ISSN: 2287-688X

Annals of
Plant Sciences

Volume 11, Issue 11 (2022) pp. 5565-5577

Research Article

Genotype by Environment Interaction Effect on Yield, and Stability of hybrid Maize (*Zea mays* L.) Genotype in Transitional Highland Agro-ecology of Ethiopia

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Abstract

Evaluating promised hybrid maize genotypes under multi-environment is pivotal for releasing best and stable commercial maize variety. The aim of the study was to investigate the effect of genotype, environment and GEI on grain yield, and stability of 15 hybrids maize genotype under five representative locations of transitional highland agroecology of Ethiopia, during the main season of 2017/2018 using AMMI and GGE biplot analysis. Based on AMMI analysis, highly significant differences of grain yield and other traits ($P \leq 0.001$) were observed due to the effect of genotype, environment, and their interaction (GEI). Genotype and GEI effects accounted for 62.7% of the total variation. Based on GGE analysis, Bako environment was the most discriminating and representative among the representative test environments. This environment could be suitable to select superior as well as broad adapted genotype. In addition, the polygon views displayed three mega environments while crossover interaction within studied genotypes. Maize breeding program might use this information to focus on maize improvement in order to develop broad and specific adaptation for transitional highland agroecology of Ethiopia. Among hybrid genotypes, 'MABK181261' was identified as more stable with a better yield. After a variety verification trial, this genotype could be released as a commercial hybrid for transitional highland agroecology of the country. Overall, the result clearly approved the effectiveness of AMMI and GGE biplot techniques for selecting stable of superior hybrid maize genotypes to mitigate climate change.

Keywords: *AMMI, Genotype by Environment, GGE-biplot, Zea mays.*

Introduction

Maize is one of stable crop, which millions of Ethiopians depend on for their daily calories. It grows from low land to high land agro-ecology of county. Farmers have been using different commercial maize hybrids which was developed and released by National Maize Breeding Research like BH540, BH546, BH547 for low to mid altitude while BH660 and BH661 for transitional high land of Ethiopia. It is important to select superior and stable hybrids from advanced variety trials planted on multilocation for transitional highland agroecology of Ethiopia. Genotype by environment interaction is the differential performance of genotypes across the environments, especially in the tropics where seasonal and spatial variability is large [Mushayi, M. *et al.*, 2020-Li, Z. *et al.*, 2018]. Experiments in single environment (location or year) do not cause general conclusions to be drawn about the genotypes being studied. As a result, multi-environment trials are needed to select a reliable and superior hybrid. The over approach of the conducted trial series was thus to substitute testing in multiple year-by location combinations by

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DOI: http://dx.doi.org/10.21746/aps.2022.11.11.7

testing in a number of extreme environments that were representative for agro-ecological conditions [Matana, Y. *et al*., 2020; Eze, C.E. *et al*., 2020]. When genotypes being evaluated rank differently in different environments (locations and/or years), genotype by environment interaction is important from the perspective of breeders. The stability of suitable genetic characters is critical for the production of improved varieties that can be used commercially under broad agroclimatic conditions. An evaluation of cultivar yield offers useful knowledge regarding their behavior in particular environments [Matana, Y. *et al*., 2020; Badu-Apraku, B. *et al*., 2015b; ranković-Radojčić, D. *et al*., 2018]. Each cultivar reacts specifically to changing climatic and soil conditions; some of them exhibit high G x E interaction, while in others it is low.

One of the primary objectives in maize breeding is always to increase yield. Yield is a very complex quantitative trait, which expression is the result of the genotype, environment as well as G x E interaction. Maize grower needs hybrids that stable and high yielder across the environment. However, different maize genotypes typically display differential responses to varying environmental conditions. As a result, the major challenge for maize breeders has always been the selection of superior genotypes for narrow or wide adaptation and the identification of the best testing sites that could be used to identify superior and stable genotypes [Badu-Apraku, B. *et al*., 2015a]. So, yield stability and superior of maize genotype evaluate at different environments can guide breeder to develop maize breeding for high yielder [Matana, Y. *et al*., 2020]. G x E interaction is often analyzed by the additive main effects and multiplicative interaction model [Oldfield, E.E. *et al*., 2019]. The primary objectives of this study were to thus (1) to evaluate the yield performance and stability of maize genotypes for transitional high land of Ethiopia (2) to study the influence of genotype by environment interaction on yield of genotypes.

Materials and Methods

Germplasm Used (Genetic Materials)

Thirteen advanced maize genotypes which were selected from different observation trials with two commercial check hybrids were used. Seeds for 13 genotypes and 2 commercial checks maize hybrids were produced at nursery of breeding blocking through hand pollination at Bako National Maize Research Center (**Table 1**).

Description of Locations

Thirteen advanced maize genotypes with two commercial check hybrids were evaluated at five enviroments vs Bako, Arsi negele, Haramaya, Pawe and F/Selam (**Table 2 and Figure 1**). These are among of representative maize growing area for transitional highland altitude agroecology of Ethiopia.

