Journal of Natural Sciences Research
ISSN 2224-3186 (Paper) ISSN 2225-0921 (Online)
Vol.6, No.13, 2016

Genotype by Environment Interaction and Yield Stability of Maize (Zea mays L.) Hybrids in Ethiopia

Lalise Ararsa[1*] Habtamu Zeleke [2] Mandefro Nigusse[3]
1. Bako Agricultural Research Center, Ethiopia
2. Haramaya University, Ethiopia
3. Oxfam, Ethiopia

Abstract

Maize (Zea mays L.) is one of the most important food and feed crops in Ethiopia. Taking the importance of the crop for food security, twelve maize hybrids were evaluated at eight locations using randomized completed block design with three replications. The objectives of the study are to identify the most stable hybrids across locations for grain yield and yield related traits. Additive Main Effects and Multiplicative Interactions (AMMI) model were employed to determine grain yield stability. The combined analysis of variance showed that genotypes (G), environments (E) and their interaction (GEI) were found to be highly significant for grain yield. The hybrid 35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1/CML202 (G3) was found to be the most stable genotype. In addition, the first two principal component axis (IPCA1 and IPCA2) were significant ($P < 0.01$) and cumulatively contributed 65.5% of the total variations of GEI. The significant effects of IPCA1 and IPCA2 in the ANOVA indicated that the AMMI model was the best fit for the data set. Hence, the genotypes can be recommended according to the specific adaptation area.

Keywords: Additive Main Effects and Multiplicative Interaction, Genotype x Environment Interaction, Hybrid, Stability

INTRODUCTION

Maize is one of the most important cereal crops grown in the Ethiopia. The total annual production and productivity exceeds all other cereal crops. In terms of area coverage, it is only superpassed by tef [*Eragrostis tef* (Zucc.) Trotter] (Mosisa *et al*., 2012; CSA, 2014). Considering its importance, wide adaptation, total production and productivity, maize is regarded as one of the high priority food security crops in Ethiopia. Ethiopia's current average national maize yield is 3.43 metric tons per hectare where as the developing and developed countries average yields are 2.5 and 6.2 metric tons per hectare, respectively (CSA, 2015).

Cultivar performance is a function of the genotype and the production environment where it grows. Environmental factors have great influence on qualitative and quantitative traits. Consequently, performance tests of potential varieties are conducted in multiple years and locations (Bernardo, 2002). This is because, besides the genotype and environment main effects, performance of cultivars is also determined by the GEI (genotype x environment interaction) Genotype x environment interaction refers to the differential response of cultivars to environmental changes (Hallauer and Miranda, 1988). Various causes have been described as sources of GEI in Sub-saharan Africa maize growing environments; for instance, temperature, rainfall, drought, length of growing season, sub-soil pH and socio-economic (sub-optimal input application) (Banziger *et al*., 2004). Biotic factors are also among the contributing factors for the presence of GEI (Butran, 2004). The relative magnitude of GEI provides information concerning the likely area of adaptation of a given genotype. It is also useful in determining efficient methods of using time and resources in a breeding program (Ceccarelli, 1989).

In crop improvement programs usually tests of performance across a wide range of environments is conduced to reduce the effect of GEI and to ensure that the selected genotypes have a high and stable performance across several environments. Various studies have been conducted to analyze the effect of GEI on maize varieties in Ethiopia. However, the changing environmental conditions of Ethiopia, the expansion of maize to new agro-ecologies coupled with inadequate maize varieties available for the different environments require a rigorous and continuous study of GEI for a dynamic crop improvement program.

Thus, this study was designed to analyze GEI and evaluate stability of 10 new and 2 existing hybrid maize genotypes across mid altitude and sub-humid agro-ecologies at eight environments or locations and to determine the pattern of grouping of the genotypes and the environments based on grain yield response. Hence, the objective of this study was to: Evaluate the performance and determine stability of hybrids and assess the magnitude of genotypes x environment interaction on yield.

MATERIAL AND METHODS

The experiment was conducted in 2014 during main cropping season (June to Nov) at eight locations (Awassa, Bako, Haramaya, Jimma, Pawe, Assosa, Finoteselam, and Harosebu). The description of test environments is given on Table 1.

