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ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION ANALYSIS OF COFFEE GERMPLASMS FROM SOUTHERN ETHIOPIA

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ABSTRACT: Additive main effects and multiplicative interaction (AMMI) analysis is a recently recommended effective method to study the genotype by environment ($G \times E$) interaction pattern of multi-environment varietal trials. This work deals with modeling and examining the $G \times E$ interaction pattern of the multi-environment trials of 43 genotypes and eight environments from Southern Ethiopia coffee (*Coffea Arabica L.*) collections using a randomized complete block design (RCBD) with four replications. The work further attempts to predict yield based on the AMMI model and evaluate and recommend high performing and adaptable varieties. The AMMI model with the first two interaction principal component axes (AMMI2) is found to be appropriate and parsimonious for the data. Environments e5, e6, e7, e8 and e3 are found to be high potential environments, where genotypes having high-yield (greater than 14 qt/ha) and resistant to Coffee Berry Disease (CBD) are associated. Among the 43 genotypes, 1, 9, 2, 3, 32, 12 and 25 are found to have the best performance with 3, 32, 12 and 25 being highly stable. Among the high-yielding genotypes, 33, 4, 23, 34 and 27 are found to be highly unstable and particularly adapted to environments 5, 6, 7 and 3, respectively.

Key words/phrases: Additive main effects and multiplicative interaction (AMMI), *Coffea arabica L.* genotype by environment interaction, stability

INTRODUCTION

Coffee (*Coffea arabica L.*) is a highly valuable export commodity in the world. More than 50 developing countries, 25 of them in Africa, depend on coffee as a major export commodity, with 17 countries earning 25% of their foreign exchange from the commodity. Coffee generated USD 18 billion for the exporting countries (Raina *et al*., 1998). Until 2000, coffee contributed 80% of Burundi's, 67% of Ethiopia's, 55% of Uganda's and 30% of Nicaragua's foreign currency earnings (Tadesse Woldemariam, 2002). The labor intensive tree crop also provides much employment in rural areas and is the means of livelihood for over 15 million people in Ethiopia.

The Southern regional state of Ethiopia is the second largest producer and supplier of Arabica coffee in the country and shares 46% of the national market (Simayehu Tafesse *et al*., 2008). Coffee grows in all parts of the region, particularly in Gedeo, Sidama, Bench Maji, Shaka, Kembata-Tembaro and Gamo Goffa areas where it is produced in large amount. The average yield of coffee in the region is 500 kg/ha for local or landrace cultivars while 800 kg/ha for the released Coffee Berry Disease (CBD) resistant cultivars. Though the region is highly endowed with suitable environments and immense genetic diversity for coffee production, the productivity of coffee per unit area remains very low as compared to world average. This is attributed mainly due to the lack of improved cultivars for central and eastern coffee growing areas of the region, shortage of improved agronomic practices and prevalence of diseases, mainly CBD and coffee wilt disease (CWD).

Previous studies on coffee have shown that there is a differential response of yield when grown under different conditions and environments, and hence is an indication of the existence of genotype by environment $(G \times E)$ interaction (Carvalho *et al.,* 1969; Colin-Maher, 1973; Srinivasan *et al.,* 1979; Walyaro, 1983; Mesfin Ameha and Bayetta Belachew, 1997). These and other findings (*e.g.,* Samonte *et al.,* 2005; Naveed *et al.,* 2007) indicate that G×E interaction has been an observable fact in many multi-environment varietal trials which create problem to

conclusively recommend high performing varieties for appropriate direction and policy making of breeding programs. Therefore, explicit studies of the G×E interaction pattern of multi-environment trials of coffee will help to increase the likelihood of screening very promising and adaptable varieties.

