

Research Article

Grain Yield Stability Analysis of Kabuli Chickpea (*Cicer Arietinum* L) Advanced Genotypes in Bale and East Bale, Southeastern Ethiopia

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Abstract

Chickpea (*Cicer arietinum* L) production in Ethiopia is highly constrained by diverse biotic and abiotic stresses, and its full genetic potential has not been exploited yet. Chickpea grain yield is one of the complex quantitative traits influenced by prevailing environmental conditions. As a result, multi-environmental yield trials are indispensable to detect wide adaptable and high yielding cultivars in the breeding program. To this end, a total of 12 advanced chickpea genotypes were evaluated against two standard checks (Arerti and Harbu) across two locations (Sinana and Ginnir) from 2019 to 2021 main cropping season. Pooled analysis of variance for grain yield showed significant differences ($p \leq 0.01$) among the main effects of genotypes and environments and ($p \leq 0.01$) for $G \times E$ interaction effects. This indicates that either the genotypes differentially responded to the changes in the test environments or the test environments discriminated the genotypes or both. The first two principal components accounted for cumulative of 84.88% interaction effects, indicating that the majority of interaction effects were within two principal components. Additive Main effect and Multiplicative Interaction (AMMI) biplot enabled identification of adapted genotypes, G5 (FLIP-09-287C) and G2 (FLIP-09-155C). GGE biplot analysis suggested the presence of one mega environment and enabled identification of high seed yielding and broadly adapted genotypes G5 (FLIP-09-287C). Therefore, FLIP-09-287C can be released as wide adaptable Kabuli type chickpea variety for potential growing areas of Bale and East Bale as well as other similar agro-ecologies.

Keywords

AMMI, *Cicer Arietinum* L., GGE, Grain Yield, Stability

1. Introduction

Chickpea is one of the most important food legumes and chief source of dietary protein playing a vital role in mitigating protein malnutrition across the world [3]. Ethiopia is the largest producer, consumer and exporter of chickpea in Africa, annually producing above 515,000 metric tons on about 241,000 hectares of land with an average productivity of

around 2 tons/ha [7]. However, the production and productivity of chickpea is highly constrained by diverse biotic and abiotic stresses to exploit its full genetic potential (>5 tons/ha).

The development of superior varieties in terms of grain yield, quality, stress resistance, and yield stability is an im-

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portant consideration in plant breeding programs. Chickpea breeding program has been focusing mainly on developing high yielding varieties, with good level of resistance to major biotic and abiotic stresses. However, yield is a complex quantitative trait, often controlled by many genes, influenced by prevailing environmental conditions, with each gene having a small effect. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials [14]. Genotypic responses in trials involving many environments are crucial in cultivar evaluation and recommendation [13]. Because crop grain yield is not determined by genotype and management practices alone but also by environmental Interaction (GEI). Therefore, to select superior genotypes, the investigation of GEI in Multi- Environmental Trials (MET) is inevitable [2]. A mega environment can be defined as a group of locations that consistently share best cultivar(s) [23].

Genotype-by-Environment Interaction simply refers to inconsistent phenotypic performance of genotypes across environments. It potentially presents limitations on selection and recommendation of varieties for target set of environments when it is associated with a significant genotypic rank change over environments [12, 17]. The multivariate approaches for the analysis of GEI are numerous; some of the current ones are: Joint Regression [10, 6]. Kang Modified Rank Sum [11]. and the Additive Main effects and Multiplicative Interaction (AMMI) analysis, the AMMI Stability Value (ASV) [18]. the Genotype Selection Index (GSI) and Genotype main effect plus Genotype by Environment (GGE) biplot [22].