Twelve maize genotypes of were included in the study. The genotypes used in the study consisted of four single crosses and eight three-way crosses. Descriptions of the genotypes are given in Table 2. The experiments were laid out in the randomized complete block design (RCBD) with three replications at eight locations. Each plot comprised two rows of 5.1m length with plant spacing between rows and within row 0.75m and 0.30m, respectively. Two seeds per hill were planted and later thinned to single plant per hill, at 2 leaf stage (V-2 stage) and then thinned to one plant per hill providing a uniform stand of about 44,444 plants/ha. Other management practices were done as per the recommendation made for crop at each location.

Table 2.Description of the testing locations used to evaluated 12 maize hybrids during 2014 cropping season

Location	Altitude (masl)	Annual Rainfall (mm)	Soil type	Locations
Bako	1650	1200	Nitosol	Mid altitude sub-humid
Jimma	1764	1572	Eurtic nitosol	Mid-altitude sub-humid
Hawassa	1700	964	Andosol	Mid altitude sub-humid
Pawe	1200	1586	Nitosol	Lowland to mid-altitude
Haramaya	1980	850	Fluvisol	High altitude sub-humid
Assosa	1547	1141	Fluvisol	Mid altitude sub-humid
Finoteselam	1935	950	Slightly Nitosol	High altitude sub-humid
Harosebu	1515	1100	NA	Mid altitude sub- humid

NA = Not available

Analysis of variance for grain and related traits for each location was done with the PROC GLM procedure in SAS (2009) versions 9.1.3 with genotype being considered fixed effects and replication within environment being as random effect least significant difference (LSD) tested were used for mean separation. Bartlett's (1974) test was used to assess the homogeneity of error variances prior to combine analysis over locations. Genotype by environment interaction was quantified using pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, genotype x environment interaction and pooled error

AMMI stability value (ASV) (Gauch and Zobel, 1996) and Purchase (1997) were performed by using GenStat Release 15.1 (2012) statistical software. Since AMMI model does not make provision for a quantitative stability measure, AMMI stability value (ASV) (Purchase, 1997) would be essential in order to quantify and rank genotypes according to their yield stability:

AMMI Stability Value (ASV) = $$\sqrt{\left[\frac{IPCA1sumofsquares}{IPCA2sumofsquares}(IPCA1score)\right]^2} + [\mathbf{IPCA2}]$$

In effect the ASV is the distance from zero in a two dimensional scatter gram of IPCA1 (Interaction Principal Component Analysis axis 1) scores against IPCA2 scores. Since the IPCA1 score contributes more to G x E sum of squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total G x E sum of squares. To compare between the stability analyses procedures, Spearman's coefficient of rank correlation (rs) was used.

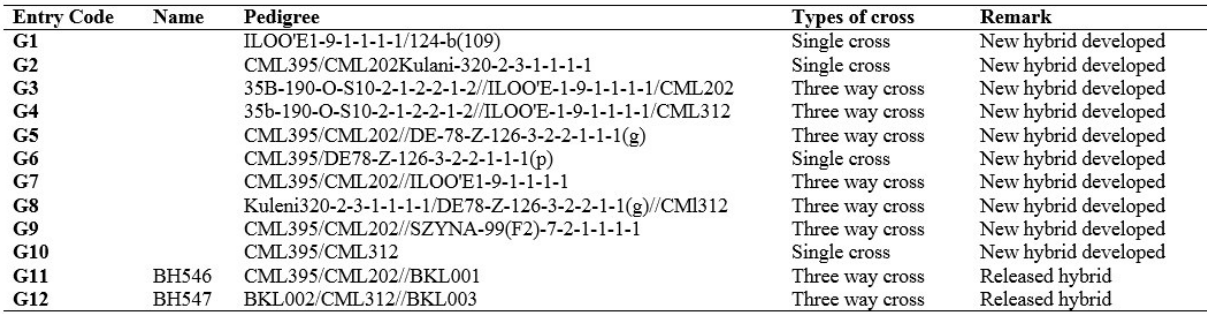
Yield stability index (YSI)

A new approached known as YSI was calculated by the following formula:

YSI = RASV + RY

Where RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes (RY) across environments. YSI incorporate both mean yield and stability is a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and stability (Farshadfar, 2008).

