

Research Article

Genotype × Environment Interaction Studies of Promising Teppi Coffee (*Coffea arabica* L.) Genotypes in Southwestern Ethiopia

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Coffee is the stimulant crop plant that belongs to the genus *Coffea*, in the family Rubiaceae. The yield variation and pattern of the crop varied within short geographic distance and thus attributed to low productivity and unpredictable production. The objective of this study was to determine the extent of genotype × environment interaction on yields of promising Teppi coffee genotype. In this study, seventeen Arabica coffee genotypes, representing coffee growing areas of Teppi, southwestern Ethiopia were evaluated at six environments. This study was conducted by using completely randomized block design with two replications. The extent of genotype × environment interaction was analyzed by using additive main effect and multiplicative interaction model and genotype main effect and genotype × environment interaction biplot analysis model. The analysis of variance for yield revealed the presence of highly significant differences ($P < 0.01$) within genotypes, environments and genotype by environment interaction. From the total sum of squares of genotype × environment interaction of yield, environment accounted for 51% while genotypic and GEI effects were 20.5% and 25.32%, respectively. Generally, genotypes with superior performance and suitable environments for coffee were identified. However, further researches have to target hybridization of those superior genotypes with elite lines in feature Arabica coffee breeding program.

1. Introduction

Coffee is a useful stimulant beverage plant that belongs to the genus *Coffea*, in the family Rubiaceae. The genus *Coffea* contains around 124 species [1]. The crop is commonly grown in tropical and subtropical agroecological zones [2]. Arabica coffee (*Coffea arabica*) originated in Ethiopia where it grows wild in the natural forests of southwestern parts of the country, and there is a great genetic diversity in the region [3].

Arabica coffee is an essential commercial crop in the national economy of Ethiopia. It is still Ethiopia's number one export item [4]. It accounts for 25 to 30 percent of total export earnings. However, at present the crops contribution to total export earnings has increasingly declined due to increased exports of other agricultural and industrial commodities like gold, flowers, khat (*Catha edulis*), textiles, and leather products [5].

Eastern Africa have suitable lands for Arabica coffee production. Ethiopia has potential to produce huge amounts of differentiated high-quality green coffee, which is liked for its unique flavor and taste. According to Central Statistical Agency [6], the estimated area of land covered by coffee in Ethiopia is about 700474.69 ha. On the other hand, many growing locations in the country did not benefit from this huge potential, as they should have. In the same way, despite the consequences of coffee plays central role in the national economy and in spite of the fact that the country is home of *C. arabica*, the country's coffee production is characterized by low productivity about 619 kg ha⁻¹ [7], which is below global productivity of 790.7 kg ha⁻¹ [8]. This could be because of a number of factors, among which lack of recommended genotypes to specific and wider ranges of production areas is one.

In cultivar development plan, multi-location performance trial across diversified environments is undertaken to understand the nature of genotype \times environment interaction (GEI) in that specific set of genotypes and environments under study. By doing so, genotypes that have affinity to doing well in a wider range of environment and specific adapting genotypes would be identified so that they can be recommended based on situations. [9]. From earlier study in Ethiopia, indigenous coffee cultivar has its own specific adaptation region. So that the coffee growing environment is subdivided into different coffee growing regions to reduce the effect of GEI.

The extent of GEI helps to know about the probable area of adaptation of specific genotypes. It is also useful in determining efficient methods of using time and resources in a breeding program. Previous studies of GEI on *C. arabica* have illustrated significant interaction of genotypes with environment for yield and yield-related traits [10–12]. In addition, Montagnon et al. [13] reported the presence of strong GEI in *C. canephora* with some stable genotypes for bean yield. Mesfin and Bayetta [14] also reported that *C. arabica* varieties that show superior performance at one site of coffee growing region did not show good performance at other locations of a dissimilar geographic region. Montagnon et al. [13] also identified that the existence of significant interaction affects genotypes performance across different coffee growing agroecologies.

Although some studies were done in the Ethiopia, there is no information about the GEI of promising Teppi coffee genotypes in diverse agroecologies of Southwestern Ethiopia. So, this study was done with the objective of determining the extent of GEI on yield of some promising Teppi coffee genotypes in Southwestern Ethiopia.

2. Materials and Methods

2.1. Description of the Study Area. The study was done at three locations, namely, Teppi, Gemadro, and Godare, for two cropping seasons (Table 1).

2.2. Genetic Materials Used and Experimental Design. Seventeen coffee genotypes were used in this study (Table 2). The genotypes consisted fourteen selections screened from previous trials, which originally were collected from coffee growing areas of Teppi and its surroundings were planted along with three checks (Geisha, Catimor J-19, and Catimor J-21). The genotypes were planted in June 2013. The experiments were conducted by superimposing on first and second bearing trees, which were grown under the shade trees of *Sesbania sesban* and *Albizia schimperiana* simultaneously at recommended space. It was arranged in randomized complete block design with two replications. A plot consisted of a double row with ten trees per row and had border on both sides of the block to reduce border effects. Spacing between rows and plants was 2 m \times 2 m and spacing between blocks was maintained at 4 m. All necessary field supervision was done as per the recommendation [15].

