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GGE Biplot Analysis of Genotype by Environment Interaction and Yield Stability Analysis of Arabica Coffee (*Coffea arabica* l.) Diallel Genotypes in South Western Ethiopia

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Abstract

Coffee is the major source of income earner or a significant cash crop for both producing and consuming-countries. In order to increase production and productivity of coffee, identification of adaptable, stable and high yielding genotypes under different environmental conditions prior to release as a variety is the first steps in plant breeding. Half diallel crosses among limmu coffee (Coffea arabica L.) comprising 17 including genotypes conducted for the objectives to determine the magnitude of genotype by environment interaction (GEI) and identify the stable genotype among diallel coffee genotypes by using GGE biplot analysis. The genotypes were evaluated for bean yield across three environments for two years (2016/17-2017/18) using a randomized complete block design (RCBD) with three replications. Combined analysis of variance revealed highly significant ($p < 0.01$) differences among environments, G × E interaction effects and genotypes for all the bean yield. The environment and GEI were found to be the most significant causes of yield accounted 69.4% and 10.5% of overall variation, respectively. The GGE biplot analyses identified promising genotype C45 (L55/01 x L45/01) which possess both highest average bean yield and stability across the environments as compared to other genotypes. Therefore, this genotypes should be used in breeding programs new hybrid variety development after further testing its repeatability.

Keywords: - Environments GGE Biplot Stability Yield

1. Introduction

Coffee is the second most valuable traded commodity after petroleum and produced in more than 80 countries including Ethiopia (Musoli *et al*., 2009). Arabica coffee (*Coffea Arabica* L.) is originated in southwestern parts of Ethiopia and the most widely cultivated among the three coffee species due to its quality, rich aroma, and low caffeine content than the others(Santos *et al.,* 2016). The coffee sector contributes about 4–5% to the country's Gross Domestic Product (GDP); it creates hundreds of thousands of local job opportunities (EBI, 2014) and providing 20–25% of the foreign exchange earnings (ECFF, 2015).

In Ethiopia, 758,523.29ha of land was allocated for coffee production and 482560.571 tons of clean coffee were obtained with the national average productivity of 0.64 tones ha^{-1} in 2019/20, which is quite low (CSA, 2020). Different biotic and abiotic factors might contributed for low productivity of coffee. Among these, lack of high yielding improved varieties for each agro ecological zones and lack of suitable varieties that exhibit stable performance across wide ranges of environments are the major constraints in coffee production and productivity in Ethiopia (Bayeta, 2001; Yonas and Bayeta, 2008).

Identifying the most stable genotypes is an important objective in many plant-breeding programs for all crops, including coffee. The performance of a genotype is determined by three factors: genotypic main effect (G), environmental main effect (E) and their interaction (Yan et al., 2007). Genotype by environment interaction (GEI) has been and still, is a major factor limiting the success of germplasm selection and identification of superior genotypes for use in plant breeding programs. It is an important to minimize the usefulness of the genotype means across locations or environments for selecting and advancing superior genotypes to the next stage of selection (De Leon et al., 2016).

Different scholars Walyaro (1983); Afework (2017); Lemi et al. (2018); Lemi (2021) and Alemu et al. (2022) have been reported the presence significant genotype-environmental interactions for coffee bean yield studied on different materials in different locations at different times. In the study of bean yield stability of coffee cultivars tested at multi locations in Ethiopia within the domain of the main coffee growing ecologies of the country, showed a significant effect of location x genotype interaction indicating differential response of genotypes across the many different locations (Mesfin and Bayeta, 1997). However, Lemi (2021), reported in his study the coffee genotypes which showed top yielding performance and stability with an ideal environment.

Adaptability and yield stability are important measures for effective cultivation of a crop species in different agro-climatic regions including coffee bean yield. Among different methods of measuring the stability of genotypes the most commonly used used to identify the stable genotype(s) are .additive main effects and multiplicative interaction (AMMI) model (Gauch,1992), genotype main effects in addition to genotype by environment interaction (GGE) biplot (Yan et al.,2000).

