Analysis of Genotype x Environment Interaction for Grain Yield in Maize Hybrids

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Abstract

Maize is an important staple crop for millions of people in Sub-Saharan Africa. The crop grows in a wide range of environmental conditions. The present study was performed to analyze the genotype-by-environment (G×E) interaction for grain yield of fourty two single cross hybrids grown in three environments located at different agro-ecological zones of Kenya. The maize genotypes were grown in randomized complete block design with three replicates in 2006 and 2007. Grain yield data of the single cross hybrids was analysed using the additive main effects and multiplicative interaction (AMMI) and GGE biplot methods. The additive main effects and multiplicative interaction model (AMMI) analysis of variance (additive main effects) showed significant effects for genotypes, environment and the genotype by environment interaction. The total proportion contributed by environment and G x E interaction accounted for 78% and 10% of the total variation. The results also showed that 64.5% of the total variation was contributed by the environment while the genotype and interaction was associated with 20.7% and 10.3% of the total variation, respectively. The most stable genotype in the high yielding group in this study was CML312/TZMI 711 (X20), followed by genotypes TZMI 102/CML384 (designated as X33), and CML312/TZMI 712 (X21). The genotype CML312/TZMI 711 (designated as X20) could be used for broad selection since it was found to be the most ideal genotypes with both high mean yield and high stability. In the biplot analysis, X20 was also close to the origin, had the shortest vector from the ATC and with large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability) implying it had the least contribution to genotype by environment interaction (GEI). Through the stability analysis, the superior genotypes identified could also be used as references for genotype evaluation and also included in further testing in both early and later stages of selection.

1. Introduction

Maize is an important staple crop for millions of people in Sub-Saharan Africa (Sibiya et al., 2011). The application of quantitative genetics in maize breeding enables the development of superior genotypes whose genetic parameters have been estimated thus maximizing the gains from selection (Vieira et al., 2012). This also enables the identification of pleiotrophic effects which largely contribute to the genotypic variation with regard to quantitative traits (Wisser et al., 2011). The maize genotype possesses different kinds of gene actions that interact differently in the inheritance of the various plant attributes. Maize crop also grows on a wide range of environmental conditions with regard to water balance, solar radiation, and temperatures (Hill et al., 1997). This differential response of maize germplasm to these varied agro ecological zones (AEZ) contributes to the genotype by environment interaction (GEI) which often hampers the identification of high yielding and stable maize hybrids (Akcura et al., 2011). The GEI interaction variance can be controlled by increasing the number of test environments.

The GEI makes genotypes to perform differently in different environments especially in the stress prone Sub Saharan Africa (SSA) with highly variable weather conditions (Sibiya et al., 2011). This has complicated the breeding and selection for important traits due to cross interaction among the hybrid ranks in different environments (Carson et al., 2002; Beyene et al., 2011; Mitrovic et al., 2012). Thus, promising genotypes with wide adaptation are barely selected. The GE components contribute to noise reducing the heritability of the traits

affecting breeding progress due to inaccurate selections especially in single environments. Through GEI studies, stable genotypes which are adapted to specific target areas and potential candidates for promising hybrid combinations could be identified (Abay et al., 2009). The identification of stable maize varieties (the response of crosses across several environments) could help to enhance the farmers' acceptability or adoption of elite new varieties since the stable maize genotypes tend to utilize the resources in higher performing environments to produce above average maize varieties in all the environments (Jong and Brewbaker, 2005).

The GEI analysis has been performed using different methods, such as, stability analysis following additive main effects and multiplicative interaction model (AMMI), principal component analysis and linear regression analysis, analysis of variance (ANOVA) and GGE biplot analysis (Abay et al., 2009; Miranda et al., 2009; Akcura et al., 2011; Mitrovic et al., 2012). The ANOVA explains only main effects and gives no information on individual genotypes and localities which are components of the interaction (Mitrovic et al., 2012). The AMMI allows for large set of technical interpretations and uses a principal component (autovector) to interpret cultivar performance by integrating the use of ANOVA and PCA. The AMMI analyses combine additive components in a single model for the main effects of genotype and environment as well as multiplicative components for the interaction effect. The graphic analyses bring out phenotypic stability, genotypic behavior of the cultivars and environments which optimize performance (Miranda et al., 2009). The AMMI model displays main effects of genotypes and environment and their interactions. It also estimates the genotype responses and separates noise from real sources of variation through partitioning of the GEI. It also contributes to improved cultivar evaluation, recommendations and selection of test sites (Abay et al., 2009). It is useful in summarizing and approximating patterns of response which exist in the original data (Akcura et al., 2011). The GGE biplot analysis is another method which integrates the genotype and genotype by environment effects in the evaluation of cultivars. The GGE which uses graphic axes identifies superior cultivars in the mega environments (Akcura et al., 2011). Mega environments comprise groups of locations which consistently share the same test cultivars (Abay et al., 2009). It also combines ANOVA and PCA by partitioning together sum of squares of genotypes and sum of squares of genotype by environment interaction using the PCA method. It is also used for the presentation and estimation of genotypes in different environments (Miranda et al., 2009).

