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Genotype by Environment Interaction Analysis of Arabica Coffee Bean Yield

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Arabica Coffee is the most important and backbone of Ethiopian economy, which accounts for an average 60% of export earnings. Coffee is a perennial crop which can be harvested multiple times of years, and it is known to be affected with a characteristic biennial, which is more pronounced in the species Arabica coffee. The immediate objective of this study was to assess its Genotype by Environment interaction (GEI). The data for this study came from coffee variety field trials conducted by Jimma Agricultural Research Center (JARC) over 7 years during 2005-2011 in south west Ethiopia across 3 coffee growing areas (Jimma, Agaro, and Metu). The experimental design of the trial was RCBD with 4 replications and 17 Arabica coffee genotypes. Combined ANOVA and AMMI model were used for GEI analysis. All analyses were done with the help of R statistical package. The combined analysis of variance revealed that the genotype, environment, and GEI effects are highly significant (P-values<0.001). GEI accounted for 16.2% of the total sum of squares and was about 2 times larger than that of genotypes. The AMMI procedure revealed that AMMI-5 was the best truncated AMMI model that can sufficiently explain the information contained in GEI. The first three interaction principal components (IPC1, IPC2 and IPC3) retained by Gollob's F-test for graphical display accounted for 64.2% of GEI. The major factor that influence yield performance of Arabica coffee in Ethiopia is the environment, and among 17 Arabica coffee genotypes, G1, G2, G3, G7, G8, G9 and G12 have the best performance with G1, G2, G3, G8 and G12 being relatively stable across the test environments. It was recommended to use information from GEI analysis to investigate yield performance of Arabica coffee genotypes across environment.

Key Words: Arabica Coffee,GEI, AMMI

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INTRODUCTION

Arabica coffee is most important and consumed widely as non-alcoholic stimulant beverage in the world (Nuhu, 2014), and backbone of Ethiopian economy, which accounts for an average 60% of export earnings. Coffee is a perennial crop which can be harvested multiple times of years, and it is known to be affected with a characteristic biennial (Argaw *et al.*, 2018).

Arabica coffee grows in Ethiopia in several places at various altitudes ranging from 550 -2750 meters above sea level (Quintin *et al.*, 2013). The major producing

areas are concentrating in the southwestern part of Ethiopia where Arabica coffee originated and diverse (Kassahun, 2008; Taye *et al*, 2011a). Arabica coffee grows under very diverse environments including annual rainfall (1000 – 2000 mm), temperature (minimum 8 – 15 ^{0}C, maximum 24 – 31 ^{0}C) and soil type, and this has a lot contribution to the high genetic diversity and as though high yield variability within Arabica coffee in the country (Mesfin and Bayetta, 1987). Yonas (2005) pointed out that there is strong variation within southwestern region of Ethiopia due to climatic and edaphic variations along altitudinal gradient. Environment and genotype have roles in determining the yield of Arabica coffee and they are also important factors for breeding purpose (Alemseged and Tesfaye, 2012). Since Ethiopia has both wide genetic diversity and diverse environment for growing Arabica coffee, conducting multi-location trial over years is important to assess GEI and identify stable genotype which can increase productivity of Arabica coffee in the country (Yonas, 2014a).

Data collected in multi-location trials are intrinsically complex, having three fundamental aspects: structural patterns, nonstructural noise and relationships among genotypes, environments, and genotypes and environments considered jointly (Crossa, 1990). For the analysis of such data especially for GEI interaction, various statistical methodologies have been extensively reviewed and documented (Zelalem, 2011; Degene, 2016). Among these statistical methodologies, the most commonly used statistical techniques for analyzing multi-environment trial (MET) data are the combined analysis of variance (ANOVA) and linear regression techniques. However, they are open to criticism due to the fact that they do not discern patterns of the underlying genotype by environment interaction, and the assumptions of normality, independency and constant variance may not be always satisfied (de Resende, 2007).

In previous studies, a number of parametric statistical procedures have been elaborated over the years to analyze genotype by environment interaction and yield stability over environment. These statistical methods broadly categorized in to two classes, univariate and multivariate models. Univariate models encompass a range of models, such as combined ANOVA, regression slope, deviation from regression, environmental variance, and Kang's yield-stability (Eberhart & Russell, 1966). Multivariate models are more powerful and flexible to investigate GEI, and they have gotten special attention in theory and application (Zobele *et al*, 1988; Girma *et al*, 2000). These models are linear-bilinear models such as, AMMI, Site Regression (SREG), Genotypic Regression (GREG), Completely Multiplicative Model (COMM) and Factor Analytic (FA).

