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Research Paper

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

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Conducting multi-location trials along with the commercial varieties and genotype by environment (G x E) data analysis are vital to breeders to develop superior genotypes and to meet the challenges posed by environmental factors. This research was undertaken to evaluate maize hybrids for yield, to assess the effect of G x E on grain yield, and determine the yield stability of hybrids across major maize growing areas of Ethiopia. A total of 24 maize hybrids including standard checks (BH547, BH547, BH661 and Limu) were evaluated at six locations (Bako, Jimma, Pawe, Ambo Wendogenet and Asosa) in randomized complete block design (RCBD) with three replications during the 2020 cropping season. The hybrids had significant differences for grain yeild at all locations. The mean squares for genotype, location and G x E were significant. The analysis of variance from Additive Main Effects and Multiplicative Interaction (AMMI) model for grain yield showed significant ($P<0.01$) effect of environment, genotype, G x E, PC1 and PC2. Environment, genotype, and G x E interaction accounted for about 58.64, 11.78, and 22.03% of the total sum of squares, respectively. The two principal components axes (PC1 and PC2) contributed 62 % to the total sum square of G x E. The SXM1910007hybrid had the highest yielding of all genotype with mean grain yield of 8.68 t/ha that had showed dynamic stability. The two hybrids, WE3106 and WE7131 had mean grain yield of 8.06 t/ha and 7.98t/ha, respectively, which was higher than best commercial checks. These hybrids along with other two hybrids (WE3105and 3XM1900476) were identified as most stable hybrids for yield by AMMI stability value, yield stability index and other stability parameters.

Keywords: AMMI, AMMI stability value, Maize hybrids, Yield stability index, Commercial check.

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INTRODUCTION

Maize is the second most widely produced crop in the world and it is the most important cereals in Sub-Saharan Africa (SSA) and a staple food for an estimated 50% of the population[1]. Maize grain yields have doubled from around 1.6 t/ha in 1990 to 4 t/ha in recent years, which are the highest level in sub-Saharan Africa after South Africa (FAOSTAT, 2022).Maize is therefore an important cereal for the economic wellbeing and food security of hundreds of millions of households in SSA (Fisher *et al*., 2015).Despite its importance in the region, maize yields in SSA are still the lowest compared with other regions of the world (Masuka *et al*., 2017).

In Ethiopia, maize ranks first among cereals in terms of total production and grain yield (4.18 t/ha), and second to teff (Eragrostis teff) in area of productionamong all the cereals (CSA, 2021). Ethiopia is a significant maize producer in Africa. The maize sector in Ethiopia has experienced a significant transformation over the past two decades. Important factors for the increased productivity include Increased availability and use of modern inputs (e.g. improved hybrid seeds and inorganic fertilizers), better extension services and increasing demand (Tesdeke Abate *et al*., 2015). Despite the recent progress, maize national average grain yield in Ethiopia is still very low relative to the potential of the crop and world’s average due to lack of well-adapted and improved cultivars and due to genotype by environment (GE) interaction. (Legesse *et al.,* 2020).The national average yield of maize is higher than Africa’s average(2.21 t/ ha), the figure is lower than the world’s average yield (5.80 t/ha) (FAO, 2022).

Stability of performance is special importance in Ethiopia and similar countries where environmental conditions vary considerably and means of modifying the environment are far from adequate. In addition, low cultivar turnover and genotype environment interaction (GEI) predominantly contribute to low yield in small-scale farming systems (Demiselew et al., 2016, Legese *et.al* 2018). Analysis of GE interaction becomes indispensable for breeders and varietal experimentation. Each cultivar reacts specifically to changing climatic and soil conditions; some of them exhibit high GE interaction, while in others it is low. The estimation of G x E interaction and yield stability analysis of Ethiopian maize has been addressed by other workers (Mosisa and Habtamu, 2008; Solomon et al., 2008Demisew et al., 2016a; Legesse et al., 2018; Desalegn, 2019; Legesse et al., 2020, Mohammed, 2020). However, no information is available on the G x E interaction and stability in grain yield performance of these hybrids that are newly developed by the Bako national maize research. In these study tests of performance of new maize hybrids 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. With this the objectives of this study were to assess the effect of genotype by environment interaction on yield stability of maize hybrids and evaluate their performances for agronomic traits in maize growing areas in Ethiopia.

