype	Environments														Mean
	AT16	AT17	GF16	HU16	KB16	MK16	MK17	MK18	MS16	NA15	NA17	NA18	PW16	SK17	
DAB 497	1922.7	2367.0	884.2	630.2	861.5	1666.2	3420.5	2317.4	1904.2	2006.9	3352.3	3355.0	1143.7	730.1	1897.3^{efg}
DAB 317	2444.8	2078.3	939.5	965.9	844.0	2766.7	2519.6	2521.7	2703.4	2781.4	3037.0	2064.4	1373.3	1274.6	2022.5^{de}
DAB 482	2083.0	1991.9	943.5	986.0	797.3	2742.1	1946.0	2773.1	1969.1	1580.5	2563.5	3192.6	1227.7	294.2	1792.2^{g}
DAB 523	2519.9	2314.1	831.5	859.4	556.1	1920.3	2843.2	2860.8	3201.7	2679.8	3433.0	2612.2	1191.0	650.9	2033.9^{de}
DAB 512	2346.8	2064.3	607.9	695.6	940.7	2181.5	3758.1	2663.1	2744.2	2044.8	2500.1	3228.3	1184.4	660.8	1972.9^{def}
DAB 513	2389.3	2963.5	1106.3	1082.6	751.9	2599.1	4222.4	2631.3	2940.5	2320.2	3575.7	2782.4	1333.8	908.6	2257.7^{ab}
DAB 496	2737.5	3243.3	1093.2	957.2	876.9	1750.7	4244.6	1982.1	2837.7	2519.9	3439.6	2801.9	1443.6	628.7	2182.6^{bc}
DAB 478	2473.2	2673.1	763.3	906.1	882.4	2238.1	3212.1	2521.6	2116.3	2299.4	3415.7	3004.4	1002.4	805.8	2022.4^{de}
DAB 544	2793.9	3203.0	1027.3	1112.5	1400.1	2392.0	3198.9	2666.9	3316.5	2450.5	4073.0	2410.7	1308.4	1357.1	2336.5^{a}
DAB 525	2879.4	2595.3	1143.6	833.5	1111.5	2749.7	3036.5	3099.2	2616.9	2289.9	3586.3	2817.0	1317.4	995.8	2219.4^{abc}
DAB 545	2537.6	1618.1	901.2	907.7	1305.4	2078.0	2148.1	2668.8	1851.1	1987.2	2636.1	3607.6	1454.9	801.5	1893.1^{efg}
DAB 540	1769.8	2488.0	1044.4	647.2	694.2	1814.9	2766.1	2611.8	2449.9	1974.0	3301.9	2917.5	1146.0	514.1	1867.1^{fg}
DAB 532	2818.1	2365.1	805.5	1087.5	1365.9	2378.5	3265.0	2630.7	2165.6	2453.7	3271.1	2875.4	936.9	653.1	2076.6^{cd}
DAB 481	2360.2	2384.0	999.7	969.9	1158.4	2024.8	3220.1	2827.2	3350.2	2776.2	3993.9	3177.3	1222.3	804.2	2233.5^{ab}
Melkedima	2571.2	2859.5	839.7	769.1	1526.7	2759.9	3482.2	2803.4	3138.1	2674.7	3639.4	2861.0	1514.6	636.9	2291.2^{ab}
Red kideny	1561.2	2083.2	579.9	691.2	1044.0	1767.9	3246.4	1949.6	2198.2	2237.6	3557.0	2422.1	840.2	510.5	1763.5^{g}
Mean	2388.0	2455.7	906.9	881.4	1007.3	2239.4	3158.1	2595.5	2594.0	2317.3	3336.0	2883.1	1227.5	764.2	

