

Genotype-by-Environment Interaction of Maize Testcross Hybrids Evaluated for Grain Yield Using GGE Biplots

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Abstract

Genotype-by-environment interaction (GEI) occurs when Performance of genotypes differs across environments because of the effect of the environment on trait expression. Information on GEI would guide breeding strategy for either specific or broad adaptation. The purposes of this study were to determine the GEI and grain yield stability of maize testcross hybrids across five environments in Ethiopia based on GGE biplot analysis. 86 maize testcross hybrids and two standard checks were evaluated in 8×11 alpha lattice design with two replications across 5 test environments in 2010. Combined analysis of variance showed that the effects of genotypes (G), environments (E) and GEI were significant for grain yield. Genotype, environment and GEI interaction explained 7.44%, 80.64% and 11.92% of the variation in grain yield, respectively. The GGE model showed that the first and second principal component axis accounted for 64.49% and 19.61% of variability, respectively. The pattern of GEI interaction was a crossover type as revealed by differential yield ranking of the genotypes across environments. Hybrid G23 was the best performer in environments E1, E2 and E3. Hybrid G33 was identified as best-performing with best specific adaptation in environment E4, while hybrid G66 and G73 had best adaptation in E5. Test environment E1 was identified as the ideal test environment for selecting superior hybrids. Hybrid G23 and G24 were high yielding and stable across environments and should be further evaluated in multi-environment trials to facilitate their registration and commercialization.

Keywords

Maize, testcross hybrids, genotype-by-environment interaction, stability, GGE biplot

1. Introduction

Maize (*Zea mays* L.) is the most widely cultivated staple food crop that supports household and national food security in sub-Saharan Africa (SSA) [1]. Despite the enormous potential and crucial role that maize plays in SSA, its production and average yield per hectare are low when comparing to the global average production [2]. The major constraints affecting maize production and productivity in SSA are inadequacy of broadly adapted varieties, drought, low soil nitrogen, and vulnerability to diseases and pests [3]. Among the cereal crops, maize ranks second in area coverage and first in total annual production and productivity in Ethiopia [4]. Maize is grown by smallholder farmers under diverse agro climatic conditions in Ethiopia. Production environments of maize in Ethiopia are highly variable for rainfall, temperature, soil characteristics and biotic and abiotic stress factors; all of which interact to influence performance of the maize crop [5]. Genotype by environment interaction (GEI) is expected for traits of economic importance, such as grain yield and disease resistance [6-7].

Plant breeders conduct multi-environment trials (MET) to evaluate the performance and adaptation of genotypes across a range of environments at advanced stages of variety development and to select testing sites that best represent the target environment [8-9]. Selection of genotypes based on performance in single environment is not effective because of complex quantitative trait such as grain yield is highly influenced by environment interaction effects [10]. This implies the need for the extensive evaluation of genotypes in many locations over years before their release. The GEI phenomenon is said to occur when genotype performance differs over environments [11]. This is because genotypes exhibit different levels of phenotypic expression under different environmental conditions resulting in crossover performances [12]. The presence of a significant GEI challenges the identification of genotypes that are superior across target production environments and suitable test locations that can be used to identify superior and stable genotypes [13-14]. GEI causes low correlation between phenotypic and genotypic values, thereby reducing genetic gain from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance [15]. The occurrence of GEI makes it useful to measure both performance and stability for genotypes being evaluated in breeding programs [16]. Information on GEI would guide breeding strategy for either specific or broad adaptation. Identifying widely adapted and stable genotypes across a wide range of environments is the most ideal way to minimize GEI although the presence of GEI can be exploited by selecting superior genotypes for specific target environments would be useful to farmers [11]. Analysis of variance (ANOVA) only tests the significance of the GEI but it does not provide information into particular pattern of genotype or environment that gives rise to GEI [17].

Various biometrical methods have been proposed to study stability and GEI of traits for multi-environment trial data, for example, Finlay and Wilkinson's regression coefficient [18], Eberhart and Russell's sum of squares deviations from regression [19], Perkins and Jink's regression coefficient [20], Shukla's stability variance [21] and Kang's yield stability (YSi) [22]. All these methods are univariate stability models based on regression and variance estimate [23]. Multivariate stability statistics include the additive main effects and multiplicative interaction (AMMI) model [24], and genotype main effects plus GEI (GGE) model [8, 25] to analyze and visualize the nature and magnitude of G x E for multi-environment trial data. GGE biplot has been suggested to be a better model for identifying the most superior cultivar in a given environment and the most suitable environment for each cultivar, the comparison of any pair of cultivars in individual environments, the best cultivars for each environment and mega-environment differentiation and the average yield and stability of the genotypes [25-26]. Furthermore, the discriminating power—representativeness view of the GGE biplot was effective in evaluating test environments, which was not possible with AMMI analysis [9]. The GGE biplot analysis is based on principal component analysis and graphically displays the two-way (genotype x environment) data matrix and allows visualization megaenvironment analysis ('which - won - where' pattern), genotype evaluation (mean vs. stability), and test environment evaluation (discriminating power vs. representativeness) [9, 17]. The objectives of this study were to determine the GEI and grain yield stability of maize testcross hybrids across five environments in Ethiopia based on GGE biplot.