2.3. Data Collected

2.3.1. Yield of Clean Coffee in Kg Ha⁻¹. The total fresh cherry yield was harvested from all the trees in a plot and measured in gm. That was used to compute mean yield per trees. The clean coffee yield in kg ha⁻¹ was obtained by multiplying the yield of the fresh cherry by percent out-turn [16].

2.4. Statistical Analysis

2.4.1. Analysis of Variance (ANOVA). The joint analysis of variance over environments was analyzed by the PROC GLM method in SAS [17] version 9.3 software. Prior to conduct combined analysis, homogeneity of variances between environment was checked by Bartlett's test. The effects of the genotypes, locations, and years as well as their interactions were determined by using SAS version 9.3.

The following statistical model was used for combined analysis of variance over locations:

$$X_{ijk} = \mu + \tau_i + \varepsilon_j + \gamma_{ij} + \rho_{k(j)} + \varepsilon_{ijk}, \quad (1)$$

where μ = general mean, τ_i = effects of genotype i , ε_j = effects of environment j , γ_{ij} = effects of genotype \times environment interaction, $\rho_{k(j)}$ = the k^{th} block effect within location j ; and ε_{ijk} = residual variation or error assumed to be normally distributed with mean 0 and variance σ^2 (i.e., $\varepsilon_{ijk} \sim N(0, \sigma^2)$).

2.4.2. AMMI Model. Additive main effect and multiplicative interaction (AMMI) model, which combines standard analysis of variance with PCA [18], was used to investigate GEI. In AMMI model, the contribution of each genotype and each environment to the GEI was assessed by use of the biplot graph display in which the means of genotypes are plotted against the scores of the IPCA1 [18]. It was done by using GEA-R [19] version 4.0. The AMMI model is as follows:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}, \quad (2)$$

where Y_{ge} = the yield for genotype (g) in environment (e); μ = the grand mean; α_g denotes genotype deviation; β_e = environment deviation; λ_n = the singular value for component n ; γ_{gn} is the eigenvector value for g ; and δ_{en} = the eigenvector value for e and the residual term is ρ_{ge} .

2.4.3. GGE Biplot Analysis. The GGE biplot method is composed of two concepts, the biplot concept and the GGE concept, which were used to visually analyze the genotypes at different environments. The GGE biplot analysis was done by using Genotype \times Environment Analysis with-R [19] version 4.0. The general model for GGE biplot is as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \varepsilon_i 1 \eta_j 1 + \lambda_2 \varepsilon_i 2 \eta_j 2 + \varepsilon_{ij}, \quad (3)$$

where Y_{ij} = the performance of the i^{th} genotype in the j^{th} environment; μ = the grand mean; β_j = the main effect of the

TABLE 1: Description of the study location.

Location	Altitude	Latitude	Longitude	Temperature		Rain fall (mm)
				Min (°C)	Max (°C)	
Teppi	1220 m.a.s.l	7° 3'	35°'	16	30	1678
Gemadro	1200 m.a.s.l	7° 28'	35° 24'	14	28	1900
Godare	1000 m.a.s.l	7° 0'	35° 10'	15	31	1400

TABLE 2: Descriptive information of genetic materials used.

Genotype code	Genotypes name	Place of origin (collection site)
G1	Accession 3/82	Feseye Genet, Oloncho
G2	Accession 28/82	Shecko, Southwestern Ethiopia
G3	Accession 29/82	Shecko, Southwestern Ethiopia
G4	Accession 32/82	Shecko, Southwestern Ethiopia
G5	Accession 37/82	Shecko, Southwestern Ethiopia
G6	Accession 39/82	Shecko, Southwestern Ethiopia
G7	Accession 42/82	Teppi to Shecko, Southwestern Ethiopia
G8	Accession 44/82	Teppi to Shecko, Southwestern Ethiopia
G9	Accession 45/82	Teppi to Shecko, Southwestern Ethiopia
G10	Accession 48/82	Teppi to Shecko, Southwestern Ethiopia
G11	Accession 235/71A	Teppi to Shecko, Southwestern Ethiopia
G12	Accession 17/79	CIFC Oeiras Portugal
G13	Accession 20/79	CIFC Oeiras Portugal
G14	Accession 22/79	CIFC Oeiras Portugal
G15	Catimor J-19	Released varieties for low land
G16	Catimor J-21	Released varieties for low land
G17	Geisha	Released varieties for low land

Source: JARC coffee breeding and genetics division data base.

environment j : λ_1 and λ_2 = singular value for IPCA1 and IPCA2, respectively; ε_{i1} and ε_{i2} = eigenvectors of genotype i IPCA1 and IPCA2, respectively; η_{j1} and η_{j2} = eigenvectors of environment j for IPCA1 and IPCA2, respectively; and ε_{ij} = residual associated with genotype i and environment j .

