

# Stability Analysis of Coffee (*Coffea arabica* L.) Bean Yield Using GGE Biplot in South Western Ethiopia

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**Abstract:** Coffee is the largest export crop, and the backbone of the Ethiopian economy. The experiment were conducted at Metu, Gore and Chora for two consecutive years with the objective of determining the nature and magnitude of genotype x environment interaction, to classify environment based on genotype performance and identifying stable genotypes on coffee yield by using GGE biplot analysis. A total 17 advanced coffee genotypes were laid out using randomized complete block design with three replications. The analysis of variance for coffee bean yield revealed the presence of highly significant difference ( $P < 0.01$ ) among genotypes, environments and genotype by environment interaction. Results of GGE biplot showed that the first two principal components (PC1 and PC2) justified 65.66% of the sum of squares with PC1=49.12% and PC2=16.54% of the GGE sum of squares. The six test environments were divided into four different coffee growing mega-environments. Among the test location Metu2 and Gore2 were the most representative and most discriminating environment while Chora2 was less powerful to discriminate genotypes or less desirable as a testing location for coffee bean yield. Genotype G5 (236/71), followed by G8 (872/74) and G12 (227/71) were stable and high yielder across coffee growing environments and it recommended for mega environment production.

**Keywords:** Bean Yield, Discriminating, Genotype x Environment Interaction, Stable

## 1. Introduction

Coffee (*Coffea arabica* L.) belongs to the genus *Coffea* in the Rubiaceae family, and is the only allopolyploid (tetraploid) ( $2n=4x=44$ ) coffee species and self-fertile at approximately above 95% [15, 24]. *Coffea arabica* L. is the most widely consumed and highly preferred international beverage mainly for its best quality and is also one of the most important agricultural commodities in the world contributing to more than 60% of the world coffee production [26]. Coffee is the largest export crop, and the backbone of the Ethiopian economy. The livelihood of a quarter of the Ethiopian population depends directly or indirectly on the different processes of production and marketing along the coffee value-chain [10].

Understanding the relationship between crop performance and environment has long been a key issue for plant breeders and geneticists. Crop performance, the observed phenotype, is a function of genotype (variety), environment, and GEI. GEI is said to occur when different cultivars or genotypes respond differently to diverse environments [30]. Researchers agree that GEI is important only when it is significant and causes significant change in genotype ranks in different environments, i.e., different genotypes are superior in different environments. The relative magnitude of GEI provides information about the likely area of adaptation of a given genotype. It is also useful in determining efficient methods of using time and resources in a breeding program. Previous studies of G x E interaction on Arabica coffee have illustrated significant interaction of genotypes with environment for yield, yield related traits and

quality traits [9, 16, 19, 35].

Several statistical models have been used to study and interpret G x E interaction, explore the performance of genotype in response to the environment and estimate yield [8, 17]. The GGE biplot methodology Genotype main effect (G), plus genotype by environment interaction (GE) of is a recent addition to the tools for analyzing multi-environment trials [32]. Many authors have acknowledged it to be very efficient. The GGE Biplot approach has strongly captured the imagination of plant breeders and production agronomists. The GGE biplot is a multi-faceted tool in quantitative genetic analyses and plant breeding. In addition to dissecting GEI, GGE Biplot helps analyze genotype-by-trait data, genotype-by-marker data, and diallel cross data [27, 30, 32, 36].

The objectives of this study are therefore to assess the G x E interaction pattern of the multi-environment trials of coffee genotypes from Southwestern Ethiopia and model the data

using GGE biplot analysis, and to select and recommend high yielding stable and adopted genotypes.

## 2. Materials and Methods

Seventeen coffee genotypes including the standard checks were evaluated at Gore, Mettu and Chora from 2015-2016 main cropping seasons (Table 1). The experiments were super-imposed on five year old coffee variety trials at these locations. Randomized Complete Block Design (RCBD) with three replications was used throughout the testing locations. The plots consisted of ten trees per row and both of the intra and inter row spacing were 2m in each location. All cultural practices, such as, slashing, applications of fertilizers DAP (81 kg/ha) and UREA (125 kg/ha), weeding, herbicide application (1-4 Liter ha<sup>-1</sup> Round up) and pruning were done properly, and timely as per the recommendation [14, 37].