The Additive Main Effects and Multiplicative Interaction Model (AMMI) were found suitable to handle both the main effects and GEI in multi-location yield trials. The AMMI model combines regular analysis of variance for additive effects with principal component analysis for multiplicative structure within the interaction. AMMI biplot is considered to be an effective tool to diagnose GEI patterns graphically. AMMI analysis is commonly being used in GE interaction data analysis in many crops to identify superior genotypes for specific or wide adaptation. In common bean crops [1, 9] used AMMI analysis to identify superior genotypes for specific or wide adaptation.

The GGE model (GGE biplot) was proposed by [22], allowing visual examination of the relationships among the test environments, genotypes, and the genotype-by-environment interactions (G×E interaction). The GGE biplot displays the genotype main effect (G) and the genotype by environment interaction (GE) in two-way data. It is an effective tool for mega environment analysis (“which-won-where” pattern), whereby specific genotypes can be recommended to specific mega environments, to identify the mean performance and stability of genotype, and environmental evaluation. Therefore, the main objective of the present study was to analyze the grain yield stability of Kabuli-type chickpea advanced pipelines in the breeding program to identifying best per-

forming genotype.

2. Materials and Methods

2.1. Plant Materials and Experimental Design

Twelve chickpea pea genotypes were examined in Randomized Complete Block Design (RCBD) with four replications in two different environments (Sinana and Ginnir) and three consecutive growing seasons comprising a total of six growing environments, where each year at each location was considered as a separate environment. All the genotypes were planted on a plot, which had 1.2 width and 4-meter length each plot consisting of four rows each row being 0.3m spaced apart. Data on seed yield and hundred seed weight were recorded from the two central rows of each plot, where the total harvestable area was 2.4m².

2.2. Data Analysis

The *additive main effect* and *multiplicative interaction* (AMMI) analysis was performed using the model suggested by [4], as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^h \lambda_n \alpha_{ni} Y_{nj} + R_{ij}$$

Where, Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment, μ is the grand mean, g_i is the mean of the i^{th} genotype minus the grand mean e_j is the mean of j^{th} environment minus the grand mean, λ_n is the square root of the Eigen value of the principal component Analysis (PCA) axis, α_{ni} and Y_{nj} are the principal and the principal component scores for the PCA axis n of the i^{th} genotype and j^{th} environment, respectively and R_{ij} is the residual. The Genotype by environment Interaction biplot was plotted for the 12 chickpea genotypes tested at 6 environments. The regression of yield for each variety on yield means for each environment was computed with the CropStat 7.2 program.

AMMI Stability Value (ASV): -ASV is the distance from the coordinate point to the origin in a two dimensional of IPCA1 score against IPCA2 scores in the AMMI model is analyzed by the method suggested by [18].

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

Where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$, the weight given to the IPCA1 value by dividing the IPCA1 sum squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. The smaller IPCA score indicates a more stable genotype across environments.

Genotype Selection Index (GSI): was calculated for each genotype, which incorporates both mean grain yield and sta-

bility index in a single criterion by the method suggested by [8].

$$GSI_i = RY_i + RASV_i$$

Genotype and Genotype by Environment Interaction biplot

analysis: GGE model was used to investigate GEI. Stastical analysis was performed by using statistical packages – Gen-Stat Discovery Edition 4 and breeding view present in the breeding Management system tool (BMS).

Table 1. Lists of Genotypes and their source.

Code	Genotypes	Source	Code	Genotypes	Source	Environment
G1	DZ-2012-CK-0262	DZARC	G7	DZ-2012-CK-0259	DZARC	E1= Sinana 2019
G2	FLIP-09-155C	DZARC	G8	FLIP-98-58C	DZARC	E2= Ginnir 2019
G3	DZ-2012-CK-0278	DZARC	G9	FLIP-09-98	DZARC	E3= Sinana 2020
G4	FLIP-09-159C	DZARC	G10	ILC-93	DZARC	E4= Ginnir 2020
G5	FLIP-09-287C	DZARC	G11	Harbu	DZARC	E5= Sinana 2021
G6	FLIP-85-17C	DZARC	G12	Arerti	DZARC	E6= Ginnir 2021

DZARC = DebreZeit Agricultural Research Center, SARC = Sinana Agricultural Research Center.