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal component analysis of the genotype by environment interaction. It has proven useful and widely used for understanding complex GEI (van Eeuwijk, 1995; Girma, 2000 Zelalem, 2011; Dejene, 2016). The results can be graphed in a useful bi-plot that shows both main and interaction effects for both genotypes and environments. This study is, therefore, greatly intended to assess the effect GEI of Arabica coffee yield to look into the performance of Arabica coffee genotypes across environment by using AMMI model

DATA AND METHODS

The data for this study came from coffee variety field trials conducted by Jimma Agricultural Research Center (JARC) over 7 years in south west Ethiopia. The field trial was conducted across three locations (Jimma, Agaro and Metu). The experimental design of the trial was RCBD with 4 replications and 17 Arabica coffee genotypes.

The locations have different soil type and altitudes and could also possibly be differentiated with their mean seasonal rainfall and temperature. Seven year coffee bean yield data collected during 2005 to 2011 were used in this study.

The Independent variables used for GIE analysis were Block, Genotype and the Environment where the Environment is a specific year-location combination, whereas CBY was the dependent (study) variablemeasured with kgha^{-1}. The location-year combinations and the assigned Environment and Genotype code are given in Table 1 and Table 2.

Combined analysis of variance

Preliminary ANOVAs can be carried out for individual experiments to assess variation among environments for experimental error and, possibly, genotypic variance. Combined ANOVAs for a complete set of experiments or its subsets can be performed with different objectives, such as:

- Verification of the occurrence (i.e. significance) of different effects;
- Estimation and comparison of mean values for levels of fixed factors (in particular, genotype mean values across the region or within sub regions); and
- Estimation of the size of genotypic and genotype-environmental variance components (possibly as a step towards estimation of genetic parameters).

The ANOVA may also represent one step in the analysis of adaptation or in the assessment of yield stability measures. In the analysis of combined experiment of data from several environments, the first requirement

Table 1: Brief summary of Environments and assigned code

Location(Year)	Environment Code	Location(Year)	Environment Code
Agaro(2005)	E1	Metu(2009)	E12
Agaro(2006)	E2	Metu(2010)	E13
Agaro(2007)	E3	Metu(2011)	E14
Agaro(2008)	E4	Jimma(2005)	E15
Agaro(2009)	E5	Jimma(2006)	E16
Agaro(2010)	E6	Jimma(2007)	E17
Agaro(2011)	E7	Jimma(2008)	E18
Mutu(2005)	E8	Jimma(2009)	E19
Metu(2006)	E9	Jimma(2010)	E20
Metu(2007)	E10	Jimma(2011)	E21
Metu(2008)	E11		

Table 2: Brief summary of Arabica coffee Genotype and assigned code

Genotype Name	Genotype Code	Genotype Name	Genotype Code
Dessu(check)	G1	39/77	G10
744(check)	G2	39/82	G11
21/81A	G3	4/84	G12
235/71A	G4	43/70	G13
29/82	G5	5/81	G14
3/77	G6	51/'84	G15
32/82	G7	64/84	G16
36/82	G8	20/81	G17
38/82	G9		

is to assess the homogeneity of the error variance at the various environments. If the errors are homogeneous, the analysis can proceed. However, if the error variances are heterogeneous, the data will be transformed to produce homogenous variance or the locations may be separated into groups within which the variance is homogenous. In multi-environment yield trials of G genotypes (i=1,2,…,g), E environments(j=1,2,…e) and r replicates(l=1,2,…,r) arranged in RCBD, the liner model for the conventional combined analysis variance(ANOVA) is

$$Y_{jir} = \mu + G_i + E_j + GE_{ji} + B_{jr} + \epsilon_{jir} \quad [1]$$

where,

Y_{jil} is the observed yield response of the i^{th}genotype of the j^{th} environment

μ is the overall mean yield of genotypes at all possible environments.

G_i is the effect of i^{th} genotype; thus $\sum_1^g Gi = 0$

E_j is the effect of the j^{th} environment and $\sum_1^e E_i = 0$

GE_{ji} is the interaction effect of the i^{th} genotype in the j^{th} environment.

B_{jr} is the effect of the i^{th} replication in the j^{th} environment, and

ϵ_{jir} is random error term with mean 0 and variance σ^2_{jir} and distributed as NID (0, σ^2_{jir})

The Additive Main Effect and Multiplicative Interaction effect Model (AMMI)

AMMI combines analysis of variance (ANOVA) in to a single model with additive and multiplicative

parameters. After removing the replicate effect when combining the data, the observations are portioned in to two sources: Additive main effects for genotypes and environments, and Non additive effects due to genotype-environment interaction. The AMMI model for G genotypes and E environments is given as

$$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in}\gamma_{jn} + \epsilon_{ij}\ ;\ \ \epsilon_{ij} \sim N(0,\sigma^2); i = 1,2,\dots g\ ; j = 1,2,\dots e \qquad [2]$$