2. Methods

2.1 Experimental materials

The genotypes used for the study comprised 86 testcross maize hybrids developed by crossing 43 elite inbred lines to two testers in line x tester mating design and two standard checks (BH543, three way cross hybrid and Melkassa-2, open pollinated variety) (Table 1). The inbred lines were introduced from CIMMYT-Zimbabwe and were bred for resistance to various biotic and abiotic stresses of Africa. The most important stresses against which the inbred lines were selected include diseases (maize streak virus, grey leaf spot, leaf rust and turicum leaf blight, low nitrogen, high density and drought). The two testers used are single crosses of commercial CIMMYT inbred lines of known heterotic groups; viz. CML312/CML442 (tester A) and CML202/CML395 (tester B), which are commonly used by CIMMYT and many other national maize research programs in Africa. Genotypes pedigree and codes are presented in Table 1.

2.2 Environments, Experimental Design and Data collected

The 86 experimental hybrids and two standard checks were evaluated across 5 environments (Melkassa, Ziway, Dhera, Mieso and Pawe) during 2010 in Ethiopia (Table 2). The experimental sites were representative of low-moisture stress areas of Ethiopia, except Pawe, which represented the mid-altitude sub-humid maize growing agro-ecology. The geographical coordinates, climatic conditions of the 5 environments are described in (Table 2). The experimental design was 8 x 11 alpha-lattice design with two replications at each location. Each plot consisted of one row of 5 m long with 75 cm and 25 cm spacing between rows and plants, respectively. Two seeds were planted per hill to ensure uniform and enough stand and then thinned to one plant per hill at 4 weeks after emergence to give a plant population of 53,333 plants per hectare. 100 kg/ha DAP and 50 kg/ha urea was applied at planting while 50 kg/ha urea was side dressed at knee height. The field experiment was managed as per the research recommendation of agronomic practices of the respective test locations.

Grain yield (g) of each plot was measured and grain yield ($t\ ha^{-1}$) was estimated from field weight of ears per plot, assuming a shelling percentage of 80, adjusted to 12.5% moisture content at four environments (Melkassa, Ziway, Mieso and Pawe). At Dhera, grain yield ($t\ ha^{-1}$) was computed from the weight of the shelled kernels per plot, adjusted to a moisture content of 12.5%.

2.3 Statistical Analysis

2.3.1 Analysis of Variance

Analysis of variance (ANOVA) was conducted on plot means for grain yield for individual environment using the PROC MIXED procedure of SAS [27]. Entry means adjusted for block effects generated from individual location analyses according to the lattice design [28] were used to perform combined analyses across environments using PROC GLM in SAS [28] to test the significance of GEI. In the ANOVA, genotypes were considered as fixed effects, whereas replications and blocks within replications were considered as random effects. In the combined analysis, the significance of genotype mean squares was tested using GEI mean square as the error term, whereas the GEI was tested using the pooled error.

2.3.2 GGE Biplot Analysis

GGE biplot was computed using the “GGEBiplotGUI” package of R statistical software in RStudio [29-30] to analyze the multi-environment trial data, and evaluate the adaptability and stability of the cultivars and the effects of genotype, environment, and GEI. A GGE biplot is a biplot that displays the genotypic main effect and GEI of a multi-environment trial based on principal component analysis (PC1 and PC2) derived from subjecting a two way data (Genotype x environment data) to singular value decomposition [8]. The data were not transformed (Transform = 0), nor standardized (Scale = 0) and were environment-centered (Centering = 2) [8, 3]. It was difficult to visually assess the presence of GEI and rank genotype based on stability and mean of the 88 hybrids on the GGE biplot. Therefore, for a better visualization and interpretation of GGE biplot, 40 hybrids (25 top performing and 15 low yielding hybrids across environments) and two checks were used for GGE biplot analysis.

The GGE biplot model equation is:

$$Y_{ij} - Y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is the average yield of genotype i in environment j , Y_j is the average yield across all genotypes in environment j , λ_1 and λ_2 are the singular values for PC1 and PC2, ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, for genotype i , η_{j1} and η_{j2} are the PC1 and PC2 scores, for environment j , ε_{ij} is the residual of the model associated with the genotype i in environment j .