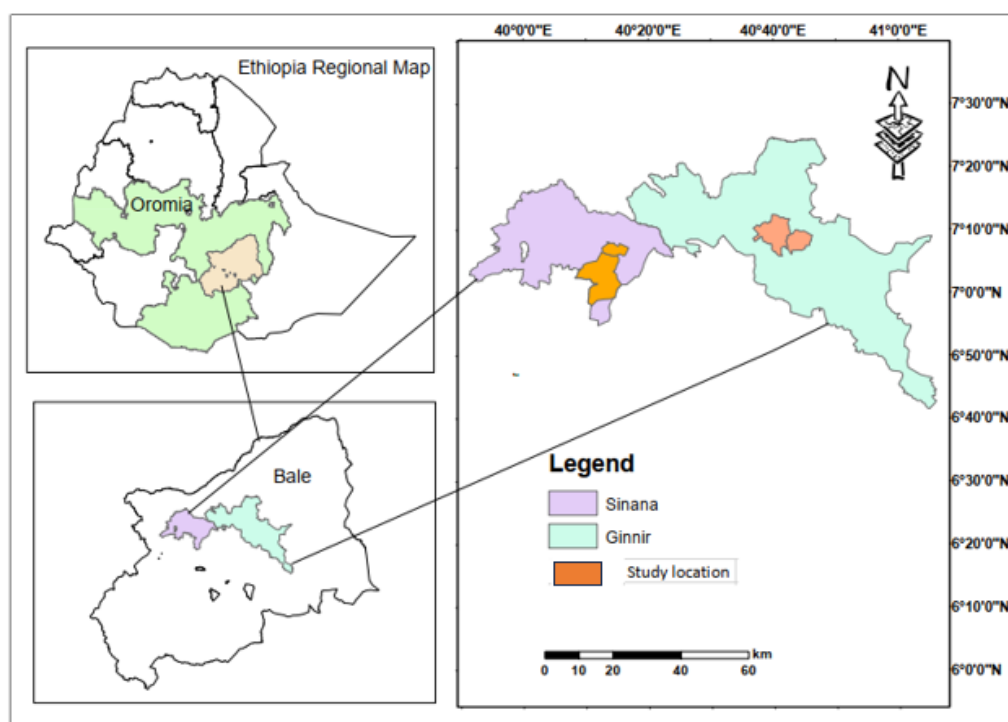


Figure 1. Description of the test locations for geographical position.

3. Results and Discussion

The combined analysis of variance and AMMI analysis is shown in Table 2. The AMMI model analysis of variance (ANOVA) for grain yield showed highly significant differences ($P \leq 0.01$) for genotypes, environments and genotypes

by environments interactions. The first principal component axis of genotype by environment interaction ($G \times E$) was also highly significant ($P \leq 0.01$). The first and second principal component explained about 73.36% and 11.51% of the genotype by environment interaction ($G \times E$), respectively. This is in agreement with the findings of [5, 19] who suggested that $G \times E$ pattern is collected in the first principal components of analysis. Similarly, other previous studies also suggested the

importance of capturing most of the genotype by environment interaction (G×E) sum squares in the first principal compo-

nent axis to attain accurate information [4, 18].

Table 2. Analysis of Variance of AMMI model for grain yield of Chickpea genotypes.

Source	DF	SS	MS	TSS explained %
Genotypes	11	19.8	1.8***	
Location	5	344.8	68.969**	
Interactions	55	23.1	0.42**	
IPCA1	15	12.9	0.861**	73.36
IPCA2	13	4.3	0.332**	11.51
IPCA3	11	3.5	0.317	
IPCA4	9	2.1	0.235	
Total	287	420.9	1.467	

The highest mean grain yield was recorded from genotype FLIP-09-287C (2.25t/ha) followed by FLIP-09-155C (1.94t/ha) and Arerti, standard check (1.81t/ha) whereas the

mean grain yield across locations ranged from 0.21t/ha for E5 to 3.28t/ha for E2. The grand mean for grain yield across locations and years was 1.65/ha (Table 3).