Given the importance of maize in Kenya and the SSA, there is need for increased maize production in order to ensure food security and also contribute to national development. The growing of high yielding and stable maize varieties will help to increase maize production and lead to improved living standards. Thus this study set out to a) to examine the yield and yield stability of single cross hybrids in three environments found in different agro-ecological environments in Kenya using (additive main effects and multiplicative interaction) AMMI and GGE biplot method b) to identify the genotypes, which could have wide or specific adaptation using the GGE biplot analysis method.

2. Materials and Methods

2.1 Introduction

The maize genotypes comprised fourty two single cross hybrids developed from seven inbred lines crossed in a full diallel. The inbred lines included CML 204, CML 312, CML 373 and CML 384 from CIMMYT (Table 1a). The rest of the inbred lines included TZMI 102, TZMI 711 and TZMI 712 from IITA (Table 1b). The maize genotypes were evaluated for grain yield performance at three sites; Kenya Agricultural Research Institute (KARI), Kiboko, University of Nairobi's Kabete Field Station and KARI-Kakamega (Table 2).

Table 1(a). The description of the CIMMYT germplasm used in the study

Inbred lines	Pedigree	Adaptation	Heterotic Group	Important Traits
CML 204	[7794]-SELF-4-1-S9-1-4-7-4-5-BB.	Mid altitude and semitropical areas of Africa	Group B	Long late maturing inbred line It has white grains and a dent texture. Good tolerance to MSV and rust
CML 312	S89500F2-2-2-1-1-B*5.	Sub-tropical areas	Group A	Tall intermediate maturing inbred line with white semi flint kernel Good resistance to GLS and *E. turcicum*
CML 373	P43SR-4'-1-2-1-B-8-1-BBB	Adapted to the subtropical areas	Group A	It has white flint textured kernels with intermediate maturity It is a tall inbred Susceptible to rust, *E. turcicum* and ear rot
CML 384		P502C1#-771-2-2-1-3-B	Group B	This is a flint textured, white grained inbred line It is a tall late maturing inbred line with good resistance to ear rot and rust

Source Pswarayi and Vivek, 2004

Table 1(b). The description of the IITA germplasm used in the study

Inbred line	Parentage	Heterotic group	Remarks
TZMI 711	National-1 variety crossed to an IITA MSV-resistant population, TZSR	B	TZSR was developed through intercrossing four populations namely TZB, TZPB, POP 21, and POP 22
TZMI 712	A mid-altitude inbred line TZMI 501 from IITA crossed to an inbred line ZSR 923 S4 bulk, from CIMMYT	B	
TZMI 102	Its pedigree is CamInb.TCSel1-13-1-1-1-B.	B	TZMI 102 was a parent of the best single-cross hybrid marketed in Plateau State of Nigeria as '8535-23'

Source: Menkir and Adepoju, 2005

Table 2. Agro-climatic description of the three experimental sites used in the study

Site	Geographic position			Mean annual Rainfall (mm)	Temperature (0°C)		Soil type
	Longitude	Latitude	Altitude		Min	Max	
KARI, Kiboko (Agro-ecological zone 5)	37° 75 E	2° 15'S	993m	548mm	17	30.6	Ferrasols to ferric luvisol on the old peneplain and eutric fluvisol at the bottom of the river valley
KARI, Kakamega (Agro-ecological zone 2)	34° 45 E	0° 16 'N	1585m	1995 mm	13	28.6	Soils are deep, friable, Basaltic loam, fertile and well drained
Kabete, University of Nairobi, Field station (Agro Ecological Zone 3)	36⁰ 44 E	1⁰ 15' S	1820m	1000 mm	16	23	Soils are well-drained, very deep, dark reddish brown, friable clay with acid humic top soil

2.2 Diallel Crosses and Evaluation of Resulting F1 Progenies and Their Parents

The crossing block was set up at KARI- Kiboko to generate the diallel crosses and multiply the seed population. Seven parents were sown in 13 rows each to allow for crossing with each line and have a self of each resulting to ninety-one rows. The seven parents were crossed in all possible combinations (diallel). After three weeks, weeding was done and buldock applied at the rate of 6 kg/ha to protect the crop from maize stalk borer. Topdressing with CAN at the rate of 60 kg Nha^{-1} was applied as a split with half applied at planting and the rest at about 10th leaf. Supplementary irrigation was also done whenever needed.