**Table 1.** List of the areas with some of their climatic and soil characteristics.

Environment code	Description	Location		Altitude (m.a.s.l)	Soil characteristics		Annual RF (mm)	Mean Temp. (°C)	
		Latitude (degree)	Longitude (degree)		Type	P <sup>II</sup>		Min	Max
E1	Chora2	8.42	36.13	1930	Nitosol	5.42	1685.7	13.1	26.2
E2	Mettu2	8.3	35.58	1580	Nitosol	5.24	1088.3	10.1	28.0
E3	Gore2	8.15	35.53	2085	Dark red		2364.1	14.4	23.7
E4	Chora1	8.42	36.13	1930	Nitosol	5.42	1694.4	13.0	26.3
E5	Mettu1	8.3	35.58	1580	Nitosol	5.24	1639.2	9.6	28.6
E6	Gore1	8.15	35.53	2085	Dark red brown		1764.2	14.4	24.9

Where, E1=Chora2 (2016), E2=Mettu2 (2016), E3=Gore2 (2016), E4=Chora1 (2015), E5=Mettu1 (2015), E6=Gore1 (2015)

Source: NMA, (2017) and JARC, center profile for other data (1995).

**Table 2.** Combined ANOVA for Coffee bean yield (kg/ha) and the percentage sum of squares of the 17 genotypes tested at different environments during 2015/16 and 2016/17 cropping season.

Source	DF	SS	SS%	MS	Pr>F
Environment (E)	5	8292628	34.46	1658526	0.0001
Replication within E (R/E)	6	591642	2.46	98607	0.0001
Genotype (G)	16	5328319	22.14	333020	0.0001
G x E	80	8210133	34.12	102627	0.0001
Residuals	96	1640952	6.82	17093.2	
Total	203	24063674	100		
Mean=857.5384			CV=15.25		

CV=coefficient of variation, DF=degree of freedom, SS=sum square, MS=mean square GxE=Genotype by environment interaction.

Data collected were analyzed using statistical analysis software 9.3 [25] by the PROC GLM procedure. Combined analysis of variance across the three tested environments were performed on plot means for bean yield to establish significant differences within the experimental factors genotypes, environment, block and Genotype X Environment. Bartlett's (1974) test was used to determine the homogeneity of error variances between environments.

The GGE biplot analysis was done using Genstat version 18<sup>th</sup> software [28]. The general model for GGE Biplot is as follow:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \epsilon_{i1} \eta_{j1} + \lambda_2 \epsilon_{i2} \eta_{j2} + \epsilon_{ij}$$

Where:

$Y_{ij}$ =The performance of the  $i$ th genotype in the  $j$ th environment;

$\mu$ =The grand mean;

$\beta_j$ =The main effect of the environment  $j$ ;

$\lambda_1$  and  $\lambda_2$ =Singular value for IPCA1 and IPCA2, respectively;

$\epsilon_{i1}$  and  $\epsilon_{i2}$ =Eigen vectors of genotype  $i$  IPCA1 and IPCA2, respectively;

$\eta_{j1}$  and  $\eta_{j2}$ =Eigen vectors of environment  $j$  for IPCA1 and IPCA2, respectively;

$\epsilon_{ij}$ =Residual associated with genotype  $i$  and environment  $j$ .

## 3. Results and Discussion

The analysis of variance for coffee bean yield revealed the presence of highly significant difference ( $P < 0.01$ ) among genotypes, environments and genotype by environment interaction (Table 2). Similar findings on the existence of genotype x environments interactions on coffee were also reported by many authors [1, 16, 18, 19, 22, 35]. Hence,