Where Y_{ji} is the mean yield of i^{th} genotype in the j^{th} environment ; m the grand mean; G_i is the i^{th} genotype effect ; E_j is the j^{th} environment effect; λ_n is eigen value of the PCA axis n; α_{in} and λ_{jn} are the i^{th} genotype j^{th} environment PCA scores for PCA axis n; ε_{ji} is the residual; n' is the number of PCA axes in the model. Ordinarily the number n' is judged on the basis of empirical consideration on F-test of significance Gauch(1988,1992). The residual combines the PCA scores from the N-n' discarded axes, where N=min(g-1,e-1). The other constraints in the model 1 are

$$\sum_i \alpha_{in}^2 = \sum_j \gamma_{jn}^2 = 1\ \forall\ n; \sum_i \alpha_{in}\alpha_{in*} = \sum_j \gamma_{jn}\gamma_{jn*} = 0,$$
$$n \neq n*; and\ \lambda_1 > \lambda_2 > \cdots > \lambda_{3n\prime} > 0$$

The model in (1) can be reparameterized as

$$Y_{ij} = \mu + G_i + E_j + Z_{ij}$$

Where $Z_{ij} = \sum_{n=1}^{n'} \lambda_n \alpha_{in}\gamma_{jn} + \epsilon_{ij}$

Let the estimate of the interaction in the (i,j)th cell of Z_{ij} be $\hat{Z}_{ij} = Y_{ij} - \mu - G_i - E_j$. Using matrix notation, denote

$\boldsymbol{Z} = (\hat{Z}_{ij})$a matrix of order GEI. Now, the estimate of the parameters of the model is

$\hat{\lambda}_n$= the non-zero eigen values of **Z'Z** (in descending order), and

$\hat{\alpha}_{in}$= the principal components of the row sum of squares and cross product matrix **ZZ'**

$\hat{\gamma}_{jn}$= the principal components of the column sum of squares and cross product matrix **Z'Z**

Using these we can write $\hat{Z}_{ij} = \sum_{n=1}^{n'} \hat{\lambda}_n \hat{\alpha}_{in}\hat{\gamma}_{jn}$

Graphical plots (Bi-plots and 3-D plots)

The model formulation for AMMI shows its interaction part consists of summed orthogonal products. Because this form the interaction lends itself to graphical display in the form so-called biplots(Gabriel,1971). Let start with AMMI and assume that either two terms suffice for an adequate description of the interaction. For AMMI the interaction consists of the sum of two products: $\alpha_{i1}^*\gamma_{j1}^* + \alpha_{i2}^*\gamma_{j2}^*$. The genotype scores, $\alpha_{i1}^*$and α_{i2}^*, are now interpreted as coordinates for planar depiction of the genotype, and the environmental scores, γ_{j1}^* and γ_{j2}^*, for a similar depiction of the environment. The score determines the end points of the genotypic and environmental vectors, which depart from the origin. Simple geometric reveals that the interaction between a genotype i and an environment j can be obtained from a projection of either vector onto the other. The reason is that the interaction according to an AMMI model with two product terms of interaction, $\alpha_{i1}^*\gamma_{j1}^* + \alpha_{i2}^*\gamma_{j2}^*$, is equal to the inner product between vectors $(\alpha_{i1}^*, \alpha_{i2}^*)$ and $(\gamma_{j1}^*, \gamma_{j2}^*)$, or the projection of either vector on to the other, times the length of the vector on which projection take place. It is easy to read from a bi-plot the relative interaction that genotypes exhibit in a particular environment.

To have a better discussion on the graphical plots IPCAs (bi-plots, three dimensional plots *ets*.) resulted from the AMMI analysis, we must consider the following points (Kempton, 1984; Kroonenberg, 1995, as cited in Rashidi *et al*., 2013):

(i) The center of bi-plot shows the mean of genotypes or environments.
(ii) A long distance of a genotype (or an environment) from the center of bi-plot indicates a large interaction with that genotype (or environment).
(iii) The long length of a genotype on the environmental vector reveals more deviation from the mean and vice versa.
(iv) The angle between the vectors of a genotype and an environments shows that the interaction is positive or negative.

AMMI1 bi-plot is constructed with additive main effects or mean yield along the abscissa and the first IPCA or multiplicative interaction on the ordinate axis. Thus, the interpretation of the bi-plot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. The Bi-plot space of AMMI1 is divided into 4 sections(quadrants) from low yielding environments in quadrants 1 (up left) and 4 (low left) to high yielding environments in quadrants 2 (up right) and 3 (low right). From the bi-plot, if the points for environment are more scattered than the point for genotypes indicating that variability due to environments is higher than that due to genotypes difference, and the reverse is true if genotypes take the situation(Zobel *et al*. 1988). On the bi-plot, the points for the generally adapted genotypes would be at right hand side of grand mean levels (this suggests high mean performance) and close to the line showing IPCA= 0 and

(this suggests negligible or no G × E Interaction).