Table 1. Genotypes pedigree and codes of 86 testcross maize hybrids and two standard checks evaluated across 5 environments in 2010

Genotype code	Pedigree
G1	[[Ent320:92SEW2-77/[DMRESR-W]EarlySel-#I-2-4-B/CML386]-B-11-3-B-2-#-B*4]/CML202/CML395
G2	[INTA-F2-192-2-1-1-1-B*7-6-B]/CML202/CML395
G3	[ZEWBc1F2-216-2-2-B-1-B]/CML202/CML395
G4	[[SC/CML204//FR812]-X-30-2-3-2-1-BBB]/CML202/CML395
G5	[ZEWAc1F2-219-4-3-B-1-B*5]/CML202/CML395
G6	[[CML141/[CML141/CML395]F2-1sx]-4-2-1-B*6]/CML202/CML395
G7	[[[Ent52:92SEW1-2/[DMRESR-W]EarlySel-#L-2-1-B/CML386]-B-22-1-B-4-#/[TIWD-EarlySelSynS1#-2-XX-2-B/[SW1SR/COMPE1-W]-126-2-1-B]-B-11-4-B-2-#]-B-2-B-1-B*5]/CML202/CML395
G8	[Syn01E2-64-2-B-2-B]/CML202/CML395
G9	[[INTA-2-1-3/INTA-60-1-2]-X-11-6-3-BBB]/CML202/CML395
G10	[[[P501c2/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-1-1-X-X-BB]-4-1-1-4-2-1-B/[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-3-#]-B-7-B-1-B*6]/CML202/CML395
G11	[PL15QPMc7-SR(BC0FS#)-balbreedbulk-31-1-4-4-2-B-3-B]/CML202/CML395
G12	[DTPWC9-F104-5-6-1-1-B*4]/CML202/CML395
G13	[(CLQRCWQ50/CLQRCWQ26)-B-47-BB]/CML202/CML395

G14	[[NC348-BB/[Ent67:92SEW1-17/[DMRESR-W]EarlySel-#I-3-3-B/CML391]-B-31-B-3-#-2-B/[NAW5867/P30-SR/NAW5867]-84-1/[NAW/P30/NAW]-3-1]-6-2-2-1-3-B-3-B]-2-1-1-BBB]/CML202/CML395
G15	[[INBRED-A/INBRED-B]-BBB-1-BBB]/CML202/CML395
G16	[[CML395/CML444]-B-4-1-3-1-B/CML444/[TUXPSEQ]C1F2/P49-SR]F2-45-7-1-2-BBB]-2-1-2-2-B*5]/CML202/CML395
G17	[[CML198/90323(B)-1-X-5-SN]-B-31-2-1-B*6]/CML202/CML395
G18	[[CML199/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-6-3-Sn]-B-23-2-2-B*8]/CML202/CML395
G19	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-1-B*7]/CML202/CML395
G20	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-B*6]/CML202/CML395
G21	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-1-B*5]/CML202/CML395
G22	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2-B*5]/CML202/CML395
G23	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-1-B*4]/CML202/CML395
G24	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-1-B*4]/CML202/CML395
G25	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-3-B*5]/CML202/CML395
G26	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1-B*4]/CML202/CML395
G27	[[CML444/CML395//SC/ZM605#b-19-2-X]-1-2-X-1-1-B*6]-2-2-2-1-B*5]/CML202/CML395
G28	[[LZ955355/LZ956441]-B-2-3-3-B-3-B*7]/CML202/CML395
G29	[[SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4]/CML202/CML395
G30	[[SYN-USB2/SYN-ELIB2]-81-1-1-1-B*6]/CML202/CML395
G31	[[TS6C1F238-1-3-3-1-2-#-BB/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-10-7(I)-X-X-X-2-BB]-1-1-2-1-1-B*6]/CML202/CML395
G32	[CML312-B]/CML202/CML395
G33	[CML442-B]/CML202/CML395
G34	[CML443-B]/CML202/CML395
G35	[CML489-B]/CML202/CML395
G36	[MAS[206/312]-23-2-1-1-B*5]/CML202/CML395
G37	[MAS[MSR/312]-117-2-2-1-B*4]/CML202/CML395
G38	[P501SRc0-F2-4-2-1-1-BBB]/CML202/CML395
G39	[P501SRc0-F2-47-3-1-1-BBB]/CML202/CML395
G40	[Z97SYNGLS(B)-F2-188-2-1-2-B*6]/CML202/CML395
G41	[ZM523A-16-2-1-1-B*4]/CML202/CML395
G42	[ZM523B-29-2-1-1-B*4]/CML202/CML395
G43	[ZM621A-10-1-1-1-2-B*6]/CML202/CML395
G44	[[Ent320:92SEW2-77/[DMRESR-W]EarlySel-#I-2-4-B/CML386]-B-11-3-B-2-#-B*4]/CML312/CML442
G45	[INTA-F2-192-2-1-1-1-B*7-6-B]/CML312/CML442
G46	[ZEWBc1F2-216-2-2-B-1-B]/CML312/CML442
G47	[[SC/CML204//FR812]-X-30-2-3-2-1-BBB]/CML312/CML442
G48	[ZEWAc1F2-219-4-3-B-1-B*5]/CML312/CML442
G49	[[CML141/[CML141/CML395]F2-1sx]-4-2-1-B*6]/CML312/CML442
G50	[[[Ent52:92SEW1-2/[DMRESR-W]EarlySel-#L-2-1-B/CML386]-B-22-1-B-4-#/[TIWD-EarlySelSynS1#-2-XX-2-B/[SW1SR/COMPE1-W]-126-2-1-B]-B-11-4-B-2-#]-B-2-B-1-B*5]/CML312/CML442
G51	[Syn01E2-64-2-B-2-B]/CML312/CML442