Many methods have been proposed to study the pattern of G×E interaction, explore the performance of genotype in response to the environment and estimate yield (Van Eeuwijk, 1995; Naveed *et al.*, 2007). The additive main effects and multiplicative interaction (AMMI) model is a preferred statistical model to analyze multi-environment varietal trials effectively and efficiently, where there is a usual occurrence of G×E interaction. It is a model which combines analysis of variance (ANOVA) for additive main effects and uses the principal component analysis (PCA) to partition the multiplicative structure of the G×E interaction (Gauch, 1988; Zobel *et al.*, 1988; Gauch and Zobel, 1996; Gauch, 2007). The ANOVA model partitions the total sum of squares (SS) into the components environment, genotype and G×E interaction without further partitioning the interaction component, making interpretation difficult or complicated in terms of significance of genotypes across different environments. On the other hand, AMMI gives a unified picture and visible pattern of the interaction component using PCA and therefore helps get easy and simplified interpretation of the results allowing to recommend high performing and adaptable genotypes to different environments.

The sum of squares (SS) produced by AMMI model, which is brought by breaking down the G×E interaction component into a visible and easily interpretable pattern, is much larger than the SS from the linear regression approach (Finlay and Wilkinson, 1963). The latter brings less pattern to the G×E interaction since it has a constraint of the model to make the PCA equal to the environment mean deviation (Gauch, 2007).

In general, AMMI model performs as good as or even better than the traditional statistical models ANOVA, PCA and linear regression (Tukey, 1949; Finlay and Wilkinson 1963; Wright, 1971) to analyze data involving multi-environmental trials when all the components genotype, environment and G×E interaction are significant (Gauch, 2007).

The objectives of this study are therefore (1) to assess the G×E interaction pattern of the multi-environment trials of coffee collections from Southern Ethiopia and model the data using appropriate AMMI model, and (2) to select and recommend high-ranked varieties with respect to yield potential and stability.

MATERIALS AND METHODS

Coffee multi-environment varietal trials of 43 genotypes were conducted at two different locations: Awada (315 kms south of Addis Ababa) and Wonago (380 kms south of Addis Ababa) in Southern Ethiopia, which have different agro-ecological characteristics such as annual rainfall, temperature and altitude (Table 1). The trials were carried out during the cropping seasons 1997–2000 in Wonago and 2003–2008 in Awada. In the study, a total of eight environments, a combination of two locations by four years were used.

Table 1. Descriptive information of the environments with their codes and climatic characteristics.

Env-code	Description	Annual rainfall(mm)	Mean temperature (°c)	
			Min	Max
e1	Wonago year 1997	694.3	8.50	25.80
e2	Wonago year 1998	1445.7	9.40	25.30
e3	Wonago year 1999	1456.4	11.50	25.60
e4	Wonago year 2000	1451.5	10.30	26.20
e5	Awada year 2003	1348.0	13.50	25.13
e6	Awada year 2004	1504.6	14.48	27.04
e7	Awada year 2005	1100.8	6.49	29.14
e8	Awada year 2006	1412.9	7.77	28.68

Altitude Awada: 1745 m above sea level, Wonago: 1850 m above sea level.

The AMMI statistical model is given as

$$Y_{ijk} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \alpha_{in} \beta_{jn} + \theta_{ij} + \varepsilon_{ijk}$$

where, Y_{ijk} is the yield of genotype i in environment j for the k^{th} replicate; μ is the grand mean; g_i is the genotype i mean deviation (genotype mean minus grand mean); e_j is the environment j mean deviation; N is the number of singular value decomposition (SVD) axes retained in the model; λ_n is the singular value for SVD axis n; α_{in} is the genotype i eigenvector value for SVD axis n; β_{jn} is the environment j eigenvector value for SVD axis n; $\theta_{ij} \sim N(0, \sigma^2_{ge})$ θ_{ij} is the genotype by environment interaction residual, $\varepsilon_{ijk} \sim N(0, \sigma^2_{\varepsilon})$ is the error term and θ_{ij} and ε_{ijk} are independent that is to say $\mathrm{cov}(\theta_{ij}, \varepsilon_{ijk}) = 0$.

Before conducting combined analyses of variance and AMMI analysis, the data were subjected to the logarithmic and square root transformations to fix failures of assumptions of ANOVA, such as normality and homogeneity of error variances among the different environments. Between the two approaches, it was found that square root transformation fixes the problem of the assumption of homogeneity of variance reasonably. Single and combined analyses of variance (ANOVA) were performed on the yield data of forty three accessions of coffee genotypes for the eight environments using the SAS statistical package (SAS Int., 2004) and R-package. The effect of G×E interaction on the yield was then determined by AMMI analyses (Gauch, 1993; 2007).