Table 1: description of maize genotypes used over five locations for this experiment. After the "Table 1"

Entry	Genotype name	Pedigree name	Source
1	MABK181250	ILOO'E-1-9-1-1-1-1-1/124-b (109)//144-7b	BNMRC
2	MABK181251	BKL003/BKL004//144-7b	>>
3	MABK181252	BKL003/BKL004//143-5-i	>>
4	MABK181253	CML395/30V53F2-20-2-1-2//142-1-e	>>
5	MABK181254	CML395/30V53F2-20-2-1-2//144-7b	>>
6	MABK181255	CML395/30V53F2-20-2-1-2//143-5-i	>>
7	MABK181256	BKL004/DE-78-Z-126-3-2-2-1-1(g)//144-7b	>>
8	MABK181257	BKL004/DE-78-Z-126-3-2-2-1-1(g)//143-5-i	>>
9	MABK181258	CML444/CML536//142-1-e	>>
10	MABK181259	CML444/CML536//144-7b	>>
11	MABK181260	CML444/CML536//143-5-i	>>
12	MABK181261	BKL004/CML536//142-1-e	>>

13	MABK181262	BKL004/CML536//143-5-i	>>
14	BH660 (S Check)	A7033/F7215//142-1-e	>>
15	BH661 (S check)	CML395/CML202/142-1-e	>>

BNMR =Bako National Maize Research Center, S Check = Standard check (commercial check)

Table 2: description of environments and geographical coordinate used to evaluate genotypes [Eze, C.E. *et al*., 2020; Ndlala, L.Z. 2018; Dao, A. 2020]. After "Table 2"

Environment	Lati (N)	Long (E)	Alti	RF (mm)	Temperature (°C)		SMgt	ST
					Max	Min		
Bako	9°06′	37°09′	1650	1598	29	12.78	opt	Nitisol
Arsi-Negele	7°20′	38°9′	1960	866	26	9.1	opt	Andosol
Pawe	11°19′	36°24′	1120	1000-1500	32.6	16.5	opt	Nitisol
F/Selam	10°42′	37°16′	1935	1125	26	13.5	opt	Nitisol
Haramaya	9°24′	42°1′	2050	NA			opt	Fluvisol

Lati = Latitude, Long = Longitude, Alti= Altitude (m.a.sl), RF = Annual rain fall, SMgt = Soil Management, ST= Soil type

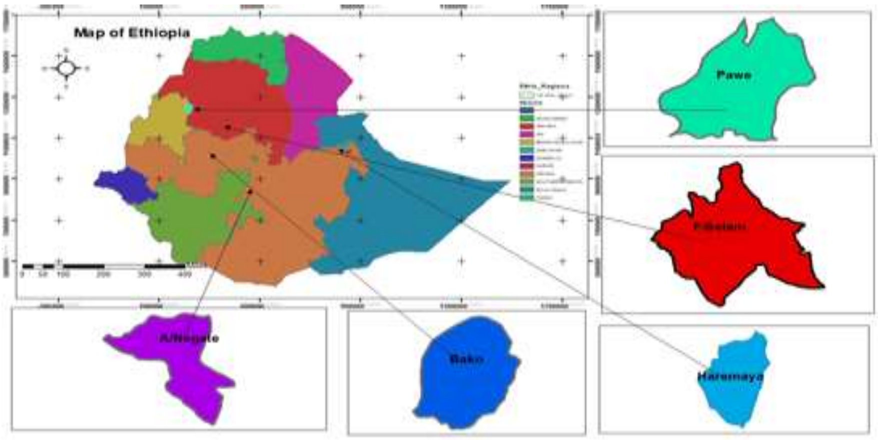

Figure 1: map of the locations (environments). After "Figure 1"

Experimental Management

Genotypes were planted in 5.1m long two-row plots with 0.75m between rows and 0.25m between plants. At the planting and flowing stages, the recommended NPS was applied. Also, pre-emergency herbicide (Grama Gold) was applied to control weeds. When it's appropriate, hand weeding rehearsals are conducted. The experiment was carried out during the rainy season.

Experimental Design and Statically Analysis

The experimental design used was alpha lattice (3 x 5) with three replications with two rows per plot for each location. Online http://www.pbstat.com/ "PBSTAT-GE: Genotype-by-environment interaction and stability analysis for plant breeding" used for data analysis. Environments were treated as a random effect in the combined analysis, whereas genotypes were treated as a fixed effect. Least square means were simultaneously generated for AMMI model. Following single site ANOVA for grain yield, the combined ANOVA and AMMI analysis of variance were done with genotypes being considered as fixed effects and replication with in environments being random mode to determine the effect of differences between genotypes, across locations and to estimate G X E interaction through stability analysis using AMMI analysis model [Zobel, R.W. *et al*., 1988; Bocianowski, J. *et al*., 2019] as follow

$$Yge = \mu + \alpha g + \beta e + \alpha \sum_{n=1}^{N} \lambda n^{y} gn^{y} en + \theta ge$$

Whereas where Yge is the yield of genotype, g, in environment, e; l is the grand mean; ag is the genotype mean deviation; be is the environment mean deviation; kn is the Eigen value of the principal component (PCA) axis, n; cgn and gen are the genotype and environment PCA scores for the PCA axis, n; N is the number of PCA axes retained in the model; and hge is the residual.

Data Collected

Data on grain yield and other important agronomic traits were collected as follows:

Days to anthesis: The number of days from emergence to when 50% of the plants in a plot start shedding pollens

Days to silking: The number of days from plant emergence to when 50% of the plants in a plot have grown 2-3 cm long silks.

Grain weight (t/ha): The weight of the ears per plot adjust to 12.5% moisture level and 80% shelling percentage to estimate grain yield in tons (t ha^{-1}) for each genotype.

Actual moisture content: Moisture content of samples from the bulk of shelled grain in each plot measured using a handheld moisture tester. Recorded at the same time as the measurement of grain weight per plot and 1000 kernel weight.

Plant aspects: Recorded on a 1 to 5 scale, where 1 means the best variety (considering general appeal of the plants per row: plant vigor, ear size, good ear placement or position, husk cover, uniformity, disease infestation, and so on), while 5 means the worst plant aspect

Ear aspects: Recorded on a 1 to 5 scale where 1 refers to the best ear aspect (considering general appeal of the ears: ear size, uniformity, bare tipness (whether the grain filled up to the tip of the ear), kernel row arrangement, ear rot infection and other acceptable characters), while 5 refers to the poorest ear aspect with undesirable characteristics.

Ear height (cm): Average height in cm of five randomly selected plants per plot measuring from the ground level to the upper most ear bearing node.

Plant height (cm): Average height in centimeter of five randomly selected plants measured from the ground level to the first tassel branch.