3. Result and Discussion

3.1. Bean Yield Mean Performance of Coffee Genotypes at Individual Environment. The mean yield of genotypes at different environments ranged from 320.85 kg ha⁻¹ for accession 39/82 at Godare during 2016/17 to 1130.97 kg ha⁻¹ for Geisha at Teppi during 2017/18 cropping season. During 2016/17 cropping season, the genotypes exhibited the maximum bean yield at Teppi while lowest general average yield was observed at Godare compared to other environments. At Gemadro, the top mean performance of the genotype was recorded for genotype Catimor J-19 followed by accession 28/82 and accession 3/82, exhibiting the maximum mean yield with average values of 845.16, 826.12, and 772.57.07 kg ha⁻¹, respectively during 2016/17 cropping season. Geisha (904.72 kg ha⁻¹), Catimor J-19 (574.13 kg ha⁻¹), and accession 17/79 (552.04 kg ha⁻¹) exhibited higher average yield at Godare during 2016/17 cropping season. On the other hand, during 2017/18 cropping season, genotypes Geisha (1130.97 kg ha⁻¹), Catimor J-19 (1126.6 kg ha⁻¹), and accession 22/79 (1134.8 kg ha⁻¹) showed higher yield at Teppi. Accessions 32/

82 (1059.5 kg ha⁻¹), 28/82 (1021.45 kg ha⁻¹), and 42/82 (1002 kg ha⁻¹) at Gemadro, and Geisha (1052.93 kg ha⁻¹), accession 22/79 (701.01 kg ha⁻¹), and Catimor J-21 (691.18 Kg ha⁻¹) at Godare exhibited the highest mean yield. The mean performance of genotypes was different from one environment to another. This indicates that different genotypes react differently to a particular environment. Similarly, different researchers [10, 11, 21] reported that different coffee genotypes responded differently to diverse agroecology of southwestern Ethiopia.

3.2. Combined Analysis of Variance over Locations. The analysis of variance for coffee bean yield revealed the presence of highly significant difference ($P < 0.01$) between genotypes, environments, and their interaction (Table 3). The existence of considerable GEI indicated that the genotypes showed inconsistent performances across the tested environments. This could be due to unpredictable variations of weather and soil characteristics. The presence of considerable GEI showed the differential performance of coffee genotypes across environments. This means different genotypes react differently to a particular environment. Related results were reported by Yonas et al., Afework, and Lemi et al. [10–12].

The total variations explained by environment genotype and GEI were 51%, 20.5%, and 25.32% (Table 3). The high proportion of the environment sum of squares means the

TABLE 3: Combined ANOVA for bean yield (kg ha⁻¹) and the percentage contribution of sum of squares of 17 genotypes tested at six environments.

Source	DF	SS	(%) SS	MS	F value	Pr > F
Env	5	4341571.73	51	868314.35	316.08	<0.0001
Rep(Env)	6	8652.51	0.102	1442.08	0.52	0.7881
Gen	16	1747311.24	20.5	109206.95	39.75	<0.0001
Env * Gen	80	2156697.73	25.32	26958.72	9.81	<0.0001
Error	96	263728.35	3.1	2747.17		
Total	203	8517961.56	100			
		Mean = 683.9	CV (%) = 14.85			

Note: CV = coefficient of variation, DF = degree of freedom, SS = sum of square, MS = mean square.

major factor that manipulates yield performance of coffee genotypes is the environment. The GEI is highly significant ($P < 0.01$) scoring 25.32% of the total sum of squares implying the call for investigating the nature of degree of difference reaction of the genotypes to environments. The presence of GEI shows that the performance of one genotype might be superior to the other genotypes in one environment but inferior in another environment. It complicates interpretation of the results. As a result, it is difficult to identify consistently superior genotypes across environments. Similarly, Afework [11] reported that the highest variation explained was due to environment and GEI.

In general, from the combined ANOVA (Table 3), superior genotypes across environments cannot be identified by considering their mean yield performance because GEI is highly significant. Because of the interactions between genotypes and environments, yield of genotypes tested across environments fluctuated. Therefore, it was a problem to identify varieties consistently giving high yields in locations with diverse environmental conditions. The existence of highly significant GEI decreases the usefulness of genotypes. The suitable statistical analyses are required for quantifying GEI. Furthermore, the conventional analysis of variance determines the values of each variation source and the significance of the contribution of each component, but it does not partition the interaction into a number of components and hence other types of analyses have to perform. For this reason, such multi-environment trial data along with considerable GEI require measures of stability analysis. That helps to get more information on the GEI as well as to evaluate the adaptation regions of the genotypes according to their favorable interaction. Similarly, previous researchers [12, 22] reported the significant effect of GEI on *C. arabica* in Ethiopia.