AMMI2 biplot The IPCA 1 versus IPCA 2 biplot (i.e. AMMI 2 biplot) explain the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment (Rashidi *et al*., 2013). The interpretation for AMMI3 (3-dimentional plot) follows like AMMI2 interpretation.

RESULTS

Before conducting any analyses of genotype by environment interaction, the data were subjected to data transformation to fix failures of assumptions of normality and homogeneity of error variances among the different environments. The box plots of coffee bean yield measurements over year in (Figure 1a) shows a high degree of skewness and outliers towards high coffee yield measurements. This suggests that the data should be treated with some transformations unless the assumption of normality and constant variance may be seriously despoiled. In this study, the natural logarithm and square root transformation were checked, and the square root transformation found to be plausible transformation for coffee bean yield measurements (Figure 1b), so that any analyses of genotype by environment interaction were done on the square root transformation.

Combined Analysis of Variance

After confirming the presence of significant differences among genotypes for coffee yield at the specific environments, combined analysis of variance was done. The combined analysis of variance in Table 3 shows that there were significant differences among environments ($p<0.001$) and genotypes ($p<0.001$) for coffee bean yield, indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. The GEI was highly significant ($p<0.001$) reflecting the differential response of genotypes in various environments. The total variation explained was 49.5% for environment, 7.2 % for genotype and 16.2% for GEI. The high percentage of the environment is an indication that the major factor that influence yield performance of coffee genotypes in Ethiopia is the environment. The percentage of variation explained by GEI was relatively large as compared to the variation explained by main effect of genotype.

Additive Main effects and Multiplicative Interaction (AMMI) analysis

The AMMI procedure has been used in order to further investigate the nature of GEI and explore the information contained in it. The result of this procedure was presented in Table 4 with the combined analysis of variance. As mentioned earlier, the environment and genotype main effects are significant, accounting for 49.5% and 7.2% of the total variation in the data set, respectively. It has also been found that 16.2% of total variation was attributed to the genotype by environment interaction.

GEI was further partitioned by principal component analysis. The Gollob F-test that has been used to measure significant of the GEI interaction components, and it shows that the first five IPCAs were significant (P-value<0.01). This indicates that the total information contained in GEI that has 320 degree of freedom can be sufficiently explained using only 155 degree of freedom which captures 80% of the total sum square of GEI, leaving only 20% of sum square of GEI as a noise.

At 1%, Table 4 shows that these principal components (PCA1, PCA2, PCA3, PCA4 and PCA5) captured about 29.1%, 20%, 15.1%, 9% and 7% of variation due to GEI sum of squares, respectively. Together they accounted for 80% of GEI sum of squares. However, most of the variation was explained by the first three principle components (PCA1, PCA2 and PCA3) which accounted for cumulative 64.2%. Over all, the contribution of environment, genotype and the first three principal components to the treatment sum square (the sum of sum of squares of genotype, environment and GEI) was around 92%, indicating the reasonableness and parsimoniousness of AMMI model with the first three interaction principal components in partitioning the treatment sum of squares.Estimates for the genotypic and environmental scores of AMMI-3 (scores of PCA1, PCA2 and PCA3) with their corresponding average coffee bean yield are given in Table 5. The PCA scores of a genotype from AMMI analysis indicate the stability or adaptation of a genotype across environments. The larger the PCA score, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The closer the PCA scores near zero, the more stable or adapted a genotype is over all test environments. Environment scores from AMMI analysis relating to interaction also have meaningful interpretation. Environments with large PCA scores are more discriminating of genotypes, while environments with PCA scores near zero exhibit little interaction across genotypes and low discrimination among genotypes.

Genotype and environment combinations with PCA scores of the same signs produce positive specific