Result and Discussion

AMMI Analysis

Environment, genotypes, genotype by environment, and genotype by environment interaction all showed highly significant differences (P00.1) in the combined AMMI across environments. (**Table 4**). Due to the presence of a highly significant genotype by environment interaction for grain yield of the cultivars, AMMI revealed that there was significant G x E for grain yields. This emphasizes the importance of extensive testing of these cultivars in a multi-environment before recommending them to farmers. [Wolde, L. *et al*., 2018], [Abakemal, D. *et al*., 2018] and [Mengesha, W. *et al*., 2019] were reported significant for grain yield for maize that tested at multi- environment. The test environment accounted for 55.78% of total variation in grain yield, while genotype 7.88 % and G x E 14.55 %t contributed, indicating a much broader range of environmental main effects than genotypic main effects. G x E has a larger magnitude sum of squares than genotype effects, indicating that there are more differences in genotypic response across environments. This suggested that Ethiopia's transitional highland agroecology has a diverse of environmental conditions. A large contribution of the environment affecting yield stability was reported by many researchers [Eze, C.E. *et al*., 2020; Nzuve, F. *et al*., 2013; Wolde, L. *et al*., 2018 and Abakemal, D. *et al*., 2018]. Analysis of multiplicative effects (Table 4) indicated that the AMMI model with test environment contributed 55.78 % from total variation of sum square for grain yield while G and G x E sources of variation accounted for 7.88 % and 14.55%. This means that the maize genotypes and the five environments were very different. Other studies have found that location accounts for the majority of total variation in multi-environment trials, while genotype and G x E account for only a small portion of total variation [Matana, Y. *et al*., 2020; Eze, C.E. *et al*., 2020 and Abakemal, D. *et al*., 2018].

Table 3: AMMI analysis for grain yield. After "Table 3"

Source of Variation	df	Sum of squares	Mean Squeres	Total variation explained %	G x E explained%	Probability
ENV	4	767.45	191.86**	55.78	-	0.0001
GEN	14	108.45	7.74**	7.88	-	0.00001
G x E	56	200.19	3.57**	14.55	-	0.01
IPCA1	17	137.01	8.06**	-	68.4	0.00001
IPCA2	15	31.70	2.11^{ns}	-	15.8	0.34
IPCA3	13	22.63	1.74^{ns}	-	11.3	0.530
IPCA4	11	8.85	0.80^{ns}	-	4.40	0.94
IPCA5	9	0	0^{ns}	-	-	1
Residuals	150	299.76	1.99	21.79	-	NA

df=degree of freedom, ns non-significant (P> 0.05), IPCA Interaction Principal Components ** Significant at P < 0.01

Performance of Genotype in Specific Environment and Mult-Enviromnent

In Table 4, AMMI revealed that the first two hybrids (G11, G12) were the best performers in each environment, while CK1 was the worst performer. The genotype by environment interactions explains the differences in grain yields t-ha^{-1} (t-ha^{-1} = tons per hectare) between selected genotypes in five environments. This is also referred to as crossover genotype by environment interaction [Matana, Y. *et al.*, 2020; Eze, C.E. *et al.*, 2020; Kebede, D. *et al.*, 2019; Tena, E. *et al.*, 2019; Nzuve, F. *et al.*, 2013 and Yan, W. *et al.*, 2006]. Bako 10.63 t-ha^{-1} (MABK181259), A/ Negele 9.04 t-ha^{-1} (MABK181255), Pawe 6.62 t-ha^{-1} (MABK181261), F/selam10.3 t-ha^{-1} (MABK181262), and Haromaya 7.43 t-ha^{-1} (MABK181259) were the highest yielders for each individual location. However, BH660 (check1) produced the lowest yielder for five individual locations: Bako (5.52 t-ha^{-1}), A/Nagel (4.41 t-ha-1), Pawe (3.51 t-ha^{-1}), F/Selam (4.87 t-ha^{-1}) and Haromaya (3.6 t-ha^{-1}). Identification of high yielding and stable maize hybrids in multi-environment trials is critical for commercial hybrid success in Ethiopia's transitional high land agroecology. In all trials, the average GY of all genotypes evaluated in multi-environment was higher than the best commercial check (BH661), with the exception of MABK181254. These implies possibility of fast releasing and overtake of new maize hybrids for transitional high land agroecology of Ethiopia to exploits available of maize inbred line germplasm to maximize production and productivity. Wender [Rezende, W.S. *et al.*, 2020] and Y Matana [Matana, Y. *et al.*, 2020] also reported similar result that grain yield of some hybrids evaluated over location was higher than grain yield of commercial check. From total studied genotypes, seven genotypes had more than grand mean (6.55 t-ha^{-1}) of grain yield. This study approves Legesse [Wolde, L. *et al.*, 2018] which the grain yield of maize genotype varied based on the interactions of genotypes x environments within across test environments. Based on IPCA1 scores, genotype MABK181251, MABK181252, MABK181257, MABK181259, MABK181260 and MABK181262 had negative interaction with the environment, in opposite direction genotype MABK181250, MABK181253, MABK181254, MABK181255, MABK181256, BH660 and BH661 had positive interaction with environment in **Table 5.** Genotype MABK181255 (0.66) had highest positive interaction with environment whereas, genotype MABK181261 (0.13) had the lowest positive interaction. Relatively, the lowest and the highest negative interaction with environment expressed from MABK181259 (-1) and MABK181257 (-0.05) respectively. Genotype MABK181257, MABK181258, MABK181259 and MABK181262 had negative interaction with environment for both IPCA1 and IPCA2. However, genotype MABK181250, MABK181254, MABK181256, BH660 and BH661 had positive interaction with for IPCA and IPCA2. In AMMI analysis, positive interactions of IPCA scores of genotypes indicate environmental stability. These genotypes showing high positive interaction with the environments have the ability to exploit specific agroecological condition of the environments so that best suited to those environments [Kebede, D. *et al.*, 2019; Tena, E. *et al.*, 2019].