AT16=Alemtena in 2016; AT17 = Alemtena in 2017; GF16 = Goffa in 2016; HU16=Haramaya in 2016; KB16=Kobo in 2016; MK16= Melkassa in 2016; MK17=Melkassa in 2017; MK18=Melkassa in 2018; MS16=Meiso in 2016; NA15=Negelle Arsi in 2015; NA17=Negelle Arsi in 2017; NA18=Negelle Arsi in 2018; PW16=Pawe in 2016; SK17=Sirinkain2017

Genotypes G6 (DAB 513) and G7 (DAB 496) emerged as top performers in Melkassa (2017), achieving exceptional yields of 4222.4 and 4244.6 kg/ha, respectively. Conversely, the check cultivar *ACOS red* displayed poor performance, recording the lowest yield (580 kg/ha) at Goffa in 2016. Seven genotypes (G9, G15, G6, G14, G10, G7, and G13) yielded above the average mean (2053.9 kg ha^{-1}) and the remaining nine were below the average yield. Overall, G9 (2336.5) records the highest in terms of average yield across environments followed by G15 (2291.2), G6 (2257.7), and G14 (2233.5) (Table 4). Notably, the yield of four genotypes was statistically indistinguishable from the leading genotype G9 (DAB544). In contrast, G16 (*ACOS red*) and G3 (DAB 482) consistently produced the lowest yields across all environments. A study by Philipo *et al*., (2021), Mutari *et al.* (2022), and Firew *et al.* (2019) revealed that genotypes of common beans displayed varying grain yield performance across different locations.

GGE biplot analysis

The GGE biplot graphically depicts the genotype main effect plus genotype-by-environment interaction G + (G × E), and simultaneously represents the mean performance and stability and facilitates the identification of suitable genotypes for specific mega-environments in multi-environment trial analysis (Yan *et al*., 2000; Yan WeiKai, 2011). The first two principal components extracted from the singular value decomposition of the environment-centered genotype data captured 62.14% of the total variation, of which the first principal component explained 42.21% while the second principal component explained 19.93%.

Mean performance and stability of genotypes seed yield

The "mean vs. stability" view in a GGE biplot helps assess genotypes based on both average performance (mean) and consistency across environments (stability) (Yan & Kang, 2003). The biplot visualizes performance and stability graphically with the help of Average Environment Coordinates (AEC). The line passing through the arrowhead and origin is AEC abscissa and the line perpendicular to it at the origin is ordinate (Bishwas *et al*., 2021). Genotypes with higher yield per hectare positioned themselves to the right of a vertical line, indicating above-average performance. Conversely, those positioned to the left fell below the average. The length of the line connecting them to the AEC reflects stability. Shorter lines indicate stable genotypes with consistent performance, while longer lines suggest higher instability with fluctuating performance across environments.

Figure 2 shows genotypes G4, G14, G15, and G9 are above average yielders with more stability whereas G2, G6, G7, and G2 are above average yielders with lower stability. Moreover, G12, G5, and G8 are stable but are below average yielders and G1, G3, G11, and G16 are both less stable and below average yielders. Firew *et al.* (2019) also evaluated genotypes using the Mean vs stability GGE biplot and identified a genotypes that had high-yielding and stable performance by deploying AEC.

Experimental sites discriminating power and representativeness on genotypes seed yield

Figure 3 shows the discriminating power and representativeness of the experimental sites on the grain yield of the common bean genotypes. Environments with longer vectors from the origin indicated stronger discrimination of high yielding genotypes, while shorter vectors implied weaker discriminating power (Yan and Kang, 2013). Among environments, MK17 has a comparatively longer length ensuring it has a higher discriminating ability followed by MS16, AT17, NA17, and MK16 as shown in Figure 3. The experimental site vector with a small angle from the average environmental axis (AEA) provides a more representative environment for evaluating the seed yield of different genotypes. MS16, NA15, and NA18 vectors had a small angle with the AEA, thus more representative compared to the other sites, whereas MK16, MK17, and MK18 had a larger angle with the AEA and therefore the least representative sites among the experimental sites.