G52	[[INTA-2-1-3/INTA-60-1-2]-X-11-6-3-BBB]/CML312/CML442
G53	[[[P501c2/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-1-1-X-X-BB]-4-1-1-4-2-1-B/ [[[K64R/G16SR]-39-1/[K64R/ G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-3-#]-B-7-B-1-B*6]/CML312/CML442
G54	[PL15QPMc7-SR(BCOFS#)-balbreedbulk-31-1-4-4-2-B-3-B]/CML312/CML442
G55	[DTPWC9-F104-5-6-1-1-B*4]/CML312/CML442
G56	[(CLQRCWQ50/CLQRCWQ26)-B-47-BB]/CML312/CML442
G57	[[NC348-BB/[Ent67:92SEW1-17/[DMRESR-W]EarlySel-#I-3-3-B/CML391]-B-31-B-3-#-2-B// [[NAW5867/P30-SR// NAW5867]-84-1/[NAW/P30/NAW]-3-1]-6-2-2-1-3-B-3-B]-2-1-1-BBB]/CML312/CML442
G58	[[INBRED-A/INBRED-B]-BBB-1-BBB]/CML312/CML442
G59	[[CML395/CML444)-B-4-1-3-1-B/CML444/[TUXPSEQ]C1F2/P49-SR]F2-45-7-1-2-BBB]-2-1-2-2-B*5] /CML312/CML442
G60	[[CML198/90323(B)-1-X-5-SN]-B-31-2-1-B*6]/CML312/CML442
G61	[[CML199/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-6-3-Sn]-B-23-2-2-B*8]/CML312/CML442
G62	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-1-B*7] /CML312/CML442
G63	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-B*6]/ CML312/CML442
G64	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2-B*5]/CML312/CML442
G65	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2-B*5]/CML312/CML442
G66	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-1-B*4]/CML312/CML442
G67	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-1-B*4]/CML312/CML442
G68	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-3-B*5]/CML312/CML442
G69	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1-B*4]/CML312/CML442
G70	[[CML444/CML395//SC/ZM605#b-19-2-X]-1-2-X-1-1-B*6]-2-2-2-1-B*5]/CML312/CML442
G71	[[LZ955355/LZ956441]-B-2-3-3-B-3-B*7]/CML312/CML442
G72	[[SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4]/CML312/CML442
G73	[[SYN-USB2/SYN-ELIB2]-81-1-1-1-B*6]/CML312/CML442
G74	[[TS6C1F238-1-3-3-1-2-#-BB/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-10-7(I)-X-X-X-2-BB-1]- 1-1-2-1-1-B*6]/CML312/CML442
G75	[CML312-B]/CML312/CML442
G76	[CML442-B]/CML312/CML442
G77	[CML443-B]/CML312/CML442
G78	[CML489-B]/CML312/CML442
G79	[MAS[206/312]-23-2-1-1-B*5]/CML312/CML442
G80	[MAS[MSR/312]-117-2-2-1-B*4]/CML312/CML442
G81	[P501SRc0-F2-4-2-1-1-BBB]/CML312/CML442
G82	[P501SRc0-F2-47-3-1-1-BBB]/CML312/CML442
G83	[Z97SYNGLS(B)-F2-188-2-1-2-B*6]/CML312/CML442
G84	[ZM523A-16-2-1-1-B*4]/CML312/CML442
G85	[ZM523B-29-2-1-1-B*4]/CML312/CML442
G86	[ZM621A-10-1-1-1-2-B*6]/CML312/CML442
G87	BH543
G88	Melkassa-2

Table 2. Description of the five environments used to evaluate the maize testcross hybrids

Location	Location code	Annual rainfall (mm)	Altitude (m.a.s.l)	Latitude	Longitude	Soil type
Melkasa	E1	710	1550	8 ⁰ 24' N	39 ⁰ 21' E	sandy-clay-loam
Ziway	E2	640	1637	7 ⁰ 56' N	38 ⁰ 35' E	silt
Dhera	E3	520	1680	8 ⁰ 20' N	39 ⁰ 23' E	sandy-clay
Mieso	E4	560	1470	9 ⁰ 12' N	40 ⁰ 52' E	clay-loam
Pawe	E5	1579	1120	11 ⁰ 09' N	36 ⁰ 03' E	clay