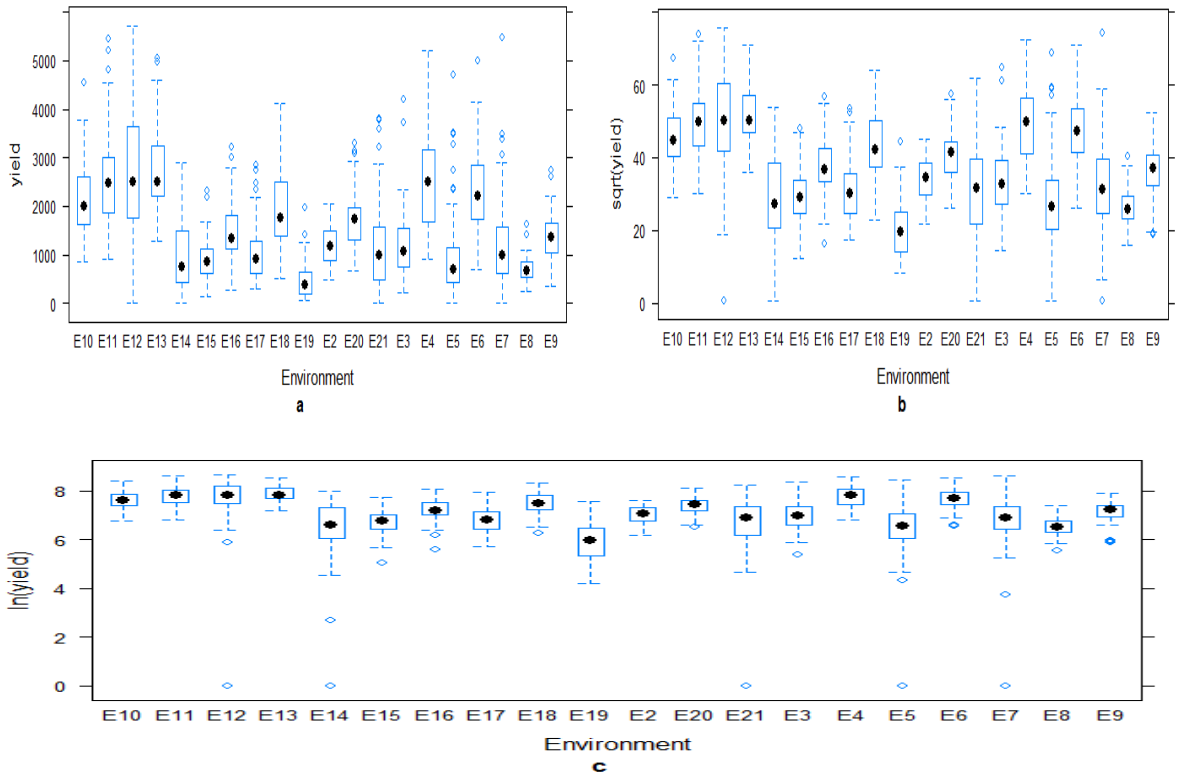


Figure 1: Box-plot of coffee yield measurements :(a) actual yield, (b) Square root transformation and (c) Logarithm transformation

Table 3: Combined ANOVA for coffee bean yield and the percentage sum of squares of the 17 genotypes tested at 21 environments (three locations over a period of seven years)

Source	DF	SS	%SS	MS	F-value	p-value
Environments(E)	20	126169	49.5	6308.5	33.6	<0.001
Block(B(E))	63	11819	4.6	187.6	3.3	<0.001
Genotypes(G)	16	18481	7.2	1155.1	20.3	<0.001
Interactions(GEI)	320	41208	16.2	128.8	2.3	<0.001
Error	1008	57333		56.9		
Total	1427	255011		178.7		

interaction effect, whereas combination of opposite signs have negative specific interactions. For example, E3 and G1 have positive specific interaction effect while E2 and G2 have negative specific interaction effect. Environment which have same signs of interaction PCA scores discriminate genotypes similarly, for instance E2 and E8; and Environments with opposite sign of interaction scores discriminate genotypes differently, for example E2 and E3(Table 5).

To further explain the GEI and stability, a bi-plot and three dimension plot with IPCAs scores were used. AMMI bi-plot of the first two principle component axes is a powerful way of detecting important score of GEI. This analysis represents stability of the genotypes across environments in terms of principle component analysis. It is used to see generally adapted genotypes that offer stable performance across environments, as well as genotypes that perform well under specific conditions. In this study, the first two principal component axes (PCA1 and PCA2) which capture around 50% of the

Table 4: Combined analysis of variance (ANOVA) according to the AMMI model and Gollob's tests of interaction PCAs

Source	DF	SS	MS	Total variation explained (%)	GEI explained (%)	Cumulative (%)
Total	1427	255011	178.7			
Treatment	356	185858	522.1***		72.9	
Environments(E)	20	126169	6308.5***	49.5		
Block nested in E	63	11819	187.6***	4.6		
Genotypes(G)	16	18481	1155.1***	7.3		
Interactions(GEI)	320	41208	128.8***	16.2		
IPCA1	35	12005	343***	4.7	29.1	29.1
IPCA2	33	8232	249.5***	3.2	20.0	49.1
IPCA3	31	6216	200.5***	2.4	15.1	64.2
IPCA4	29	3663	126.3***	1.4	9.0	73.1
IPCA5	27	2852	105.6**	1.1	7.0	80
IPCA6	25	2220	88.8*	0.9	5.4	85.4
IPCA7	23	2018	87.8*	0.8	5.0	90.3
IPCA residuals	117	4001	34.2			
Error	1008	57333	56.9			