Table 4: Grain yield mean Performance for Individual location and all studied traits multi-environment

Genotype name	**Individual location for GY $^{t-h1}$**					**Across locations for all traits**						
	BAKO	ARSI NEGELE	PAWE	F/SELAM	HARAMAYA	GY $^{t-h1}$	AD	SD	PH	EH	EA	PA
MABK181250	8.18	6.49	5.96	5.68	6.55	6.57	89.07	93.64	276	155.4	2.17	2.56
MABK181251	9.04	5.3	5.38	7.44	4.71	6.37	89.65	93.87	280.5	155.6	2.42	2.41
MABK181252	7.77	5.35	5.14	8.14	5.11	6.3	90.07	93.89	275.4	161.3	2.5	2.53
MABK181253	7.56	7.11	3.77	6.72	6.25	6.28	90.03	93.99	266.2	151.4	2.25	2.48
MABK181254	4.77	5.47	5.03	6.19	4.57	5.21	90.07	94.1	271.9	155.6	2.38	2.46
MABK181255	7.34	9.04	4.07	6.53	4.37	6.27	89.41	93.67	280.7	175.2	2.58	2.61
MABK181256	7.39	7.71	5.34	7.34	6.81	6.92	88.98	93.53	266.9	159.5	2.5	2.51
MABK181257	8.82	6.75	3.83	7.29	5.39	6.42	89.17	93.43	275.5	161	2.38	2.56
MABK181258	9.2	5.84	5.21	8.11	6.43	6.96	89.41	93.69	269.1	165	2.5	2.38
MABK181259	10.63	4.41	4.61	9.42	7.43	7.3	89.93	93.89	270.7	151.1	2.17	2.38
MABK181260	9.18	5.61	5.31	8.4	7.34	7.17	89.6	93.64	275.4	153.9	2.46	2.41
MABK181261	9.44	8.22	6.62	7.99	6.65	7.78	89.65	93.57	273.3	160	2.54	2.51
MABK181262	9.09	6.98	5.57	10.3	6.93	7.77	89.26	93.5	267	154.7	2.13	2.48
BH660 (S Check)	5.57	7.07	3.51	4.86	3.6	4.92	90.79	94.08	265	158.1	2.42	2.75
BH661 (S check)	6.94	7.88	4.15	5.41	5.51	5.98	89.36	93.67	274.8	155.4	2.46	2.73
MEAN	8.06	6.62	4.9	7.32	5.84	6.55	89.63	93.74	272.5	158.2	2.39	2.51
MAX	10.63	9.04	6.62	10.3	7.43	7.78	90.79	94.08			2.42	2.75
MIN	5.57	4.41	3.51	4.86	3.6	4.92	88.98	93.53	266.9	5	2.5	2.51
LSD 0.05	3.05	1.63	2.13	1.8	0.92	0.88						
CV (%)	33.24	14.58	20.9	22.19	13.54	22.3						

						2						

GY =grain yield, AD= anthesis date, SD= silking date, PH= plant height, EH= ear height EA= ear aspect PA= plant aspect

Table 5a AMMI adjusted mean grain yield (t-ha^{1}) IPCA score of genotypes and ASV of 15 genotypes tested across five environments in Ethiopia. After "Table 5"

Genotype name	Mean GY (t-ha^{1})	IPCA1	IPCA2	ASV
MABK181250	5.92	0.18	0.30	-0.71
MABK181251	5.90	-0.40	0.07	-0.31
MABK181252	5.79	-0.33	0.29	0.21
MABK181253	5.66	0.22	-0.27	0.09
MABK181254	4.75	0.27	0.85	0.29
MABK181255	5.83	0.66	-0.47	0.23
MABK181256	6.24	0.32	0.15	0.16
MABK181257	5.88	-0.08	-0.49	-0.02
MABK181258	6.31	-0.38	-0.02	-0.11
MABK181259	6.56	-1.00	-0.25	-0.06
MABK181260	6.43	-0.45	0.07	-0.06
MABK181261	7.12	0.13	-0.01	-0.21
MABK181262	7.08	-0.38	-0.02	0.64
BH660 (S Check)	4.56	0.64	-0.01	0.03
BH661 (S check)	5.43	0.61	-0.17	-0.16

Table 5b: continues

ENV	Mean GY (t-ha^{1})	DIM1	DIM2	DIM3
1(Bako)	8.06	-0.55	-0.50	-0.43
3(Arsi Negele)	6.61	1.00	-0.32	0.14
4(Pawe)	4.89	0.08	0.64	-0.25
5(F/Selam)	7.32	-0.57	0.02	0.62
6(Haramaya)	2.92	0.05	0.15	-0.08

GGE Biplot Analysis

The GGE biplot can be thought of as a graphical representation of matrix multiplication. As a result, fifteen hybrids, including two commercial checks, were evaluated at the five sites shown in **Figures 2, 3, 4, and 5**. GGE biplot analysis gathered a lot of useful information from various biplot graphs [Matana, Y. *et al.*, 2020; Eze, C.E. *et al.*, 2020; Abakemal, D. *et al.*, 2018]. The x-axis was the first principal component (PC1) scores, and the y-axis was the second principal component (PC2) scores. Biplot's total variation in relation to G and GEI explained 80.1 percent of the variance (Figure 2). PC1 explained 65.4 percent of genotype by GGE from total variation, while PC2 explained 14.7 percent. Two principal components (PC1 & PC2).