Genotype main effects in addition to genotype by environment interaction (GGE) biplot GGE bi-plot analysis considers both genotype and GEI effects and graphically displays GEI in a two-way table (Yan and Hunt, 2001). It is an effective method based on principal component analysis (PCA) to fully explore a multi-environment trial (MET) data. It allows visual examination of the relationships among the test environments, genotypes and the GEI (Sime and Tesfaye, 2020). Therefore, the objectives of this study was to determine the magnitude of genotype by environment interaction (GEI) among diallel coffee genotypes and to identify the stable genotypes from the diallel coffee genotypes by GGE biplot analysis.

2. Materials and Methods

2.1. Description of the study area

The field experiments were conducted in three coffee growing environments in south western Ethiopia (Jimma, Agaro and Gera) for two consecutive years (2016/17 and 2017/18). The description of study areas with some climatic and soil characteristics are presented in Table 1.

Table 1. Summary of ecological description of the study sites

Locations	Altitude (m.a.s.l)	Latitude	Longitude	Min.Temp (^{0}C)	Max.Temp (^{0}C)	Rain fall(mm)	RH(%)	Soil type	P^H
Jimma	1753	7^{0}40'00"N	36^{0}47'00"E	11.6	26.3	1572	67	Reddish brown/ nitosols	5.2
Agaro	1650	7^{0}50'35"N	36^{0}35'30"E	12.4	28.4	1616	-	Mollicnitosols	6.2
Gera	1940	7^{0}7'0"N	36^{0}00'00"E	10.4	24.4	1878.9	75.03	Loam	-

Source: Jimma Agricultural Research center; (center profile)

2.2. . Experimental Materials

Limmu coffee genotypes were collected from Limmu-kossa in 2001 and 2003 G.C. Among collected genotypes five elite advanced pure lines were selected as parents and crossed in a half diallel fashion in 2014 and resulted ten hybrids by p(p-1)/2 and 15 diallel genotypes by p(p+1)/2 formula where p is number of parental lines. The total entries (Five parental lines and their respective 10 F1 hybrids) along two checks were sown in polythene tubes filled with a finely prepared mixture of top-soil and sand soil in December 2014 and then transplanted to Jimma agricultural research centers, Agaro and Gera agricultural research sub-centers. The experiments were laid down by randomized completely block design with three replications. One-row plot consisting of six plants and a spacing of 2m x 2m were used area. Summary of all experimental materials (parents, their crosses and the checks) described in Table 2.

Table 2. List of experimental materials with designations used for the study

S.No	Codes of materials	Genotype label	Name
1	P_1	P_1	L20/03
2	P_2	P_2	L67/01
3	P_3	P_3	L03/01
4	P_4	P_4	L55/01
5	P_5	P_5	L45/01
6	$P_1 \times P_2$	C12	L20/03 x L67/01
7	$P_1 \times P_3$	C13	L20/03 x L03/01
8	$P_1 \times P_4$	C14	L20/03 x L55/01
9	$P_1 \times P_5$	C15	L20/03 x L45/01
10	$P_2 \times P_3$	C23	L67/01 x L03/01
11	$P_2 \times P_4$	C24	L67/01 x L55/01
12	$P_2 \times P_5$	C25	L67/01 x L45/01
13	$P_3 \times P_4$	C34	L03/01 x L55/01
14	$P_3 \times P_5$	C35	L03/01 x L45/01
15	$P_4 \times P_5$	C45	L55/01 x L45/01
16	hybrid check at Jimma and Agaro (Check1)	CH1	Ababuna
	hybrid check at Gera (Check1)	CH1	Gawe
17	pure line check at Jimma and Agaro (Check2)	CH2	Dessu
	Pure line check at Gera (Check2)	CH2	74110

2.3. Data collected

Total fresh cherries were harvested per plot or from all trees during the first two years (2017 and 2018) bearing season and weighed in grams per plot basis and converted in to clean coffee (kg ha^{-1}) by multiplying the yield of the fresh cherry by the fraction of out-turn.

