Genotype by Environment Interaction and Yield Stability of Drought Tolerant Mung Bean [*Vigna radiata* (L.) Wilczek] Genotypes in Ethiopia

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Abstract: *A multi-environment evaluation of mung bean genotypes was conducted in six environments across Ethiopia to select promising genotypes. This study was conducted to estimate the magnitude of genotypes by environment interaction (GEI) and seed yield stability of the selected drought-tolerant mung bean genotypes across different environments. A total of fifteen mung bean genotypes were used. Out of these, two released varieties were used as standard checks. The field experiments were conducted during the 2019 main cropping season at six locations namely Humbo, Gofa, Melkassa, Konso, Jinka, and Kako using a randomized complete block design with three replications. Data were subjected to analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI), and GGE bi-plot analysis. A combined analysis of variance revealed significant variations among the genotype, environments, and GEI for yield and yield-related traits, indicating that seed yield was significantly affected by these factors. Analysis of variance from the AMMI model indicated the contribution of environment, genotype, and GEI was 59.6%, 16.8%, and 14.8% of the total variation in seed yield, respectively. Sum squares of the first and the second interaction principal component axis (IPCA) explained 47.4% and 7.4% of the GEI variation, respectively. The IPCA1 mean square was highly significant (P≤0.01) and that of IPCA2 was significant (p≤0.05), indicating the adequacy of the AMMI model with the first two IPCAs for cross-validation of the seed yield variation. The magnitude of the GEI sum squares was 4.4 times that of the genotypes sum squares for seed yield, indicating the presence of substantial differences in genotypic responses across the environments. The results for the AMMI, Yield stability index (YSI), AMMI Stability Value (ASV), and GGE biplot, analyses depicted that the genotypes G6 (NLLP-MGC-24), G13 (Acc006), and G3 (NLLP-MGC-15) were identified as stable and high yielders across the environments and should be considered for variety release. AMMI1 biplot showed Kako was the potential and favorable environment for mung bean production, while Humbo was an unfavorable for mung bean production.*

Keywords: *AMMI Stability Value*, GGE biplot, Kako, Gofa, Yield Stability Index

1. Introduction

Mung bean [*Vigna radiata* (L.) Wilczek] is an important self-pollinated pulse crop of Asia and can be grown in sandy and loam soils, with a pH range of 6.2 to 7.2. Multi-environment trials allow breeders to select the best-performing genotype for their target areas by assessing the relative performance of genotypes under a variety of locations and environmental conditions (Zu, 2010). Genotypes tested in different locations and over years have significant fluctuations in yield due to variations in soil fertility, unpredicted rainfall, and the presence of other biotic and abiotic stresses (Kang, 1993). Differential response of genotypes to different environmental conditions is termed genotype by environment interaction (GEI). In this context, genotypes across environments may be classified as stable when the classification of genotypes remains constant in various environments and there is significant interaction due to the differences in the magnitude of the responses; or complex when the classification of the genotypes is different from one environment to another, which is quite common and has greater importance in plant breeding (Mohammadi and Amri, 2013). The magnitude of an environment, genetics, and their interaction effects are a serious problem for the yield and stability of genotype

across environments because it reduces the efficiency of the genetic gain. Comestock and Moll (1993) suggested that GE interaction reduces the genetic progress in plant breeding programs by minimizing the association between phenotypic and genotypic values. Hence, GE interaction must be either exploited by selecting a superior genotype for each specific target environment or avoided by selecting a widely adapted and stable genotype across a wide range of environments (Ceccarelli, 1996).

Genotypes x environment interactions exist, when the responses of the genotypes to different levels of environmental factors fail to respond similarly (Allard and Bradshaw, 1964). Major constraints in breeding pulses such as mung beans are the high genotype x environment (GxE) interactions and the low genetic diversity in the primary gene pool (Jitendra *et al*., 2011). Researchers working in the area of plant breeding have the trend of evaluating genotypes in multi-environments, representing favorable and unfavorable growing conditions, to estimate and understand the stability of the genotype across environments. Hence, Tiwari *et al*. (2000) and Mehla *et al*. (2000) suggested testing varieties over a large number of environments is necessary to observe GEI effects

Grain yield performance is not the only parameter for selection as a genotype with the highest grain yield and would not be necessarily stable and adaptable across locations and years. The plant breeders need to identify adaptable and stable high-yielding genotypes with other desirable traits under varying environmental conditions as a desirable variety (Showemimo *et al*., 2000; Mustapha *et al*., 2001).

In Ethiopia, G x E interaction studies have been conducted on different food legumes, thus on cowpea (Tariku *et al*., 2018), common bean (Asrat *et al*., 2008; Nigussie *et al*., 2012), soybean (Asrat *et al*., 2009), faba bean (Gemechu *et al*., 2002; Gemechu and Musa, 2002; Musa and Gemechu, 2004; Gemechu *et al*., 2006; Mulusew *et al*., 2008; Tamene *et al*., 2015; Asnakech *et al*., 2017; Tadele *et al*., 2017; Tekalign *et al*., 2019), field pea (Mulusew *et al*., 2009; Mulusew *et al*., 2014), and mung bean (Asrat *et al*., 2012). However, information on the effect of genotype, environment, and GEI on mung bean yield with drought-tolerant traits is limited in Ethiopia. There

have been only limited studies on the use of the GGE biplot study for mung bean genotypes evaluation in Ethiopia. In these areas, more studies are needed to help mung bean farmers choose the right genotypes. Therefore, the present study was conducted to estimate the magnitude of genotypes by environment interaction effect and to evaluate the performance and stability of promising drought-tolerant mung bean genotypes for wider and /or specific recommendations for cultivation under farmers' conditions in Ethiopia.

2. Materials and Methods
2.1. Description of the study areas
The field experiments were conducted during the 2019 main cropping season at six locations namely Humbo, Gofa, Melkassa, Konso, Jinka, and Kako. The geographical locations and mean rainfall and temperatures of the study area over several years (2009 to 2019) are presented in Table 1. The weather data were collected from the nearby stations, respective woreda, and zonal Bureau of Agriculture and research centers (Personal Communication).

2.2. Experimental materials
A total of fifteen selected genotypes were used. Out of these, two released varieties were used as standard checks and thirteen genotypes were selected from the drought experiment where 60 genotypes were tested (Table 2). Genotypes were sourced from Melkassa Agricultural Research Center as well as our collections from southern Ethiopia.

2.3. Experimental design and procedures
The experiments were laid out using a randomized complete block design with three replications. During planting, blended NPSB fertilizer at the rate of 100 kg ha^{-1} was applied. Agronomic management practice namely, weeding was carried out uniformly for all experimental units. Experiments were planted from early June to early July of the 2019 cropping season at each location. The plot size was 4 m long, 0.3 m between rows, and 0.05 m between plants. Each experimental plot had an area of 6.0 m^2. It consists of five rows accommodating 80 plants per row. The distance between plots and replications was 1 m and 2 m, respectively. The data were collected from the middle three rows, which have a 3.6 m^2 net plot area.