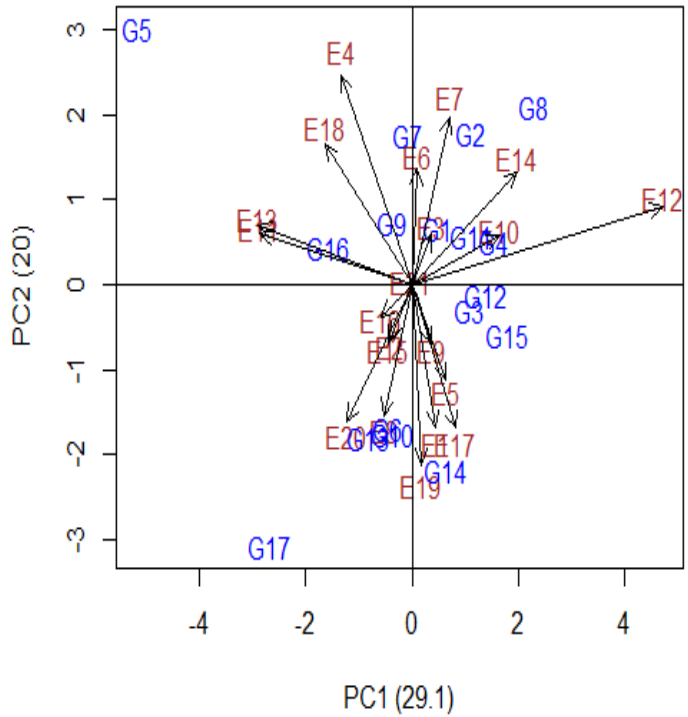
***p-value<0.001; **p-value<0.01;*p-value<0.05 IPCA=Interaction Principal Component Axis

Table 5: IPCA1, IPCA2 and PCA3 scores for genotypes and environment with their corresponding estimated mean

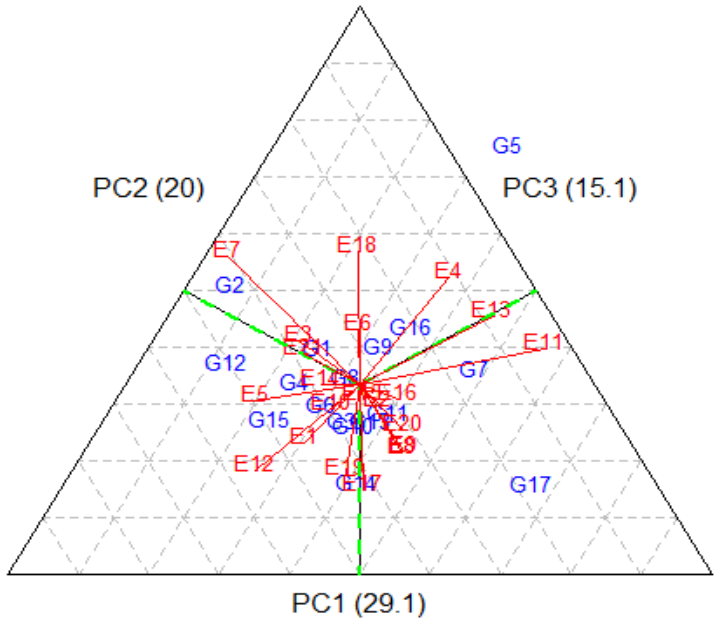
Env	Mean	PCA1	PCA2	PC3	Gen	Mean	PCA1	PCA2	PCA3
E1	21.20	0.451	-1.869	-1.140	G1	41.06	0.499	0.670	-0.680
E2	34.08	-0.415	-0.723	0.067	G2	42.23	1.129	1.774	-2.482
E3	33.83	0.367	0.671	-1.336	G3	37.39	1.093	-0.295	0.617
E4	49.91	-1.342	2.738	1.154	G4	36.52	1.541	0.507	-0.289
E5	28.34	0.632	-1.259	-2.328	G5	34.58	-5.174	3.019	-1.004
E6	46.95	0.093	1.516	0.024	G6	31.69	-0.447	-1.696	-1.508
E7	32.63	0.707	2.200	-3.002	G7	39.97	-0.077	1.750	3.170
E8	26.36	-0.534	-1.714	0.631	G8	38.85	2.300	2.087	1.885
E9	36.35	0.365	-0.778	1.585	G9	39.52	-0.356	0.721	0.199
E10	45.07	1.658	0.635	0.873	G10	31.07	-0.370	-1.754	-0.570
E11	49.81	-2.874	0.668	2.345	G11	36.90	1.115	0.573	1.898
E12	49.10	4.725	1.021	1.785	G12	42.55	1.381	-0.130	-2.403
E13	51.71	-2.891	0.781	0.847	G13	31.76	-0.820	-1.799	-0.542
E14	28.70	1.980	1.476	0.916	G14	33.79	0.644	-2.182	0.535
E15	29.33	-0.456	-0.775	-0.351	G15	36.15	1.803	-0.597	-0.767
E16	37.38	-0.593	-0.422	0.474	G16	34.44	-1.586	0.438	-0.179
E17	31.02	0.834	-1.875	0.943	G17	33.09	-2.674	-3.086	2.122
E18	43.71	-1.645	1.837	-1.693					
E19	20.67	0.182	-2.360	-0.206					
E20	40.71	-1.242	-1.793	-0.004					
E21	30.94	-0.001	0.025	-1.584					