Table 3.Description of maize hybrids tested in eight locations during 2014 cropping season for the study



Entry Code	Name	Pedigree	Types of cross	Remark
G1		ILOO'E1-9-1-1-1-1/124-b(109)	Single cross	New hybrid developed
G2		CML395/CML202Kulani-320-2-3-1-1-1-1	Single cross	New hybrid developed
G3		35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML202	Three way cross	New hybrid developed
G4		35b-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML312	Three way cross	New hybrid developed
G5		CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)	Three way cross	New hybrid developed
G6		CML395/DE78-Z-126-3-2-2-1-1-1(p)	Single cross	New hybrid developed
G7		CML395/CML202//ILOO'E1-9-1-1-1-1	Three way cross	New hybrid developed
G8		Kuleni320-2-3-1-1-1-1/DE78-Z-126-3-2-2-1-1(g)//CMl312	Three way cross	New hybrid developed
G9		CML395/CML202//SZYNA-99(F2)-7-2-1-1-1-1	Three way cross	New hybrid developed
G10		CML395/CML312	Single cross	New hybrid developed
G11	BH546	CML395/CML202//BKL001	Three way cross	Released hybrid
G12	BH547	BKL002/CML312//BKL003	Three way cross	Released hybrid

Source: Bako National Maize Research Center

RESULTS AND DISCUSSIONS

Analysis of Variance

Combined Analysis of Variance Across Locations

Variances of homogeneity from results of the Bartlett test revealed that the mean squares of individual environments were homogenous and so a combined ANOVA could be done. The three way and single cross maize hybrids had the highest yields across environments as indicated on Table 3.Genotype(G3) had the highest yield (8.84 t/ha) followed by (G2) (8.09 t/ha) and the local check (G11) (7.74 t/ha) and (G4) (7.74 t/ha.The single cross hybrid maize (G10) and (G6) and the three way cross hybrid (G9) had the lowest average yield, with yields of 5.55 t /ha, 6.51 t/ha and 6.84 t/ha respectively. In terms of yield, hybrids performed best at Bako, Jimma, Harosebu, Hawassa and Harmaya while they performance was low at Assosa, Finoteselam and Pawe for yield (Table3).

Additive Main Effects and Multiplicative Interaction (AMMI) Analysis

The AMMI analysis of variance for grain yield showed that most of the total sum square was explained (84.13%) environment sum square and the rest to genotypic effects (11.26%) and the genotype x environment interaction (11.14%) (Table 4). The large sum square and highly significant mean square of environment indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. These result was in agreement with the findings Taye *et al.*, (2000); Kaya *et al.*, (2002); Alberts, (2004); Solomon *et al*,. (2008); Abdurhaman, (2009) and Worike *et al.*, (2013). This indicated that the devastating influence of environments on the yield performance of maize hybrid Alberts, (2004) and Solomon *et al.,* (2008) reported a similar result in that all the genotypes, environmental and genotype x environment effects were declared significant in the ANOVA of AMMI.

Table 4. Mean grain yield (t/ha) of 12 maize hybrids evaluated at eight locations during 2014 cropping season

No	Genotype	Locations									
		Assosa	Bako	Haramaya	Hawassa	Pawe	Jimma	Finoteselam	Harosebu	GM	R
1	ILOO'E1-9-1-1-1-1/124-b(109)	6.18	8.22	7.51	8.15	5.30	9.55	5.74	8.79	7.21	7
2	CML395/CML202Kulani-320-2-3-1-1-1-1	6.25	11.04	8.03	7.38	4.64	11.16	5.26	10.97	8.09	2
3	35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML202	7.08	11.85	8.73	8.37	6.06	11.61	4.53	11.24	8.84	1
4	35b-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML312	5.91	11.27	7.50	7.19	5.44	10.31	4.42	9.86	7.74	4
5	CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)	5.98	9.88	7.49	7.54	5.20	10.02	4.25	9.47	7.48	5
6	CML395/DE78-Z-126-3-2-2-1-1-1(p)	5.59	6.63	7.05	7.55	3.69	9.23	3.96	8.66	6.51	11
7	CML395/CML202//ILOO'E1-9-1-1-1-1	5.08	10.76	6.61	6.38	5.00	9.35	3.92	8.82	6.93	8
8	Kuleni320-2-3-1-1-1-1/DE78-Z-126-3-2-2-1-1(g)//CMl312	5.42	10.77	7.01	6.71	4.97	9.81	3.69	9.34	7.24	6
9	CML395/CML202//SZYNA-99(F2)-7-2-1-1-1-1	5.61	9.18	6.81	7.54	6.04	8.73	3.45	7.77	6.84	10
10	CML395/CML312	4.36	7.80	5.54	6.34	4.85	7.39	3.07	6.40	5.55	12
11	CML395/CML202//BKL001(check1)	6.06	10.68	7.64	7.45	5.29	10.36	3.03	9.90	7.74	3
12	BKL002/CML312//BKL003(check2)	4.93	11.68	6.36	6.23	5.84	8.98	1.75	8.28	6.92	9
	EM	5.70	9.98	7.19	7.24	5.19	9.71	3.92	9.12	7.26	
	CV%	11.7	22.62	21.00	19.95	17.07	6.36	21.33	7.50		
	SE(M)	0.45	5.09	2.28	2.09	0.79	0.38	0.48	0.56		
	LSD	1.13	3.82	2.56	2.45	1.50	1.05	1.42	1.17		