Table 3. Mean grain yield (t/ha) of Chickpea genotypes x site over three years, 2019-2021.

Genotype Code	Genotype	Environment (Year x Location) t/ha						Mean
		E1	E2	E3	E4	E5	E6	
G1	DZ-2012-CK-0262	1.66	3.16	2.03	0.14	0.30	1.79	1.51
G2	FLIP-09-155C	2.60	3.49	2.59	0.22	0.25	2.50	1.94
G3	DZ-2012-CK-0278	1.77	3.19	2.51	0.11	0.24	1.86	1.61
G4	FLIP-09-159C	2.36	3.22	2.20	0.30	0.32	1.74	1.69
G5	FLIP-09-287C	3.56	4.47	2.64	0.33	0.26	2.23	2.25
G6	FLIP-85-17C	1.86	2.58	2.29	0.38	0.06	1.74	1.48
G7	DZ-2012-CK-0259	1.76	3.74	2.08	0.22	0.30	2.61	1.79
G8	FLIP-98-58C	1.25	3.00	1.56	0.20	0.12	1.76	1.31
G9	FLIP-09-98	1.40	2.65	1.51	0.30	0.13	1.57	1.26
G10	ILC-93	1.41	3.14	2.48	0.17	0.11	1.99	1.54
G11	Harbu	1.57	2.97	2.01	0.31	0.19	2.28	1.55
G12	Arerti	1.90	3.72	2.72	0.34	0.31	1.89	1.81
	Mean	1.93	3.28	2.22	0.25	0.21	1.99	1.65
	LSD 0.05	0.17	0.95	0.42	0.04	0.05	0.12	0.17
	CV (%)	7.2	24.2	15.7	12.9	17.9	4.9	21.9

3.1. AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

AMMI stability value (ASV), proposed by [18] quantifies and ranks genotypes according to their yield stability. In the present study, AMMI stability value discriminated genotypes G3, G12, G1, G7, and G6 as stable ones, whereas those with the second-lowest ASV, G10, G2, G11, G8, G4 and G8 were considered to be moderately stable. [16] suggested that the most stable genotypes would not necessarily have the best

yield performance; hence there is a need for pursuing approaches that incorporate both mean yield and stability in a single index. For the simultaneous selection of yield and stability, a new approach known as genotype selection index (GSI) was recommended by [8]. Genotype with the least GSI is considered as the most stable with high grain yield. Accordingly, G5 and G2 were found to be the best genotypes since they gave the highest mean seed yield and showed moderate stability (Table 4).

Table 4. Mean grain yield, and Stability parameters for 12 Chickpea genotypes.

Code	Genotypes	Mean	Rank	Slope	MS-DEV	IPCA1	IPCA2	ASV	Rank ASV	GSI
G1	DZ-2012-CK-0262	1.51	9	0.94	0.809	0.122	0.010	0.367	3	12
G2	FLIP-09-155C	1.94	2	1.13	0.098	-0.315	0.020	0.944	8	10
G3	DZ-2012-CK-0278	1.61	6	1.01	0.333	0.042	-0.130	0.181	1	7
G4	FLIP-09-159C	1.69	5	0.96	0.106	-0.221	-0.338	0.744	4	9
G5	FLIP-09-287C	2.25	1	1.36	0.000	-1.090	0.096	3.272	12	13
G6	FLIP-85-17C	1.48	10	0.84	0.100	0.160	-0.572	0.747	6	16
G7	DZ-2012-CK-0259	1.79	4	1.11	0.010	0.098	0.693	0.753	5	9
G8	FLIP-98-58C	1.31	11	0.88	0.095	0.342	0.205	1.047	10	21
G9	FLIP-09-98	1.26	12	0.77	0.681	0.346	-0.171	1.053	11	23
G10	ILC-93	1.54	8	1.01	0.055	0.251	0.037	0.753	7	15
G11	Harbu	1.55	7	0.91	0.133	0.324	0.139	0.983	9	16
G12	Arerti	1.81	3	1.10	0.113	-0.061	0.011	0.182	2	5