Materials and Methods

Description of Study Area

The experiment was conducted at six locations representing major maize-growing agro-ecologies of Ethiopia. These locations vary in altitude, temperature, total annual rainfall and soil types.

Table 1. Description of the study locations

Location	Altitude (m.a,s.l)	Soil type	Rainfall (mm)	Geographical position		Temperature	
				Latitude	Longitude	Maximum	Minimum
Bako	1650	Nitisol	1598	9°06’	37°09’	29	12.78
Asosa	1547	Nitisol	1276.2	100° 02'	340°31’	33	21
Jimma	1753	Nitosol	1561	7 0° 46’	360° 00’	23	18
Pawe	1120	Nitisol	1250	110°19’	36°24’	32.6	16.5
Wondo Genet	1780	Alluvial	1128	7° 19’	38° 38’	26	11
Ambo	2175	Vertisol	1265.7	8^{o} 57’	37^{o} 51’	25.6	11.7

Source: Ethiopian institute of agricultural research (2020)

Planting Materials, Trial Management and Experimental Design

Twenty maize hybrids with four commercial cheacks (BH546 BH 547 BH661 and Limu) were evaluated in the multi-location trial. These hybrids were developed or adapted by the National Maize Research Program of the Ethiopian Institute of Agricultural Research (EIAR) based at Bako Agricultural Research Center (BARC).The trial was conducted during the 2020 main cropping season in randomized complete block design (RCBD) with three replications. Each hybrid was planted in a two-row plot of 5 m long with spacing of 0.75 m between rows and 0.25 m between plants within a row. Two seeds were sown per hill for each genotype and later thinned to one plant at three to four leaf stages to get the generally recommended total plant population of 53,000 plants per hectare. Planting was done immediately after the onset of the main rainy season after an adequate soil moisture level to ensure good germination and seedling development. The NPS fertilizer at the rate of 150 kg /ha was applied once at planting time at all locations as per the recommendation (MoA, 2018), while 200 kg/ha Urea at Ambo and Pawe and 250 kg/ ha Urea at Bako, Wendo Genet Jima and Asosa was applied in split, half at thinning and the remaining half at knee height.

Table 2. Maize hybrids tested across six locations in 2020 main growing season.

Entry	Hybrids	Pedigree	Source
1	WE6103	CKDHL0089/CML395//CKLTI0036-B-B	CIMMYT
2	WE7124	CKDHL0089/CKDHL0295//CKLTI0348-B-B	CIMMYT
3	CZH15568	CZH15568	CIMMYT
4	WE2108	CML312/CML442//CKDHL0411-B-B-B	CIMMYT
5	CZH15587	CZH15587	CIMMYT
6	WE7117	CKLTI0139/CKLMARSI0029//CKDHL120312-B-B-B	CIMMYT
7	BH 661	CML395/CML202//142-1-e	Bako
8	SXM1910008	BKL004/BKL003	Bako
9	BH 546	CML395/CML202/BKL001	Bako
10	BH 547	CML312BK/BKL002/BKL003	Bako
11	SXM1910173	SC22/124- b(113)	Bako
12	Limu	Limu	Pioneer
13	WE3105	CML444/CML442//CKDHL0295-B-B-B	CIMMTY
14	CZH15523	CZH15523	CIMMTY
15	3XM1900476	CML488/CML489/CML536	Bako
16	SXM1910007	CML444/CML536	Bako
17	WE3106	CML312/CML395//CKDHL0089-B-B-B	CIMMYT
18	WE7131	CKDHL0089/CKDHL0323//CKLTI0045-B-B	CIMMYT
19	WE7126	CML395/CML444//CKLTI0348-B-B	CIMMYT
20	WE7119	CKDHL0500/CKLTI0137//CKDHL120312-B-B-B	CIMMYT
21	WE7128	CKDHL0089/CML395//CKLTI0368-B-B-B	CIMMYT
22	WE1101	CML395/CML444//CML539-B-B-B	CIMMYT
23	WE6105	CKDHL0089/CKDHL0295//CKLTI0344-B-B	CIMMYT
24	WE6106	CKDHL0089/CKDHL0323//CKLTI0200-B-B-B	CIMMYT

CIMMYT= International Maize and Wheat Improvement Center.