3. Results and discussion

3.1 Analysis of variance

The combined analysis of variance across environments for grain yield of the 88 maize genotypes tested in five environments showed highly significant differences ($p < 0.001$) among genotypes (G) and environments (E), implying a substantial variation among genotypes and locations (Table 3). The significant variation observed among the genotypes for grain yield, indicated that adequate genetic variability existed among the hybrids to allow significant progress from selection. Similarly, analysis of variance revealed significant G x E interaction (GEI), which indicated that the performance of these genotypes were not consistent across locations and the need to identify genotypes with high yield and stability across the test environments. Significant G x E interactions for grain yield in maize was also reported in several studies [7, 32-33]. A large grain yield variation revealed by E which explained 80.64 % of the total G + E + GEI variation, while G and GEI sources of variation accounted for 7.44 % and 11.92 % of the total variation, respectively. The high proportion of the contribution of the E effects than those from G and G x E interaction indicated that the test environments were variable. These results are in agreement with previous findings of Oyekunle and Badu-apraku [34], Badu-apraku et al. [35], Ndhlela et al. [36], Badu-Apraku et al. [3] and Badu-Apraku et al. [37], who reported that the largest proportion of total variation is attributed to environments and relatively smaller sources of variation to G and GEI. The large effects of environments in this study underscore the importance of testing the best hybrids in diverse agro-ecologies to identify the most stable and high-yielding maize hybrids. The E portion in multi-environment trial (MET) has been shown to be the largest contributor among all the sources of variation, but only G and GEI are relevant and considered simultaneously in genotype evaluation [25, 38]. However, a large G x E interaction effect compared to genotype effect suggests the possible existence of diverse mega-environments with different winner genotypes [38]. Mega-environment was defined as group of locations that consistently share the same best cultivars [31]. The variance of GEI main effects was nearly twice that of genotypic main effects, mainly caused by hybrids' rank changes at different locations, suggesting a crossover type of adaptation [31]. A higher G x E variance compared with G variance for maize grain yield has been commonly reported [39, 40].

25 best performing, 15 low-yielding testcrosses hybrids and two standard checks were selected from across site analysis. The yield performance data of these hybrids across five environments is presented in Table 4. Mean grain yield across the 5 environments for the 40 testcrosses hybrids ranged from 3.6 to 6.9 t/ha. The best six high-yielding hybrids across environments were G23 (6.9 t/ha), G24 and G73 (6.7 t/ha), G50, G56 and G72 (6.6 t/ha). Twenty five test-crosses hybrids had higher grain yield than the best standard check, G87.

3.2 Genotype and genotype x environment interaction (GGE) biplot analysis of performance and stability

The presence of significant G and GEI justified the use of GGE biplot analysis to decompose the GEI and to determine stable and high-yielding hybrids. The GGE biplot analysis was used to visualize the best genotypes at each environment, assess G x E interaction and evaluate the stability of the genotypes. The results of GGE biplot analyses for grain yields of 25 top-yielding testcrosses hybrids, 15 lowest yielding and two standard checks tested across five environments are presented in Figures 1, 2, and 3. The first two principal components (PC1 and PC2) obtained by singular value decomposition of environment-centered data of grain yield explained 84.1 % of the total effect it had on the grain yield variation with PC1 and PC2 accounted for 64.49 % and 19.61 % of variability, respectively (Figure 1).

Table 3. Combined analysis of variance for grain yield (t ha⁻¹) of 88 maize genotypes grown at five environments

Source	DF	SS	MS	F	Pr > F	% contribution to SS
Genotype (G)	87	214.94	2.46	2.18	<.0001	7.44
Environment (E)	4	2320.65	580.16	79.22	<.0001	80.64
G x E (GEI)	348	343.01	0.99	2.2	<.0001	11.92
Pooled Error	331	195.29	0.59			
G+E+GEI	439	2878.6				

Table 4. Mean grain yield (t ha⁻¹) of selected hybrids and two checks across 5 environments in Ethiopia

hybrids/ checks	Environments					Mean Across
	E1	E2	E3	E4	E5	
G3	6.5	4.7	3.8	3.6	5.4	4.8
G4	7.6	3.0	2.3	3.4	7.7	4.8
G5	6.5	3.9	3.1	3.3	5.6	4.4
G7	9.1	1.9	2.2	3.7	6.3	4.6
G9	7.7	3.0	3.1	3.9	6.1	4.8
G11	8.9	4.7	3.2	4.1	8.5	5.9
G14	5.2	3.4	1.7	3.3	4.4	3.6
G17	7.4	3.4	2.9	3.0	6.4	4.6
G18	7.0	4.0	2.6	3.3	6.1	4.6
G21	10.0	4.8	2.7	4.4	8.1	6.0
G22	8.8	4.7	3.2	4.2	8.9	5.9
G23	12.4	5.4	2.7	4.2	9.8	6.9
G24	12.2	6.2	2.5	3.6	9.1	6.7
G25	10.3	4.5	2.6	3.9	10.4	6.3
G27	9.5	6.1	3.0	3.9	8.4	6.2
G30	9.2	3.6	2.7	3.4	11.3	6.0
G33	11.6	5.9	2.6	3.9	7.1	6.2
G34	7.2	4.6	1.3	2.3	6.2	4.3
G35	6.9	3.2	1.6	3.2	6.6	4.3
G37	10.3	5.0	4.1	4.1	7.0	6.1
G38	6.2	3.8	1.9	3.0	8.8	4.7
G43	9.1	5.4	3.0	3.9	8.9	6.1
G45	10.1	5.0	3.8	5.0	6.3	6.0
G50	11.4	5.6	3.4	4.7	7.9	6.6
G56	8.9	5.3	3.2	5.9	9.7	6.6
G59	7.1	3.0	2.3	3.0	7.0	4.5
G60	10.1	5.0	4.0	5.6	7.8	6.5
G64	11.2	5.3	1.5	5.1	7.0	6.0
G66	9.1	5.5	3.0	3.2	11.4	6.4
G67	8.9	5.7	3.3	3.5	9.4	6.2
G69	8.7	5.9	3.7	3.8	8.9	6.2
G70	9.4	4.8	3.4	3.4	10.3	6.3
G72	11.4	5.0	4.0	4.0	8.7	6.6
G73	10.9	5.8	2.7	3.3	11.1	6.7
G75	7.4	2.4	1.4	2.7	5.3	3.8
G76	7.3	3.2	1.7	3.7	4.6	4.1
G77	9.7	4.4	3.1	4.6	7.9	5.9
G79	6.2	4.1	1.7	4.0	6.6	4.5
G84	11.0	4.3	3.2	5.8	7.8	6.4
G85	8.2	6.6	1.4	4.0	10.2	6.1
G87	7.5	4.2	1.8	3.9	8.8	5.2
G88	6.9	2.8	2.4	3.8	4.7	4.1
Means	8.8	4.5	2.7	3.9	7.8	5.5