For all of the trials, a randomized complete block design (RCBD) with four replications was used. Each plot comprised of 10 trees with an area of 36 m² and 2 m by 2 m spacing. Unless further description is given, the 43 genotypes are coded as a sequence of the numbers 1 to 43. Description on the codes is given in Table 2.

Further detailed results of the AMMI analysis are interpreted using informative biplots, two dimensional graphs which show the main effects and G×E interactions. For instance, Figure 2 shows the first interaction principal component axis (IPCA1) of both genotype and environment versus the mean yield of both components while Figure 3, shows the pattern of the G×E interaction based on the plot of the IPCA1 and second interaction principal component axis (IPCA2) of both genotype and environment.

Table 2. Descriptive information on the names and codes of the 43 coffee genotypes.

Genotype name	Genotype code	Genotype name	Genotype code
75227	1	3070	23
1377	2	85200	24
2181	3	85259	25
3677	4	85265	26
85190	5	85237	27
3670	6	85241	28
3470	7	2777	29
85260	8	85232	30
2081	9	85213	31
1681	10	85257	32
85264	11	85188	33
85238	12	85245	34
3270	13	2077	35
85246	14	85193	36
85181	15	85252	37
85296	16	744	38
85269	17	85180	39
3977	18	85263	40
85196	19	85195	41
2970	20	3170	42
1870	21	85294	43
85288	22		

RESULTS AND DISCUSSION

The AMMI analysis result for the varietal trials of the eight environments (Table 2) showed a very high significant difference ($p<0.001$) of the environment, genotype and G×E interaction components. The proportion of treatment sum of squares explained by environment, genotype and G×E interaction is 75.6, 8.7 and 15.7, respectively. These results indicate that environmental factors have significant influence on the performance of genotypes. This conclusion is in agreement with many findings that show large proportion of the environment and the G×E interaction component (Gauch and Zobel, 1996; Dixon and Nukenine, 1997; Naveed *et al.*, 2007).

The very high differential response of genotypes across the different environments and the interaction of the G×E component indicate the importance of partitioning this component using AMMI model fitting method. The first two principal components explained about 74 percent of the G×E interaction component (Table 3). This means the contribution of environment, genotype and the first two principal components to the treatment sum square is around 96,

indicating the reasonableness and parsimoniousness of AMMI model with the first two interaction principal component axes hereafter called AMMI2, in partitioning the treatment sum of squares effectively (Gauch, 2007; Girma Taye *et al*., 2000).

Figure 1 gives information on the first five top-ranked genotypes using AMMI model as compared to unadjusted means. Visual inspection of the plot indicates how AMMI model ranked most of the top-ranked genotypes in a different pattern than the unadjusted means across the different environments. For instance, genotype 1 in environments 2, 1 and 3 which had ranks of 1, 3 and 5, respectively, is now ranked as the first top genotype in all of the three environments. Detailed information on the differential rank of genotypes across the different environments for the first 15 top-ranked genotypes using the fitted AMMI model and unadjusted means is shown in Table 4. Out of 63 different rankings within the different environments only 12 (highlighted in the table) are found to have comparably similar ranks with the unadjusted means. This implies that statistical noise or systematic error is seriously affecting the ranking, thereby showing the advantage and reliability of fitting the data using AMMI model (Aina *et al.,* 2007). This result is in harmony with many findings (*e.g.,* Crossa *et al*., 1990; Dixon and Nukenine, 1997; Girma Taye *et al*., 2000; Samonte *et al.,* 2005). Information on the mean yield of the 43 genotypes including the mean scores of the IPCA1 and IPCA2 is displayed in Table 5.

Table 3. AMMI analysis for 43 southern Ethiopian coffee genotypes grown under eight environments.