3.3. AMMI Analysis. The AMMI analysis of variance showed highly significant differences ($P < 0.01$) for environments, genotypes, and their interaction (Table 4). The F-test was highly significant ($P < 0.01$) for the first five interaction principal component analyses (IPCA). The IPCAs were put in order according to their decreasing significance. The AMMI analysis of variance for bean yield showed that most of the total sum of squares was explained by environment (52.65%) followed by genotypic (21.19%) and then by GEI (26.16%) illustrated in Table 4. This indicated that the environments used were diverse, with large

differences that caused most of the variation in yield, confirming the significant influence of environments on the yield performance of coffee. Similarly, Afework, Lemi et al., and Demissie et al. [11, 12, 22] reported the related results. (Table 5)

The Gollob test discovered that the first five IPCAs were significant ($P < 0.01$), indicating that the total information contained in GEI can be explained using these IPCAs. Out of the total IPCAs, the first five IPCAs axes explained 100% of the GEI sum of squares. The first IPCA1 captured about 44.11% of the interaction sum of squares, while the second IPCA explained 27.03% of the GEI sum of squares. This is related to the findings of Yonas et al., Lemi et al., and Demissie et al. [10–12, 22] who reported significance of the 4 to 6 IPCAs in *C. arabica* for bean yield evaluation.

The AMMI model performed by using the first two IPCAs and the rest of the IPCAs mostly capturing noise showed that IPCA 1 against IPCA2 is generally informative. The pattern in GEI of the given coffee data set was also predicted by using the first two PCAs of genotypes and environments, since IPCA1 and IPCA2 cumulatively accounted for 71.14%, which was greater than half of a total GEI.

3.4. AMMI 2 Biplot Analysis. The AMMI 2 biplot is performed by using the genotype and environment score of the first two successive AMMI components [23]. The first IPCA captured 44.11%, while the second IPCA captured 27.03%. The first two successive IPCAs cumulatively captured 71.14% of sum of square of the GEI of studied genotypes. From earlier yield experiment of GEI in *C. arabica*, [22] identified that the first two IPCAs explained 74% of AMMI total interaction sum of squares, [11] reported 58.55%, and [12] reported 63.3%.

The genotypes and environments located far away from the center are more reactive or unstable, while genotypes that are positioned closer to the biplot center have superior stability achievement [24]. Hence, genotypes 32/82, 45/82, 235/71A, 17/79, 20/79, and Catimor J-19 were plotted relatively close to the origin in the AMMI 2 biplot indicating their related yielding potential to all environments. Therefore, genotypes 32/82, 17/79, and Catimor J-19 were considered as a high yielding and widely adopted genotypes indicating their minimum contribution to the total GEI variance. On the other hand, genotypes like Geisha, Catimor

TABLE 4: AMMI analysis of variance for mean bean yield (kg ha⁻¹) of 17 coffee genotypes tested across six environments in 2016/17 and 2017/18.

SV	DF	MS	SS	Explained (%)	Cumulative (%)	F
Env	5	868314.3* *	4341571.7	52.65	52.65	325.16
Gen	16	109207* *	1747311.24	21.19	73.84	40.89
Env * Gen	80	26959* *	2156697.7	26.16	100	10.09
PC1	20	47560.01* *	951200.3	44.11	44.11	18.13
PC2	18	32388.9* *	583000.3	27.03	71.14	12.34
PC3	16	19085.6* *	305369.13	14.16	85.29	7.27
PC4	14	13925.6* *	194958.71	9.04	94.34	5.31
PC5	12	10180.9* *	122169.33	5.67	100	3.88
Residuals	102	2670.4	272380.9	0	0	

Note: **, * significant difference at $P < 0.01$ and $P < 0.05$, DF = degree of freedom, SS = sum of squares, MS = mean square, IPCA = interaction principal component axis and SV = source of variation.

TABLE 5: Mean bean yield (kg ha⁻¹) of 17 coffee genotypes tested across six environments during 2016/17 and 2017/18 cropping season at different locations over years.