2.3 Field Evaluation

The single crosses generated through the diallel crosses at Kiboko were evaluated at KARI-Kiboko, Kabete Field Station and KARI-Kakamega. Fifty entries that included 42 hybrids, seven parents and commercial checks were planted. In Kabete field station and KARI Kiboko, each entry was planted in a single row while in KARI Kakamega there were two rows per entry. The rows were 5m long and the plants were planted at inter- and intra-row spacings of 0.75 m and 0.25 m, respectively. Between replicates, a one metre path was left to allow for easy movement during data taking. Two seeds per hill were sown and later thinned to one plant per hill.

2.4 Grain Yield Data Collection Among the Single Cross Hybrids

At maturity, all the cobs in a row for each entry were harvested. The harvested cobs were then adjusted to 13% moisture content while assuming an 80% shelling percentage. The moisture content was then determined from a seed sample of ten randomly selected cobs.

2.5 Data Analysis

The means of all parameters recorded was done using the SAS program (SAS, 1996). The least significant differences (LSD) were used to separate these means at significance level of 5%. The genotype by environment interaction was analysed using the AMMI and GGE biplot analysis embedded in the Genstat program (Genstat 14th Edition).

i)   GGE model: $Y_{ij} - \mu - \beta_j = a_i + j_{ij} \ldots$

ii)   AMMI model: $Y_{ij} - \mu - \beta_j - a_i = j_{ij} \ldots$

Where Y_{ij} is the measured mean of ith genotype in jth environment, μ is the grand mean, a_i is the main effect of ith genotype, β_j is the main effect of jth environment, j_{ij} is interaction between ith genotype and jth environment.

3. Results and Discussion

3.1 The AMMI Analyses of Variance

The AMMI analysis of variance (additive main effects) showed significant effects for genotypes, environment and the genotype by environment interaction, GEI (Table 3). This implies that different hybrids could be selected for the different agro ecological zones (Derera et al., 2008). Other studies have reported significantly different G×E interactions for grain yield in maize (Carson et al., 2002; Makumbi, 2005; Menkir and Ayodele, 2005). The relative magnitudes of the different sources of variation varied greatly as shown by their variance components on Table 3. The results also showed that 64.5% of the total variation was contributed by the environment and GEI were associated with 20.7% and 10.3% of the total variation respectively. The large sum of squares for environments indicated that the environments included in the study were diverse with large differences among environmental means causing most of the variation in grain yield. From this study, the use of the AMMI model was justified and it effectively partitioned the sum of squares (Mwololo et al., 2009).

Table 3. Combined analysis of variance for grain yield data in maize genotypes across three environments

Source	df	SS	MS	Total variation (%)
Total	293	10143	34.6	
Treatments	146	9696	66.4***	95.6
Genotypes	48	2096	43.7***	20.7
Environments	2	6552	3276***	64.6
Interactions	96	1049	10.9***	10.3
IPCA	49	925	18.9***	9.1
IPCA	47	123	2.6	1.2
Residuals	0	0		
Block	3	121	40.4***	1.2
Error	144	325	2.3	3.2

NB: The block source of variation refers to blocks within environments.

***= significance level at p<0.001.

3.2 The Grain Yield Adaptability and Yield Stability

The grain yield adaptability and yield stability of the single cross hybrids derived from the seven maize inbred lines were visually assessed using the GGE biplot analysis. In this study, the first two principal components explained a total of 78.17% GGE variation (PC1 50.91%, PC2 27.26%, Figure 1, Table 4). The first principal component (PC1) represented on the x axis and across its value was used to estimate yield in that the genotypes which had higher PC1 values were considered to be more productive. The second principal component which