Where; Gm=Genotype mean, EM=Environment mean; R=Rank Genotype by environment interaction effects were further partitioned in to interaction principal component axes (IPCA) by using AMMI model. The first two IPCA axes explained the total G X E interactions. The first principal components axis (IPCA1) captured about 39.86% of the interaction sum of squares and the second interaction principal component axis (IPCA2) explained 25.64% of the G x E sum of squares. The mean square for IPCA1 and IPCA2 were and cumulatively accounted for 65.5% of the G x E interaction.

The two interaction principal component axes of the interaction were significant for the model. Thus, the AMMI with only the two interaction principal component axes was the best predicative model, which is harmony with Zobel *et al.*, (1988) and Annicciarico, (2002). The further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. Hence the interaction of the 12 genotypes with eight environments was best predicted by the two interaction principal components.

Table 4. Analysis of variance and tests of interaction principal components in AMMI for grain yield (t/ha) of 12 maize genotypes tested across in eight locations of Ethiopia

Source	DF	SS	MS	Sum of square explained		
				% Total	% G x E	G x E cumulative (%)
Treatments	95	1610.2	16.95**	84.13		
Genotypes	11	181.3	16.48**	11.26		
Environments	7	1249.5	178.5**	77.60		
Rep within Env	16	34.3	2.14ns	2.13		
G x E	77	179.4	2.33**	11.14		
IPCA1	17	71.5	4.21**		39.86	
IPCA2	15	46	3.07**		25.64	65.5
Residuals	45	61.9	1.38ns		34.50	
Error	176	269.4	1.53	14.08		
Total	287	1913.9	6.67			

ns and ** non-significant and significant at $P \leq 0.01$, respectively. Grande mean=7.26, R-squared=0.84 CV=17.
DF = Degree of Freedom SS = Sum of Square and MS = Mean Square G x E= Genotype x Environments

As Gauch and Zobel, (1996); Yan *et al*., (2000); Annicchiarico, (2002) that AMMI model can be predicate by using the first two IPCAs. Hence the results showed that the number of the terms to be included in an AMMI model cannot be specified *a priori* without first trying AMMI predicative evaluation. The IPCA 1 and IPCA 2 axes explained 39.86% and 25.64% of the total GEI. They were both significant ($P<0.01$)(Table 4) and this indicate that the AMMI2 model is the best fit for this data set.

The AMMI Model 2-Biplot

The IPCA1 and IPCA2 sum of square, mean square are explained in PCA analysis. If IPCA1 and IPCA2 means square are significant and residual mean square is non-significant, the steps may be continued for development of biplot. The AMMI bipolt is developed by placing both genotype and environment mean value on the x-axis and the respective IPCA axis on the y-axis.

Tables 4 and 5 present the AMMI analysis data with the IPCA1 and IPCA2 score for the environments and the hybrids, respectively. It indicates the names and graph ID, of the environments and the hybrids, when interpreting the AMMI 2 biplot (Figure 1). On Figure 1, the IPCA1 scores for both the hybrids (oval shape) and the environments (triangle shape) were plotted against the mean yield for the hybrids and the environments. On the same graph, the association between the hybrids and the environments can be clearly seen. The IPCA scores of a genotype in the AMMI analysis are indication of the stability or adaptation across environments. The greater the IPCA scores, negative or positive, (as it is a relative value), the more specifically adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

According to the result of the analysis (Table 5), Pawe and Harosebu were favorable environments with environmental index positive and significant. The environments like Assosa, Jimma and Finotselam were poor (unfavorable) environments with negatively significant environmental index; while Bako, Haramaya and Hawassa are average environments. Estimation of environmental indices were used to classify environments in to three classes *viz*. positive and significant as good (favorable environments), positive or negative and non-significant as average to the environments and negatively significant as poor (unfavorable) environments (Solomon *et al*., 2008).