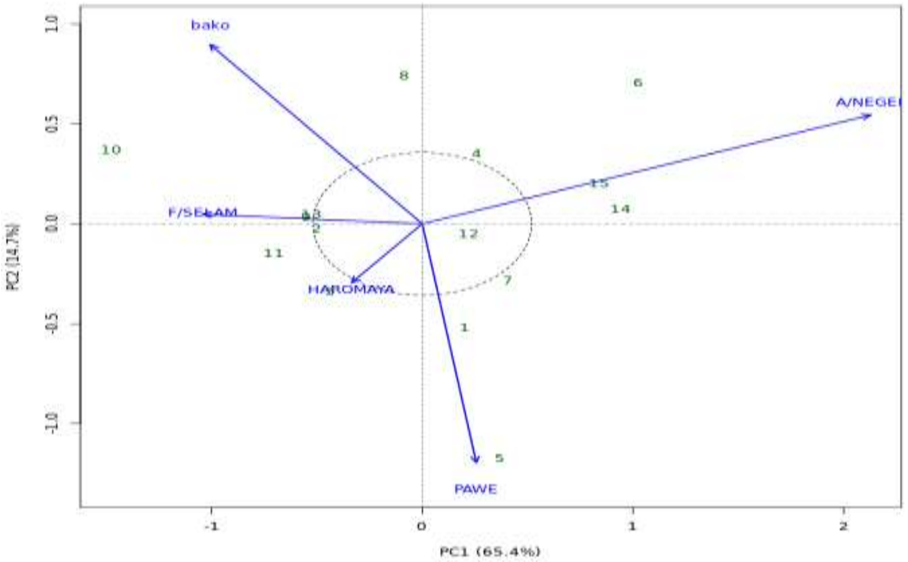

Figure 2: AMMI biplot: PC1 vs PC2. After "Figure 2"

explained more than half of the G x E interpretation, so the best AMMI model can be predicted by using the first two PCs to explain two interpretable explanation patterns Yan [Yan, W. *et al.*, 2000], Yan and Tinker [Yan, W. *et al.*, 2006]. The vector view of the GGE biplot is shown in **Figure 4**, in which the environments are connected to the biplot origin vs the vectors. This perspective aids in comprehending the environment's interrelationships. The length of the vector that approximates the standard deviation with each test environment, according to Yan [Yan, W. *et al.*, 2006], is a measure of the environment's ability to discriminate genotypes. As a result, the F/Selam vector is abnormally short in comparison to the plot size. Thus, genotypic differences based on projections onto vectors of such an environment may be unreliable, reflecting only noise. The polygon view of the GGE biplot is useful for visualizing the multi-environment trial dataset's "which-won-where" pattern. PC1 accounted for 62.7 percent of variation, while PC2 accounted for 17.5 percent **(Figure 5).** Demisew [Abakemal, D. *et al.*, 2018], Hortense [Mafouasson, H.N.A. *et al.*, 2018] and Legesse [Wolde, L. *et al.*, 2018] also reported the variation of PC1 was much greater than PC2 in their studies of maize hybrids. Grain yield was explained by 80.4 percent of total variation on both axes. A polygon was created by connecting genotypes that were the farthest from the biplot origin, enclosing all hybrids within it. Starting at the biplot origin, perpendicular lines were drawn to each side of the polygon. The biplot's rays divided the plot into six sections, with five environments appearing in one sector and the remaining one appearing in a different sector, as shown in **Figure 5**. The sectors had different high yielding vertex genotypes, such as MABK181261, MABK181255, MABK181253, MABK181254, MABK181259, and MABK181262, which are located at the polygon's corner and have the longest vectors. In comparison to other hybrids, these genotypes were among the most responsive to the environments in their respective directions. When a test environment is divided into mega Environments, it means that different environments have different high yielding genotypes for those sectors, indicating crossover G x E [Yan, W. *et al.*, 2007]. Based on this, the polygon views divided the test environment into three mega environments, with Bako, Pawe and Haromaya in best genotype MABK181262 group I, F/Selam MABK181259 group II and A/Negele in best genotype 6 (group III). Eliyas [Tena, E. *et al.*, 2019] also used GGE-biplot models and classified eight environments into two mega-environments for sugar cane genotypes evaluation for yield.

To avoid random GEI, genotype evaluation in mega environment should be based on both mean performance and stability [Yan, W. *et al*., 2003]. As a result, the genotypes MABK181261 and MABK181262 were identified as high yielders in the AMMI analysis. However, MABK181261 was identified as stable. only MABK181261 was chosen as the ideal genotype because it met both of the criteria. Demissew [Abakemal, D. *et al*., 2018] also selected three maize hybrids for high land mid altitude of Ethiopia using the same criteria. Genotype MABK181262 is the highest yielding vertex hybrid in all the test environments that share the sector with it. Whereas MABK181259 was the highest yielding found in separate sector at F/selam site.

The environment -vector view of the GGE biplot with the average -environment axis was shown in **Figure 3.** The AEA lines pass through the average environment and the biplot origin, and the average environment (represented by the small circle at the end of the arrow) contains the average coordinates of all test environments. Through discriminating and representativeness by GGE biplot analysis, testing environments were used to distinguish environments that select high yielder genotypes in sets of environments. The biplot's concentric circles help to visualize the length of the environment vectors, which is proportional to the standard deviation within each environment and is a measure of the environments' discriminating ability as well as representativeness [Yan, W. *et al*., 2006]. A test environment with a smaller angle with AEC is the most representative of the others. Thus, Pawe's vector is very short, ensuring that all genotypes perform similarly. Consequently, it no information or gave little information about genotype difference [Matana, Y. *et al*., 2020; Wolde, L. *et al*., 2018]. Bako has long vectors and small angles, and when combined with absicca, which is more discriminating genotypes and representative of test environments, the result is ideal for genotype selection. With AEC, however, A/NEGEL has a long vector and a large angle. Abssicca cannot be used to select the best performing genotypes, but it can provide information on genotypes that are unstable [Yan, W. *et al*., 2007]. The discriminating test environments of A/NEGEL and F/SELAM are not representative, but they are useful for selecting specific adapted genotypes and discarding unstable genotypes. The performance of genotypes can be easily