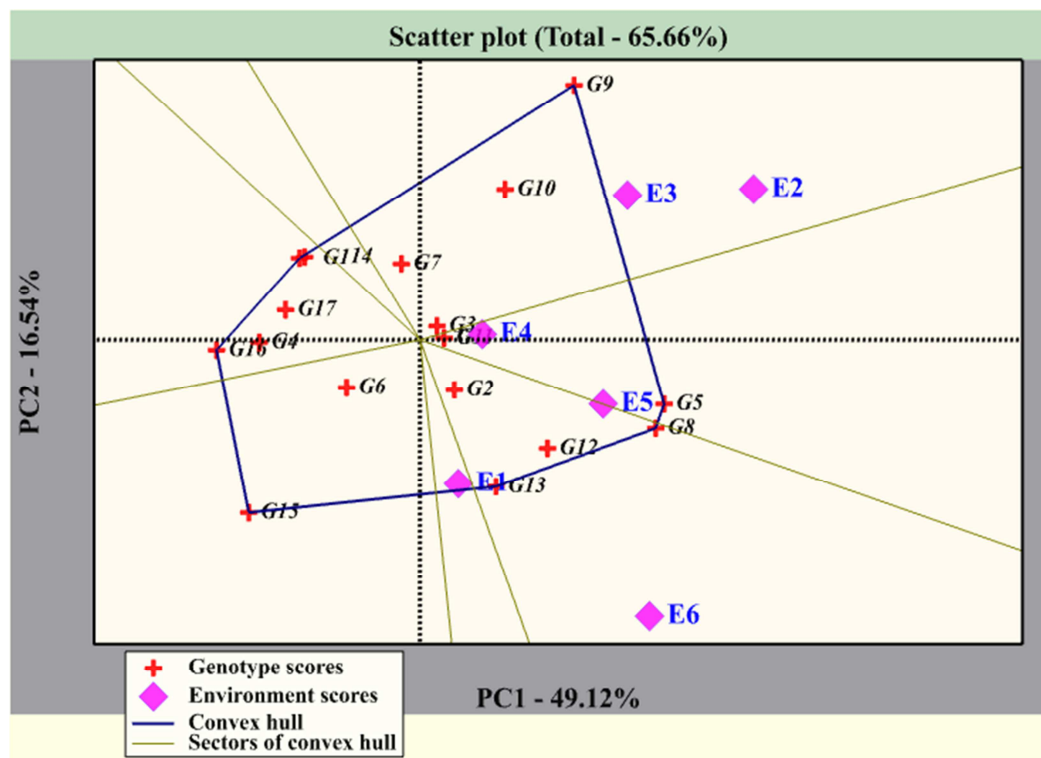
genotype  $\times$  environment interaction was highly significant for grain yield indicating that we can proceed and calculate phenotypic stability. Various stability statistics and concepts have been developed to analyze and interpret GEI [3, 11, 17]. Yan *et al.* (2000) proposed methodology known as genotype main effect and genotype by environment interaction (GGE) biplot for graphical display of G  $\times$  E interaction pattern of multi-environment data with many advantages. GGE biplot is an effective method based on principal component analysis (PCA) to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the G  $\times$  E interactions. GGE biplot analysis considers both genotype (G) and G  $\times$  E interaction effects and graphically displays G  $\times$  E interaction in a two way table [33]. GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from subjecting the environment centered data to singular-value decomposition [5].

### 3.1. The “Which-Won-Where” Patterns

The GGE biplot is an invaluable statistical tool for examining the performance of genotypes tested in different environments. The polygon view of the GGE biplot (Figure 1) indicated the best genotype in each environment. The “which-won-where” view of the GGE biplot is an effective visual tool in mega-environment analysis [29]. The term mega environment analysis defines the partition of a crop growing region into different target zones [7].

The partitioning of G  $\times$  E interaction through GGE biplot

analysis showed that IPCA 1 and IPCA 2 accounted for 49.12% and 16.54% of sum of squares, respectively with total of 65.66% variation for yield (figure 1). The six environments fell into four sectors with different winner genotypes and the bi-plot showed that eight vertex genotypes, G9, G5, G8, G13, G15, G16, G11 and G4. There are seven rays (figure 1), which divided the biplot into seven sections. The genotypes fell into seven sections but all the tested environments fell into four sections. The vertex genotype of each sector is the one that gave the highest yield for the environments which fall within that sector. The GGE biplot identified four different coffee growing mega-environments. The first environment containing the highest yielding environment E2 and E3 in Mettu2 and Gore2 area, respectively with a vertex genotype G9; the second environment containing the higher yielding environment (E5) in Mettu1 area with winner genotype G8 (872/74) and G5 (236/71) and low yielding E4 in Chora1 area; third environment includes medium yielding environment E6 in Gore1 area; and fourth environment containing low yielding E1 environments in Chora2 area with the winner genotype G13 (678) (figure 1). It had also been observed that no environments fell into sectors where genotype G15, G16 and G17 were the vertex genotypes, indicating that these genotype were not the best in any of the test environments. Similarly, Lemi *et al.*, (2018) identified four different *C. arabica* growing mega-environments, in sesame [34] and in lentil [12] identified three different growing mega-environments.