Source	df	SS	MS	Contribution of each Component to the total SS (in %)
Treatment	343	1593.810	4.65***	77.30
Environments	7	1204.996	172.14***	58.40
Reps with in envs	24	31.500	1.31	1.53
Genotype	42	138.786	3.30***	6.73
Genotype x Env.	294	250.028	0.85***	12.13
IPCA 1	48	112.864	2.35***	5.50
IPCA 2	46	72.206	1.57***	3.50
IPCA 3	44	30.726	0.70***	1.49
IPCA 4	42	18.612	0.44**	0.90
IPCA 5	40	8.854	0.22ns	0.43
IPCA 6	38	6.743	0.19ns	0.33
IPCA 7	36	0.023	0.00ns	0.00
Residual	10008	435.960	0.43	21.15

, * indicate probability level of significance at 0.01 and 0.001 respectively, ns indicates non-significance.
df, degrees of freedom; SS, sum of squares; MS, mean squares

Table 4. Adjusted (r1) and unadjusted (r2) ranks of the first 15 top-ranked genotypes within the eight environments

Genotype	e1		e2		e3		e4		e5		e6		e7		e8	
	r1	r2	r1	r2	r1	r2	r1	r2	r1	r2	r1	r2	r1	r2	r1	r2
V-1	3	1	1	1	5	1	6	1	4	3	4	3	3	2	1	2
V-9	8	11	12	3	*	*	8	2	*	*	*	*	1	1	5	1
V-2	*	*	10	7	*	*	7	2	11	11	11	11	5	8	4	3
V-3	11	4	3	5	4	6	*	*	12	12	12	12	7	12	15	9
V-32	6	2	10	4	2	3	*	*	9	8	9	8	*	*	*	*
V-39	*	*	*	*	*	*	*	*	6	5	6	5	*	*	2	6
V-20	*	*	*	*	*	*	*	*	5	7	5	7	4	7	*	*
V-33	*	*	*	*	*	*	*	*	3	4	3	4	2	3	13	3
V-12	*	*	*	*	*	*	*	*	7	6	7	6	*	*	*	*
V-25	*	*	2	6	8	9	7	6	*	*	*	*	*	*	*	*
V-4	*	*	*	*	*	*	*	*	2	2	2	2	14	14	14	12
V-23	*	*	*	*	*	*	*	*	1	1	1	1	*	*	*	*
V-34	*	*	*	*	*	*	*	*	8	9	8	9	11	13	*	*
V-27	*	*	2	8	2	1	3	9	*	*	*	*	*	*	*	*
V-38	7	5	*	*	6	4	12	10	15	14	14	14	*	*	*	*

All stars represent data out of range.

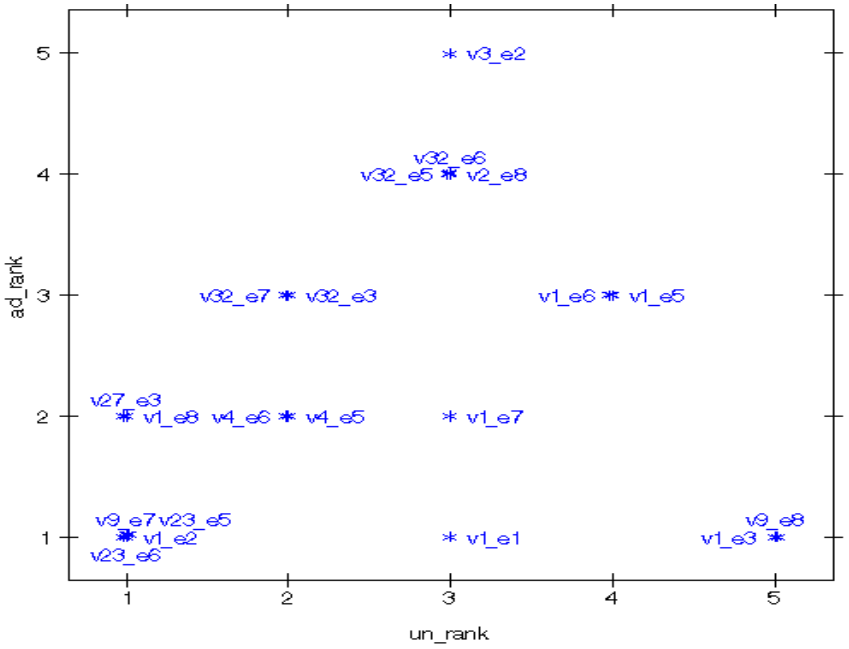

Fig. 1. Plot of the first five top ranked AMMI adjusted (ad_rank) and unadjusted (un_rank) genotypes (v, refers to genotype and the numbers after the underscore sign represents the number of the genotype).