Table 1: Description of the experimental sites

| Experimental sites | Soil Type | Geographical location | | | Rainfall (mm) | Temperature (°C) | |
		Altitude (m.a.s.l)	Latitude (N)	Longitude (E)		MinT (°C)	MaxT (°C)
Humbo	Vertisols	1390	6° 39'	37° 48'	710-1337	18.3	21.0
Gofa	Cambisols	1276	6°19′	36°56′	800-1200	17.5	20.0
Melkassa	Andosols	1550	8°30'	39° 24'	763	15.73	27.31
Konso	Vertisols	1432	5°23'	37°20'	787	18.4	30.70
Jinka	Cambisols	1420	5° 47'	36° 38'	1381	16.61	27.68
Kako	Cambisols	1407	5° 39'	36° 41'	637.3	23.1	38

Table 2: List of genotypes used

Genotypes	Genotypes code
NLLP-MGC-01	G1
NLLP-MGC-12	G2
NLLP-MGC-15	G3
NLLP-MGC-20	G4
NLLP-MGC-22	G5
NLLP-MGC-24	G6
NLLP-MGC-27	G7
VC1973A	G8
NM94 (VC6371-94)	G9
VC6368(46-40-4)	G10
NLLP-MGC-06	G11
Acc002	G12
Acc006	G13
N-26 (Standard check)	G14
NVL-1 (Standard check)	G15

2.4. Data collection

The quantitative data were collected according to the descriptor of the mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980). The data collected on the plot basis were; days to flowering (days), days to maturity (days), hundred seed weight (g), and seed yield per hectare (kg). The data collected on a plant basis were; plant height (cm), number of pods per plant, five plant pod numbers, and number of seeds per pod.

2.5. Data analysis

Different statistical packages were used to analyze the data. GenStat Software 16th edition (GenStat, 2014) was used for the analysis of variance of the individual location and the combined data over

locations, AMMI, and GGE biplot analysis. GEA-R (Genotypic by Environment Analysis with R for Windows) Version 4.1 was also used (Angela *et al.*, 2016). The AMMI model was used based on the recommendation of Choukan (2010) who suggested that the additive main effects and multiplicative interaction (AMMI) are an effective alternative method for assessing the suitable genotype. The author also proposed that the GGE biplot is an effective tool for the Mega-environment analysis (which-won-where pattern), genotype evaluation, mean performance and stability, and environment evaluation to discriminate among genotypes in the targeted environment.

2.5.1. Analysis of variance

The analysis of variance of each location and combined data over location were performed using a mixed linear model to assess the differences among genotypes as per Gomez and Gomez (1984). The combined analysis of variance across the environment was analyzed by using GenStat Software 16th edition (GenStat, 2014) to determine the differences between genotypes across the environment, among environments, and their interaction. Bartlett's test was used to assess the homogeneity of error variances before combined analysis over the environments (Bartlett, 1947). In the combined analysis of variance, the location was used as random while genotypes were a fixed variable.

2.5.2. additive main effect and multiplicative interaction model analysis

The Additive Main effect and Multiplicative Interaction (AMMI) model analysis proposed by Zobel *et al*. (1988) was used for analyzing the magnitudes of GEI. The seed yield data were

analyzed using this model because AMMI partitions the sum of squares into the interaction principal component (IPC) axis. The AMMI analysis of variance summarizes most of the magnitude of GEI into one or a few interaction principal component axes (IPCA). The AMMI model equation is indicated below [1].

$$Y_{ij} = \mu + G_i + E_j + (\sum K_n V_{ni} S_{ni}) + Q_{ij} + e_{ij} \qquad [1]$$

Where

- Y_{ij} = the observed yield of genotype i in environment j
- μ = grand mean
- G_i = additive effect of the ith genotype (genotype means minus the grand mean)
- E_j = additive effect of the jth environment (environment mean deviation)
- K_n = eigenvalue of the interaction principal component (IPCA) axis n
- V_{ni} and S_{ni} = scores for the genotype i and environment j for the PCA axis n
- Q_{ij} = residual for the first n multiplicative components
- e_{ij} = error

2.5.3. GGE biplot analysis

The GGE biplot has many visual interpretations that additive main effects and multiplicative interaction do not have; particularly it allows visualization of any crossover G x E interaction. GGE biplot is close to the best additive main effects and multiplicative interaction model in most cases (Yan and Ma, 2006). Moreover, the GGE biplot is more logical for biological objectives in terms of explaining the first principal component score, which represents the genotypic level rather than the additive level (Yan *et al.,* 2000). The GGE biplot is built on the first two major components of a principal component analysis (PCA) using the Site Regression (SREG) model. When the first component is highly correlated with the main effect of the genotype, the proportion of the yield is considered to be due only to the characteristics of the genotype. The second component represents the part of the yield due to the G×E (Yan, 2011). The model for a GGE biplot (Yan, 2002) is based on singular value decomposition of the first two principal components [2].

$$Y_{ij} - \grave{i} - \hat{a}_j = \ddot{e}l\ \hat{i}il\ \varsigma jl + \ddot{e}2\ \hat{i}i2\ \varsigma j2 + \varepsilon ij \qquad [2]$$

Where

- Y_{ij} = the measured mean of genotype i in environment j
- $\grave{I}$ = grand mean
- $\hat{A}_j$ = main effect of environment j,
- $\grave{i}+\hat{a}_j$ = mean yield across all genotypes in environment j
- $\ddot{e}1$ and $\ddot{e}2$ = singular values for the first and second principal components, respectively
- $\hat{i}i1$ and $\hat{i}i2$ = eigenvectors of genotype i for the first and second principal components, respectively
- $\varsigma 1j$ and $\varsigma 2j$ = eigenvectors of environment j for the first and second principal components, respectively
- $\mathring{a}ij$ = residual associated with genotype i in environment j.

2.5.4. Stability analysis

The AMMI stability parameters (Guach and Zobel, 1988; Zobel *et al*., 1988) and GGE biplot by using GenStat Software 16th edition (GenStat, 2014) were computed for grain yield and the GEI analyses of variance. Accordingly, regression coefficient (bi) and deviation from linear regression (S^2di) from Eberhart and Russell's (1966) model and interaction principal component axes (IPCA) scores of genotype and environment and AMMI Stability Value from the AMMI model were computed as per the established standard procedures for each model. The pooled deviations mean square was tested against the pooled error mean square by F-test to evaluate the significance of the differences among the deviations of genotypes from their expected performances. Hence, to test whether there is a significant difference among the genotypes concerning their mean grain yields, genotypes mean square and regression mean square were tested against the pooled error mean square using the F-test.

2.5.5. AMMI stability value (ASV)

Since the AMMI model does not make provision for a quantitative stability measure that guides us to rank genotypes in terms of their yield stability. The AMMI stability values (ASV) were calculated to study the stability of genotypes across the environments following the formula of Purchase (1997) expounded by Purchase *et al.* (2000) was applied to quantify and rank genotypes according

to their yield stability. Therefore, AMMI stability value (ASV) was computed to quantify and rank genotypes according to their yield stability by using Microsoft office excel 2007. The larger the absolute value of IPCA, the greater the adaptability of a specific variety for a certain environment. Conversely, lower ASV values indicate greater stability in different environments (Farshadfar *et al.*, 2011).

$$ASV = \sqrt{\left[\left[\frac{IPCA\ 1\ Sum\ of\ squares}{IPCA\ 2\ Sum\ of\ squares}(IPCA\ 1\ scores)\right]^2 + [IPCA\ 2\ scores]^2\right]}$$ [3]

Where

- ASV = AMMI's stability value
- SS = sum of squares
- IPCA1 = interaction of principal component analysis one
- IPCA2 = interaction of principal component analysis two.

The ASV is the distance from zero in a two-dimensional scatter graph of IPCA1 (Interaction Principal Component Analysis Axis 1) scores against IPCA2 (Interaction Principal Components Analysis Axis 2) scores. Since the IPCA1 score contributes more to the GEI sum of squares; it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GEI sum of squares.

2.5.6. Yield stability index (YSI)
YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Bose *et al.*, 2014; Tumuhimbise *et al.*, 2014). The yield stability index was calculated using the following formula below [4].

$$YSI = RASV + R \qquad [4]$$

Where

- RASV = the ranking of the AMMI stability value
- R = the ranking of mung bean genotypes yields in all environments.

3. Results and Discussion
3.1. Combined analysis of variance across environments
The combined analysis of variance showed significant differences in the environment, genotype, and genotype-by-environment interactions (Table 3). The result revealed that there were significant variations among genotype, environments, and GEI for yield and yield-related traits, indicating that the environment had a great impact on seed yield potentials of the tested genotypes.