Gen	Environments						Mean	Rank
	E1	E2	E3	E4	E5	E6		
3/82	840.7 ^{abc}	772.57 ^{ab}	511.2 ^{b-e}	895.1 ^{cd}	943.7 ^{a-e}	340.86 ^g	717.34	6
28/82	691.2 ^{gf}	826.13 ^a	506.9 ^{b-e}	691.6 ^{fg}	1021.45 ^{ab}	498.4 ^{cde}	707.6	8
29/82	415.95 ^j	648.7 ^{bcd}	405.97 ^{f-i}	934.4 ^{bc}	886.5 ^{c-f}	578.71 ^c	645.03	12
32/82	889.1 ^{ab}	705.64 ^{bcd}	449.3 ^{d-g}	850.2 ^{cde}	1059.5 ^a	584.85 ^c	756.42	3
37/82	732.3 ^{ef}	579.78 ^{def}	375.22 ^{hi}	600.4 ^g	640.6 ⁱ	431.93 ^{efg}	555.02	16
39/82	618.6 ^h	607.17 ^{def}	320.85 ⁱ	572.4 ^g	636.5 ⁱ	304.25 ^{fg}	519.54	17
42/82	473.0 ^j	661.2 ^{bcd}	450 ^{b-f}	770.0 ^{def}	1002 ^{abc}	340.27 ^g	622.70	14
44/82	543.8 ⁱ	545.61 ^{ef}	330.13 ⁱ	953.8 ^{bc}	834.2 ^{efg}	371.52 ^{fg}	596.5	15
45/82	789.8 ^{cde}	495.96 ^f	446.2 ^{d-g}	741.5 ^{ef}	919.63 ^{b-e}	501.45 ^{cde}	649.09	11
48/82	762.3 ^{de}	635.2 ^{cde}	427.4 ^{e-h}	679.3 ^{gf}	782.6 ^{fgh}	551.49 ^{def}	623.05	13
235/71A	649.8 ^{gh}	745.26 ^{abc}	529.4 ^{bcd}	767.1 ^{def}	738.54 ^{ghi}	542.86 ^{cd}	662.11	9
17/79	782.6 ^{cde}	742.34 ^{abc}	552.04 ^{bc}	951.95 ^{bc}	907.23 ^{b-f}	508.23 ^{cde}	740.74	4
20/79	654.2 ^{gh}	640.91 ^{cde}	241.86 ^{ef}	879.5 ^{cd}	937.78 ^{a-e}	489.04 ^{cde}	661.37	10
22/79	725.7 ^{ef}	583.63 ^{def}	388.7 ^{ghi}	1034.4 ^{ab}	862.2 ^{d-g}	701.01 ^b	716.07	7
Cat J-19	904.25 ^a	845.16 ^a	574.13 ^b	1126.6 ^{ab}	963.1 ^{a-d}	547.2 ^{cd}	810.06	2
Cat J-21	830.6 ^{bcd}	753.32 ^{abc}	459.8 ^{c-g}	941.9 ^{bc}	685.1 ^{hi}	691.18 ^b	726.95	5
Geisha	903.22 ^a	748.39 ^{abc}	904.72 ^a	1130.97 ^a	760.2 ^{ghi}	1052.93 ^a	916.74	1
Mean	718.02	679.23	471.1	848.33	857.7	529.04	683.9	
CV (%)	13.95	14.28	10.20	13.34	16.29	14.86		
LSD _(5%)	70.799	126.31	96.9	128.47	125.77	104		

Cat = Catimor, CV = coefficient of variation, E = environment, E1 = Teppi 2016/17, E2 = Gemadro 2016/17, E3 = Godare 2016/17, E4 = Teppi 2017/18, E5 = Gemadro 2017/18 E6 = Godare 2017/18, LSD = least significance difference.

J-21, 42/82, 44/82, 37/82, 29/82, and 22/79 were far away from center of biplot. Genotypes 3/82, 28/82, 39/82, and 44/82 were relatively distant from the origin and have considerable contribution to the GEI variance considered as specifically adopted to their individual favorable environments (Figure 1).

The AMMI 2 biplot showed that E1 (Teppi 1), E4 (Teppi 2), E5 (Gemadro 2), and E6 (Godare 2) were far from the origin indicating that these environments contributed higher amount of variation to the total GEI. However, because of their longest distance between their marker and the origin, genotypes inconsistency at this environment may not exactly reflect the average genotypes performance across environments. On the other hand, E3 (Godare 1) and E2 (Gemadro 1) are located close to the origin indicating their lower contribution to the GEI variance. It shows that they

are the least discriminating and stable environments (Figure 1).

In AMMI 2 biplot analysis, the genotypes that are close to each other on the graph tend to have related performance and those that are close to environments show their better adaptation to that particular environment. Hence, genotypes 37/82, 39/82, and 48/82 were relatively adapted to environment E1 (Teppi 1). Genotypes 22/79, 29/82, and 44/82 were relatively adapted to environment E4 (Teppi 2). Only Geisha adapted to environment E6 (Godare 2), genotypes 3/82, 28/82, 32/82, 45/82, and Catimor J-19 were relatively adapted to environments E2 (Gemadro 2), genotypes 235/71A and Catimor J-21 were relatively adapted to environment E3 (Godare 1), and genotypes 42/82 and 20/79 were relatively adapted to environment E5 (Gemadro 2) (Figure 1).