**Figure 1.** “Which won where” or which is best for what view based on genotype by environment interaction yield data of 17 genotypes evaluated in six environments.

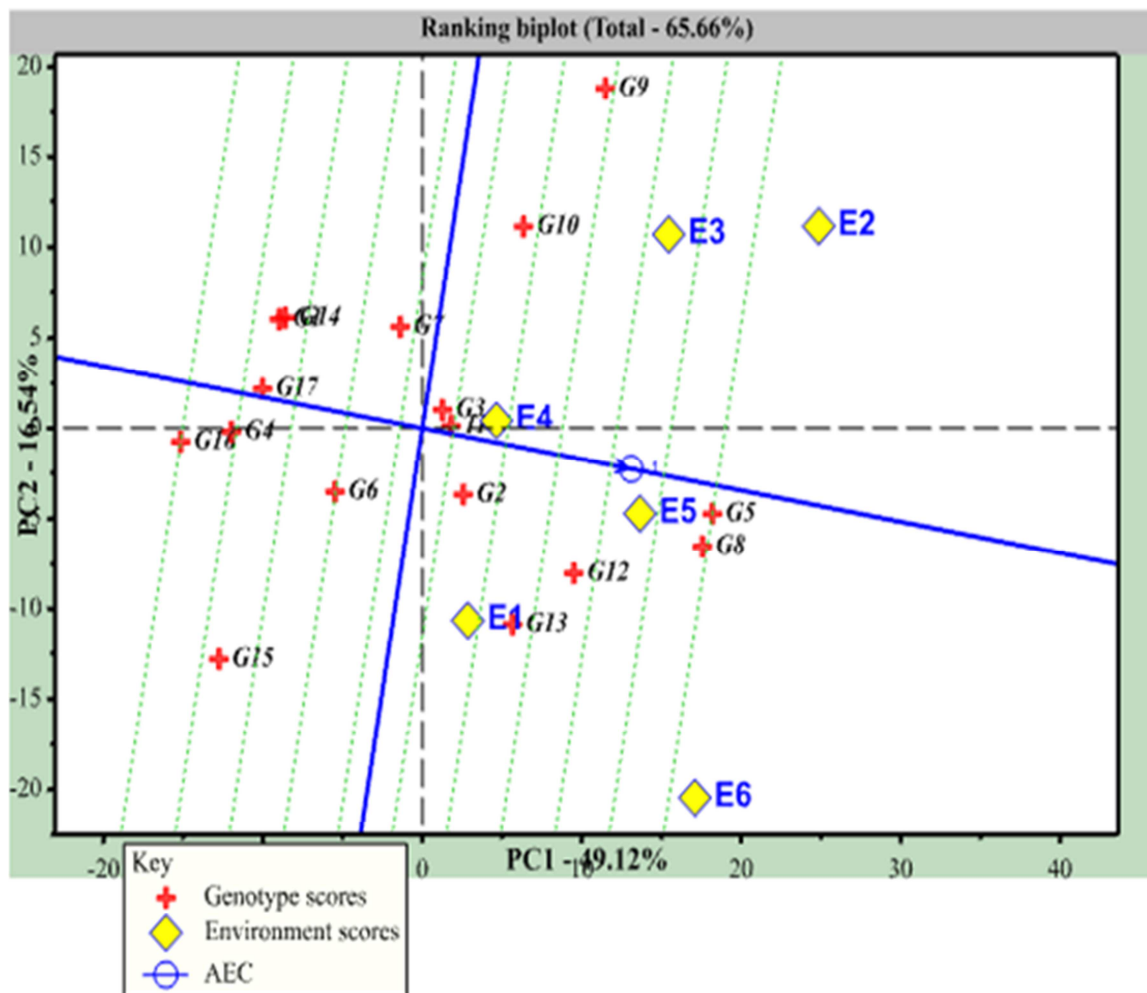
Where, E1=Chora2, E2=Mettu2, E3=Gore2, E4=Chora1, E5=Mettu1, E6=Gore1, G1=P-28, G2=233/71, G3=744, G4=P-23, G5=236/71, G6=P-30, G7=P-16, G8=872/74, G9=243/71, G10=363/73, G11=74140, G12=227/71, G13=678, G14=G15=P-17, G16=229/71, G17=74110.