As presented in Table 3, days to maturity, five plant pods, seeds per pod, and a hundred seed weights were significantly (P ≤0.01) influenced due to genotype, environments, and genotype x environment interaction. Pods per plant and seed yield per hectare were significantly (P ≤0.01) affected due to genotype. The environment had exerted a significant (P≤0.01) effect on days to flowering. The results also depicted that GEI for days to flowering, days to maturity, plant height, five plants pod number, number of pods per plant, hundred seed weight and seed yield per hectare were highly significant (P ≤0.01), while it had brought significant (P ≤0.05) effect on plant height, indicating that the environment had a great impact on the seed yield potential of the tested genotypes (Table 3). Generally, the result signifies that the studied phenological and other yield-related traits of mung bean genotypes were influenced by environmental factors and it also indicated the presence of genetic variability among the tested genotypes. This result agreed with the previous findings of Lal *et al*. (2010) on fifteen mung bean genotypes at 10 locations and found that the genotype by environment interaction and both variances due to genotypes and environments were significant, which coincides with the reports of several researchers (Dhillion *et al*., 2009; Tyagi and Khan, 2010) on soybean, Kan *et al*. (2010) on chickpea, Nigussie *et al*. (2015) on common bean, Yeyis *et al*. (2014) on field pea, Akande (2009), and Tariku *et al*. (2018) on cowpea genotypes.

Moreover, this study revealed that the magnitudes of the GEI sum square were about 4.4 times that of the genotypes sum squares for seed yield, indicating that there were considerable differences in genotypic responses across environments thereby differential responses of genotypes across environments were observed. This result agreed with the work of Dyulgerova and Dyulgerov (2019), who reported that the magnitude of the GEI sum of squares was two times larger than that of genotypes, indicating that there was a substantial difference in genotypic response across environments. The larger sum of squares of GEI

compared to the genotype indicated larger differences in genotypic response across environments, indicating that there was a considerable variance in genotypic response across environments. Therefore, GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance and minimizing the association between genotypic and phenotypic values (Crossa, 1990). The GEI in the current analysis was a cross-over type whereby a change in the ranking of genotypes for a target environment because of the difficulty to interpret seed yield based on genotype and environment means alone. This finding is in line with the previous report of Asrat et al. (2009) on soybean.

3.2. Comparison of mean seed yield across the environments

The average environmental seed yield across genotypes ranged from 507 kg ha^{-1} at E2 (Humbo) to 2081 kg ha^{-1} at E4 (Kako) with the overall environmental mean yield of 1164 kg ha^{-1}, while the average genotype seed yield across environments ranged from 696 kg ha^{-1} for the genotype (G4) to 1375 and 1580 kg ha^{-1} for G13 and G8, respectively (Table 4). This indicates that the tested genotypes had inconsistent performance across the tested environments. In this study, most of the tested genotypes gave relatively good seed yield performance and could be suggested that there is an opportunity to get high-yielding mung bean genotypes for future variety development. The large variation due to the environments in our study also confirmed the high diversity of weather conditions during growing seasons and also the locations had different soil types, temperatures, and rainfall as well as altitude, directly affecting the performances of the genotypes. Hence, the selection and development of mung bean varieties in the future should follow environment-specific approaches.

The results of the present study are in agreement with the work of Tariku et al. (2018) on the cowpea genotype, who reported that the performance of cowpea genotypes was different from location to location, similar to that of Aremu et al. (2007) in cowpea. Ranking based on the genotype-focused scaling assumed that stability and mean yield was equally important (Yan, 2002). The best candidate genotypes were expected to have a high mean seed yield with stable performance across all test locations. However, such genotypes are very rare to find in practice. Therefore, high-yielding and relatively stable genotypes can be considered as a reference for genotype evaluation (Yan and Tinker, 2006).

In this study, the mean values of seed yield and yield-related traits are presented in table 5. The highest mean seed yield (1580 kg ha^{-1}) was recorded for the genotype (G8) and the least (696 kg ha^{-1}) was recorded for the genotype (G4), with an overall mean of (1164 kg ha^{-1}). Overall mean values for days to flowering ranged from 40.42 days for the genotype (G5) to 59.77 days for the genotype (G14). Days to maturity ranged from 66.72 to 98.98 days. Genotypes (G6, G13, G14, and G15), respectively took 96.33, 98.98, 97.72, and 98.39 days to attain their physiological maturity. Plant height ranged from 37.57 cm for (G8) to 48.79 cm for (G15). The number of pods per five plants ranged from 38.5 for (G11) to 96.6 for (G3). In this study, the maximum pods per five plants of 96.6, 94.9, and 88.7, respectively were also recorded for the genotypes (G3, G2, and G8) while the minimum number of pods per five plants of 38.5 and 44 were recorded for G11 and G15, respectively. Pods per plant varied from 14.03 for G13 to 25.14 for G5. Seeds per pod ranged from 9.29 for G11 to 12.35 for G1. Hundred seed weight ranged from 3.66 g for the genotype (G5) to 5.94 g for G11.

Table 3: Mean square of combined ANOVA for eight traits of 15 mung bean genotypes

Source	DF	DTF	DTM	PH	FPP	PPP	SPP	HSW	SY
Genotype (G)	14	581.04**	3307.60**	147.34**	6180.2**	232.0*	11.613**	6.3254**	743921*
Environment (E)	5	32.70*	26.993**	751.17**	4840.3**	978.6**	45.428**	2.6136**	15313847**
GEI	70	0.01**	0.004**	151.14*	242.1**	50.9**	1.449**	0.0272**	655105**
Error	178	25.54	3.524	20.95	642.1	118.1	3.163	0.3648	561079

*, ** = significant at 5% and 1% probability level, respectively, SV = source of variation, DF = Degree of freedom, GEI = genotype by environment interaction, DTF= days to flowering, DTM days to maturity, PH= plant height, FPP= five plants pod, PPP= number of pods per plant, HSW= hundred seed weight, SPP= the number of seeds per pod

Table 4: Mean Seed yield (kg ha^{-1}) **of 15 mung bean genotypes at six environments and stability indicators of AMMI analysis**

Genotype	E1	E2	E3	E4	E5	E6	Mean	IPCAg[1]	IPCAg[2]
G1	939	421	1101	3143	421	939	1161	-19.98967	5.99378
G2	1072	572	1237	2922	572	1072	1241	-14.48429	7.06782
G3	1320	791	1289	1509	1325	1320	1259	11.77525	17.02819
G4	944	364	583	979	364	944	696	11.49340	7.04205
G5	1709	446	1584	878	446	1709	1129	21.74822	-8.60742
G6	1437	593	1011	2499	760	1437	1290	-5.21787	1.15422
G7	2037	633	911	1237	633	1704	1192	16.79039	-11.77015
G8	1550	693	1112	3881	693	1550	1580	-25.16245	-3.87765
G9	1301	584	999	1979	584	1301	1125	1.11140	2.62966
G10	1453	557	1484	813	557	1453	1053	21.12314	0.73750
G11	1188	454	1111	904	587	1188	905	16.64242	6.21678
G12	1063	459	1022	2201	459	1063	1044	-4.66412	5.19843
G13	2098	306	1276	2833	306	1432	1375	-9.17042	-21.46960
G14	1071	457	1315	3298	457	1071	1278	-20.64006	3.65807
G15	1612	275	1188	2138	275	1278	1128	-1.35534	-11.00170
Mean	1386	507	1148	2081	563	1297			
IPCAe[1]	13.36480	8.13392	8.80096	-54.21802	10.28095	13.63738			
IPCAe[2]	-25.23624	13.09221	2.23948	-2.14545	20.72911	-8.67911			

E1 = Gofa, E2 = Humbo, E3 =Jinka, E4 = Kako, E5 =Konso, E6 = Melkassa, G1 = NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 = VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1