3.3 Polygon view of GGE biplot (which-won-where)

Genotype and Genotype x environment interaction evaluation based on GGE biplot analysis used to determine ‘which-won-where’ pattern to identify genotypes that had wide and/or specific adaptation across/to locations [41]. Figure 1 represents the polygon view showing the “which-won-where” pattern of GEI. The polygon is formed by joining

the vertex genotypes that are located farthest away from the biplot origin while the rest are inside the polygon with perpendicular lines radiating from the origin of the biplot divide the biplot into different sectors. The best performing genotype (winning genotype) for an environment or set of environments in a sector is the vertex genotype [42]. The polygon view of the GGE biplot provides a good visualization of crossover $G \times E$ interactions [25]. When environments fall into different sectors of the polygon, there are specifically adapted high yielding cultivars for each sector [9]. This shows crossover GEI and thus environments could be divided into mega environments [26]. From polygon view of GGE biplot, the polygon divided into eight sectors, with the five environments appearing in three sectors and the 42 hybrids falling in all the seven sectors (Figure 1). Three environments, E1, E2 and E3, fell in the first sector with three hybrids (G23, G24 and G27) where G23 was the vertex genotype implying that this genotype was the winning genotype (highest performing) for these environments. Out of 9 hybrids in sector 2, hybrid G33 was identified as best-performing with best specific adaptation in environment E4. Sector 3 comprised one environment (E5) with 12 genotypes where G66 and G73 were the highest yielder. The vertex hybrids G45, G76, G14 and G36 had no environments in their sectors indicating that these genotypes would be considered poorly adapted in all test environments.

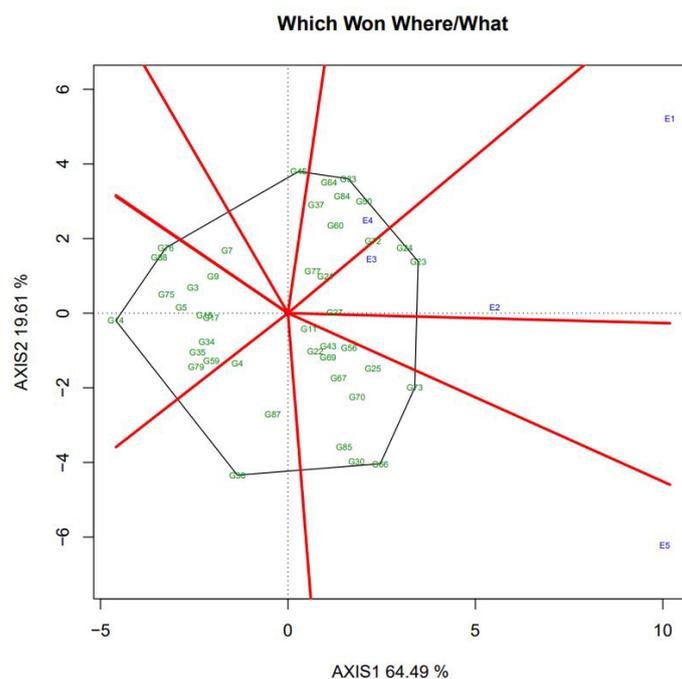


Figure 1. The polygon (which-won-where) view of genotype main effects plus genotypic x environment interaction effect (GGE) biplot of selected maize hybrids tested in five environments for grain yield.