### 3.2. Ranking of Genotypes Based on Mean Yield and Stability Performance

In GGE biplot methodology, the estimation of yield and stability of genotypes were done by using the average environment (tester) coordinate (AEC) methods [27, 36]. The line passing through the biplot origin is called the average environment (tester) coordinate (AEC), which is defined by the average PC1 and PC2 scores for all environments [31]. More close to concentric circle indicates higher mean yield. The AEC ordinate separates genotypes with below average means from those with above average means. Accordingly, genotypes with above average means or highest yielder were G5 (236/71), G8 (872/74), G12 (227/71), G2 (233/71), G13 (678), G11 (74140) and G3 (744) (figure 2).

The line, which passes through the origin and is

perpendicular to the AEC with double arrows, represents the stability of genotypes. Either direction away from the biplot origin, on the axis, indicates greater G x E interaction and reduced stability. For selection, the ideal genotypes are those with both high mean yield and high stability. In the biplot, they are close to the origin and have the shorter vector from the AEC. A longer projection to the AEC, regardless of direction, represents a greater tendency of the GEI of a genotype that means less stability across environments. Thus, genotypes G3, G8, G11, G12 and G5 were the most stable. On the other hand, the genotypes G9, G10, G15, G13 and G10 were far from AEC (long vector) indicating their least stability (figure 2). These results are in agreement with that obtained on rice [2], on coffee [16], on bread wheat [21] and on wheat [23].



**Figure 2.** Average environment coordination (AEC) views of the GGE biplot based on environment focused scaling for the means performance and stability of genotypes.

E1=Chora2, E2=Mettu2, E3=Gore2, E4=Chora1, E5=Mettu1, E6=Gore1, G1=P-28, G2=233/71, G3=744, G4=P-23, G5=236/71, G6=P-30, G7=P-16, G8=872/74, G9=243/71, G10=363/73, G11=74140, G12=227/71, G13=678, G14=P-17, G15=P-17, G16=229/71, G17=74110.