Table5: Mean values of seed yield and yield-related traits of 15 mung bean genotypes

Genotypes	DF	DM	PH	FPP	PPP	SPP	HSW	SYLD
G1	42.56	69.39	42.98	53.9	14.86	12.35	4.528	1161
G2	53.22	67.72	42.02	94.9	20.19	11.07	4.028	1241
G3	45.22	67.72	40.06	96.6	22.36	10.24	4.25	1259
G4	40.69	69.39	37.82	63.2	14.81	10.63	4.667	696
G5	40.42	68.39	40.77	59.4	25.14	11.57	3.656	1129
G6	51.38	96.33	43.49	47.4	15.47	10.51	4.089	1290
G7	44.31	66.72	40.28	62	20.36	10.74	4.694	1192
G8	45.22	68.12	37.57	88.7	23.64	10.07	3.683	1580
G9	51.22	68.39	40.08	79.9	20.25	10.96	4.294	1125
G10	45.36	69.39	41.27	74.4	20.86	11.35	4.333	1053
G11	41.56	66.72	38.63	38.5	17.47	9.29	5.944	905
G12	42.69	68.727	38.69	75.4	15.31	9.63	4.52	1044
G13	57.56	98.98	43.74	61.5	14.03	10.24	4.222	1375
G14	59.77	97.72	41.74	47.5	15.36	11.51	4.639	1278
G15	55.56	98.39	48.79	44	20.36	10.18	5.361	1128
Mean	47.78	76.14	41.20	65.82	18.70	10.69	4.46	1164
SD	4.48	1.71	4.18	23.12	9.92	1.62	0.55	8.27
CV (%)	2.3	2.5	11.1	28.5	16.4	16.6	13.6	28.3

CV = Coefficient of variation, SD = standard deviation, G = genotype, DF = days to flowering, DM = days to maturity, PH = plant height, FPP = five plants pod, PPP = number of pods per plant, HSW = hundred seed weight, SPP = seed per pod. G1 = NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 = VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1.

3.3. Stability analysis

3.3.1. Additive main effects and multiplicative interaction analysis

The AMMI analysis of variance for seed yield (kg ha-1) of 15 mung bean genotypes tested at six environments is presented in Table 6. Considering the additive component of the analysis, genotype had brought significant (P≤0.01) effects on seed yield, while the environment significantly (P≤0.001) affected seed yield. A similar result was reported by Kocaturk *et al*. (2019) on soybean genotypes, who reported that significant (P≤0.01) effects were observed due to environment, genotype, and G×E interaction for the seed yield and yield components. In this study, the environment accounted for the largest part of the variation in seed yield (59.6%) followed by genotype (16.8%). This finding is supported by the works of (Asrat *et al*., 2009; Kocaturk *et al*., 2019) on soybean, and Tamene *et al*. (2013) on field pea, that demonstrating the environment accounted for the largest part of the variation in seed yield followed by the genotype. Similarly, Yan and Kang (2003) reported the environment was considered as the predominant source of variation. In the current study, the largest variation in seed yield was explained by environments, which indicated the presence of different environments that can be sub-grouped into mega-environments. This result is in agreement with the work of Dessalegn *et al*. (2018) on finger millet, who reported that the difference in seed yield across environments implies that the environments are highly variable. This indicated the presence of different environments that can be sub-grouped into mega-environments, since, the largest variation in seed yield was explained by environments.

Regarding the multiplicative component, genotype by environment interaction significantly (P≤0.01) influenced seed yield. According to the result of AMMI, (14.8%) was explained due to GEI effects on the variation in the total sum of squares (Table 6). This finding conforms to the report of Kocaturk *et al*. (2019) on soybean, who reported that the GE interaction explained (20.84%) of the total variation. The highest share of the total sum squares was contributed by environment and genotype total sums of squares as compared to the GEI, with large differences among environmental means causing most of the variation in seed yield

of mung bean. This finding also coincides with the previous works on cowpea (Akande, 2009; Sarvamangala *et al*., 2010; Nunes *et al*., 2014; Tariku *et al*., 2018), Zali *et al*. (2012) in chickpea who reported that the larger contribution of GEI than genotype effect for the observed yield variation was due to large contribution of the environment in GEI.

The AMMI model extracted two significant Interaction Principal Component Axis (IPCAs) from the interaction component (Table 6). The multiplicative component of the AMMI further revealed that the mean squares were highly significant (P≤0.01) for the first interaction principal component axis (IPCA1) and significant (P≤0.05) for the second interaction principal component axis (IPCA2). Hence, these two IPCAs (IPCA1 and IPCA2) captured 47.4% and 7.4% of the interaction of sum squares, respectively accounting for a total of 54.8% of the total GEI sum of squares. Moreover, the IPCA1 mean square was greater than that of IPCA2, indicating the presence of differences in seed yield performance of the genotypes as a result of GEI. This finding is in agreement with the previous reports by Tamene *et al*. (2013) for field pea, Hagos and Fetien (2013) for bread wheat, and Ashraf *et al*. (2016) on flax. The first and the second IPCA together explained 54.8% of the variability in seed yield of mung beans due to GEI. This indicated that the first two IPCAs had exerted a significant contribution to the variations in GEI.

In this study, the two IPCA's accounted for greater than 50% of the interaction of sum square and were significant. Therefore, the AMMI model with the first and second multiplicative terms was adequate for cross-validation of seed yield variation explained by GEI that can easily be visualized with the aid of the biplot whereas, the residual was considered as noise. The results were in agreement with the several authors who took the first two IPCAs for GGE biplot analysis for different crops (Zobel *et al*., 1988; Mohammadi and Mahmoodi 2008; Asrat *et al*., 2009; Hagos and Fetien, 2013; Tamene *et al*., 2013; Kilic, 2014; Pržulj *et al*., 2015; Dyulgerova and Dyulgerov, 2019) which showed a similar magnitude of GEI variance revealed by the first two principal components of GEI and indicated that AMMI with the first two multiplicative terms was the best predictive model.

Table 6: AMMI ANOVA for seed yield (kg ha⁻¹) of 15 mung bean genotypes

Table 6: AMMI ANOVA for seed yield (kg ha^{-1}) of 15 mung bean genotypes

Source	DF	SS	MS	Sum of squares explained (%)	GxE Interaction explained (%)	Cumulative explained (%)
Total	269	238218571	885571			
Treatments	89	132841482	1492601***	33.6		
Genotypes	14	10414899	743921**	16.8		
Environments	5	76569237	5313847***	59.6		
Block	12	30842052	2570171ns	5.79		
Interactions	70	45857346	655105**	14.8		
IPCA 1	18	37882199	2104567**		47.4	47.4
IPCA 2	16	5250316	328145*		7.4	54.8
Residuals	36	2724831	75690*	1.7		
Error	168	74535037	443661			

E = Environments, G = Genotypes, SS = Sum of Squares, MS = Mean Squares, DF = Degree of Freedom, IPCA1 = Interaction Principal Component Analysis Axis 1 scores, IPCA2 = Interaction Principal Components Analysis Axis 2 scores.

3.3.2. *GGE biplot analysis*

The GGE biplot displays the genotypic main effect (G) and genotype by environment (G x E) interaction of a genotype by the environment data set (Yan *et al*., 2000). The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 75.22% and 14.06% of the GGE sum of squares, respectively (Figure 1).

3.3.3. *Mean performance and stability of genotypes*

Desirable genotypes are those located close to the ideal genotype. Genotypes G8, G6, and G15 can be thus used as benchmarks for the evaluation of mung bean genotypes since they are placed near the ideal genotype and found near the first concentric circle, and thus are desirable genotypes. This finding is in line with the reports by Muez *et al*. (2015), who found outstanding genotypes near to the ideal genotype in wheat. Based on the average environmental coordination (AEC) method, genotypes (G4, G10, and G11) were the most unstable and undesirable genotypes across the tested environment since these genotypes had a larger distance from the origin of the biplot and were found far distant from the first concentric circle (Figure 1).