2.4. Statistical Analysis

The analysis of variance was carried out for each location over two years using SAS version 9.3 and before combining the data, the assumption of (ANOVA) normality test was executed the for coffee bean yield. Genotype -by- environment interaction impact that was detected in ANOVA table that led to the GEI and stability analysis was done by using GGE biplot (Olivoto et al., 2019). The GGE biplot is a biplot that displays the GGE part of MET data. GGE biplot analysis was used to carry out the usage of the genotype via environment analysis in R software v 4.4.2 (Yan and Kang. 2003). The GGE biplot was built according to the formula given by Yan et al. (2000):

$Yij - \mu - bj = l1ci1hj1 + l2ci2hj2 + eij$

Where, Yij= the performance of the ith genotype in the jth environment; μ= the grand mean; bj=the main effect of the environment j; l1and l2= singular value for IPCA1 and IPCA2, respectively; ci1 and ci2= eigen vectors of genotype i for IPCA 1 and IPCA2, respectively; hj1andhj2= eigen vectors of environment j for IPCA1 and IPCA2, respectively; eij = residual associated with genotype i and environment j

3. Results and Discussion

3.1. Analysis of Variance (ANOVA)

The combined analysis of variance (ANOVA) was performed to describe the main effect and quantify the interaction within and between the sources of variation. Combined ANOVA showed highly significant difference (P<0.01) among locations, genotypes and their interaction (GEI) for bean yield indicating the presence of variability among the genotypes and the yielding potential of these genotypes varied from one environment to another. Out of the total effect (sum square) of variations, considerable extent of variation was due to location and genotype by environment interaction which accounted 69.4 and 10.5%, respectively. This may indicated that the environment was highly contributed on the coffee yield. In line to this, different scholars

Mesfin and Bayetta (1987); Yonas et al. (2014); Lemi (2021) and Alemu et al (2022) were reported the presence significant GEI in different materials Coffee Arabica tested at different time. For example, Lemi (2021) reported in his study from the total variation, about 41.63% and 32.32% variation was explained for environments and GEI, respectively. Highly significant difference and greater contribution of GEI among diallel coffee genotypes in south western Ethiopia also reported by Alemu et al. (2022).

Table 3. Combined analysis of variance for coffee bean yield across six environments

SOV	DF	SS	MS	Explained SS (%)	F value	pr(>F)
Environment(ENV)	5	95227709	19045542	69.4	191.51	1.34e-72***
Reps(ENV)	12	1301192	108433	0.9	1.09	3.70e-01ns
Genotype (GEN)	16	7265024	454064	5.3	4.57	1.06e-07***
GEN:ENV	80	14373028	179663	10.5	1.81	5.32e-04***
Residuals	192	19094655	99451	13.9		
CV (%)	39.5					
Mean	798.2					

Note: Value with *** indicated highly significant difference at 0.001 probability level, ns= non-significant, SOV = Source of variation, DF= degree of freedom, SS = sum of square, MS = Mean square, CV = Coefficient of variation (%)

3.2. GGE biplot analysis

Analysis of GGE biplot analysis show the components which-won-where pattern, ranking of cultivars on the basis of yield and stability, and correlation vectors among environments.

3.1.1. Which-Won-Where pattern

The visualization of which won where pattern is an important to know the existence of different mega environments within an agro-ecology. It is important because evaluations of test locations and genotypes are most useful when conducted within a mega environment (Yan et al., 2007). The perpendicular lines to the polygon sides divide the biplot into sectors, each having its own winning cultivar/genotypes. The winning genotype for a sector is the vertex genotype at the intersection of the two polygon sides whose perpendicular lines form the boundary of that sector; it is positioned usually, but not necessarily, within its winning sector (Yan, 2002).