Env=environment; Gen=genotype

total GEI sum squares in bi-plot analysis and the 3-dimensional plots (PCA1, PCA2 and PCA3) that explained about 64% of the total GEI sum of squares are presented in Figure 2. On these AMMI plots, genotypes and environment having PCA values close to zero (near the origin) have small interaction effects, whereas those having large positive or negative PCA values (distant from zero) largely contribute to GEI



(b) 3-dimentional plot



(a) Bi-plot

Figure 2: Bi-plot (a) and 3-dimensional plot (b) of interaction principal components analysis (PCA): IPCA1 versus IPCA2 (a) and IPCA1 verses IPCA3 verse IPCA3 (b) for bean yield (kgha-1) for17 coffee genotype grown in 21 environments

interaction. According to Figure 2b, G5 and G17 are relatively far apart from the origin, indicating strong interaction effects and G1, G3, G4, G5, G6 G8, G9, G10 and G12 appeared close to zero(the center of the axes) , and therefore are relatively more stable. Among the 21 environments, E7, E18, E4, E13, E11 and E12 exhibited larger interactions (i.e. they are relatively far apart from the origin) and were more discriminating of genotypes, whereas the environment E8, E9, E10, E14, E15, E16, E8, E19 and E21 relatively exhibited negligible interaction and low discrimination (Figure 2a&b).

Figure 2: Bi-plot (a) and 3-dimensional plot (b) of interaction principal components analysis (PCA): IPCA1 versus IPCA2 (a) and IPCA1 verses IPCA3 verse IPCA3 (b) for bean yield (kgha^{-1}) for17 coffee genotype grown in 21

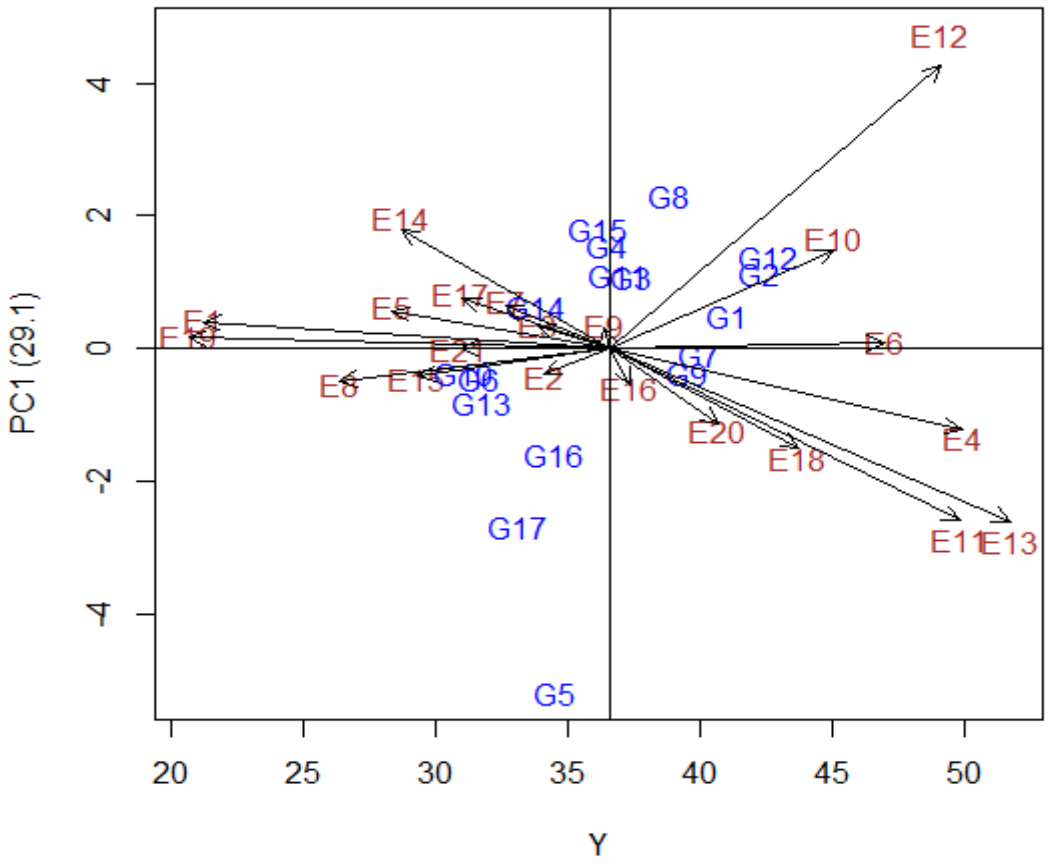


Figure 3: Bi-plot of the first interaction principal component axis (IPCA1) versus means yield for17 coffee genotype grown in 21 environments