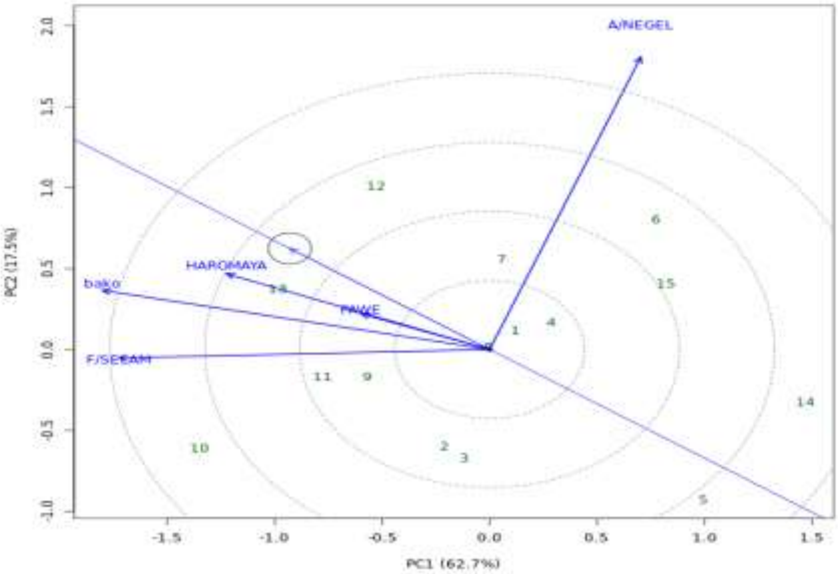

Figure 3: the GGE biplot's discrimination and representativeness view to show the test environments' discriminating ability and representativeness. After "Figure 3"

identified in a test environment with high representativeness and discriminating ability [Yan, W. *et al*., 2007]. Only one test environment (Bako) is both representative and discriminating, making it a good place to find genotypes that are generally adapted. The same result with many authors Y Matana [Matana, Y . *et al*., 2020]; Legesse [Wolde, L. *et al*., 2018], Demissew [Abakemal, D . *et al*., 2018], SALEEM [Saleem, R . *et al*., 2016] and Dagnechew [Lule, D. *et al*., 2014] who's used GGE biplot for identifying locations for both high representativeness and discriminating hybrids.

Stability of Genotype

Within a single mega environment, genotypes should be evaluated for both mean performance and stability across environments. The average environment coordination (AEC) view of the GGE biplot is shown in **Figure 5**. According to Yan [Yan, W. *et al*., 2006], the AEC abscissa is a single arrowed line that points to higher mean yield cross environments. Thus, the highest mean yield was MABK181262, followed by MABK181261, MABK181259, and so on. MABK181262 vs MABK181259 (an acute angle) indicates that the two genotypes responded similarly in all environments and that the difference between them was proportional. An obsute angle (e.g., MABK181261 vs BH660) indicates that the genotypes reacted inversely, with the MABK181261 outperforming the BH660 and vice versa. Differences in genotypes contributed more to G than GE in both cases. A right angle indicates that genotypes responded to the environment independently, implying that the differences were primarily responsible for G x E (eg MABK181261 vs MABK181262, MABK181253 vs MABK181251 and MABK181254 vs BH660). AEC ordinate is the double arrowed line. It indicates a higher level of variability (poor stability in both directions). As a result, G1 was extremely stable, whereas MABK181259 was extremely unstable.

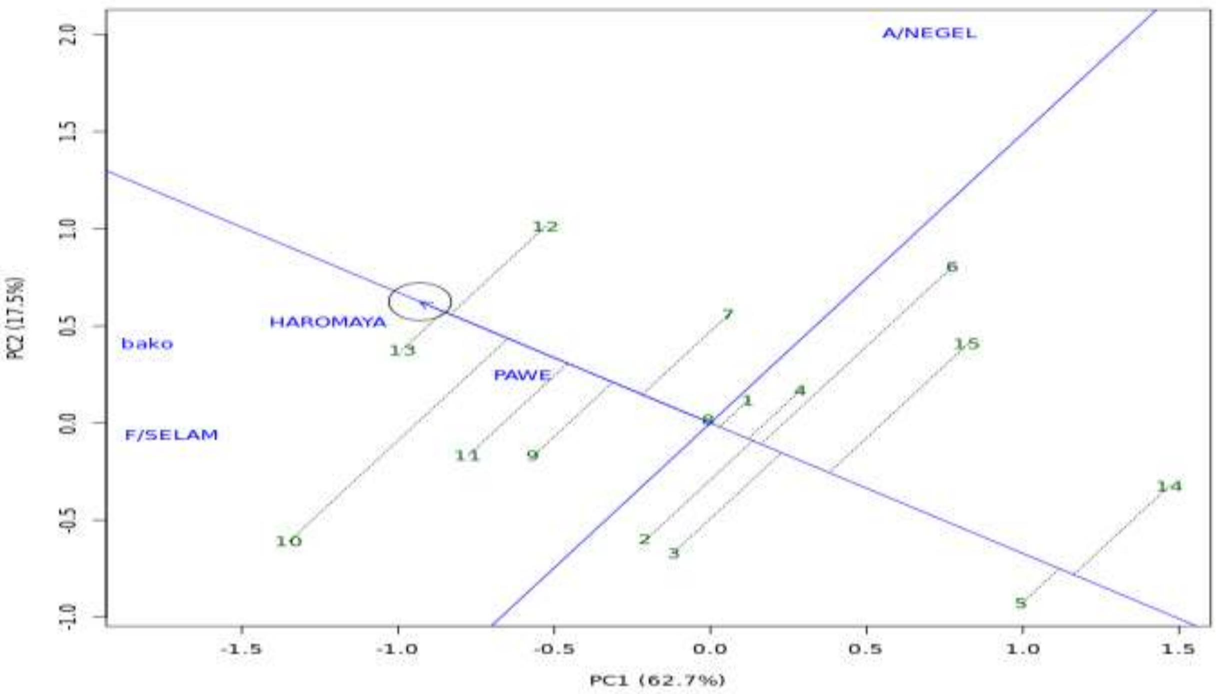

Figure 4: GGE biplot: Mean vs Stability. After “Figure 4”