The first interaction principal component axis (IPCA) and mean grain yield (tons/ha) were used to construct an AMMI biplot graph to gain sufficient information on the stability of individual genotypes in different test environments (Figure 2). The result of AMMI Biplot analysis with IPCA1 against mean grain yield (tons/ha) indicated that some of the test genotypes showed good stability for grain yield in most test environments.

The characterization of each promising genotypes to mean grain yield and contribution to genotype by environment interaction (G×E) by mean of IPCA-1 indicated that genotype FLIP-09-287C (G5) were specifically adapted to high yield-

ing environments Mata (MT) (Figure 2). But with respect to their contribution to genotype by environment interaction (G×E) (the IPCA-1 Score, that is, stability), FLIP-09-287C (G5) were intermediately stable genotypes. However, FLIP-09-155C (G2), FLIP-09-159C (G4) and Arerti (G12) were shown to have a higher stability for yield than any other genotypes because these genotypes were positioned near the origin of the biplot (Figure 2). However, any genotype to be considered as best genotype should be able to combine good grain yield and stable performance across a range of growing environments. In this regard, FLIP-09-287C (G5) was relatively high yielding and stable genotype.

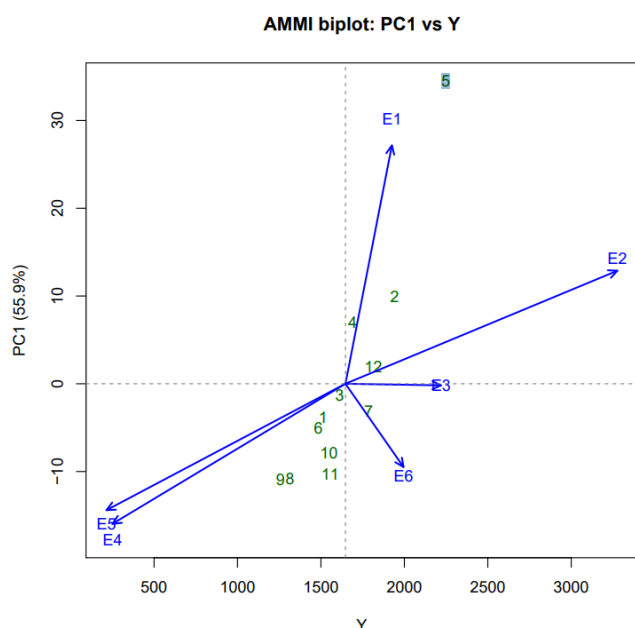


Figure 2. AMMI Biplot of Interaction Principal Component Axis (IPCA1) against mean grain yield ton/ha of 12 chickpea genotypes evaluated across 6 environments.

3.2. Genotype and Genotype by Environment Interaction (GGE) Biplot Analysis

“Which-won-where” grain yield performance of the 12 chickpea genotypes across test environments is presented in Figure 3. This explicitly displays the which-won-where pattern of genotypes. Each of the environments is located on one of the six sectors found in the biplot. The genotype(s) vertex in these sectors may have higher or the highest yield compared to other parts in all environments. The longest vector of the polygon on the sector 5 which is also the closest to E1 was FLIP-09-287C (G5), suggesting that it was high yielding and well adaptable to E1, E2, E3, E4 and E5. The vertex genotype for E4 sector was DZ-2012-CK-0259 (G7) suggesting it was the most adaptable genotype in this environment. The genotype in each sector is also adaptable for environment whose marker fell into corresponding sector so that environments within the same sector share the same winning genotype. No environment fell into the sector with G1, G3, G6, G8, G9, G10 and G11 which indicates that they were the poorest genotypes in some or all of the environments.