GGE biplot was constructed by plotting the first two principal components PC1 and PC2 derived from subjecting environment center yield data to singular value decomposition (Yan et al., 2000). In the current study, the first two principal components of GGE biplot pattern explained 84.59% (PC1 = 62.95% and PC2 =21.64%) of the GEI variation for grain yield of the genotypes evaluated at six environments (Fig 1). The polygon view of the GGE biplot pattern in this study showed that, all the environmental indicators positioned into one segments or sections of biplot which may indicate the presence of a given genotype which performed best across environment. Inline to this, Khan et al (2021) stated that the positioning of all environmental indicators into one section of biplot directed that a unique genotype performs best under all tested environments where as different genotypes gained different environments if the environmental indicators were positioned into a different segment of biplot. However in contrast to this Lemi (2021) and Sime and Tesfaye (2020) reported four different sectors and two different sectors of environments in coffee Arabica and bread wheat, respectively were suggested in their study.

Genotypes that attached with a vertex of the polygon in a sector where all environmental markers drop in suggested, such genotype provided greater yield and perform best across environment. However, the genotypes placed at the polygon vertex in a section of biplot where there is no environmental indicator are treated as poorly perform genotypes under all tested environments (Oladosu et al., 2017). In this study, the polygon view of which-where-pattern formed six different convex hull on which genotypes namely C45 (L55/01 x L45/01), C12 (L20/03 x L67/01), C34 (L03/01 x L55/01), C25 (L67/01 x L45/01), P2 (L67/01) and P5

(L45/01) were found at vertex of biplot. Genotype C45 (L55/01 x L45/01) was the best performed genotype across locations. The vertex genotype P5 (L45/01) was the poorest genotype in all of the test environments, since it had the longest distance from the origin of the biplot on the opposite side of the environments. In agreement to this result, Sime and Tesfaye (2020) reported both the best and poorest genotypes in bread wheat whereas Lemi (2021) stated the best performed genotypes in coffee Arabica genotypes.

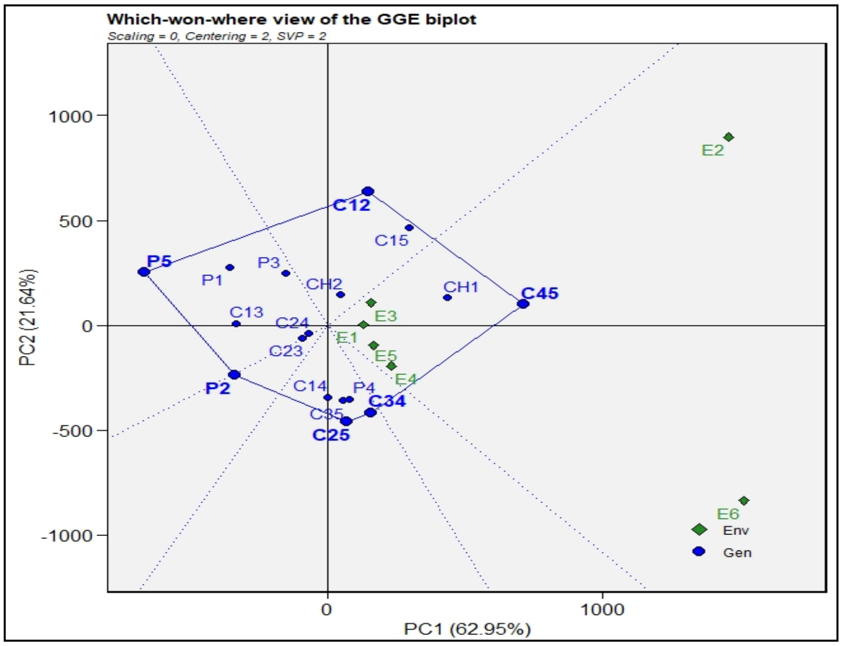

Figure 1. Polygon view of GGE biplot Polygon for which won where pattern of genotypes and environments