Table 5. Mean yield and mean IPCA1 and IPCA2 scores of 43 coffee genotypes.

Genotype	Mean yield in qt/ha	prin1	prin2	Genotype	Mean yield in qt/ha	prin1	prin2
1	21.35	0.22	-0.19	23	15.66	0.71	0.52
2	17.35	0.28	-0.10	24	10.33	0.08	-0.45
3	17.28	0.05	0.09	25	15.92	-0.08	-0.03
4	15.87	0.60	0.37	26	14.28	-0.17	0.61
5	14.63	-0.15	0.18	27	14.84	-0.46	-0.19
6	13.42	-0.34	-0.19	28	12.03	-0.38	-0.04
7	8.73	-0.52	0.23	29	14.08	-0.11	0.29
8	11.81	-0.50	-0.06	30	12.24	0.16	0.21
9	18.04	0.23	-0.79	31	14.53	0.02	-0.26
10	14.21	-0.14	-0.06	32	16.94	-0.02	0.33
11	13.31	-0.24	0.28	33	16.44	0.78	-0.04
12	16.23	0.12	0.38	34	14.95	0.47	0.16
13	12.96	0.63	-0.47	35	12.79	-0.19	0.14
14	10.24	-0.56	0.29	36	10.43	-0.40	-0.63
15	13.22	0.16	-0.38	37	14.39	0.17	-0.11
16	12.02	-0.18	-0.22	38	14.65	-0.24	0.39
17	13.78	-0.28	0.26	39	16.93	0.34	0.14
18	13.42	0.28	0.08	40	12.50	0.17	0.40
19	11.14	-0.31	-0.43	41	14.17	0.37	-0.31
20	16.75	0.43	0.06	42	11.89	-0.48	0.23
21	10.17	-0.51	-0.19	43	12.66	-0.01	-0.30
22	11.25	0.01	-0.19				

1qt=100 kg

Summary information on the performance, stability and adaptability of the 43 genotypes to the 8 different environments and $G \times E$ interaction is presented in the biplot (Fig. 2). In this figure, the IPCA1 scores of both the genotypes (1 to 43) and the environments $\left(e_i \; i = 1,...,8\right)$ were plotted against the mean yield for the genotypes and the environments, respectively. The associations between the genotypes and the environments can be seen clearly from such figure. The IPCA scores of a genotype in the AMMI analysis are an indication of the stability or adaptation over environments (see Gauch and Zobel, 1996). The greater the IPCA scores (either positive or negative) the more specific is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotypes are over all the

environments sampled (Alberts, 2004). The biplot discriminates four differentially characterized environments as quadrant I, II, III and IV. Environments 5, 6, 7 and 8 are visible in quadrant II and environment 3 is visible in quadrant IV; these environments are referred to as high potential environments. Environments 1, 2 and 4 are visible in quadrant III and are referred to as low potential environments.

Most of the best performing genotypes are predominantly seen in quadrants II and IV, where environments with high potential are persistently seen; whereas most of the genotypes with the worst performance are predominantly seen in quadrants I and III, associated with the low potential environments. One of the reasons for the high-potential environments which are seen in quadrant II, could be the agro-climatic characteristics of these environments, having relatively higher temperatures, lower rainfall and altitude as compared to the other environments. The high potential environment e3, which plots in quadrant IV, is distinguished as having high temperature, high altitude and rainfall as compared to the other environments. This combined agro-climatic property of e3 is the reason for the associated genotypes in this environment to become high yielders (genotypes with yield greater than or equal to 14 qt/ha) and highly resistant to CBD. Most of the genotypes plotting in quadrant II in association with environments e5, e6, e7 and e8 are high yielders having moderate resistance to CBD. On the other hand, the low-potential environments, e1, e2, e4 are characterized climatically as having high altitude, moderate rainfall and low temperature as compared to the other environments. Most of the genotypes associated with these environments and plotting in quadrant I and III are comparatively low yielders (genotypes with yield less than 14 qt/ha) and are less tolerant to CBD, those genotypes falling in quadrant I, being highly susceptible to CBD.