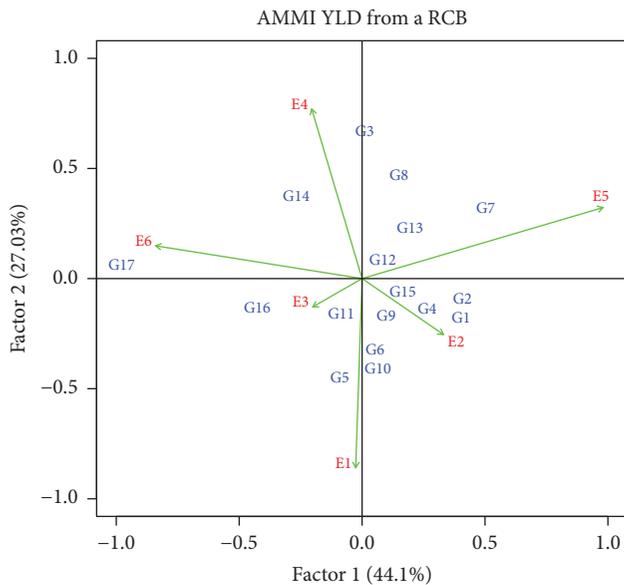


FIGURE 1: AMMI biplot of IPCA1 against IPCA2 for bean yield of 17 coffee genotypes tested at six environments. Note: E1 = Teppi1, E2 = Gemadro1, E3 = Godare1, E4 = Teppi2, E5 = Gemadro2, E6 = Godare2. G1 = 3/82, G2 = 28/82, G3 = 29/82, G4 = 32/82, G5 = 37/82, G6 = 39/82, G7 = 42/82, G8 = 44/82, G9 = 45/82, G10 = 48/82, G11 = 235/71A, G12 = 17/79, G13 = 20/79, G14 = 22/79, G15 = Catimor J-19, G16 = Catimor J-21, and G17 = Geisha.

3.5. GGE Biplot Analysis

3.5.1. The “Which-Won-Where” Patterns. The partitioning of GEI through GGE biplot analysis showed that IPCA1 and IPCA2 accounted for 52.51% and 17.59% of sum of squares, respectively, with 70.1% variation for yield (Figure 2). The six environments fell into two sectors with different winner genotypes and the biplot showed five vertex genotypes, Geisha, Catimor J-19, 42/82, 39/82, and 37/82. There are rays, which divided the biplot into five sections. The genotypes fell into five sections but all the tested environments fell into two sections. The genotypes that fell on vertex of all sectors were the ones that performed the highest yield in those environments, which fell within that sector. In this study, GGE-biplot analysis identified two different coffee growing mega-environments. The first environment contains E1 (Teppi 1), E2 (Gemadro1), E4 (Teppi 2), E3 (Godare 1), and E6 (Godare 2) with a vertex genotypes Geisha and Catimor J-19; the second environment contains the environment E5 (Gemadro 2) with 32/82 the winner genotype. It had also been observed that no environments fell into sectors where genotypes 37/82, 42/82, and 39/82 were the vertex genotypes, indicating that these genotypes were not adapted in any of the test environments. Some authors also reported related findings in the country; Lemi [21] identified four different *C. arabica* growing mega-environments and Afework [11] identified four different *C. arabica* growing mega-environments.

3.5.2. Mean Performance and Yield Stability of Genotypes. Yield performance and stability of the genotypes were evaluated by an average environment coordination method.

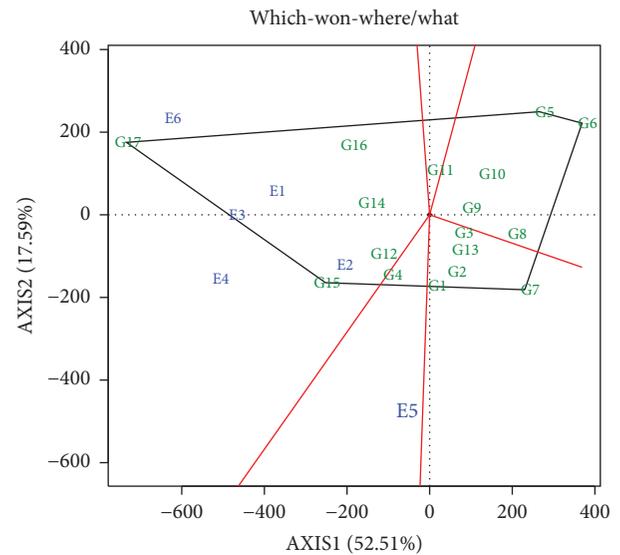


FIGURE 2: Which-won-where or which is best for what view based on genotype by environment interaction yield data of 17 genotypes evaluated in six environments. Note: E1 = Teppi1, E2 = Gemadro1, E3 = Godare1, E4 = Teppi2, E5 = Gemadro2, E6 = Godare2. G1 = 3/82, G2 = 28/82, G3 = 29/82, G4 = 32/82, G5 = 37/82, G6 = 39/82, G7 = 42/82, G8 = 44/82, G9 = 45/82, G10 = 48/82, G11 = 235/71A, G12 = 17/79, G13 = 20/79, G14 = 22/79, G15 = Catimor J-19, G16 = Catimor J-21 and G17 = Geisha.