Test environments should be selected based on their ability to differentiate genotypes and represent the target environments (Aruna *et al.*, 2016; Bhartiya *et al.*, 2017). MS16 was identified as a perfect test environment in this study due to its longer vector and smallest angle with the ideal environment, signifying its superior discriminatory power and strongest representativeness of the overall test environment set.

Which-won-where model

The GGE-biplot's polygon offers a visual representation of GEI patterns in multi-environment seed yield trial data. This view explicitly highlights the "which-won-where" scenario, identifying the top-performing genotype for each specific environment. The polygon view of the GGE biplot was drawn by joining the markers located farthest from the origin such that all other markers are included within the polygon (Bishwas *et al.*, 2021; Yan, 2011). Perpendicular lines are drawn from the origin, intersecting each side of the polygon and extending beyond its perimeter. This partitions the biplot space into distinct sectors, effectively segregating the various environments (Wolde *et al.*, 2020). In this polygon, the environments fell into four sections and the genotypes into five sections. Environments that fall into different sectors have different best genotypes. Genotypes positioned near the biplot origin are less responsive to environmental changes (Yan & Rajcan, 2002). The vertex genotypes in this trial were G1, G2, G3, G7 and G9. These genotypes were the best or the poorest in some or all environments since they had the furthest position from the biplot's center (Yan & Kang, 2003). Castiano *et al*. (2023) and Mutari *et al*., (2022) also conducted a GGE biplot analysis in common bean cultivars and identified mega environments.

From Figure 4, G9 was more adapted to the NA17, GF16, NA15, AT16, SK17, MS16, KB16, and HU16 environments. The G2 performed well PW16, MK16, and MK18 environments. G7 was adapted to MK17 and AT17 environments, and G3 performed well in the NA18 environment. When genotypes form the vertices of polygons without any environments clustered in their corresponding sectors, they are considered unadapted to all test environments (Goa *et al*., 2022), as seen with genotype G1. Genotypes positioned near the origin, such as G13, G8, and G4, displayed a more stable performance across environments. These genotypes may be preferable for breeding programs seeking broad adaptation, especially if environmental variation is unpredictable.

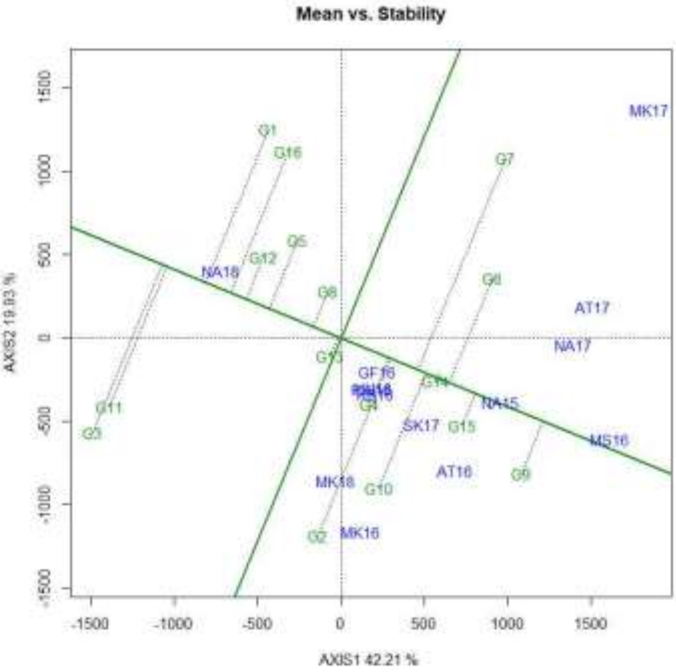

Figure 2. “Mean vs. Stability” view of the GGE biplot of 16 common bean genotypes across 14 test environments.