Data Analyses

Data of each location were subjected to analysis of variance separately (Table 3) and the combined analysis of variance was calculated as indicated in table 3. The homogeneity of error variances test was verified using Bartlett test for the trait evaluated and the combined analyses of the variance across locations were computed using R software 4.1 versions. The mean comparison of the hybrids was done by LSD test at 5% probability levels.

Table 3. Outline of analysis of variance for individual locations

Sources	DF	SS	MS	Expected MS
Replication (R)	(r - 1)	SSr	MSR	$ϭ^2e + gϭ^2r$
Genotypes (G)	(g - 1)	SSg	MSG	$ϭ^2e$ +rϭ2g
Error (e)	(r - 1) (g - 1)	SSe	Mse	$ϭ^2e$

SS_r =sum square of replication, SS_g = sum square of genotypes, SS_e= sum square of error, MS_e =mean squares due to error, MS_G = mean squares due to genotypes, MS_R = mean squares due toreplications.

The statistical model for combined analysis of variance was as outlined by (Gomez and Gomez, 1984). Yijk = µ + Gi + Ej + GEij + Bk(j) + ϵijk Where, Yijk, is the total variation of the response variable, µthe grand mean, Gi the treatment/genotype effect, Ej the location effect, Bk(j) the effect of the replication within location, GEij the interaction effect between genotype vs. location and ϵijk the residual.

Table 3. Combined Analysis of Variance Over location

Source	Df	MS	ExpectedMS	F- ratio
Total	ERG-1			
Environment (E)	E–1	MS_E	$\sigma^2e + g\sigma^2R(E) + RG\sigma^2E$	MSE/MSGE
Rep/Env't (R)	E(R-1)	MSR	$\sigma^2e + g\sigma^2R(E)$	
Genotype(G)	(G -1)	MSG	$\sigma^2e + g\sigma^2GE + ER\,\sigma^2G$	MSG/MSGE
Gx E Interaction	(E-1) (G-1)	MSGE	$\sigma^2e+g\sigma^2GE$	MSGE/MSe
Pooled Error(e)	E (G-1) (R-1)	MSe	σ^2e	

G=number of geno types, E=number of environments, MSE=means quares due to environments,MSR=meansquaresduetoblock(locations),MSG=meansquaresduetogenotypes, MSGE = mean squares due to G x E and MSe = mean squares due to residual and R =number of replications.

Additive Mean Effect and Multiplicative Interaction (AMMI) Model

The AMMI analysis uses analysis of variance (ANOVA), followed by a principal component analysis (PCA) applied to the GxEsums of squares from the ANOVA (Kempton, 1984).
The AMMI model equation is: $Y_{ger} = \mu + \alpha_g + \beta e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \varepsilon_{ger} + \rho_{ge}$; where, $Y_{ger}$is the observed yield of genotype (g) in environment (e) for replication (r); (Zobel *et al*. 1988).

Additive parameters*:* μ is the grand mean; αg is the deviation of genotype g from the grand *mean,* βe is the deviation of the environment e;

Multiplicative parameters*: λn is the singular value for IPCA, γgn is the genotype eigenvector* for axis n, andδ_{en} is the environment eigenvector; ε_{ger} is error term and ρ_{ge} is PCA residual.
Accordingly, genotypes with low magnitude regardless of the sign of interaction principal component analysis scores have general or wider adaptability while genotypes with high magnitude of IPCA scores have specific adaptability.

AMMI Stability Value (ASV):ASV is the distance from the coordinate point to the origin *in a* two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the GXE interaction sum of squares, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$\square\square\square = \sqrt{\frac{\square\square\square 1\square\square\square\ \square\square\square\square\square\square\square}{\square\square\square\square 2\square\square\square\ \square\square\square\square\square\square\square}(\square\square\square\square\ 1\ \square\square\square\square\square)]^2 + (\square\square\square\square\ 2\ \square\square\square\square\square\ )]^2}$$

Where, *SS IPCA*1 / *SS IPCA*2 is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments (Purchase, 1997).Genotypes with the lowest ASV are identified bytheir shortest projection from the biplot origin and consideredthe most stable.