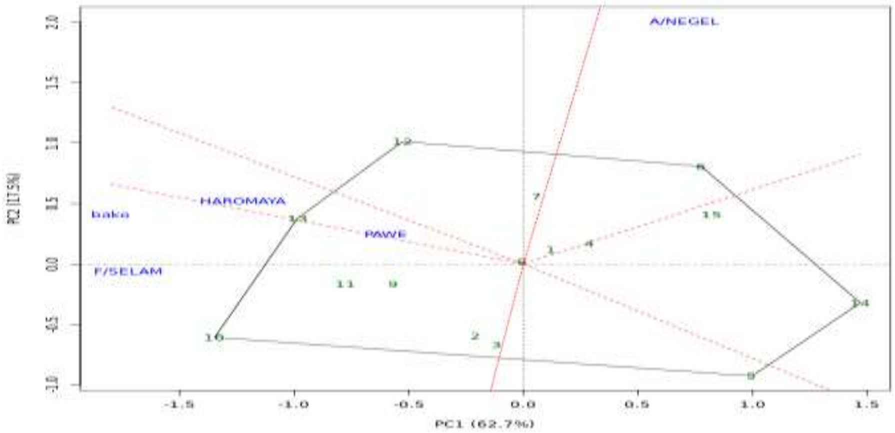

Figure 5: GGE biplot: which-won-where. After "Figure 5"

Conclusion

Except for MABK181254, all genotypes evaluated in multi-environment had higher average grain yields than the best commercial check (BH661). For the next variety trial evaluation, we have identified best candidate of maize hybrid (MABK181261), which is a stable and high yielder for Ethiopia's transitional maize high land agroecology. According to the GGE biplot model, only the Bako environment was chosen for both representative and discriminating genotype selection, indicating that it is an appropriate environment for selecting generally adapted genotypes. The test environment was divided into three mega environments by polygon views: Bako, Pawe, and Haromaya. The biplot's rays divided the plot into six sections, with five environments appearing in one sector and one appearing in a different sector. The sectors had different high yielding vertex viz, Genotypes MABK181261, MABK181255, MABK181253, MABK181254, MABK181255, MABK181254, MABK181259, and MABK181262 located at the polygon's corner are vertex genotypes with the longest vectors. In comparison to other hybrids, these genotypes were among the most responsive to the environments in their respective directions. Overall, this study discovered the possibility of fast releasing and overtake of new maize hybrids for transitional high land agroecology of Ethiopia to exploits available of maize inbred line germplasm to maximize production and productivity. MABK181261 to be a stable and high yielder as compared to commercial check, and it was suggested that it be released for further yield tests as a commercial hybrid substitute.

Acknowledgment

We thank researchers and technicians from collaborative research center from Pawe, Hawasa, Pawe, Haramaya and F/Selam for experimental management and data collection.

References

1. Mushayi, M., Shimelis, H., Derera, J., Shayanowako, A.I. and Mathew, I. Multi-environmental evaluation of maize hybrids developed from tropical and temperate lines. *Euphytica* 216.5 (2020): 84.
2. Nyombayire, A., Derera, J., Sibiya, J. and Ngaboyisonga, C. "Genotype x environment interaction and stability analysis for gran yield of diallel cross maize hybrids across tropical medium and highland ecologies." *Journal of Plant Sciences* 6.3 (2018): 101-106.
3. Li, Z., Coffey, L., Garfin, J., Miller, N.D., White, M.R., Spalding, E.P., De Leon, N., Kaeppler, S.M., Schnable, P.S., Springer, N.M. and Hirsch, C.N. "Genotype-by-environment interactions affecting heterosis in maize." *PloS one* 13.1 (2018): e0191321.
4. Matana, Y., Nur, M. and Romadhon, M.R. "Stability of fruit and bunch of mapanget tall and Indonesia coconut hybrid with several planting distance using AMMI model and GGE biplot analysis." *Earth and Environmental Science* 418 (2020): 012034.