Table 5. IPCA1 and IPCA2, scores and environmental index for eight locations sorted on environmental means yield

Environments	Graph ID	EN index	EN. Mean	IPCA1	IPCA2
Bako	BK	2.72ns	9.98	1.85949	-0.2346
Haramaya	HU	-0.07ns	7.19	-0.4147	0.10839
Hawassa	HW	-0.03ns	7.24	-0.9558	-0.4529
Assosa	AS	-1.56**	5.70	-0.5284	-0.1609
Jimma	JM	-2.07**	9.71	0.01966	0.61421
Pawe	PW	2.45**	5.19	0.06229	-1.4055
Finoteselam	FS	-3.34**	3.92	-0.186	0.54874
Harosebu	HS	1.87**	9.13	0.14342	0.9825

** ns highly significant at probability level 0.05, 0.01 and non significant respectively.
EN index = environmental index, EN. Mean = environmental mean, IPCA1=interaction principal component axis first and IPCA2=interaction principal component axis second

When observing the environments it is clear that there is a good variation in the different environments sampled and they are spread from the lower yielding environments in quadrant I and IV to the high yielding environments in quadrant II and III. The environments showed that high variability in both the main effect and interaction of IPCA1 scores as shown on Figure 1. The highest yielding environments are Bako (BK), Jimma (JM) Harosebu (HS), Hawssa (HW) and Haramaya (HU) and these are the most favorable environments for all genotypes with similar yield response and, have differences in their IPCA1 interactions. Finoteselam (FS), Assosa (AS) and Pawe (PW) are the least favorable environments for all genotypes with differences in their IPCA1 interactions and yield response.

The genotypes have considerably less variation on the mean yields of 7.26 t/ha than the environments. The genotypes 35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML202(G3), CML395/CML202Kulani-320-11(G2), CML395/CML202//BKL001(G11), 35b-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML312(G4) and CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)(G5) are specifically adapted to higher yielding environments. By considering only the IPCA1 scores, the genotypes ILOO'E1-9-1-1-1-1/124-b(109)(G1) and CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)(G5) were unstable genotypes, and also adapted to the higher yielding (more favorable) environments. It is clear that there is a good variation in the different environments. Bako (1), Jimma (5) and Harosebu (8) were the most discriminating environments as indicated by the longest distance their marker and the origin (Figure 1). Among the environments closer relationships were observed between Assosa(4), Haramaya (2), Hawassa(3), Finoteselam(7), Jimma(5) and Harosebu(8).

Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield performance. Those genotypes that are clustered to closer to center tend to be stable, and those plotted far apart are unstable in performance. Accordingly, the genotypes CML395/DE78-Z-126-3-2-2-1-1-1(p)(G6), BKL002/CML312//BKL003(G12), CML395/CML312(G10) and 35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML202(G3) (G3) were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The genotypes positioned closer to the origin of the biplot which indicate their stability performance across environments are CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)(G5), Kuleni320-2-3-1-1-1-1/DE78-Z-126-3-2-2-1-1(g)//CMl312G(8), 35b-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML312(G4) and CML395/CML202//BKL001(G11). The closer association between CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)(G5) and CML395/CML202//BKL001(G11) showed similar response of the genotypes to the environments.

The projection of the genotypes point to environmental vectors shows that there is specific interaction between genotypes and environment. Thus, the first two IPCA axes were plotted one to another to help investigate the G X E interactions pattern of each genotype (Figure 2). Among environments, Bako had the best yield potential and a good stability. Hybrids G3, G2 and G11 had the best association with Bako, Hawassa, Assosa, Haramaya, Finoteselam, Harosebu and Jimma. Hybrids G7, G8 and G4 had best association with Pawe.