E1= Jimma 2016/17 E2= Jimma 2017/18 E3 = Agaro 2016/17 E4= Agaro 2017/18

E5 = Gera 2016/17 E6 = Gera 2017/18

3.1.2. Average yield and stability performance

The mean yield performance and stability of genotypes was evaluated by an average environment coordination (AEC) method (Yan, 2001; 2002). The mean yield performance and stability of the 17 genotypes were plotted using average environment coordination (AEC) method as shown in Figure 2. In the AEC system, AEC X axis (PC1) passes through the biplot origin with an arrow indicating the positive end of the axis and indicates the mean performance of genotypes. The genotypes were ranked along the average environment to coordinate/abscissa axis (AEC X-axis) with an arrow indicating the highest value based on their mean performance across all environments. The AEC ordinate (vertical) separates genotypes with below-average means (located left side of biplot origin) from those with above-average means (located right side of biplot origin). Thus, in this study genotypes with above-average means were C45, CH1, C15, C34, C12, C35, C25, C14 and CH2 whereas genotypes below-average means were P5, P1, C13, P2 and P3 (Fig 2). Similar results were reported by Tena et al. (2019) for sugar yield, Sime and Tesfaye (2020) for bread wheat and Lemi (2021) for Arabica coffee; these authors generally reported that the genotypes on the left side of the ordinate had less yield performance relative to the grand mean yield.

The ATC Y-axis passes through the biplot origin and is perpendicular to the ATC X-axis indicates the stability axis (PC2). Based on these, statistically, the stable genotypes located near the AEC X axis (PC1) with PC2 scores of almost zero. In other ways, genotypes stability is explored by the length of their projection from AEC abscissa (horizontal axis). The genotype that falls on the AEC abscissa (horizontal axis) and had almost zero projection onto the AEC ordinate (vertical axis) are considered to be most stable while genotype with the longest contact in either direction with the AEC abscissa is consider to be less stable across the environments or vice versa. The best genotype is the one with the highest yield and stability across environments. In other ways, best genotype have large PC1 rankings (high mean yield) and small PC2 scores (high stability). Thus, in this study, C45 (L55/01 x L45/01) and CH1(Check1) which had higher PC1 and smaller PC2 rankings had been recognized as high bean yield and stable across locations (Fig 2). Therefore, genotypes C45 (L55/01 x L45/01) and CH1(Check1) with high yield and stable could be recommended as promising variety for south western and similar agro-ecology of coffee growing areas.

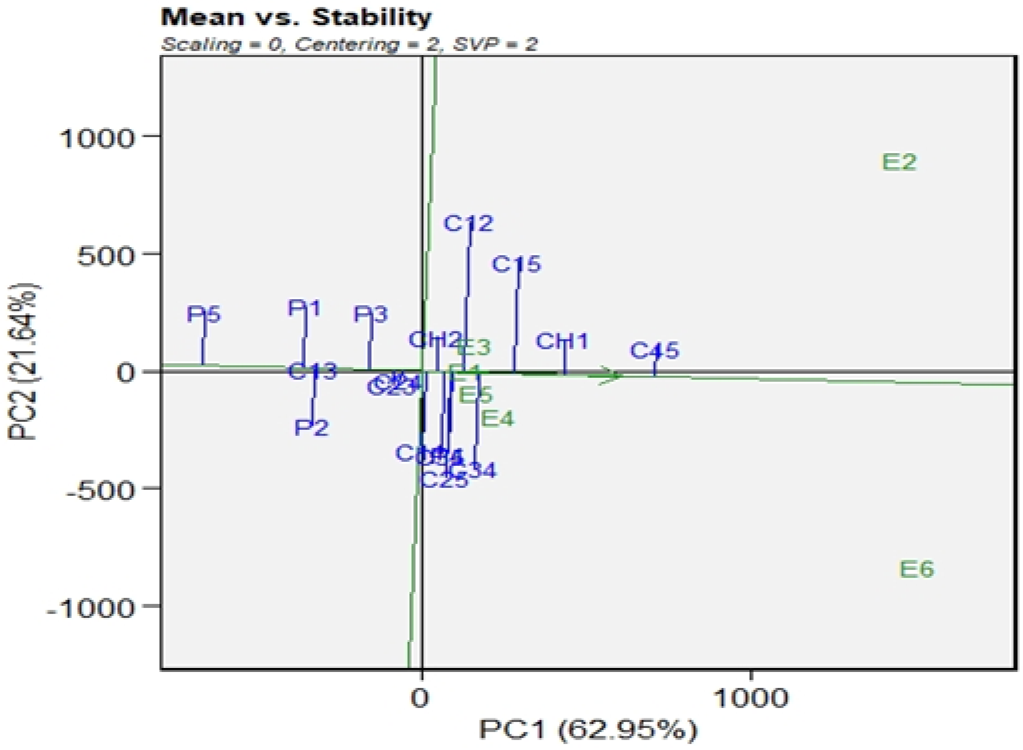

Figure 2. Average environment coordination (AEC) views for GGE biplot based on environment focused scaling for the means performance and stability of genotypes