The other interesting result from Figure 2 is that no closely associated genotypes are available for the first and second environments, indicating that these environments might not be important for any of the selected candidate genotypes. This implies that such types of environments are not suitable for growing coffee. Among the high potential environments, environment eight is exceptionally high yielding and uniform for most of the genotypes. Although low yielding, environment 4 is the next stable environment in its potential for most of the genotypes; it has some particularly adaptable and closely associated varieties, such as genotypes 7, 14 and 21.

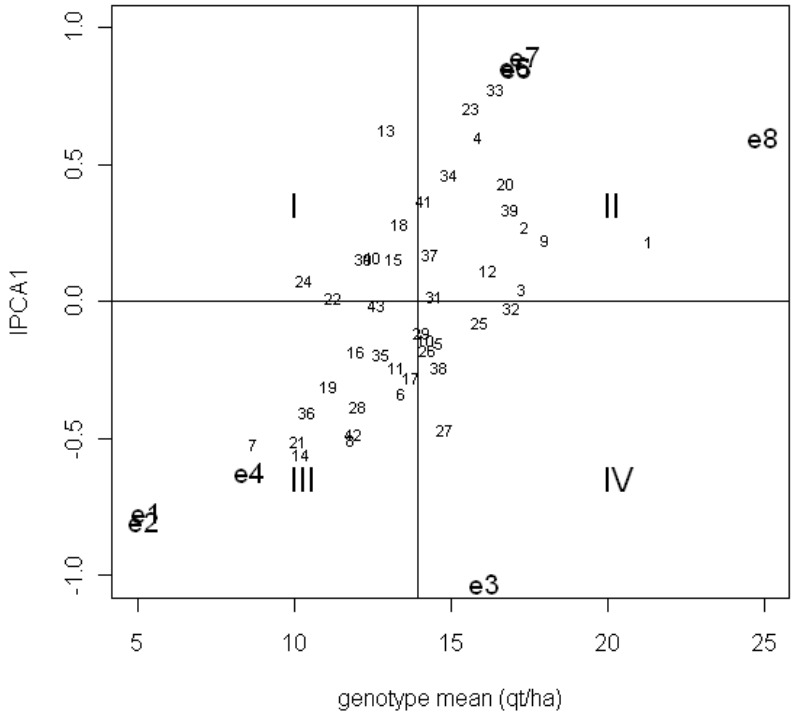

Fig. 2. AMMI biplot of mean yield of 43 coffee genotypes and eight environments versus the first interaction principal component axis.

The high yielding genotypes in order of their performance are: 1, 9, 2, 3, 32, 39, 20, 33, 12, 25, 4, 23, 34, 27, 38, 5, 31, 37, 26, 10, 41, 29. Among these, genotypes 1, 9, 2, 3, 32, 12, 25, 38, 5, 31, 37, 26, 10, and 29 are reasonably stable, genotypes 3, 32, 12, 25, 31, 10 and 29 are most stable and genotypes 33, 4, 23, 34 and 27 are highly unstable. The results indicate the specific adaptability of the genotypes 33, 23, 4 and 34 to environments 5, 6 and 7 and genotype 27 to environment 3. In general, genotypes 1, 9, 2, 3, 32, 12 and 25 have the best performance, with genotype 1 being exceptionally high yielding and having acceptable stability.