The ideal genotype is the one presenting high means and is identified based on the length of the vector; thus, the longer the PC1 and PC2 without projections and the closer to the concentric circle, the better the genotype (Santos *et al*., 2017). Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero GE, as represented by the small circle with an arrow pointing to it (Yan, 2001). Thus, starting from the middle concentric circle pointed with arrow concentric circles were drawn to help visualize the distance between genotypes and the ideal genotype (Yan and Tinker, 2006). Based on this, the genotype (G13) was considered the ideal genotype and was followed by the genotype (G6). Genotypes were classified in the following order according to their performances: Genotype (G13) > (G6) ≅ (G8) > (G15) > (G9) ≅ (G2) ≅ (G14) ≅ (G7) > (G1) ≅ (G12) ≅ (G3) > (G5) > (G10) > (G11) > (G4). A position in either direction away from the biplot origin, on this axis, indicates greater GEI and reduced stability (Yan, 2002). Genotypes (G8, G6, and G15) are located on the next consecutive concentric circles, and these genotypes are considered the most desirable genotypes. On the other hand, undesirable genotypes were those very far distant from the first concentric circle; namely, genotypes (G4, G10, and G11) in Figure 1.

The ranking of fifteen mung bean genotypes based on their mean yield and stability performance is shown in Figure 2. The line passing through the biplot origin is called the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang, 2003). The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa indicating a greater G×E interaction effect and reduced stability in either direction away from the biplot origin and separates genotypes with below-average means from those with above-average means (Bhartiya *et al*., 2017). For selection, the ideal genotypes are those with both high mean yield and high stability. The

average yield of a genotype is approximated by the projections of their markers on the AEC x-axis while the stability is determined by the projection onto the AEC ordinate line (y-axis) (Yan and Rajcan, 2002). As shown in Figure 2, the genotypes further along the average tester axis (ATA), away from the biplot origin and in direction of the arrow (to the left), exhibited higher mean performance. Therefore, the genotypes that gave higher yield values were in the order of (G8) > (G13) > (G6) > (G14) > (G15); while the lowest yielding genotype was (G4). Generally, in the bi-plot, as shown in Figure 2, the genotypes G6 (NLLP-MGC-24), G15 (NVL-1), and G8 (VC1973A) can be considered as genotypes with both high yield and stable performance since these genotypes are close to the origin and have the shortest vector from the ATC. The genotypes with the highest yielding performance but relatively low stability were G7 (NLLP-MGC-27), whereas the genotype with low yield and low stability were G5 (NLLP-MGC-22) and G10 (VC6368 (46-40-4)). The other genotypes on the left side of the line with no arrow have yield performance greater than the mean yield and the genotypes on the right side of this line had yields less than the mean yield.

As indicated in the bi-plot (Figure 2) the genotypes, G6 (NLLP-MGC-24), G15 (Acc0013), and G8 (VC1973A) were the most stable genotypes with better mean yield performance. The genotypes G1 (NLLP-MGC-01), G14 (N-26), G10 (VC6368 (46-40-4)), G12 (Acc002), G7 (NLLP-MGC-27), and G5 (NLLP-MGC-22) can be recommended for specific adaptation, whereas genotypes G6 (NLLP-MGC-24), G9 (NLLP-MGC-09), G8 (NLLP-MGC-08), G15 (NVL-1), G11 (NLLP-MGC-06), G4 (NLLP-MGC-20), G13 (Acc006), and G3 (NLLP-MGC-15) can relatively be recommended for wider adaptation.
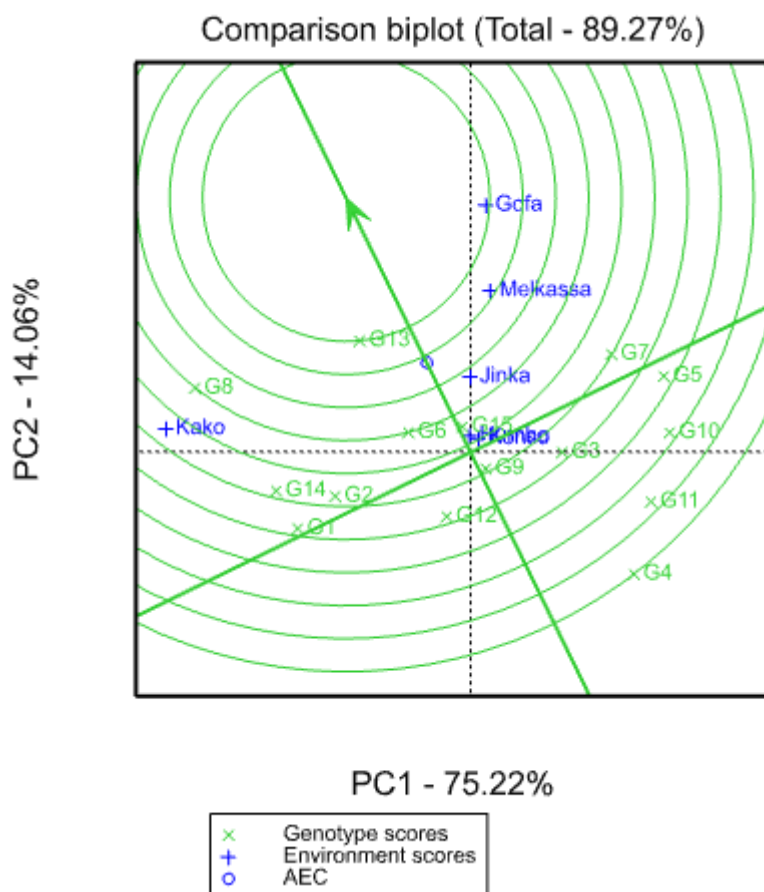