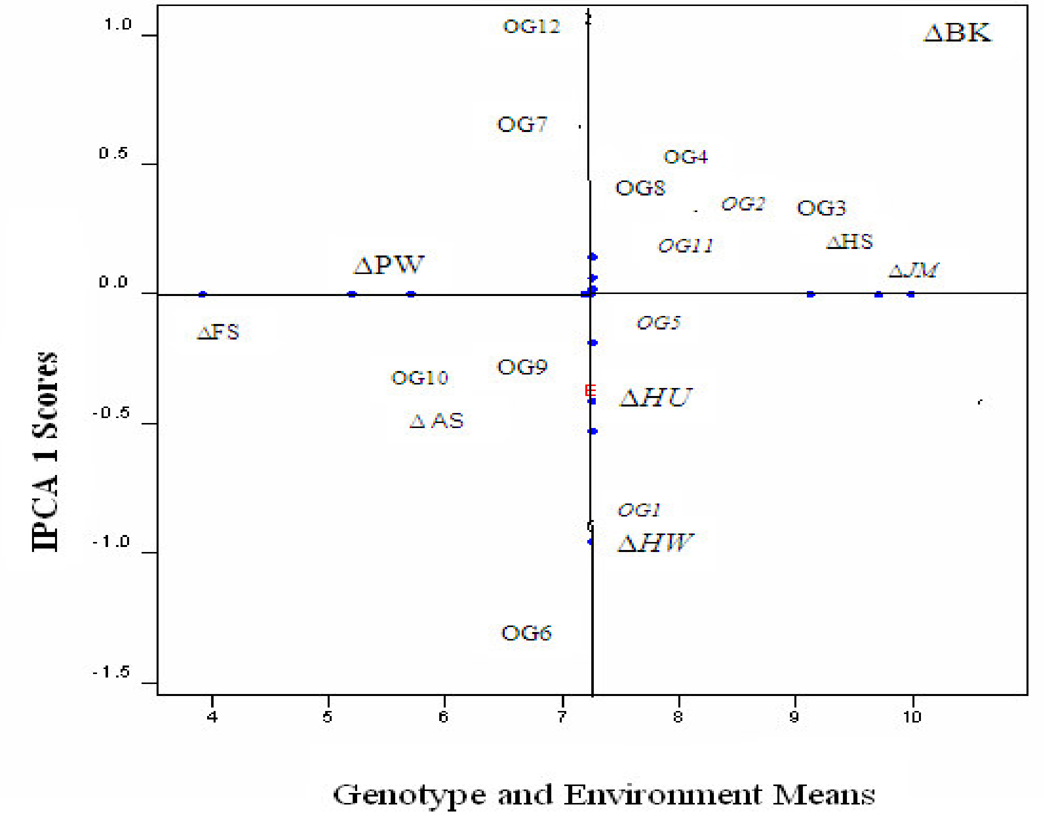


Figure 1. AMMI model 2 biplot on Grain yield(ton ha-1) the main effects and interactions

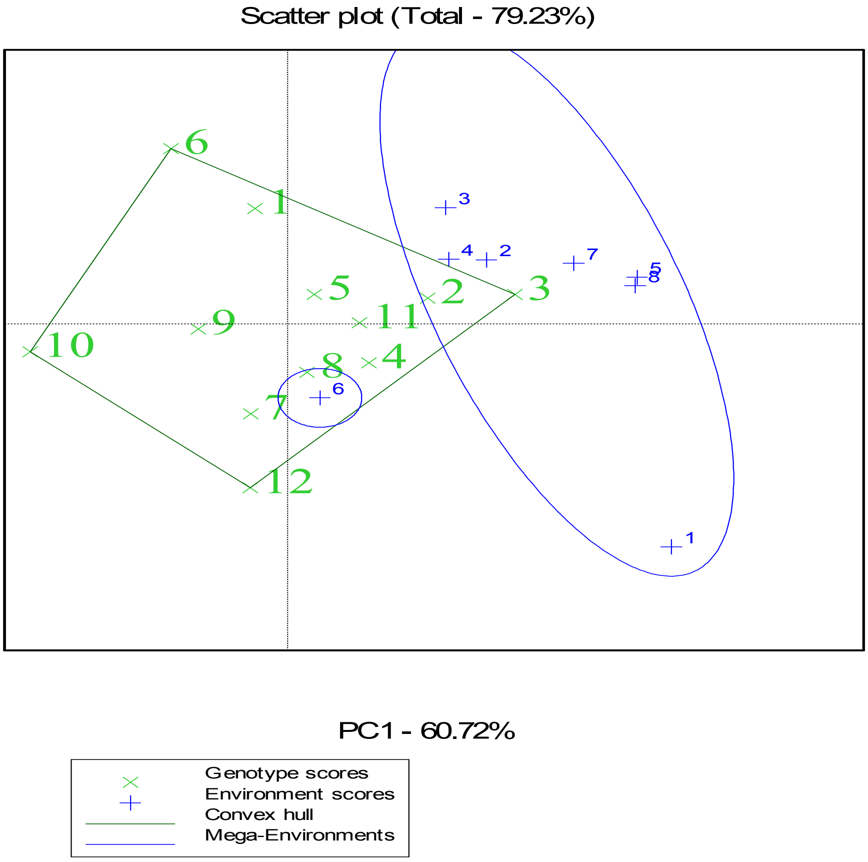


Figure2. Biplot of IPCA1 against IPCA2 for both environments and genotypes

AMMI Stability Value (ASV)