In this method, genotypes were ranked beside the average environment coordinate axis through an arrow demonstrating the uppermost value based on their mean performance across every part of environments. The average environment coordinate ordinate separates genotypes, which are above-average means and below-average means. Accordingly, genotypes with above-average means were 45/82, 3/82, 32/82, Catimor J-21, 17/79, 45/82, 48/82, Catimor J-19, and Geisha, while genotypes with below-average means were 42/82, 20/79, 37/82, 29/82, 44/82, 235/71A, 22/79, 28/82, and 39/82 (Figure 3).

The line, which passes through the center and that is perpendicular to the average environment coordinate by having double arrows, represents the consistency of genotypes. The direction of genotypes away from the biplot, basis, on the axis, shows greater GEI and instability. The better genotypes are those that perform high mean yield and similar consistency across the environment. In the biplot, they are close to the origin and have the shorter vector from the average environment coordinate. The longer projection to the average environment coordinate, without considering direction, represents a greater tendency of the GEI of a genotype that means less constancy across environments. Accordingly, genotypes 17/79, 22/79, 29/82, Catimor J-19, 45/82, 48/82, and 44/82 were the most stable. On the other hand, the genotypes Geisha, 3/82, 42/82, 39/82, and 37/82 were far from AEC (long vector) indicating their least constancy (Figure 3). These results are in accordance with the report of Lemi and Afework [11, 21] on Limmu and Ilu Abababora coffee genotypes, respectively. They found the ideal genotypes by using this mean performance and yield stability measuring parameters.

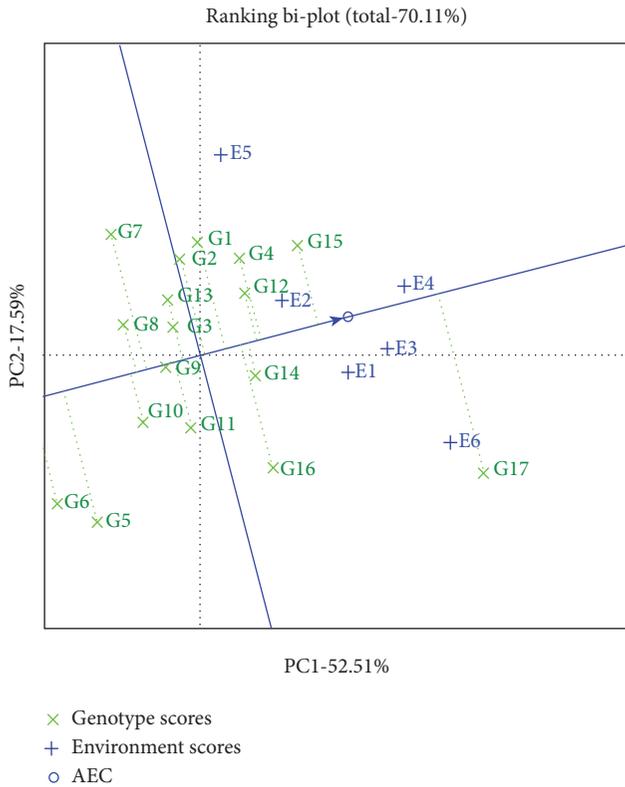


FIGURE 3: Average environment coordination views of the GGE biplot based on environment focused scaling for the mean performance and stability of genotypes. Note: E1 = Teppi1, E2 = Gemadro1, E3 = Godare1, E4 = Teppi2, E5 = Gemadro2, E6 = Godare2. G1 = 3/82, G2 = 28/82, G3 = 29/82, G4 = 32/82, G5 = 37/82, G6 = 39/82, G7 = 42/82, G8 = 44/82, G9 = 45/82, G10 = 48/82, G11 = 235/71A, G12 = 17/79, G13 = 20/79, G14 = 22/79, G15 = Catimor J-19, G16 = Catimor J-21 and G17 = Geisha.

3.5.3. Rank Genotype and Environments Relatively. An ideal genotype is one that shows superior performance in mean yield and that has high performance in constancy. The interior of the concentric circles (Figure 4) represents the situation of an ideal genotype, which is defined by a projection onto the mean-environment axis. For the reason that the units of IPCA1 and IPCA2 for the genotypes are the novel component of yield in the genotype-focused scaling, the units of the AEC abscissa and ordinate should also be the original unit of yield. Accordingly, genotypes Catimor J-19, 17/79, 32/82, and 3/82 followed by Geisha, which fell closer to the center of concentric circles, were desirable genotypes in terms of higher yield potential and constancy, compared with the rest of the genotypes. Genotypes 39/82, 37/82, 42/82, 44/82, 45/82, 235/71A, 48/82, and 29/82, followed by 20/79, were unattractive genotypes located distant from the first concentric circle of the ideal genotype. The result of the study was in accordance with Lemi and Afework [24, 11] that they had found an ideal genotype in *C. arabica* growing domain of Ethiopia.