Figure 2: GGE biplot-based genotype-focused scaling for comparison of the genotypes with the stable genotype
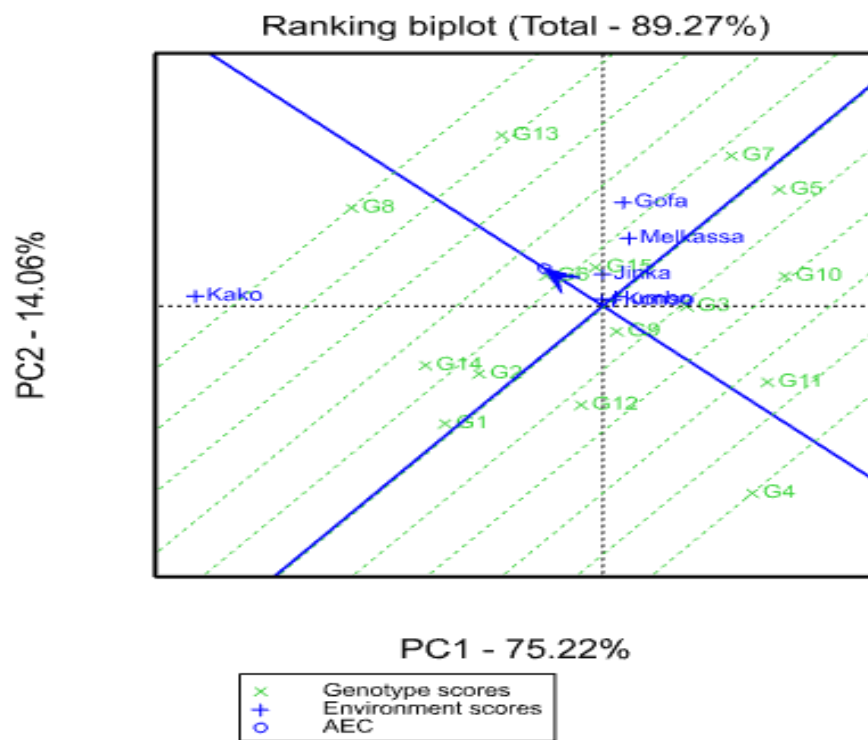
Figure 2: The AEC Views of the GGE Biplot Based on Environment-focused Scaling for the Mean Performance and Stability of Genotypes
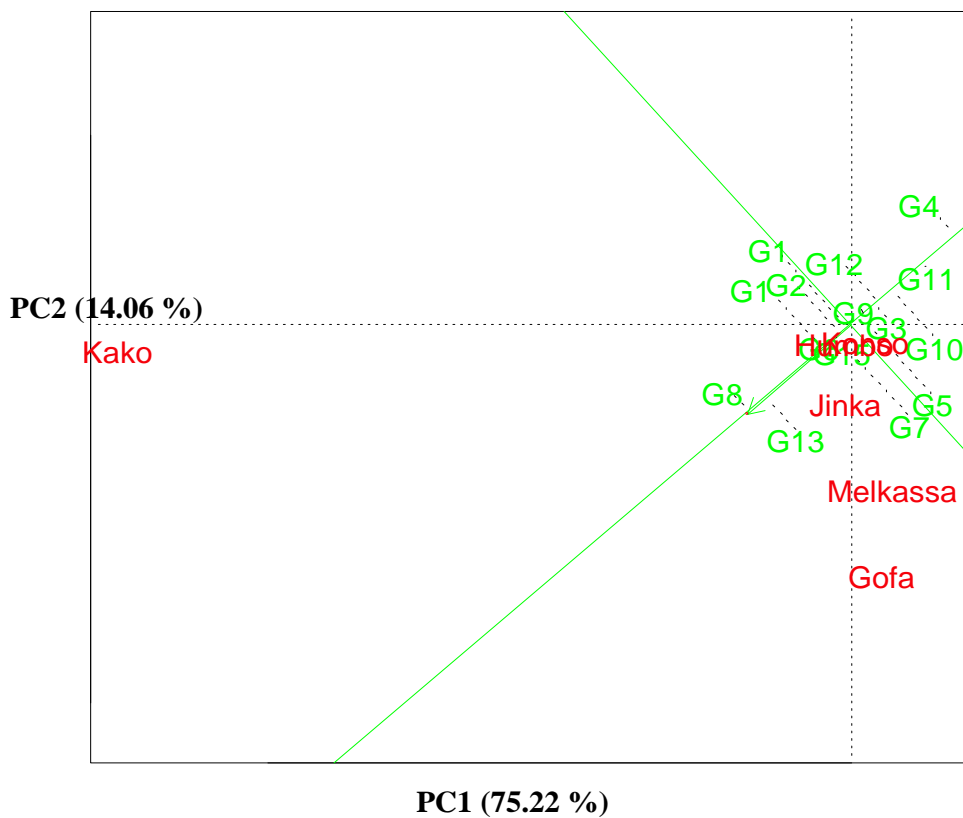

Figure 3: Mean and stability view of the GGE bi-plot for mung bean genotypes evaluated at six environments

3.3.4. 'Which-Won-Where' patterns of genotypes and environments

As indicated in Table 6, the residual mean square for seed yield was significant (P≤0.05), suggesting that the importance of constructing an AMMI biplot is very low or good for nothing. The polygon view of the GGE biplot is the best way the identification winning genotypes by visualizing the interaction patterns between genotypes and environments (Yan et al., 2000; Yan and Kang, 2003). Therefore; the GGE biplot has been used in a variety of trials to identify the best-performing genotype(s) across environments, and categorize the best genotypes for specific environments, whereby specific genotypes can be recommended to specific environments (Yan and Kang, 2003; Yan and Tinker, 2006).

Therefore, it was necessary to construct a GGE biplot for visual observation to understand which genotypes were best performed in which environment or which genotypes were stable and unstable (Figure 4). A polygon view of GGE was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. Genotypes (G8, G13, G7, G5, G4, and G1) were the vertex genotypes, having the largest distance from the origin and were more responsive to environmental changes and gave high yield except G4 were considered as specially adapted genotypes. The genotypes located on vertices of polygon performed either best or poorest in one or more environments. Therefore, these genotypes are best in the environment lying within their respective sector in the polygon view of the GGE-biplot (Yan and Tinker, 2006); thus these genotypes are considered specifically adapted. The vertex genotypes in each sector are the best genotype in environments whose markers fall into the respective sector. If a genotype at an angular vertex of the polygon falls within one sector with an environment marker (or with several markers), that means that the yield capacity of this genotype was the highest in this particular environment. Environments within the same sector share the same winning genotypes and environments in different sectors have different winning genotypes. Genotypes (G8 and G13) performed well at Kako while genotypes (G5 and G7) performed well at Gofa and Melkassa and were moderately adapted to Jinka. Two vertex genotypes, G1, and G4 had the highest yield in none of the environments (Figure 4). Genotypes

close to the origin of axes have wider adaptation (Fetein and Bjornstand, 2009). In this study, the genotypes (G3, G9, G2, G12, G15, G6, G11, and G14) were located within the polygon and were less responsive. This finding is supported by the previous works (Yan et al., 2001; Yan and Tinker, 2006), who reported that the genotypes within the polygon and nearer to origin were less responsive than the vertex genotypes.

The polygon view of the GGE-biplot analysis in (Figure 4) helps to detect cross-over and non-crossover genotype-by-environment interaction and to analyze possible mega environments in multi-location yield trials (Yan et al., 2007). The perpendicular lines were equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. Line 1 is between G8 and G13 and line 2 is perpendicular to side G13 and G7; line 3 is perpendicular to side G7 and G5; lines 4 and 5 are perpendicular to side G10 and G11; similarly, line 6 is perpendicular to side G4 and G1; while, line 7 is perpendicular to side G1 and G8. The environments fall into two quadrants while the genotypes are into four quadrants. In the GGE biplot, the vectors from the biplot center divided the graph into seven sectors.

The GGE biplot presented in Figure 4, indicating that the best performing genotypes for a specific environment and the group of environments. This finding is following the results of (Yan et al., 2007; Dessalegn et al., 2018) who reported that when different environments fell into different sectors; it shows that they had different high-yielding cultivars for those sectors, and also the presence of a cross-over interaction. The rays of the bi-plot divided the plot into seven sections. The environments appeared in three of them, revealing two mega environments. The vertex families for each quadrant represented the genotypes with the highest yield in the specific environment hence the highest yielding genotypes were identified for each sector. This finding is in agreement with the previous reports on soybean genotypes (Bhartiya et al., 2017; Ramos et al., 2017; Kocaturk et al., 2019), who reported that the GGE biplot created for soybean genotypes in seed yield was divided into six or eight sectors. When using the first two principal components, two clusters of environments (mega-environments) were formed using the GGE biplot methodology, indicating the environmental groupings, which suggests the possible existence of

different mega-environments. The polygon view of the GGE biplot indicated the presence of a crossover G x E interaction as the environments fell in different sectors of the polygon view and had different high-yielding genotypes (Yan and Kang, 2003). The current test locations could be grouped into two different mung bean-growing mega-environments. Thus, in our studies, the first mega-environment consists of environments Jinka, Humbo, Konso, Gofa, and Melkassa whereby genotypes (G5 and G7) in Gofa and Melkassa produce the highest yield (Figure 4), while the genotypes (G8 and G13) are producing the highest yield in Jinka, Humbo, and Konso.