### 3.3. Evaluation of Genotypes Relative to Ideal Genotypes

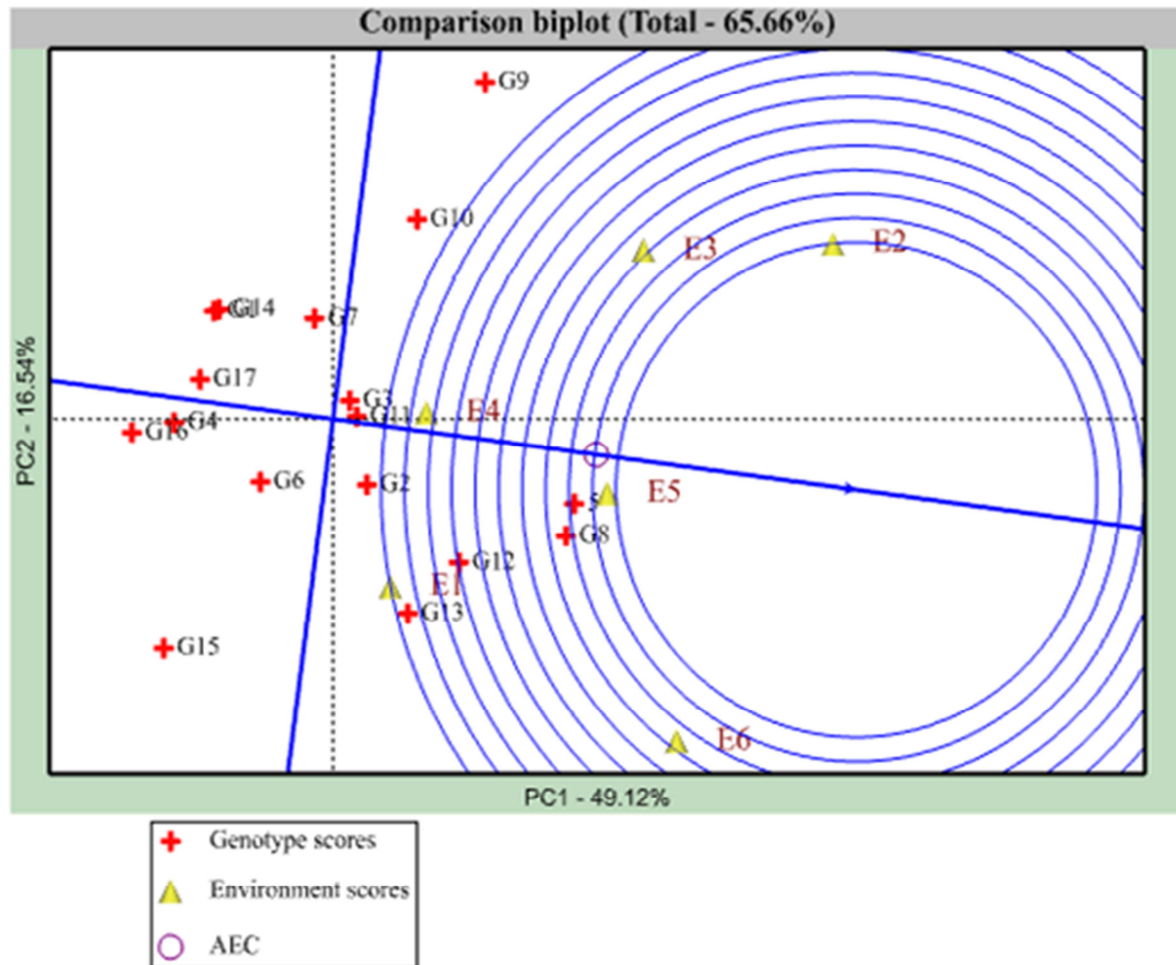
Genotype G5 (236/71), followed by G8 (872/74) and G12

(227/71) which fall closer to the center of concentric circles, were desirable genotypes in terms of high yield and stability, as compared to other genotypes (Figure 3). The center of the

concentric circles 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). Because the units of both IPCA1 and IPCA2 for the genotypes are the original unit of the yield in the genotype focused scaling, the units of the AEC abscissa (mean yield) and ordinate (stability) should also be the original unit of the yield. The unit of the distance between

genotype and the ideal genotype, in turn is the original unit of yield. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important [30]. On the other hand, genotypes G15 (P-17), G16 (229/71), G4 (P-23), G17 (74110), G6 (P-30), G1 (P-28), G14 (754) and G7 (P-16) which are located distant from the first concentric circle were undesirable genotypes (Figure 3).

Similar result was reported by many authors on different crops [2, 4, 13, 16, 20, 34].



**Figure 3.** GGE biplot based on genotype focused scaling for comparison and genotypes with the ideal genotype. Where E1=Chora2, E2=Mettu2, E3=Gore2, E4=Chora1, E5=Mettu1, E6=Gore1, G1=P-28, G2=233/71, G3=744, G4=P-23, G5=236/71, G6=P-30, G7=P-16, G8=8/72/74, G9=243/71, G10=363/73, G11=74140, G12=227/71, G13=678, G14=, G15=P-17, G16=229/71, G17=74110.

### 3.4. Evaluation of Environments Relative to Ideal Environments

E5 (Mettu-2) had the longest vector with small IPCA, which fell into the center of concentric circles was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. E3 (Gore-2) was closer to the ideal environment and considered as second powerful to discriminate genotypes. Conversely environments E1 (Chora-2), E6 (Gore-1), E4 (Chora-1) and E2 (Mettu-1) were far from the ideal environment and

considered as less powerful to discriminate genotypes (figure 4).

Discriminating ability and representativeness are the important properties of a test location. An ideal location should be highly differentiating for the tested genotypes and at the same time representative of the target location. Similar to ideal genotype, an ideal environment or location is defined and showed by the small circle with an arrow pointing to it. Meaning that the environment is more desirable and discriminating when located closer to the center circle or to an ideal environment. This result is in line with many authors [6, 30, 32, 34].