E1= Jimma 2016/17 E2= Jimma 2017/18 E3 = Agaro 2016/17 E4= Agaro 2017/18

E5 = Gera 2016/17, E6 = Gera 2017/18

3.1.3. Ranking genotypes relative to the ideal genotypes

In this model, an ideal genotype is one that has both high mean yield and high stability performances across the environments (Yan and Kang, 2003; Farshadfar et al., 2012). Desirable genotypes are those located close to the ideal genotype. From the origin through the middle of concentric circle is drawn a line to visualize the distance between genotypes and the ideal genotype (Yan and Tinker, 2006). The average-environment coordination (AEC) of GGE-biplot view to rank genotypes relative to ideal genotypes indicated in Fig 3 .The ideal genotype which is found at the center of the concentric circles can be used as a benchmark for selection. Genotypes located closer to the “ideal genotype” is more desirable than the others located farther away. Thus, genotypes C45 (L55/01 x L45/01) and CH1(Check1)were the first and second genotypes closer to concentric circle, which were the desirable genotypes higher yield ability and stability. However, genotypes like P5 followed by P1 and P2 were the farthest away from the concentric circle, which were the least desirable genotypes in terms of both yield performance and stability by GGE biplot.

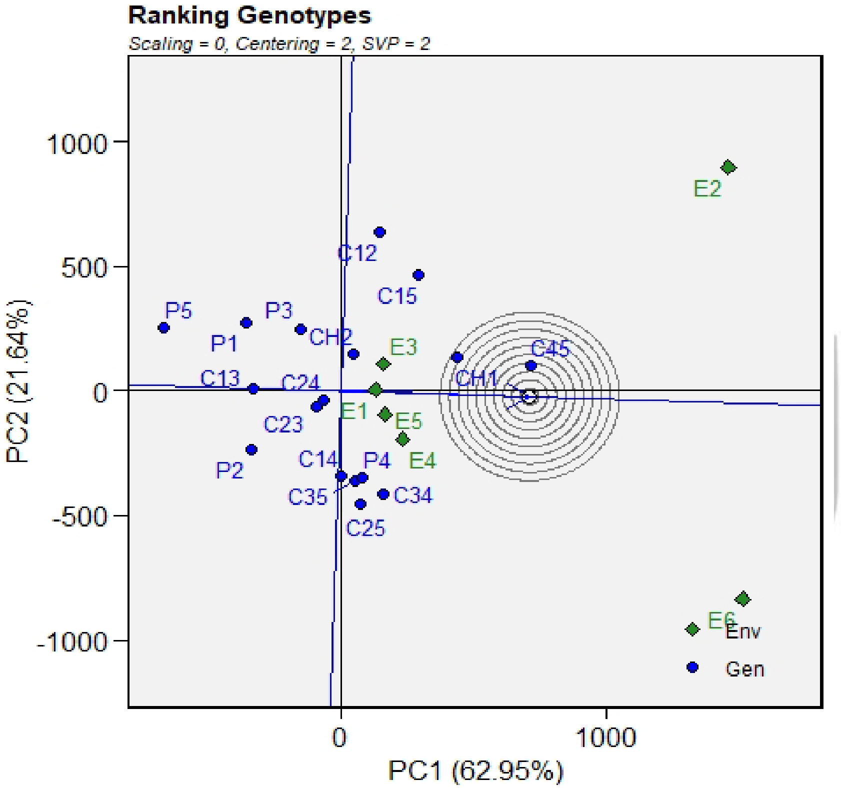

Figure 3. The average-environment coordination (AEC) of GGE-biplot view to rank genotypes relative to ideal genotypes