Cultivar Performance Measure

(Lin and Binns,1986) defined the superiority measure (*Pi*) of the i^{th}test cultivar as the MS of distance between the i^{th}test cultivar and the maximum response as:

$$\square\square = [\square(\square\square - \square)^2 * \frac{\sum_{\square=1}^{\square}(\square\square\square - \square\square - \square\square + \square)^2}{2}$$

Where *Xij*is the average response of the i^{th}genotype in the j^{th}environment, *Xi*is the mean deviation of genotype *i*, ***Mji*s** the genotype with maximum response among all genotypes in the j^{th}location, and *n* is the number of locations. The first term of the equation represents the genotype sum of squares and the second part the GE sum of squares. The smaller the value of *Pi*, the less is the distance to the genotype with maximum yield and the better the genotype. A pair-wise GEI mean square between the maximum and each genotype will be calculated. This method is similar to the one used by (Plaisted and Peterson 1959), except that, (a) the stability statistics are based on both the average genotypic effects and GEI effects and (b) each genotype is compared only with the one maximum response at each environment (Crossa, 1990).

Yield Stability Index (YSI)

The performance stability index calculated applying the sum of the ranking based on performance and ranking based on the AMMI stability amount.

□□□ = □□□□ + □□

RASV is the genotypes' rank based on the AMMI stability value, and RY is the rank of the genotypes based on mean grain yield across environment Genotypes with low YSI values are considered the best across environments (Bose *et.al.*2014)

Results and Discussion

AMMI Analysis of Variance for Grain Yield

The analysis of variance using AMMI showed the significant ($P<0.01$) effect of environment, genotype, and G x E on grain yield. Environment, genotype, and G x E accounted 58.64, 11.78 and 22.03% to the total sum of squares, respectively. The total sum of squares of the treatment, environment and the interaction effect (92.45%) was significantly larger than the error sum of squares (6%) (Table 4) indicating the observed variations were due to treatments with minimum errors made. The environment contributed the largest proportion of the variation for grain yield as compared to genotype and G x E appears to be reasonable as testing sites of major maize growing areas are known to represent different agro-ecologies. This result is in agreement with the results reported by Demisew *et al.* (2016), Legese *et al.* (2020), Gemechu *et.al.* (2021), Ye *et al*. (2021) that the contribution of environment was large to the observed variation of yield of maize. The larger sum of squares for G x E compared to the genotype indicated differences in genotypic response across test environment is large. In maize many author reported the larger contribution of GEI than genotype effect for the observed grain yield variation (Mushayi *et al.,* 2020; Ye *et al.,* 2021).

The F-test indicates highly significant variation ($P<0.001$) for PC1 and PC2. PC1 contribute 39.9 % and PC2 contribute 22.2 % to the total sum squares of GEI. The mean square of residual was highly significant and residual sum square contributed 37.86% to the total sum square of GEI (Table 4) indicating the contribution of unknown error (noise) was relatively high.

Table 4.AMMI analysis of variance for grain yield of 24 maize hybrids tested at six environments during 2020 cropping season in Ethiopia.

				Sum of square explained		
Source	D.F.	S.S.	M.S.	%Total	% G x E	% G x E cumulative
Total	431	2115	4.91			
Treatments	143	1955.4	13.67**	92.45		
Genotypes	23	249.2	10.83**	11.78		
Environments	5	1240.3	248.06**	58.64		
Rep	12	33.9	2.83			
Interactions	115	465.9	4.05**	22.03		
IPCA 1	27	185.9	6.89**		39.9	39.9
IPCA 2	25	103.7	4.15**		22.2	62.2
Residuals	63	176.4	2.8**		37.86	
Error	276	125.6	0.46	6		

= significance level at $p<0.01$. Df = Degree of freedom, SS = Sum of square, MS = Mean square, G x E = Genotype by environment interaction,** Rep (env) = replication within environments, **IPCA 1and IPCA 2=** Interaction principal component axis one **and** two.

AMMI Selections for the Highest Yielding and stable Hybrids across Six Environments

From the score of PC1 and PC2, hybrids WE3105, 3XM1900476, WE7117, WE3106, WE7131 and WE7119 had low PCA1 value near to zero score. These hybrids had smaller interactions, considered as stable and less responsive to the environmental changes. On the other hand, to determine the hybrids were stable or generally adaptable to all environments, they should attain high mean performance having greater than the grand mean and the IPCA score should be nearly zero. Thus, WE3105, WE3106, WE7131and WE7119 were considered stable based on their above the grand mean grain yield and near zero IPCA score (Table 4). Thus could exhibit wide adaptation across the testing locations. This findings agree with the work of Gauch and Zobel, (1997), Alberts, (2004), Demissew *et al*. (2016), Tadesse *et al*. (2017), Legesse *et al*.(2020), who used PCA score in their experiment identifying stable and high yielding Maize hybrids over wide range of environments.