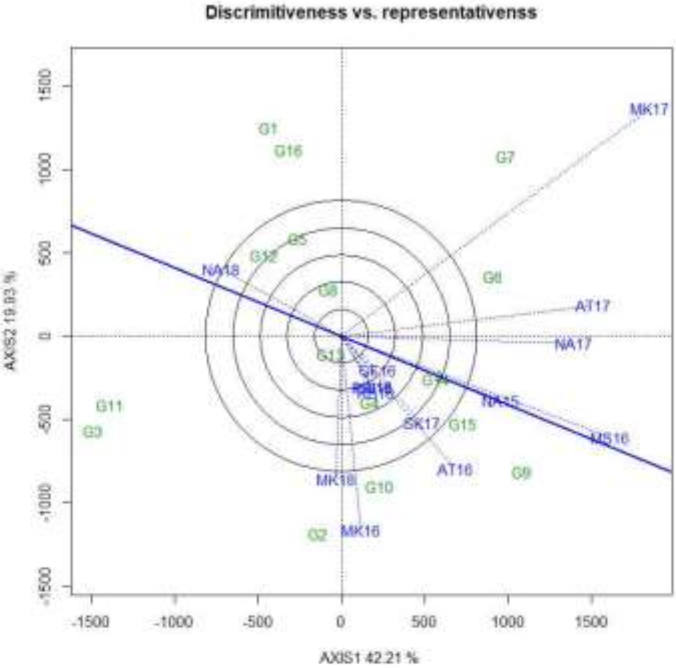

Figure 3. “Discriminativeness vs. representativeness” view of test locations based on GGE biplot of 16 common bean genotypes across 14 test environments.

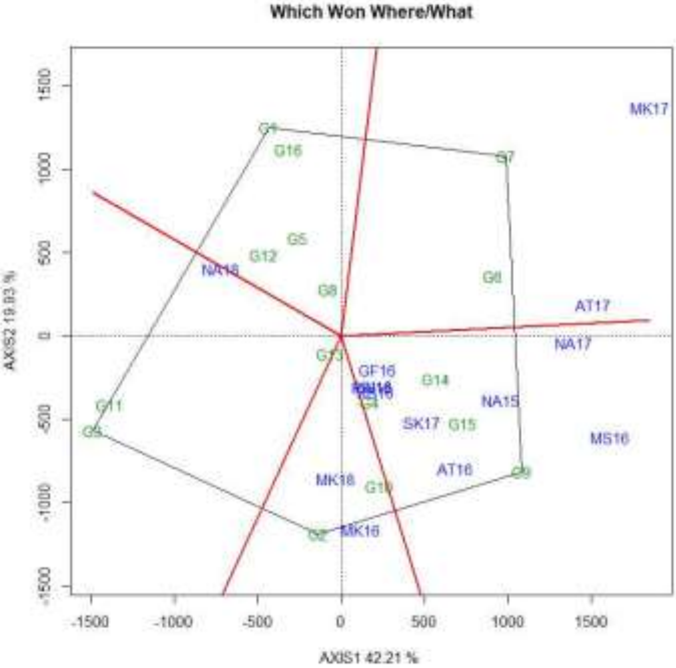

Figure 4. “Which-won-where” view of the GGE biplot of 16 common bean genotypes across 14 test environments.

AMMI Stability Value (ASV)

AMMI model excels at analyzing GEI but lacks a quantitative stability measure for genotype ranking. To overcome this limitation, Purchase *et al.* (2000) introduced the ASV measure. This allows researchers to quantify and rank genotypes based on their stability, providing a crucial tool for informed selection in breeding programs.

The ASV method, as described by Purchase *et al.* (2000), uses principal components (IPCA1 and IPCA2) derived from a statistical technique called Principal Component Analysis (PCA) to evaluate genotype stability. It calculates an ASV score based on the distance from zero in a two-dimensional graph where each axis represents an IPCA score. Genotypes with lower ASV scores are considered more stable, meaning their performance is less affected by environmental variations. In this study, genotypes G12, G13, and G8 displayed the lowest ASV scores, indicating the most stable performance across environments (Table 5). Conversely, the check variety G16 (*ACOS red*) had the highest ASV score, suggesting it was the most influenced by environmental changes and therefore the least stable genotype.