3.3.5. Discriminating and representativeness of the test environments

The IPCA scores of the genotype in the AMMI analysis signify the adaptability of the genotypes across environments and the relationship between genotypes and environments. This is supported by the reports of (Zobel et al., 1988; Gauch and Zobel, 1996). Therefore, genotypes with small scores close to zero have low interactions and were stable, whereas, genotypes with large scores have high interactions and were unstable. In the present investigation, IPCA1 alone and despite positive or negative signs, genotypes (G6, G9, and G12) had small scores close to zero and were stable, while the genotypes (G10, G3, G5, G7, G8, G11, G1, and G14) had large IPCA1 scores and far from zero were unstable (Figure 5). The genotype (G9) had a small and positive sign of IPCA1 scores and thus this genotype was stable across the environments. Oliveira et al. (2014) and Tariku et al. (2018) reported that the genotypes with lower IPCA1 scores would produce lower G×E interaction effects than those with higher IPCA1 scores and have less variable yields or more stable across environments. In the present study G3, G13, G8, G5, G7, G1, G14, and G10 had more responsive since they were away from the origin whereas the genotypes G4, G11, and G15 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G6, G9 and G12 were closest to the origin and hence had almost no interaction forces. Genotypes (G9, G11, and G4) had a positive sign of IPCA1 scores and had a shorter vector to the origin. Here the genotype (G9) is adapted to Jinka while genotypes (G4 and G11) are adapted to Humbo, genotypes (G5 and G7) are adapted to Gofa and Melkassa, while genotype (G3) is adapted to

Konso. In contrast, the genotype (G8 and G13) was adapted to Kako with a larger and negative IPCA1 score.

As shown in Figure 5, the discriminating ability and representativeness of test environments, Kako, Konso, and Gofa were more discriminating environments with longer vectors and larger angles which provides much information about differences among genotypes. These environments cannot be used for selecting superior mung bean genotypes, but are useful in culling out unstable genotypes. Environments with longer vectors are more discriminating with the genotypes whereas environments with very short vectors are little or not informative on the genotype difference (Yan, 2002; Yan et al., 2007). On the other hand, if the marker of a test environment is close to the biplot center, having a short vector, all genotypes in it are similar, and this environment is not informative about their differentiation. Environments with short spokes do not exert strong interactive forces while those with long spokes exert strong interaction.

In this study, Jinka, Humbo, and Melkassa had relatively short vectors and were close to the origin, indicating that all genotypes performed similarly and therefore it might provide little or no information about the genotypes' differences. The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Therefore, it should not be used as a test environment for mung bean genotypes. As suggested by Yan and Tinker (2006), though, identification and removal of non-informative test environments as well as identification of test environments for yield evaluation trials require multiyear data. If budgetary constraints allow only a few test environments, these test environments would be the first choice. The cosine of the angle between environment vectors is used for the assessment of approximation between environments; the smaller the angle between environment vectors; the larger the correlation between them (Yan and Holland, 2010). The smaller the angle, the more representative the environment is (Yan and Tinker, 2006; Yan et al., 2007). Representativeness of the test environment is visualized by the angle formed between the environment vector and abscissa of the average environment axis. Correspondingly, there is a strong correlation between environments Humbo

and Konso since the cosine of the angle between these two environment vectors is small. As suggested by Yan (2001), discriminating ability and representativeness are the important properties of test environments. An ideal environment should be highly differentiating for the tested genotypes and is also representative (Yan and Kang, 2003). Thus, environments Kako, Konso, and Gofa with long vectors had high discriminating power, and environments Jinka, Humbo, and Melkassa were characterized by low discriminating power (Figure 5). Hence, environments Kako, Gofa, and Konso exerted strong interaction forces while the rest three (Jinka, Humbo, and Melkassa) did less.

Therefore, the tested environments, Kako, Gofa, and Konso were more discriminating environments with longer vectors and larger angles which provides more information about differences among genotypes. Contrastingly, Jinka, Humbo, and Melkassa had relatively short vectors and were close to the origin and all genotypes performed similarly and therefore provide little or no information about the genotypes' differences (Figure 5). On the contrary, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction.
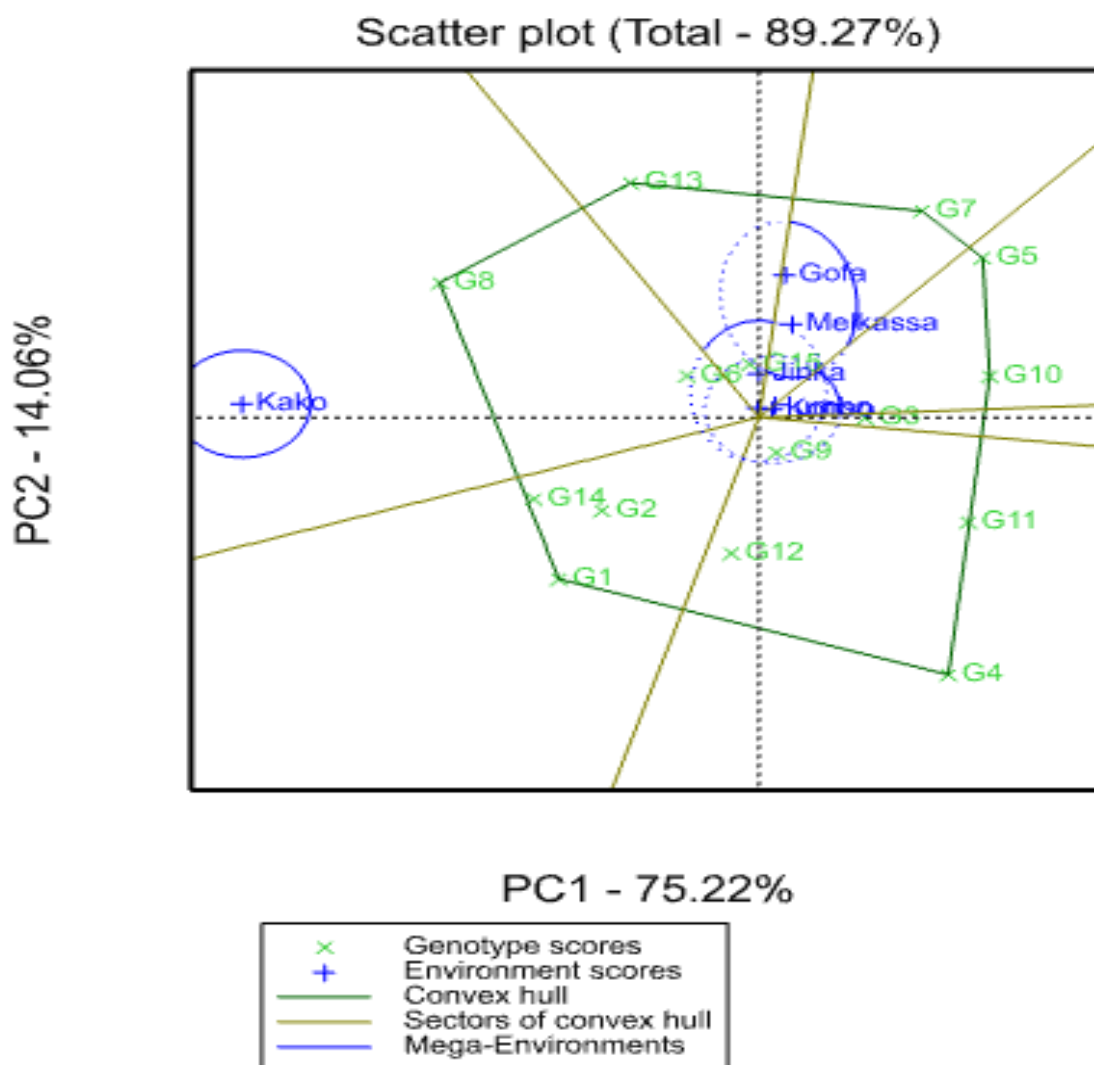