AMMI stability value score showed that hybridWE7131, WE3105 and WE7119 were among hybrids with lower ASV values and these hybrids are relatively more stable than others as suggested by purchase *et al.* (2000). Conversely, HybridSXM1910008 followed by HybridWE6106 and WE6103, were classified under the least stable hybrids. Similar results as many authors Tadesse *et al*. (2017), Chandel *et al.* (2019),Ye *et al.* (2021) who used ASV value to identify stable hybrids for different crops.

Four best hybrids selection of AMMI model

The AMMI model selected four best genotypes in each location (Table 6).The hybrid ranked differently in six different environments; in this case, Hybrid Limu ranked first at PW third in AS, hybrid WE6103 ranked first at WG second at JM. The other hybrid SXM1910008 ranked first at JM, third at WG. The selection of these genotypes in respective environments by the AMMI model is an indication of the specific adaptation of the genotypes at those particular environments.

Hybrids selected relatively in most of the environments were indicator of the best adaptation of the Maize hybrid in relation to the different environments. the highest yielding hybrid (SXM1910007) was among the four best hybrid selected by the AMMI model and had selected as 1st best genotype at three environments and as 3rd and 4nd best hybrid at one environment. This hybrids was selected at four favorable environments (environmental mean yield greater than the grand mean) and one unfavorable (environmental mean yield less than the grand mean), suggesting that it is desirable for cultivation in both environments. Similarly, the second-highest yielder genotype (WE3106) was selected at three environments. Other hybrids WE6106 and BH 661 were found three times at different environments (Table 5).

Table 5. Mean grain yield performances of hybrids along with PCA scores analyzed across six locations.

Entry	Hybrids	Grain yield	PC1	PC2	ASV	rASV
1	WE6103	7.40	0.85	1.09	1.87	22
2	WE7124	6.38	-0.79	-0.14	1.42	17
3	CZH15568	6.99	-0.36	-0.74	0.98	13
4	WE2108	6.5	0.69	0.30	1.27	16
5	CZH15587	6.67	-0.15	-0.12	0.30	4
6	WE7117	6.64	-0.11	0.43	0.48	8
7	BH 661	7.95	0.65	-0.01	1.17	15
8	SXM1910008	7.6	1.20	0.61	2.25	24
9	BH 546	7.16	0.36	-0.69	0.95	12
10	BH 547	7.16	0.60	-0.30	1.12	14
11	SXM1910173	4.85	-0.60	0.96	1.44	19
12	Limu	7.79	-0.82	-0.10	1.48	21
13	WE3105	7.53	0.04	0.25	0.26	2
14	CZH15523	7.78	0.14	-0.60	0.65	10
15	3XM1900476	7.59	0.10	-0.40	0.44	7
16	SXM1910007	8.68	0.76	-0.49	1.46	20
17	WE3106	8.06	-0.11	-0.30	0.36	5
18	WE7131	7.99	-0.11	-0.08	0.21	1
19	WE7126	6.58	0.17	-0.29	0.42	6

Table 5.continuation

20	WE7119	7.68	-0.12	-0.19	0.29	3
21	WE7128	6.63	-0.39	-0.42	0.82	11
22	WE1101	6.99	-0.79	0.15	1.42	18
23	WE6105	7.49	-0.21	0.29	0.48	9
24	WE6106	7.61	-1.00	0.79	1.96	23

PC1 and PC2= principal component one and two, ASV= AMMI stability value and rASV = Rank of AMMI stability value.

Table 6. The Ranking of first four AMMI selections per environment for grain yield (t/ha) of 24 Maize hybrids.