To verify the results obtained from inspection of Figure 2 and further explore the adaptation of genotypes and since IPCA2 scores also play a significant role (p-value<0.001) in explaining the $G \times E$ (29%), the overlaid plot of IPCA1 versus IPCA2 of both genotype and environment axes scores are displayed in Figure 3. Visual inspection of this figure indicates a moderate interaction of $G \times E$ for most of the varieties in the IPCA2 with very few exceptions (genotypes: 9, 36, 26 and 23). This gives information on the wrong classification of the genotypes 9 and 26 as reasonably stable. On the other hand, the plot indicates the overall correct interpretation of the results based on the first axis, which is expected as this component explains nearly half of the variance in the $G \times E$ interaction.

The main findings from this study are: i) study of the genotype by environment interaction pattern of 43 genotypes in eight environments and selection and modeling of the data using appropriate candidate AMMI model; the AMMI model with the first interaction principal component axes, AMMI2 which is parsimonious, is chosen as a final model which fits the data very well. ii) selection and recommendation of high performing and stabilized genotypes, including their patterns of adaptation for specific and for all of the eight environments.

From the consequent result of the data fitted and analyzed using AMMI2 model, environments e5, e6, e7, e8 and e3 are found to be high potential environments, where high-yielding genotypes (with yield greater than or equal 13.95 qt/ha) and resistant to Coffee Berry Disease (CBD) are associated. Genotypes, 1, 9, 2, 3, 32, 12 and 25 are found to have the best performance with genotypes 3, 32, 12 and 25 being highly stable. Among the high-yielding ones, genotypes 33, 4, 23, 34 and 27 are found to be highly unstable and particularly adapted to environments 5, 6, 7 and 3 respectively. Genotypes 1, 9, 2, 3, 32, 12, 25, 38, 5, 31, 37, 26, 10, and 29 are high yielders and are reasonably adapted to all of the referred environments.

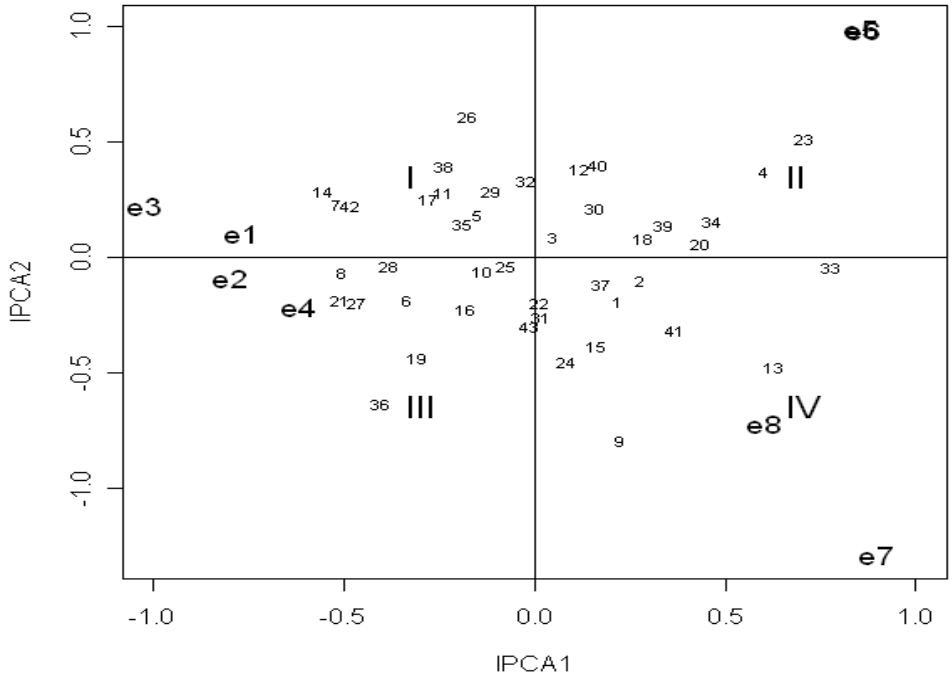

Fig. 3. AMMI biplot of the first two principal component axes.

CONCLUSIONS

This study has shown the importance of modeling data on multi-environment trials of coffee collections from two locations in Southern Ethiopia using AMMI2 to understand and effectively depict the $G \times E$ interaction pattern. It is recommended that coffee breeding programs use the information presented on the top ranked and adaptable varieties to specific and all of the eight referred environments.

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