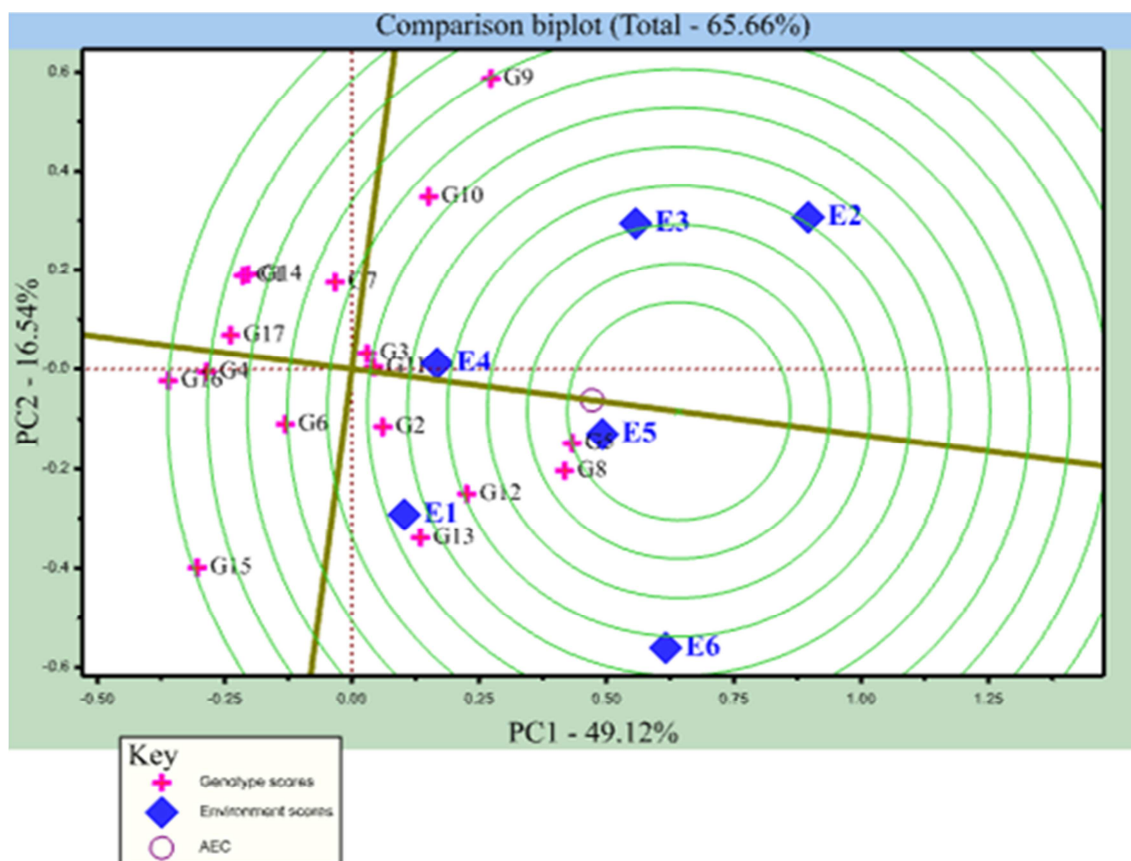


Figure 4. GGE biplot based on environment focused scaling for comparison and environment with the ideal environment.

## 4. Conclusion

GGE biplot is an important tool that allows visual examination of the relationships among the test environments, genotypes and the genotype  $\times$  environment (G $\times$ E) interactions. The partitioning of G  $\times$  E interaction through GGE biplot analysis showed that IPCA 1 and IPCA 2 accounted for 49.12% and 16.54% of sum of squares, respectively with total of 65.66% variation for yield. The current multi-location studies showed variation in the performance of 17 coffee genotypes from one environment to another. Genotype G5 (236/71), followed by G8 (872/74) and G12 (227/71) were among the best high yielding genotypes and most stable across all the tested environments suggesting that these genotypes were suitable for the agro-climatic regions evaluated in this study. E5 (Mettu2) and E3 (Gore2) were ideal environments or the most suitable taste location for coffee breeding in the region, whereas rest test environments (E1, E6, E4 and E2) were poorest for selecting cultivars adapted to the region.

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