Yield Stability Index (YSI)

Genotype stability, as assessed by ASV, focuses on consistent performance across environments, independent of yield performance (Mohammadi & Amri, 2008; Rono *et al.*, 2016). Consequently, some genotypes identified as stable by ASV may exhibit relatively low overall yields. Recognizing the importance of balancing high seed yield with genotypic stability in breeding, various authors used the yield stability index (Adjebeng-Danquah *et al.*, 2017; Milioli *et al.*, 2018). This index integrates these two key selection criteria into a single metric, enabling the identification of superior bean genotypes that demonstrate desirable yield potential and consistent performance across environments. ASV incorporates information from both IPCA1 and IPCA2, which capture most of the genotype-environment interaction (GEI) variation, it effectively reflects genotypic stability. YSI combines the rank of ASV (with the lowest value indicating the most stable genotype) with the rank of the genotype's mean yield (the highest yield gets rank one). YSI creates a single metric for simultaneous selection based on yield and stability by summing these ranks. Consequently, genotypes with the lowest YSI score are considered the most desirable, demonstrating high grain yield and consistent performance across environments. Based on YSI the most stable genotypes with high grain yield were G15, G10, G13, G14, and G9 which follow the result of AMMI stability value (Table 5).

Table 5. First and second IPCA, mean yield, ASV, and YSI

Genotypes	IPCA1	IPCA2	Grain yield	ASV	YSI
G1	-1.784	20.628	1897	20.621	23
G2	7.170	-24.800	2022	24.498	22
G3	29.009	1.047	1792	152.69	31
G4	-3.490	-14.048	2034	14.155	16
G5	1.062	14.010	1973	14.013	18
G6	-15.563	4.575	2258	28.335	16
G7	-23.895	11.875	2183	31.749	20
G8	-0.470	5.439	2022	5.437	12
G9	-11.313	-17.415	2336	19.657	11
G10	5.979	-8.020	2219	6.137	9
G11	30.094	9.339	1893	54.823	28
G12	1.089	3.016	1867	3.086	15
G13	3.563	2.904	2077	4.900	9
G14	-5.741	-5.415	2233	8.016	10
G15	-5.396	-5.960	2291	7.866	7
G16	-10.315	2.824	1763	19.510	25

Conclusion and Recommendation

The study revealed that genotype, environment, and GEI significantly impact the yield of large red bean genotypes. The fourteen environments examined in this study can be grouped into four mega environments. Notably, nine of these environments fall into one mega environment, where genotype G9 exhibited the highest yield. The environment MS16 (Meiso_2016) was identified as an ideal test environment due to its discriminating ability and representativeness. Given the exceptional yields from NA17 and MK17, further investigation is needed to understand the specific factors contributing to their superiority. Generally, selecting stable large red bean genotypes with high yields based on a single stability model is challenging. However, YSI and GGE biplot models identified three genotypes G9 (DAB544), G14 (DAB481), and G15 (Melkadima) as superior and stable for grain yield. Therefore, these two genotypes are recommended for verification trials and release in tested and similar agroecologies.

Acknowledgements

We express our sincere gratitude to Alliance Bioversity and CIAT for providing the materials used in this trial. Our heartfelt appreciations also go to the dedicated researchers at various research centers for their invaluable efforts in conducting the trials and meticulously collecting the data.

References

Abebe, Y. and Lema, Z. 2019. Common bean production, marketing, and validation of new product concepts. Research Report No 125 (Issue March).