AMMI Stability Value (ASV) is comparable with the methods of Shukla, and Eberhart and Russell on Wheat (Purchase *et al*,. 2000). This is also the finding of this study for Ethiopia maize hybrids for mid agro ecologies of Ethiopia. Table 6 indicates the AMMI 2 model IPCA1 and IPCA2 scores for each hybrid and also the ASV with that of the ranks for 12 maize genotypes tested across 8 environments of Ethiopia.

The ASV could be used if selection is to based primary on stability (Mohammadi *et al*,. 2010b). In ASV ranking method a hybrids with least ASV score is the most stable are, CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)(G5) CML395/CML312(G10),CML395/CML202//SZYNA-99(F2)-7-2-1-1-1-1(G9), CML395/CML202//BKL001(G11) and CML395/CML202//ILOO'E1-9-1-1-1-1 (G4) were the most stable. The most unstable genotypes were CML395/DE78-Z-126-3-2-2-1-1-1(p)(G6), CML395/CML202Kulani-320-2-3-1-1-1-1(G2) and ILOO'E1-9-1-1-1-1/124-b(109)(G1) presented on (Table 6).

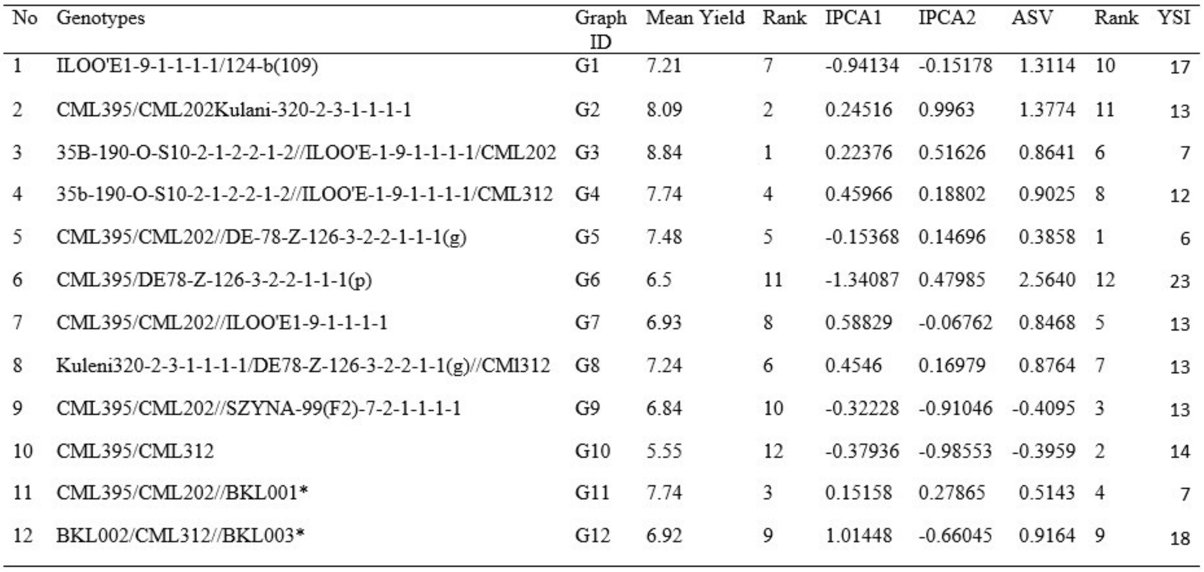
Stability index (YSI)

Stability is not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi *et al*,. 2010b), Hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why Kang (1993) introduced three selection criteria for simultaneous selection of yield and stability: rank-sum(RSM), Modified rank-sum(MRSM) and the statistics yield- stability (YSi).

ASV takes into account both IPCA1 and IPCA2 that justify most of the variation in the GE interaction, therefore the rank of ASV takes the rank one, while the highest yield mean takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability: Yield Stability index (YSI).