environments

The bi-plot in Figure 3 presents interaction PCAs score versus mean bean yield of both coffee genotypes and environments. From the bi-plot, environments are distributed from lower yielding environments in quadrants II(top left) and III(bottom left) to the high yielding environments in quadrants I (top right) and IV (bottom right). Thus, The high yielding environments classified according to the AMMI1 model were E12, E10, E6, E4, E16, E20, E18, E11 and E13. The lower yielding environments were E19, E1, E14, E5, E17, E7, E3, E9, E21, E8, E15 and E2. The environments E19 & E1, E12, and E11 &E13 are visible in quadrant I, III, and IV, respectively, and are relatively quite distant from the origin. Accordingly, E11, E12 and E13 were the most favorable season and E19 and E1 were the less favorable seasons among the 21 environments.

Furthermore, the genotypes grouped under favorable environments with above average means were G1, G12, G3, G7, G8, G9 and G12. Among them, G1, G3 were found to be relative more stable. Genotypes grouped under low yielding environments are shown on the left quadrants of the bi-plot. Thus, G5 and G17 were low yielder and the most unstable genotype identified by the AMMI model.

DISCUSSION

Genotype by Environment Interaction (GEI) analysis was done after square root transformation of the data. The combined analysis of variance revealed that the mean squares of genotypes, environments and genotype by environment interaction were highly significant. The significance of interaction indicates that there is uncertainty in measuring overall performance of

genotypes across different environments (Yonas *et al*., 2014b), or reflecting the differential response of genotypes in various environments (Girma *et al*., 2000; Zubair *et al*., 2001, as cited in Zelalem, 2011; Asnake *et al.,* 2013, as cited in Degene, 2016). The proportion of variability attributed to environment was relatively large (Table 3), and it was an indication that the major factor that influence yield performance of coffee genotypes in Ethiopia is the environment. This is in line with the work of Lemi and Ashenafi (2016) and Yonas and Tarekegn (2015) who reported genetic variation and heritability of various traits in Arabica coffee genotypes. The magnitude of the GEI sum of squares was about 2 times larger than that of genotypes, indicating sizeable differences in genotypic response across environments, and as GEI was significant therefore we can further proceed and calculate phenotypic stability (Rashidi *et al*., 2013).

GEI was further partitioned by principal component analysis (Table 4). The Gollob's test using an approximate F-statistic revealed high significant differences for IPC1, IPC2, IPC3, IPC4 and IPC5 at 1%. The first three interaction principal components (IPC1, IPC2 and IPC3) retained by Gollob's F-test accounted for 64.2% of GEI, indicating the reasonableness and parsimony of AMMI model with the first three interaction principal component axes hereafter called AMMI3, in partitioning the treatment sum of squares effectively ((Gauch and Zobel, 1988; Gauch, 1992). This is also in line with the work of Meaza *et al.* (2011) and Yonas *et al*. (2014a) who reported the possibility of developing stable coffee genotype across environments. But the investigators showed that more than 70% of GEI sum square was explained by the first two interaction principal components. The difference could be due to the nature of the data. The current study also reported that Environments E12, E10, E6, E4, E16, E20, E18, E11 and E13 are found to be high potential environments, where genotypes having high-yield (greater than grand mean). Among 17 genotypes, G1, G2, G3, G7, G8, G9 and G12 are found to have the best performance with G1, G2, G3, G8 and G12 being relatively stable. Among the high-yielding genotypes, G7 and G9 are found to be unstable and particularly adapted to environment E4. E17 and G5 found to be low yielder and highly unstable among 17 genotypes.

CONCLUSION

The major factor that influence yield performance of Arabica coffee in Ethiopia is the environment. In particular, GEI highly significant and is about 2 times larger than that of genotypes, implying further proceed of extracting the information contained in GEI to investigating the nature of differential response of genotypes across environments. Among 17 genotypes, G1, G2, G3, G7, G8, G9 and G12 were identified to have the best performance with G1, G2, G3, G8 and G12 being relatively stable across the test environments under investigation using AMMI procedure. Hence, these genotypes can potentially be released for wide adaptation across coffee producing areas that have similar agro-climatic settings.

LIST OF ACRONYMS

AMMI Additive Main Effects and Multiplicative Interaction
ANOVA Analysis of Variance
CBD Coffee Berry Disease
CBY Coffee Bean Yield
EIAR Ethiopian Institute of Agricultural Research
GEI Genotype by environment interaction
IPCA Interaction Principal Component Analysis
JARC Jimma Agricultural Research Center
MIVQUE Minimum Variance Quadratic Unbiased Estimator
PCA Principal Component Analysis
RCBD Randomized Complete Block design

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