Adams, R. M., Hurd, B. H., Lenhart, S. and Leary, N. 1999. Effects of global climate change on agriculture: An interpretative review. Climate Research, 11(1): 19–30. https://doi.org/10.3354/cr011019

Adjebeng-Danquah, J., Manu-Aduening, J., Gracen, V. E., Asante, I. K. and Offei, S. K. 2017. AMMI stability analysis and estimation of genetic parameters for growth and yield components in cassava in the forest and Guinea savannah ecologies of Ghana. International Journal of Agronomy, 2017. https://doi.org/10.1155/ 2017/8075846

Amsalu, B., Negash, K., Shiferaw, T., Tumussa, K., Tsegave, D., Claude, R. J. and Mukankusi, C. M. 2018. Progress of common bean breeding and genetics research in Ethiopia. Ethiopian Journal of Crop Science, 8(December): 114–128.

Aruna, C., Rakshit, S., Shrotria, P. K., Pahuja, S. K., Jain, S. K., Siva Kumar, S., Modi, N. D., Deshmukh, D. T., Kapoor, R. and Patil, J. V. 2016. Assessing genotype-by-environment interactions and trait associations in forage sorghum using GGE biplot analysis. Journal of Agricultural Science, 154(1): 73–86. https://doi.org/10.1017/S0021859615000106

Bhartiya, A., Aditya, J. P., Singh, K., Pushpendra, Purwar, J. P. and Agarwal, A. 2017. AMMI & GGE biplot analysis of multi environment yield trial of soybean in North Western Himalayan state Uttarakhand of India. Legume Research, 40(2): 306–312. https://doi.org/10.18805/lr.v0iOF.3548

Bishwas, K. C., Poudel, M. R. and Regmi, D. 2021. Heliyon AMMI and GGE biplot analysis of yield of different elite wheat line under terminal heat stress and irrigated environments. Heliyon, 7(January): e07206. https://doi.org/10.1016/j.heliyon.2021.e07206

Blair, M. W., Díaz, L. M., Buendía, H. F. and Duque, M. C. 2009. Genetic diversity, seed size associations and population structure of a core collection of common beans (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 119(6): 955–972. https://doi.org/10.1007/s00122-009-1064-8

Bose, L. K., Jambhulkar, N. N., Pande, K. and Singh, O. N. 2014. Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. Chilean Journal of Agricultural Research, 74(1): 1–9. https://doi.org/10.4067/S0718-58392014000100001

Botero, H. and Barnes, A. P. 2022. The effect of ENSO on common bean production in Colombia: A time series approach. Food Security, 14(6): 1417–1430. https://doi.org/10.1007/s12571-022-01290-z

Castiano, B. L., Kimurto, P. K. and Ojwang, P. O. 2023. Stability of common bean (Phaseolus vulgaris L.) genotypes for root system architecture and seed yield in multi-environments. Field Crops Research. 293(January): 108863. https://doi.org/10.1016/j.fcr.2023.108863

Cichy, K. A., Porch, T. G., Beaver, J. S., Cregan, P., Fourie, D., Glahn, R. P., Grusak, M. A., Kamfwa, K., Katuuramu, D. N., McClean, P., Mndolwa, E., Nchimbi-Msolla, S., Pastor-Corrales, M. A. and Miklas, P. N. 2015. A Phaseolus vulgaris diversity panel for Andean bean improvement. Crop Science. 55(5): 2149–2160. https://doi.org/10.2135/cropsci2014.09.0653

CSA. 2020. The Federal Democratic Republic of Ethiopia Central Statistical Agency Agricultural Sample Survey 2019/20 (2010 E.C.) Volume I Report on Area and Production of Major Crops. Statistical Bulletin. I: 121.