The least YSI is considered as the most stable with high yield mean. It is applied to identify high yielding stable genotypes in cereal crop like maize (Fan *et al*., 2007) and durum wheat (Mohammadi *et al*., 2010b). Based on the YSI (Table 6) the most stable genotypes with grain yield was hybrids G5,G11,G3 and G4 are relatively with low ASV and high yielding indicating they were stable (wide adaptable) and high yielding. Though G2 was he 2nd high yielding, it was ranks2nd highest ASV indicating that this hybrid was unstable but high yielding towards favorable environments.

Table 6. Mean yield (t/ha),rank, IPCA1 and IPCA2 scores and AMMI stability values (ASV) of 12 maize hybrids tested across eight environments of Ethiopia during 2014 cropping season



No	Genotypes	Graph ID	Mean Yield	Rank	IPCA1	IPCA2	ASV	Rank	YSI
1	ILOO'E1-9-1-1-1-1/124-b(109)	G1	7.21	7	-0.94134	-0.15178	1.3114	10	17
2	CML395/CML202Kulani-320-2-3-1-1-1-1	G2	8.09	2	0.24516	0.9963	1.3774	11	13
3	35B-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML202	G3	8.84	1	0.22376	0.51626	0.8641	6	7
4	35b-190-O-S10-2-1-2-2-1-2//ILOO'E-1-9-1-1-1-1/CML312	G4	7.74	4	0.45966	0.18802	0.9025	8	12
5	CML395/CML202//DE-78-Z-126-3-2-2-1-1-1(g)	G5	7.48	5	-0.15368	0.14696	0.3858	1	6
6	CML395/DE78-Z-126-3-2-2-1-1-1(p)	G6	6.5	11	-1.34087	0.47985	2.5640	12	23
7	CML395/CML202//ILOO'E1-9-1-1-1-1	G7	6.93	8	0.58829	-0.06762	0.8468	5	13
8	Kuleni320-2-3-1-1-1-1/DE78-Z-126-3-2-2-1-1(g)//CMl312	G8	7.24	6	0.4546	0.16979	0.8764	7	13
9	CML395/CML202//SZYNA-99(F2)-7-2-1-1-1-1	G9	6.84	10	-0.32228	-0.91046	-0.4095	3	13
10	CML395/CML312	G10	5.55	12	-0.37936	-0.98553	-0.3959	2	14
11	CML395/CML202//BKL001*	G11	7.74	3	0.15158	0.27865	0.5143	4	7
12	BKL002/CML312//BKL003*	G12	6.92	9	1.01448	-0.66045	0.9164	9	18

Four Best Hybrids Selections of AMMI model

The AMMI model selected four best hybrid in environments and presented in Table 7 the best AMMI selection for the hybrids per environment is shown. Hybrid selected in all environments is an indication of the best adaptation of the hybrids in relation to the different environments. The hybrid (G3) and (G2) was adapted to higher yielding, favorable environments, better selected in all environments as highest share indicated it was best adaptation. The G11 and G4 were the better performing in the high yielding to low yielding environments, but also stable across environments. The other hybrids that were selected did not show a distinct pattern of adaptation and more specific adapted either higher yielding environments. The AMMI model can be used to analyses the GEI and can be used to identify the superior genotypes. It can also be used in the selection of the best environments for genotype evaluation.

Table 7.The AMMI model's best four hybrid selections for mean yield in relation to the environments

Environment	Sites	Mean	Score	1	2	3	4
E1	Bako	9.980	1.8595	G3	G12	G4	G2
E8	Haro sebu	9.126	0.1434	G3	G2	G11	G4
E6	Pawe	5.193	0.0623	G3	G9	G12	G4
E5	Jimma	9.707	0.0197	G3	G2	G11	G4
E7	Finote selam	3.922	-0.186	G3	G2	G11	G4
E2	Haramaya	7.188	-0.4147	G3	G2	G11	G1
E4	Assosa	5.704	-0.5284	G3	G2	G1	G11
E3	Hawassa	7.237	-0.9558	G3	G1	G6	G9

Acknowledgement

I would thanks to Mr. Tolera Keno, the National Maize Research Coordinator for his all rounded support during the research period; and professional comments and encouragement and Oromia Agricultural Research Institute (OARI). Also Greatful to my famlies Especial thanks for my beloved, Mr. Megersa Tufa and my sweet baby boy Hundanol Megersa

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