E1= Jimma 2016/17 E2= Jimma 2017/18 E3 = Agaro 2016/17 E4= Agaro 2017/18

E5 = Gera 2016/17 E6 = Gera 2017/18

3.1.4. Discriminativeness vs. representativeness pattern of GGE biplot

Determination of a best suited (ideal) test environment is crucial for a successful breeding technique in the selection of superior genotypes. In this model, the length of an environmental vector is an estimation of discriminating power of the environment (Yan et al., 2007). The results of the present study revealed that the first principal component (PC1) and the second (PC2) respectively clarified 62.95% and 21.64% of the variance (Figure 4). The two principal component axis (PC1 and PC2) together clarified 84.59% of the total variance. So this biplot can be used for extracting interrelationships among the environments.

According to Yan and Tinker (2006) a long environmental vector represents a high capacity to discriminate the genotypes. With the longest vectors from the origin, environments E2 and E6 were the most discriminating of the genotypes. However, with the shortest vector from the origin, the environments E1, E3 and E5 provided little information about the genotype differences. Furthermore, the vector view of the GGE-biplot provides a brief summary of the interrelationships among the environments. Two environments are positively correlated if the angle between their vectors is 90°, independent if the angle is 90° (Yan and Tinker, 2006). Based on this, all environments were positively correlated because all of the angles among their vectors were smaller than 90°. If the angle formed between the test environment and the line passing through the average environment is small, it means that this test environment is representative (Yan and Tinker, 2006). Based on this, Environment2 (E2) and Environment6 (E6) showed a long vector that forms a small angle with the AEC abscissa line indicated that these environment were the most representative and discriminative (Fig 4). Although the small angle between the environments (E1, E3 and E5) and AEC abscissa line the length of these environments vector was short indicated list discriminating ability or provide little information

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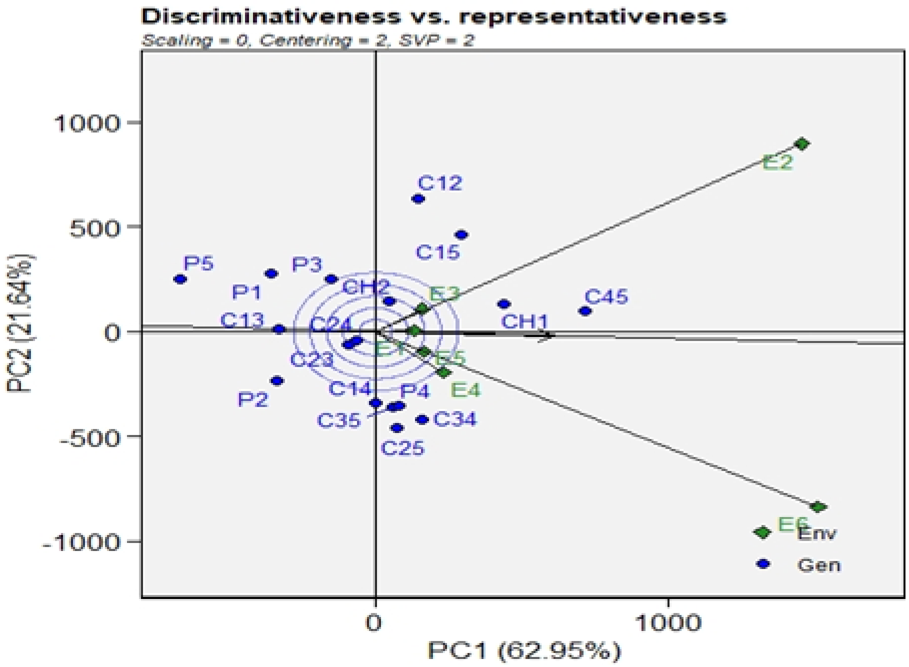

Figure 4. GGE-biplot view of ranking the test environments based on discriminating ability and representativeness

E1= Jimma 2016/17	E2= Jimma 2017/18	E3 = Agaro 2016/17	E4=Agaro 2017/18
E5 = Gera 2016/17	E6 = Gera 2017/18		

3.1.5. Ranking testing environments relative to the ideal environment

An ideal environment is a representative and has the highest discriminating power (Yan and Tinker, 2006). The ideal environment is located in the first concentric circle in the environment-focused the GGE biplot and the environments that are close to the ideal environment are defined as the desired environments (Fig 6). Thus, among the environments E6 and E2 were close to the ideal environment (concentric circle) and these environments were identified as desired environments than the others. The most acceptable is the one closest in the sketch of the ideal environment (Yan et al., 2000).