Debouck, D. G., Toro, O., Paredes, O. M., Johnson, W. C. and Gepts, P. 1993. Genetic diversity and ecological distribution of Phaseolus vulgaris (Fabaceae) in northwestern South America. Economic Botany. 47(4): 408–423. https://doi.org/10.1007/BF0290735

Delerce, S., Dorado, H., Grillon, A., Rebolledo, M. C., Prager, S. D., Patiño, V. H., Varón, G. G. and Jiménez, D. 2016. Assessing weather-yield relationships in rice at local scale using data mining approaches. PLoS ONE. 11(8). https://doi.org/10.1371/journal.pone.0161620

Diaz, L. M., Ricaurte, J., Tovar, E., Cajiao, C., Terán, H., Grajales, M., Polanía, J., Rao, I., Beebe, S. and Raatz, B. 2018. QTL analyses for tolerance to abiotic stresses in a common bean (Phaseolus vulgaris L.) population. PLoS ONE, 13(8): 1–26. https://doi.org/10.1371/journal.pone.0202342

Ebdon, J. S. and Gauch, H. G. 2002. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials. Crop Science, 42(2): 489. https://doi.org/10.2135/cropsci2002.0489

Firew, A. M., Amsalu, B. and Tsegaye, D. 2019. 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. African Journal of Agricultural Research, 14(35): 2135–2145. https://doi.org/10.5897/ajar2019.14180

Goa, Y., Mohammed, H., Worku, W. and Urage, E. 2022. Genotype by environment interaction and yield stability of cowpea (Vigna unguiculata (L.) Walp.) genotypes in moisture limited areas of Southern Ethiopia. Heliyon, 8(3): e09013. https://doi.org/10.1016/j.heliyon.2022.e09013

Habte, E., Katungi, E., Yirga, C. and Fenta, B. A. 2021. Adoption of common bean technologies and its impacts on productivity and household welfare in Ethiopia: Lessons from Tropical Legumes Project. (Issue June). https://doi.org/10.13140/RG.2.2.17130.03524

Huertas, R., Karpinska, B., Ngala, S., Mkandawire, B., Maling'a, J., Wajenkeche, E., Kimani, P. M., Boesch, C., Stewart, D., Hancock, R. D. and Foyer, C. H. 2023. Biofortification of common bean (Phaseolus vulgaris L.) with iron and zinc: Achievements and challenges. Food and Energy Security, 12(2): 1–27. https://doi.org/10.1002/fes3.406

Ligarreto–Moreno, G. and Pimentel–Ladino, C. 2022. Grain yield and genotype x environment interaction in bean cultivars with different growth habits. Plant Production Science, 25(2): 232–241. https://doi.org/10.1080/1343943X.2021.1981141

Mekbib, F. 2003. Yield stability in common bean (Phaseolus vulgaris L.) genotypes. Euphytica, 130: 147–153.

Milioli, A. S., Zdziarski, A. D., Woyann, L. G., Dos Santos, R., Rosa, A. C., Madureira, A. and Benin, G. 2018. Yield stability and relationships among stability parameters in soybean genotypes across years. Chilean Journal of Agricultural Research, 78(2): 299–309. https://doi.org/10.4067/S0718-58392018000200299

Mohammadi, R. and Amri, A. 2008. Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica, 159(3): 419–432. https://doi.org/10.1007/s10681-007-9600-6

Mutari, B., Sibiya, J., Gasura, E., Kondwakwenda, A., Matova, P. M. and Chirwa, R. 2022. Genotype x environment interaction and stability analyses of grain yield and micronutrient (Fe and Zn) concentrations in navy bean (Phaseolus vulgaris L.) genotypes under varied production environments. Field Crops Research, 286(June): 108607. https://doi.org/10.1016/j.fcr.2022.108607

Ntukamazina, N., Onwonga, R. N., Sommer, R., Mukankusi, C. M., Mburu, J. and Rubyogo, J. C. 2017. Effect of excessive and minimal soil moisture stress on agronomic performance of bush and climbing bean (Phaseolus vulgaris L.). Cogent Food and Agriculture. 3(1). https://doi.org/10.1080/23311932.2017.1373414

Pereira H.S,. Faria L.C,. Wendland A,. Costa J.G.C,. Souza T.L.P.O.& Melo L.C..2018.Genotype by environment interaction for disease resistance and other important agronomic traits supporting the indication of common bean cultivars.Euphytica. 214(1).