Figure 4: Polygon view of GGE biplot showing the relationship among environments and the specific ideal niches of the tested genotypes
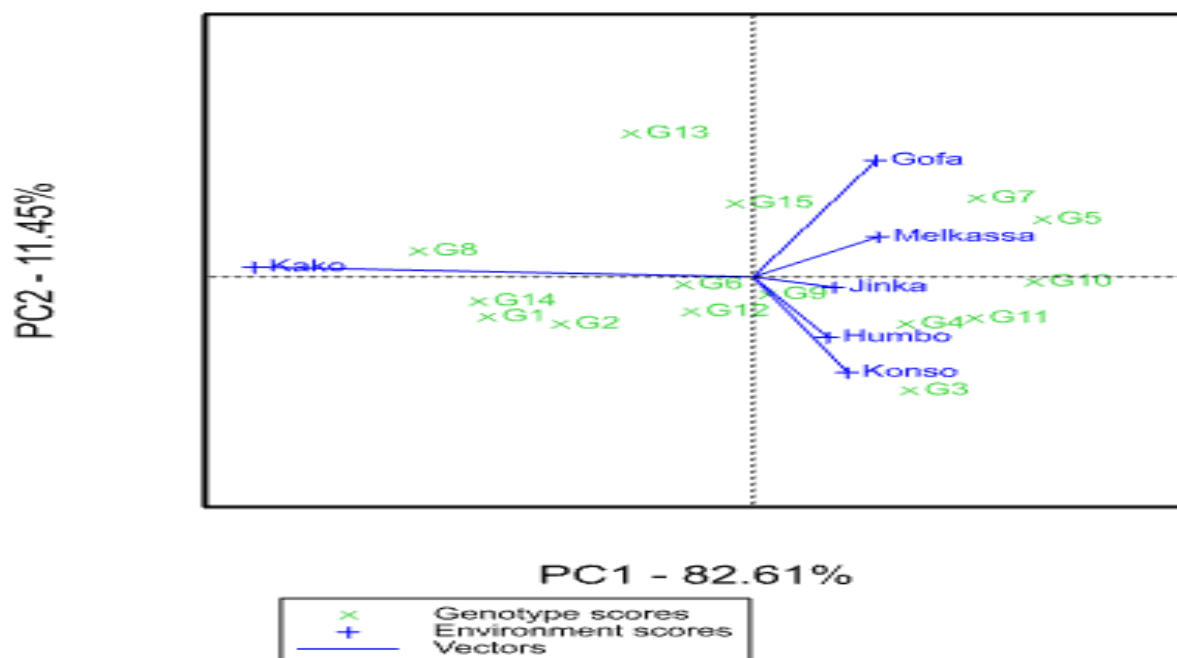
Figure 5: Discriminating power and representativeness of test environments

3.3.6. AMMI stability value (ASV) and yield stability index (YSI)

According to the ASV model, genotypes (G9), (G15), and (G12) were stable and high yielders among the tested genotypes, indicating that the yield performance and stability had the same trend in the present study (Table 7). Similarly, Annicchiarico (2002) noted the dynamic of stable genotype and yield response that is always parallel to the mean response of the tested environments. Such findings have been observed by Getachew et al. (2015) in chickpea, Nigussie et al. (2015) in common bean and Tariku et al. (2018) in cowpea. However, genotypes G10, G8, and G14 were the most unstable. These genotypes are adapted to specific and favorable environments. Likewise, Lotan et al. (2014) reported genotypes with the higher IPCA score and AMMI stability values were more specifically adapted to a certain environment. The principles of stability alone might not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance. Therefore, as per the suggestion (Hassan et al., 2012; Lotan et al., 2014), the stability per se should however not be the only parameter for selection because the most stable genotypes would not necessarily give the best yield performance.

Therefore, there is a need for approaches that incorporate both mean yield and stability in a single index. To this end; the yield stability index (YSI) method incorporates both yield and stability into a single index, reducing the problem of using only yield stability as the single criteria for the selection of genotypes. Genotypes with the least YSI values are considered the most stable with a high grain yield (Bose et al., 2014; Lotan et al., 2014). Genotypes G6 and G13 were the most stable with low YSI values and high mean performance. Therefore, the yield stability index (YSI) discriminated genotypes G6 and G13 with high adaptability and high grain yield (Table 7). Thus, according to the YSI method, the most desirable genotypes which can be considered as widely adapted and with seed yield above the grand mean (1164 kg ha^{-1}) among 15 mung bean genotypes are presented in Table 7. Similarly, Hassan et al. (2012) indicated that both yield and stability should be considered simultaneously to exploit the useful effect of GE interaction and to make the selection of the genotypes for a diverse environment. Conversely, genotypes like G1, G4, G5, G9, G10, G11, G12, and G15 had high YSI values and below the grand mean (1164 kg ha^{-1}) seed yield performance, which indicates instability of the genotypes across the tested environments.

Table 7: Mean seed yield (kg ha^{-1}) of fifteen mung bean genotypes, AMMI stability values (ASV), Ranks, yield stability index, IPCA1, and IPCA2 scores

Genotypes	IPCA1	IPCA2	ASV	R[a]	MSY	R[y]	YSI
G1	-19.98967	5.99378	6.89	11	1161	8	19
G2	-14.48429	7.06782	5.55	8	1241	6	14
G3	11.77525	17.02819	4.89	7	1259	5	12
G4	11.49340	7.04205	4.87	6	696	15	21
G5	21.74822	-8.60742	6.95	12	1129	9	21
G6	-5.21787	1.15422	3.68	4	1290	3	7
G7	16.79039	-11.77015	5.84	9	1192	7	16
G8	-25.16245	-3.87765	8.60	14	1580	1	15
G9	1.11140	2.62966	1.56	1	1125	11	12
G10	21.12314	0.73750	10.82	15	1053	12	27
G11	16.64242	6.21678	6.12	10	905	14	24
G12	-4.66412	5.19843	3.06	3	1044	13	16
G13	-9.17042	-21.46960	4.47	5	1375	2	7
G14	-20.64006	3.65807	7.60	13	1278	4	17
G15	-1.35534	-11.00170	2.08	2	1128	10	12
Grand Mean					1164		

ASV = AMMI Stability Value, R[a] = rank of ASV, MSY = means of seed yield, R[y] = rank of seed yield, YSI = Yield Stability Index, G1= NLLP-MGC-01, G2 = NLLP-MGC-12, G3 = NLLP-MGC-15, G4 = NLLP-MGC-20, G5 = NLLP-MGC-22, G6 = NLLP-MGC-24, G7 = NLLP-MGC-27, G8 = VC1973A, G9 = NM94 (VC6371-94), G10 =, VC6368(46-40-4), G11 = NLLP-MGC-06, G12 = Acc002, G13 = Acc006, G14 = N-26, G15 = NVL-1

4. Conclusion

Combined analysis of variance shows that genotype, environment, and G x E interaction are highly significant, which indicate the existence of a wide range of variation between the genotypes, environments, and interactions.

According to AMMI and GGE biplot methods, G6, G13, and G3 were identified as stable and high yielder genotypes across the environments. Besides, the results of the yield stability index and AMMI stability values identified genotypes G6, G13 and G3 as high yielding with stable performance across the environments and be recommended for diverse environments. Therefore, genotype G13, which fell into the center of concentric circles, was the ideal genotype in terms of higher yield ability and stability, compared with the rest of the genotypes. Also, genotypes, G6, G8 and G15 can be considered as desirable genotypes. In this study, genotype G13, which fell in the first concentric circle, was the ideal genotype in terms of higher-yielding ability and can be used as a benchmark for evaluation of mung bean variety development in future breeding programs. However, G1, G4, G5, G9, G10, G11, G12, and G15 were identified as least stable with high YSI and ASV values that can be recommended for specific environments.

In general, this study has provided highly valuable information on the yield stability status of the mung bean genotypes and the best environments for future improvement programs in Ethiopia. Therefore, the mung bean improvement strategy in Ethiopia should be based on the performance of the genotypes across environments. Generally, GGE biplot analysis, AMMI, and Eberhart and Russell's model revealed that genotype G13 was stable and high yielding.

Conflict of interest
The author declares that there is no conflict of interest.

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