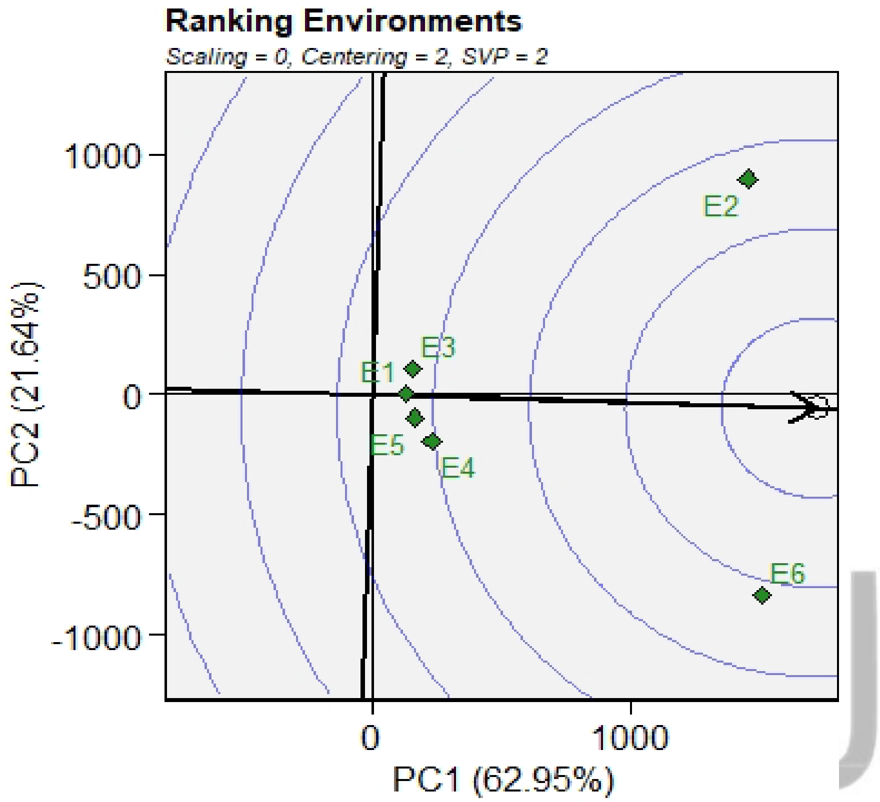

Figure 5. GGE biplot showing ranking of test environments relative to an ideal test environment

E1= Jimma 2016/17 E2= Jimma 2017/18 E3 = Agaro 2016/17 E4= Agaro 2017/18

E5 = Gera 2016/17 E6 = Gera 2017/18

4. Conclusion

A GGE biplot model is an excellent tool for visual MET data analysis. The current study determined the magnitude of genotype-by-environment interaction and stability for 17 coffee bean yield through the technique of GGE biplot analysis. The results of combined analysis of variance for coffee bean yield of 17 coffee genotypes indicated that genotype, environment and GEI were highly significant ($p<0.01$). The factors explained showed that the effect of environment and genotype by environment interaction on mean yield of genotype performance was very high which accounted 69.4 and 10.5%, respectively The GGE biplot analysis shown that the genotypes C45 was the corner genotypes and suited to all environments. In addition, environments E2 (Jimma 2017/18) and E6 (Gera 2017/18) the representative and discriminative and desirable environments. Likewise, based on mean yield and stability genotypes C45 (1st) and CH1 (2nd) were the best genotypes across locations. Therefore, these genotypes could be considered as promising genotypes in commercial variety development after extra data is added for south western and similar agro ecologies of coffee growing areas.

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