Philipo M,. Ndakidemi P.A.& Mbega E.R..2021.Environmentally stable common bean genotypes for production in different agro-ecological zones of Tanzania.Heliyon7(1),e05973.

Pour-Aboughadareh A,. Barati A,. Koohkan S.A,. Jabari M,. Marzoghian A,& Gholipoor A..2022.Dissection of genotype-by-environment interaction and yield stability analysis in barley using AMMI model and stability statistics.Bulletin of the National Research Centre. 46(1).

Purchase J.L,, Hatting H.& van Deventer C.S..2000.Genotype × environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II.Stability analysis of yield performance.South African Journal of Plant and Soil.17(3):101–107.

Ramburan S,, Zhou M.& Labuschagne M..2011.Interpretation of genotype×environment interactions of sugarcane: Identifying significant environmental factors.Field Crops Research.124(3):392–399.

Rono J.K,, Cheruiyot E.K,, Othira J.O,, Njuguna V.W,, Macharia J.K,, Owuoche J,, Oyier M,& Kange A.M..2016.Adaptability and stability study of selected sweet sorghum genotypes for ethanol production under different environments using AMMI analysis and GGE biplots. Scientific World Journal. 2016.

Roostaeia M,, Mohammadib R,& Amric A..2014.Rank correlation among different statistical models in ranking of winter wheat genotypes. Crop Journal. 2(2–3):154–163.

Sicard D,, Nanni L,, Porfiri O,, Bulfon D,& Papa R..2005.Genetic diversity of Phaseolus vulgaris L.and P.coccineus L.landraces in central Italy.Plant Breeding. 124(5): 464–472.

Stevens G.A,, Finucane M.M,, De-Regil L.M,, Paciorek C.J,, Flaxman S.R,, Branca F,, Peña-Rosas J.P,, Bhutta Z.A,& Ezzati M..2013.Global regional,and national trends in haemoglobin concentration and prevalence of total and severe anaemia in children and pregnant and non-pregnant women for 1995-2011:A systematic analysis of population-representative data. The Lancet Global Health. 1(1):16–25.

Suárez J.C,, Polanía J.A,, Contreras A.T,, Rodríguez L,, Machado L,, Ordoñez C,, Beebe S,& Rao I.M..2020.Adaptation of common bean lines to high temperature conditions:genotypic differences in phenological and agronomic performance. Euphytica. 216(2).

Tolessa T..2015.Application of AMMI and Tai's Stability Statistics for Yield Stability Analysis in Faba bean (Vicia faba L.) cultivars grown in central highlands of Ethiopia.Journal of Plant Sciences. 3(4):197.

Wolde L,, Keno T,, Abebe A,, Abakemal D,, Terefe W,& Negera D..2020.Genotype x environment interaction and stability analysis of grain yield in QPM hybrid varieties.Maydica64(3).

Yan W..2001.GGEbiplot -A windows application for graphical analysisof multienvironment trial dataand other typesof two-way data.Agronomy Journal. 93(5): 1111–1118.

Yan W,, Hunt L.A,, Sheng Q,& Szlavnics Z..2000.Cultivar evaluationand mega-environment investigationbased on the GGE biplot. Crop Science. 40(3):597–605.

Yan W,& Kang M.S..2003.GGE Biplot Analysis,A graphical tool for breeders geneticist,and agronomists. In Crop Science. CRC Press LLC CRC.

Yan W,& Rajcan I..2002.Biplot Analysisof Test Sitesand Trait Relationsof Soybeanin Ontario.Crop Science. 42(1):11.

Yan WeiKai .2011.GGE biplot vs.AMMI graphsfor genotype-by-environment dataanalysis.Journalof the Indian Societyof Agricultural Statistics. 65(2):181–193.

Zobel R.W,, Wright M.J,& Gauch H.G..1988. Statistical Analysisof a Yield Trial. Agronomy Journal. 80(3):388–393.