5. Eze, C.E., Akinwale, R.O., Michel, S. and Bürstmayr, H. "Grain yield and stability of tropical maize hybrids developed from elite cultivars in contrasting environments under a rainforest agro-ecology." *Euphytica* 216.6 (2020): 89.
6. Badu-Apraku, B., Fakorede, M.A.B., Oyekunle, M., Yallou, G.C., Obeng-Antwi, K., Haruna, A., Usman, I.S. and Akinwale, R.O. "Gains in grain yield of early maize cultivars developed during three breeding eras under multiple environments." *Crop Science* 55.2 (2015b): 527-539.
7. Badu-Apraku, B., Annor, B., Oyekunle, M., Akinwale, R.O., Fakorede, M.A.B., Talabi, A.O., Akaogu, I.C., Melaku, G. and Fasanmade, Y. "Grouping of early maturing quality protein maize inbreds based on SNP markers and combining ability under multiple environments." *Field Crops Research* 183 (2015): 169-183.
8. Branković-Radojčić, D., Babić, V., Girek, Z., Živanović, T., Radojĉić, A., Filipović, M. and Srdić, J. "Evaluation of maize grain yield and yield stability by AMMI analysis." *Genetika* 50.3 (2018): 1067-1080.
9. Oldfield, E.E., Bradford, M.A. and Wood, S.A. "Global meta-analysis of the relationship between soil organic matter and crop yields." *Soil* 5.1 (2019): 15-32.
10. Zobel, R.W., Wright, M.J. and Gauch Jr, H.G. "Statistical analysis of a yield trial." *Agronomy journal* 80.3 (1988): 388-393.
11. Wolde, L., Keno, T., Tadesse, B., Bogale, G. and Abebe, B. "Mega-environment targeting of maize varieties using Ammi and GGE bi-plot analysis in Ethiopia." *Ethiopian Journal of Agricultural Sciences* 28.2 (2018): 65-84.
12. Abakemal, D., Shimelis, H. and Derera, J. “Genotype-by-environment interaction and yield stability of quality protein maize hybrids developed from tropical highland adapted inbred lines.” *Euphytica* (2018).
13. Nzuve, F., Githiri, S., Mukunya, D.M. and Gethi, J. “Analysis of genotype nine environment interaction for grain yield in maize hybrids.” *J Agric Sci* 5(2013):75–85.
14. Mengesha, W., Menkir, A., Meseka, S., Bossey, B., Afolabi, A., Burgueno, J. and Crossa, J. "Factor analysis to investigate genotype and genotype× environment interaction effects on pro-vitamin A content and yield in maize synthetics." *Euphytica* 215.11 (2019):180.
15. Kebede, D., Dagnachew, L., Girma, M., Kassa, M., Chemeda, B., Girma, C. and Gudeta, B. (2019). “Genotype by Environment Interaction and Grain Yield Stability Analysis for FingerMillet (Eleusine coracana (L.) Gaertn) Genotypes from Western Oromia Ethiop.” *J. Crop Sci.* 6.1 (2018) :119-133.
16. Tena, E., Goshu, F., Mohamad, H., Tesfa, M., Tesfaye, D. and Seife, A Tena, E., Goshu, F., Mohamad, H., Tesfa, M., Tesfaye, D. and Seife, A. "Genotype× environment interaction by AMMI and GGE-biplot analysis for sugar yield in three crop cycles of sugarcane (Saccharum officinirum L.) clones in Ethiopia." *Cogent Food & Agriculture* 5.1 (2019): 1651925.
17. Yan, W. and Tinker, N.A. "Biplot analysis of multi-environment trial data: Principles and applications." *Canadian journal of plant science* 86.3 (2006): 623-645.
18. Yan, W., Hunt, L.A., Sheng, Q. and Szlavnics, Z. "Cultivar evaluation and mega-environment investigation based on the GGE biplot." *Crop science* 40.3 (2000): 597-605.
19. Mafouasson, H.N.A., Gracen, V., Yeboah, M.A., Ntsomboh-Ntsefong, G., Tandzi, L.N. and Mutengwa, C.S. "Genotype-by-environment interaction and yield stability of maize single cross hybrids developed from tropical inbred lines." *Agronomy* 8.5 (2018): 62.
20. Yan, W., Kang, M.S., Ma, B., Woods, S. and Cornelius, P.L. "GGE biplot vs. AMMI analysis of genotype-by-environment data." *Crop science* 47.2 (2007): 643-653.
21. Yan, W. and Kang, M.S. “GGE Bi-plot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists.” *CRC Press. Boca Raton, FL* (2003)288.
22. Saleem, R., Ashraf, M., Khalil, I.A., Anees, M.A., Javed, H.I. and Saleem, A. "GGE Biplot Analysis: Windows Based Graphical Analysis of Yield Stability and Adaptability of Millet Cultivars Across Pakistan."

Academia Journal of Biotechnology 4 (2016): 186-193.

23. Lule, D., Tesfaye, K. and Mengistu, G. "Genotype by environment interaction and grain yield stability analysis for advanced triticale (x. Triticosecale Wittmack) genotypes in Western Oromia, Ethiopia." *SINET: Ethiopian Journal of Science* 37.1 (2014): 63-68.
24. Rezende, W.S., Beyene, Y., Mugo, S., Ndou, E., Gowda, M., Sserumaga, J.P., Asea, G., Ngolinda, I., Jumbo, M., Oikeh, S.O., Olsen, M., Borém, A., Cruz, C.D. and Prasanna, B.M. "Performance and yield stability of maize hybrids in stress-prone 07 - environments in eastern Africa." *The crop journal* (2020): 107-118.
25. Bocianowski, J., Niemann, J. and Nowosad, K. "Genotype-by-environment interaction for seed quality traits in interspecific cross-derived Brassica lines using additive main effects and multiplicative interaction model." *Euphytica* 215.1 (2019): 7.
26. Eze, C.E., Akinwale, R.O. and Michel, S. "Grain yield and stability of tropical maize hybrids developed from elite cultivars in contrasting environments under a rainforest agro-ecology." *Euphytica* 216(2020): 89.
27. Ndlala, L.Z. "Evaluation of early maturing maize (*zea mays* l.) hybrids for multiple-stress tolerance." *MSc. Thesis* (2018). https://researchspace.ukzn.ac.za/handle/10413/18159
28. Dao, A., Alvar-BeltrÃ¡n, J., Guira, A., NÃ©biÃ©, L., Gnanda, A. & Sanou, J. "Biplot analysis of test environments of quinoa (Chenopodium quinoa Willd.) in Burkina Faso." *African Journal of Plant Science* 14.9 (2020): 358-371.

Source of support: Nil;

Conflict of interest: The authors declare no conflict of interests.

Cite this article as:

Getachew, G., Beyene, A., Desalegn, C., Sara, O., Temesgen, C., Zelalem, T., Bedlu, G. and Abu, E. N. "Genotype by Environment Interaction Effect on Yield, and Stability of hybrid Maize (*Zea mays* L.) Genotype in Transitional Highland Agroecology of Ethiopia." *Annals of Plant Sciences*.11.11 (2022): pp. 5565-5577.

DOI: http://dx.doi.org/10.21746/aps.2022.11.11.7