			Rank of hybrids			
Environment	Mean(t/ha)	IPCA Score	1	2	3	4
JM	7.631	1.1977	SXM1910008	WE6103	SXM1910007	BH 661
BK	9.911	1.1634	SXM1910007	CZH15523	BH 546	BH 661
AM	7.53	0.276	SXM1910007	BH 661	WE3106	WE7131
WG	4.112	0.0127	WE6103	WE6106	SXM1910008	SXM1910007
AS	7.256	-0.459	SXM1910007	WE6106	Limu	WE3106
PW	6.986	-2.1907	Limu	WE6106	WE1101	WE3106

JM=Jimma BK=Bako AM=Ambo WG=wendogenet AS= Asosa PW=Pawe

Yield Stability Index and Cultivar Superiority Measure

The hybrid selection index consider as the most stable hybrids with high mean yield. Accordingly WE7131, WE3106 and WE7119 were most stable hybrids. The yield stability index was applied to identify high yielding stable hybrids in cereal crops like maize (Fan *et al.,* 2007; Chandel *et al.*,2019), durum wheat (Mohammadi *et al*., 2010) and sugarcane (Fantaye *et.al.,*2021; Esayas Tena *et.al.,*2021). According to Lin and Binns(1986) cultivar superiority measure (Pi) the most stable hybrids were hybrids with small values of Pi. Hybrids SXM1910007, WE3106, WE7131 and BH 661 showed smaller Pi and high yield response across environments. They gave mean grain yield of 8.67, 8.06, 7.98 and 7.95 t/ha respectively. The hybrids, SXM1910173, WE7124 and WE2108 had relatively larger Pi values showing that they were not stable across location. In most cases the rank of Pi was in agreement with that of overall mean yield (Table7). The cultivar superiority measure (Pi) was used by many workers to identify stable and high yielding genotypes of different crops (Alberts, 2004; Solomon *et al*., 2008; Bose *et al.,* 2014; Seyed *et al*., 2021).

Table 7. Combined mean grain yield (t/ha) and stability measurements in 24maize Hybrids evaluated across six locations 2020.

Entry	Hybrids	Mean grain yield	RY(A)	Pi	rASV(B)	YSI(A+B)	rYSI
1	WE6103	7.40	13	3.92	22	35	21
2	WE7124	6.38	23	6.62	17	40	23
3	CZH15568	6.98	17	4.2	13	30	16
4	WE2108	6.49	22	5.58	16	38	22
5	CZH15587	6.66	18	5.14	4	22	10
6	WE7117	6.63	19	5.51	8	27	13
7	BH 661	7.95	4	2.25	15	19	7
8	SXM1910008	7.59	9	3.71	24	33	19
9	BH 546	7.16	14	3.68	12	26	11
10	BH 547	7.15	15	3.99	14	29	15
11	SXM1910173	4.84	24	14.27	19	43	24

Table 7.continuation

12	Limu	7.78	5	3.24	21	26	12
13	WE3105	7.53	11	2.79	2	13	4
14	CZH15523	7.78	6	2.43	10	16	5
15	3XM1900476	7.59	10	2.58	7	17	6
16	SXM1910007	8.67	1	0.79	20	21	8
17	WE3106	8.06	2	1.76	5	7	2
18	WE7131	7.98	3	1.89	1	4	1
19	WE7126	6.57	21	5.23	6	27	14
20	WE7119	7.68	7	2.38	3	10	3
21	WE7128	6.63	20	5.2	11	31	17
22	WE1101	6.99	16	4.89	18	34	20
23	WE6105	7.49	12	3.11	9	21	9
24	WE6106	7.6	8	4.17	23	31	18

Superiority Measure = Pi, YSI = yield stability index, rYSI=rank of yield stability index RY=rank of main grain yield Rasv =rank of AMMI stability value

CONCLUSIONS

The results of experiment indicated the presence of significant variations among the 24 maize hybrids. The combined analysis of variance of AMMI results showed that the mean squares of genotype, location and G x E were significant. Generally**,** the SXM1910007 hybrid had the highest yielding of all genotype with mean grain yield of 8.68 t/ha with dynamic stability. The two hybrids, WE3106 and WE7131 along with other two hybrids (WE3105and WE7119) were identified as most stable hybrids for yield by AMMI stability value, GGE bi plot, yield stability index and other stability parameters. The identified desirable maize hybrids could be used as candidate varieties for cultivation in major maize growing areas of Ethiopia. However, the identified hybrids need to be further evaluated under verification trial over many locations to be recommended as commercial varieties. Finally the results are crucial in directing the breeding decision following additional season evaluation of the hybrids in the same locations.

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