3.4 Mean vs. stability and genotype comparison with ideal genotype views of GGE biplot

The average environment coordinate (AEC) view based on genotype-focused singular value partitioning (SVP = 1) and mean value can be referred as the “mean vs. stability” view of GGE biplot [9]. The mean vs. stability GGE biplot of the hybrids across the test environments is presented in Figure 2. The single-arrowed line shown on the AEC abscissa points in the direction of higher mean yield of genotypes and ranks the genotypes with respect to trait performance [8, 26]. Thus, genotype G23 had the highest mean grain yield followed by G24 and G73 while genotype G14 had the lowest. The AEC ordinate divided the abscissa into two parts, thereby separating the hybrids with below-average mean grain yield from those with above-average mean grain yield [43]. The stability of each genotype are determined by its projection onto the AEC vertical axis with the most stable genotype was located on the AEC abscissa (horizontal axis) and had minimum projection on the AEC vertical axis. Hence, genotype G27, G17, G18 and G14 were the most stable hybrids. While genotypes G66, G38, G30, G85, G45, G33 and G64 had the longest projection and hence were the least stable hybrids for grain yield. However, the most stable genotypes across locations were not the highest yielding across locations. Yan and Tinker [26] reported that stability is important only when coupled with high trait mean. Hence, an ideal genotype would be one that combines both high mean yield performance and high stability across environments. The “comparison with ideal genotype” view of GGE biplot has concentric circles with the ideal genotype in the inner circle (arrow pointing to the center of innermost circle) (Figure 3). It permits to visualize the distance between each genotype and the ideal genotype; a genotype is more desirable than others if it is located closer to ideal genotype. The biplot in Figure 3 showing the ranking of cultivars based on mean yield and stability indicated that there was no single

hybrid near the center of the concentric circle that could be considered as an ideal hybrid with high grain yield and stable performance across the test environments. However, G23 and G24 located near the vertical axis in the second concentric circle can be considered as relatively stable, with high grain yields across the 5 environments could therefore be selected for broad adaptation. Hybrids G14, G38, G88, G75 and G76 were low yielding and were located far away from the ideal genotype.

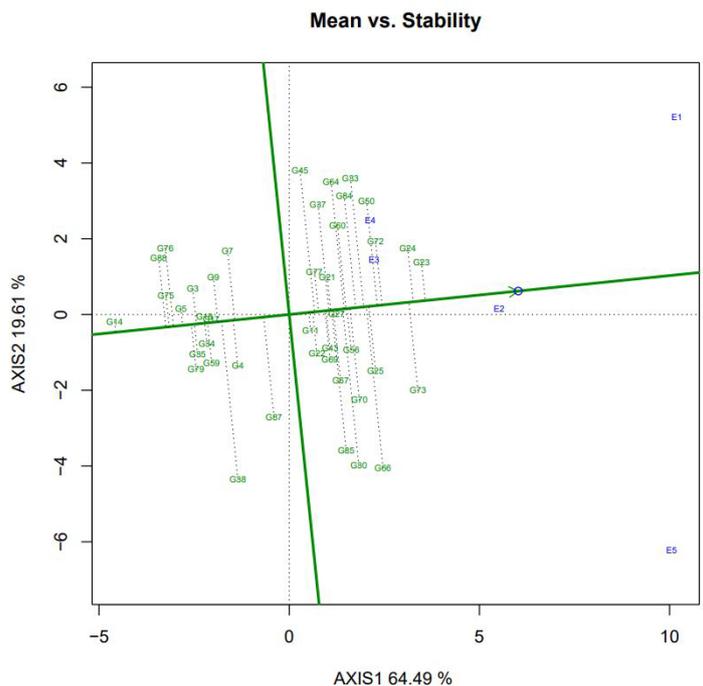


Figure 2. The mean vs. stability view of genotype main effects plus genotypic x environment interaction effect (GGE) biplot of selected maize hybrids tested in 5 environments for grain yield.

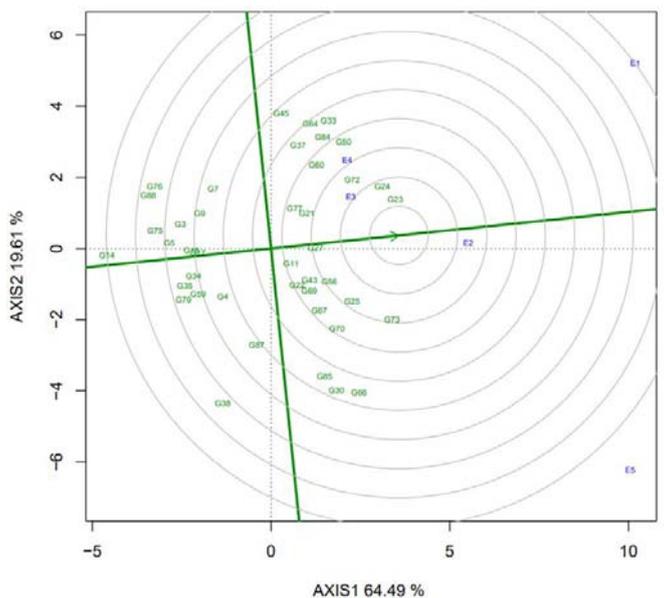


Figure 3. The genotypes comparison with ideal genotype view of genotype main effects plus genotypic x environment interaction effect (GGE) biplot of selected maize hybrids tested in 5 environments for grain yield.