In the ways of ranking environments relative to the ideal environment method, the average IPCA1 and IPCA2 scores of all environments, represented by a small circle (Figure 4),

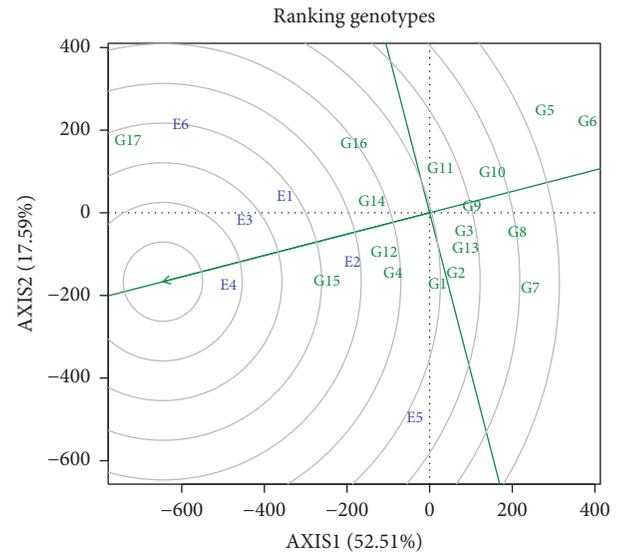


FIGURE 4: GGE biplot based on genotype-focused scaling for comparison and genotypes with the ideal genotype. Note: E1 = Teppi1, E2 = Gemadro1, E3 = Godare1, E4 = Teppi2, E5 = Gemadro2, E6 = Godare2. G1 = 3/82, G2 = 28/82, G3 = 29/82, G4 = 32/82, G5 = 37/82, G6 = 39/82, G7 = 42/82, G8 = 44/82, G9 = 45/82, G10 = 48/82, G11 = 235/71A, G12 = 17/79, G13 = 20/79, G14 = 22/79, G15 = Catimor J-19, G16 = Catimor J-21 and G17 = Geisha.

describe an average environment. Like that of ideal genotype, an ideal environment is more advantageous if it is located closer to the ideal environment. The model environment, represented by a symbol of a small circle with an arrow pointing to it, is mainly discriminating the genotypes and representativeness of the other test environments. Figure 4 indicates that E4 (Teppi2), which fell in the interior part of circles, was an ideal test environment in terms of being the most representative of the all environments and being mainly powerful to discriminate genotypes, where Gemadro2 was far from the ideal environment and considered as less powerful to discriminate genotypes.

Discriminating ability and representativeness are the important properties of an experimental location. Ideal locations have to be highly differentiating for the evaluated genotypes and simultaneously representative of the target location. Like ideal genotype, an ideal location is defined and shown by the small circle with an arrow pointing to it. It shows that experimental site is more desirable and discriminating when situated closer to the origin of concentric circle or to an ideal environment. This result is related to the findings of Lemi and Afework [11, 21] that they identified an ideal genotypes and environments as well as undesirable genotypes by using ranking genotypes and environment method.

4. Conclusion

The oscillating agroecology within a short distance in Ethiopia leads to fluctuation of coffee yield due to GEI and

thus contributes to low productivity. Therefore, testing genotypes across different environments is important to identify genotypes with low GEI, which can increase *C. arabica* productivity in the country. The large sum of squares and highly significant performance mean square of environments showed that the environments were diverse, by means of large differences among environmental means causing difference in yield. This shows the main influence of environments on yield performance of the crop. The existence of important genotypes, environments, and GEI indicates that the considerable influence of environments on *C. arabica* and the genotypes showed instability across environments, and high percentage variation of yield was due to environmental effect.

The Gollob test revealed that the first five IPCAs were significant; and the total information contained in GEI explained IPCAs. The patterns in GEI of the given coffee data set were predicted by the first two IPCAs of genotypes and environments, since IPCA1 and IPCA2 cumulatively accounted for 71.14% of the total GEI. Among the tested genotype, Catimor J-19 showed lower GEI across environments. GGE biplot identified two different mega-environments and two winner genotypes in each mega-environment. The first mega-environments contained E4 (Teppi 2), E6 (Godare 2), E3 (Godare 1), and E1 (Teppi 1) with a vertex genotype Geisha and Catimor J-19; the second environment contained E2 (Gamadro 1) and E5 (Gemadro 2). It has also been identified that genotypes 37/82 and 39/82 were not adopted in any of the test environments.

Even though no genotypes showed superior performance across the experimental site, some genotypes with better mean performance coupled with lower GEI were identified. Therefore, priority should be given to the genotypes that showed desirable performance. In this case, Catimor J-19 is the most desirable genotype for its low GEI and high yield potential. Generally, in the study, genotypes were adapted and an ideal location was identified. However, further researches have to target hybridization of those superior genotypes with elite lines in feature Arabica coffee breeding program.

Data Availability

The data used during the current study are available from the corresponding author on reasonable request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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