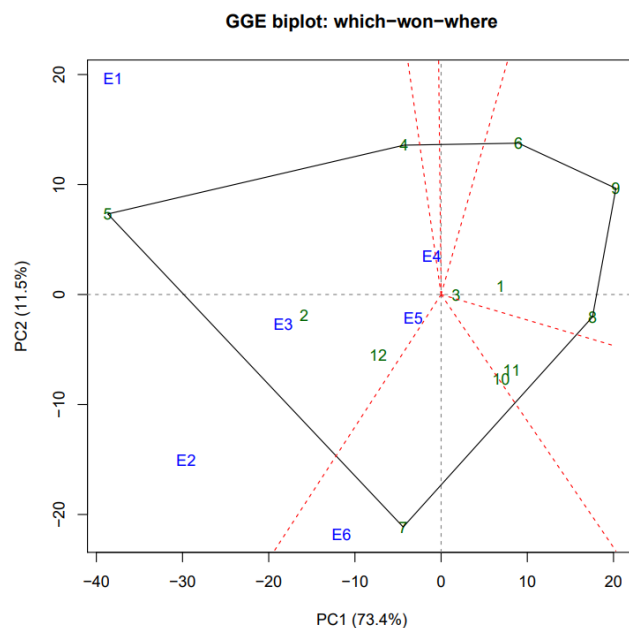


Figure 3. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments. Green and blue numbers stand for genotypes and environments, respectively.

3.3. Ranking Genotypes Relative to the Ideal Genotypes

An ideal genotype is one that has both high mean yield and high stability. The center of the concentric circles (Figure 4) represents the position of an ideal genotype, which is defined by a projection onto the mean-environment axis that equals the longest vector of the genotypes that had above-average mean yield and by a zero projection onto the perpendicular line (zero variability across environments). A genotype is more desirable if it is closer to the ideal genotype. Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation [21].

Units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype-focused scaling (Figure 4); the units of the AEC abscissa (mean yield) and ordinate (stability) should also be the original unit of yield. The unit of the distance between genotype and the ideal genotype, in turn, is the original unit of yield as well. The ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important [20]. Therefore, genotype G5 (FLIP-09-287C) which fell into the center of concentric circles was ideal genotypes in terms of higher yield ability and stability compared with the rest of the genotypes. In addition, G2 (FLIP-09-155C) and G12 (Arerti), located on the next concentric circle may be regarded as desirable genotypes.

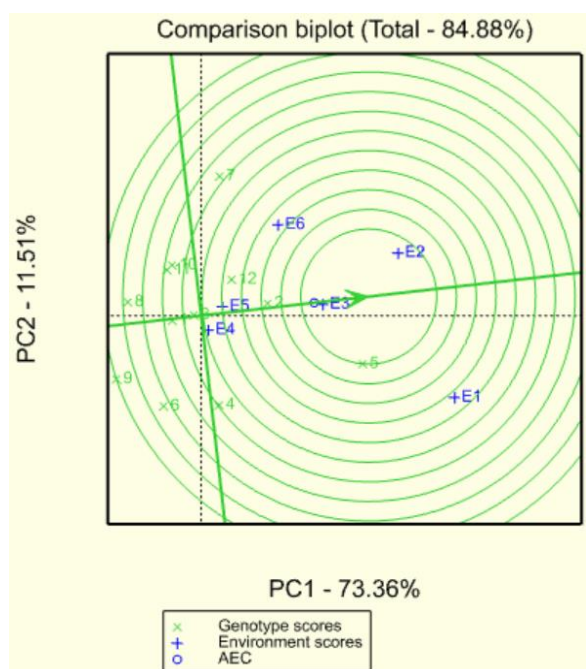


Figure 4. GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes. Green and blue numbers stand for genotypes and environments, respectively.