3.5 Discriminative vs. representativeness and ranking environments relative to an ideal environment

Evaluation of test environments is crucial to identify the most desirable genotypes for a mega environment in variety performance trial. Figure 4 represents the “discriminating ability vs representativeness” view of the GGE biplot. The discriminating power (i.e., the ability of test environment to effectively and efficiently discriminate genotypic perfor-

mance for assessed traits) is measured by the vector length of an environment [25]. Test environments with longer vectors are more discriminating of the genotypes whereas a test environment marker with a short vector provides little information about the genotypes differences [25]. Hence, among the five environments evaluated, E1 and E5 were the most discriminating of the genotypes while E3 had the shortest vector and was the least discriminating of all test environments. According to Yan and Tinker [26], the representativeness of testing environment is visualized by the angle between environment vector and abscissa of average environment axis. The smaller the angle, the more representative of the test environment would be [9]. Consequently, in the present study, E2 was found to be highly representative of the test environments, followed by E1. The ideal test environment is one that is most discriminating for genotypes and is representative of the target environments [25]. The comparison with the ideal environment view of GGE biplot (Figure 5) has concentric circles with the ideal environment in the inner circle. An environment is more desirable and discriminating when located closer to the ideal environment [44]. Therefore, the test environment E1 was highly discriminative and representative of the target environment.

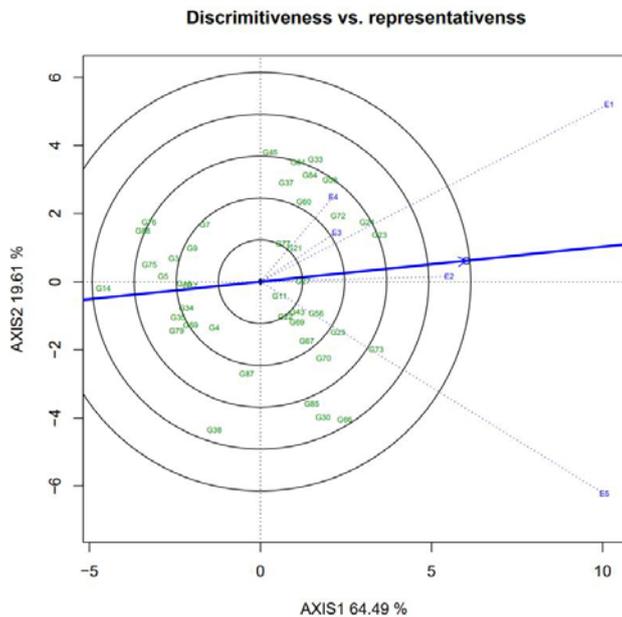


Figure 4. The “discriminating power vs. representativeness” view of the GGE biplot based on selected maize hybrids tested at five test environments.

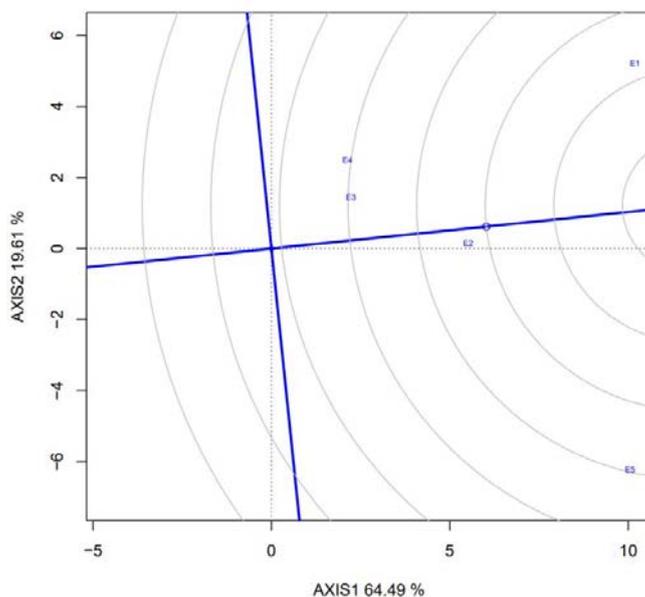


Figure 5. The comparison with the ideal environment view of the GGE biplot based on selected maize hybrids tested at five test environments.

4. Conclusion

The results of this study showed that genotypes, environments and genotype by environment interaction were significant for grain yield. GGE biplot model was effective for analyzing and visualizing pattern of GEI and identifying the most high-yielding and stable cultivar as well as discriminating ability and representativeness of the test environments. The GEI was a crossover type where a change in performance ranking of the genotypes across environments observed, which suggested the need to breed for both broad and specific adaptations. Hybrid G23 was the best performer in environments E1, E2 and E3. Hybrid G33 was identified as best-performing with best specific adaptation in environment E4, while hybrid G66 and G73 had best adaptation in E5. Test environment E1 was found to be the ideal test environments for selecting superior hybrids because of their high discriminating power and representativeness of the target environments. The GGE biplot showed that hybrid G23 and G24 were high yielding and consistent performing across the test environments. Therefore, these superior hybrids could be considered as widely adaptable hybrids and should be further evaluated in multi-environment trials to confirm the consistency of their performance and facilitate their registration and commercialization.

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