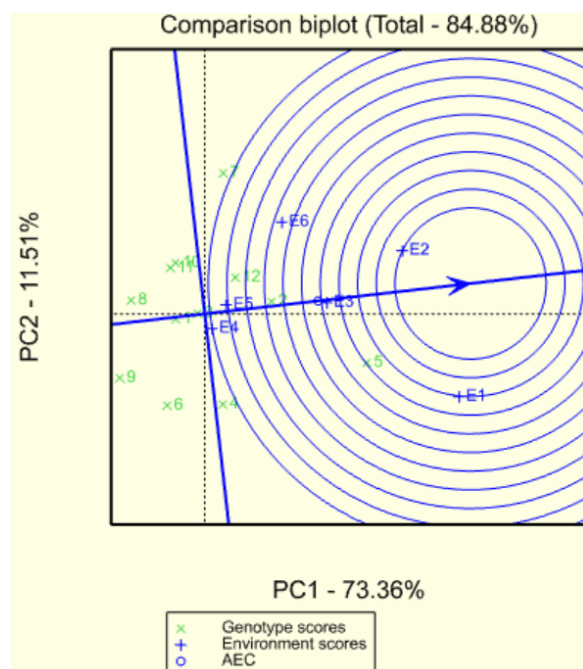


Figure 5. GGE biplot based on test environments-focused comparison for their relationships.

3.4. Ranking Environment Relative to the Ideal Environment

Rank environments with reference to the ideal environment. The ideal environment is defined as the most discriminating and representative. It generates a ranking of the test environments in terms of both criteria. An ideal environment should have a greater power of discrimination in terms of genotype main effects with high PC1 score and the most representative of all of the other environments, which is zero PC2, scores [24]. In the same way as the ideal genotype, the ideal environment is only an estimate and serves as a reference for the choice of site for multi-environment testing. Figure 5 defines an ideal test environment, which is the center of the concentric circles. This is a point on the AEA in the positive direction (most representative), with a distance to the biplot origin equal to the longest vector of all environments (most informative).

In the current study, E2 is closest to this point, therefore, having the greatest capacity for discriminating between genotypes and favored the selection of superior genotypes whereas E4 was poorest for selecting cultivars adapted to the whole environment. Recently, GGE biplot have been used to investigate adaptability and phenotypic stability of different genotypes in common bean [11, 15].

4. Conclusion

ANOVA showed significant differences among genotypes, environments, and genotypes $\times$ environments interaction (GEI) effects for grain yield of the 12 chickpea genotypes. The significant GEI indicated the inconsistent performance of genotypes. The discriminating ability and representativeness of test environments were assessed with GGE biplot and from mean yields, which showed that E2 (Ginnir 2019) was the most discriminating environment of all the others. In this study, AMMI biplot stability analysis (ASV) and genotype selection index (GSI) revealed that the most stable and high yielding genotypes was G5 (FLIP-09-287C). Additive Main effect and Multiplicative Interaction (AMMI) biplot enabled the identification of moderately adapted genotypes, G5 (FLIP-09-287C) and G2 (FLIP-09-155C). GGE biplot analysis suggested the presence of one mega environment and also enabled the identification of high seed yielding and broadly adapted genotype G5 (FLIP-09-287C). The results of the present study indicated that FLIP-09-287C showed better yield stability across all test environments and therefore, could be selected for release as wide adaptable variety in potential chickpea growing areas of Bale and East Bale, Southeastern Ethiopia and other similar agroecologies.

Abbreviations

AMMI	Additive and Multiplicative Interaction
ASV	AMMI Stability Value
GSI	Genotype Selection Index
GGE	Genotype and Genotype by Environment Interaction
GSI	Genotype Selection Index
PCA	Principal Component Analysis

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Conflicts of Interest

The authors declare that they have no conflicts of interest.

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