was represented on the y axis explained the stability of genotypes (Abay et al., 2009; Muhammadi and Amri, 2009). The average environment axis (AEA) or average tester coordinate (ATC) was presented as the line which passes through the circle and the origin of the biplot. In this study, the greatest stability in the high yielding group was related to genotypes X33, X20 and X21, while the most stable of all was X20 (Figure 1 and Table 4). The genotype X20 could be used for broad selection since it was found to be the most ideal genotypes with both high mean yield and high stability. In the biplot analysis, X20 is close to the origin and has the shortest vector from the ATC implying that it has the least contribution to GEI (Muhammadi and Amri, 20009). Through the stability analysis, superior genotypes could be identified from multi location trials (Sharma et al., 2010).
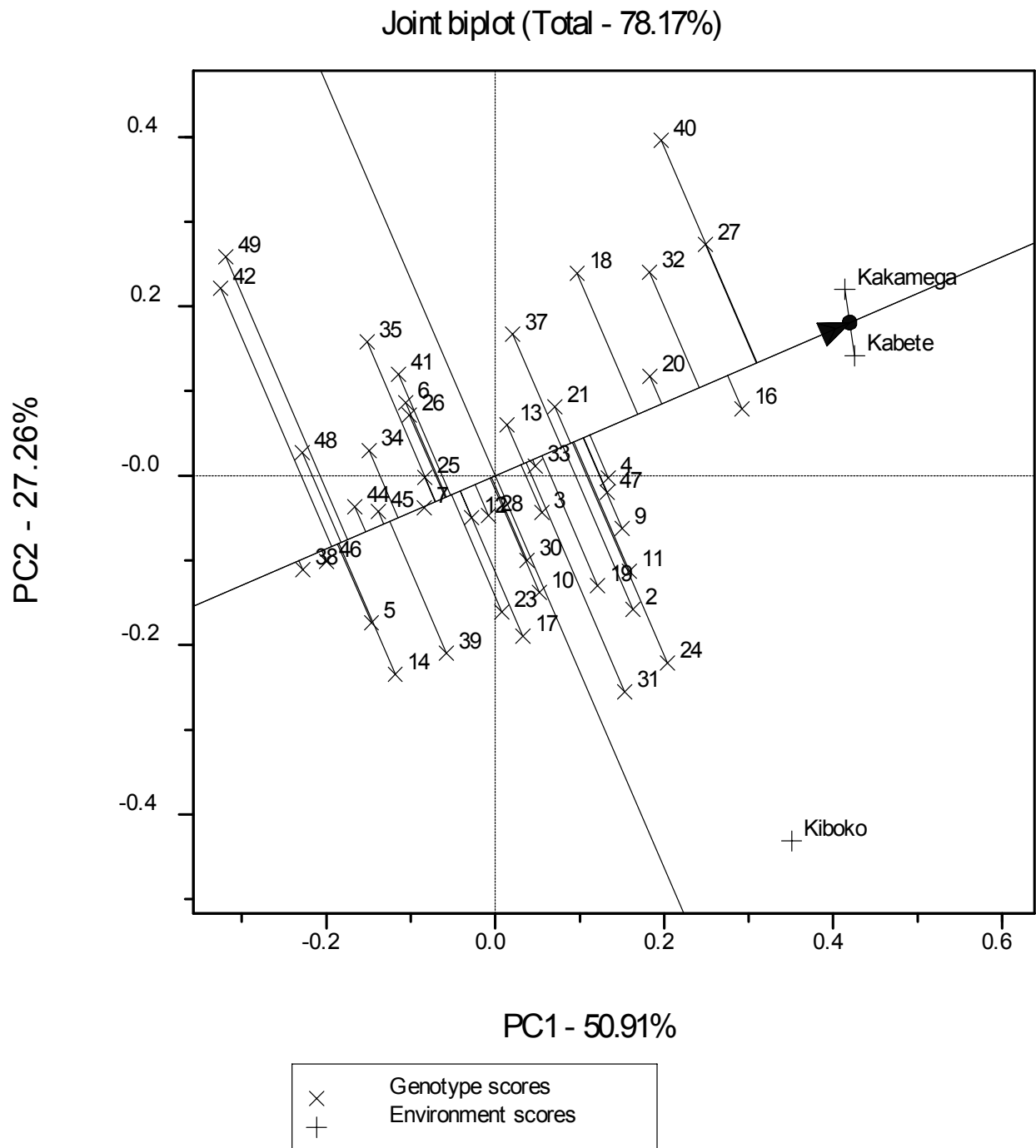

Figure 1. GGE-biplot showing ranking of 42 maize genotypes based on yield and stability performance across three environments; Kiboko, Kabete and Kakamega. Their parentage of genotypes is listed on Table 4

Table 4. The genotypes and the parentage used in the experiment

Genotype	*Parentage	Genotype	Parentage
X2	CML204/CML312	X26	CML384/TZMI 102
X3	CML204/CML373	X27	CML384/TZMI 711
X4	CML204/CML384	X28	CML384/TZMI 712
X5	CML204/TZMI 102	X30	TZMI 102/CML204
X6	CML204/TZMI 711	X31	TZMI 102/CML373
X7	CML204/TZMI 712	X32	TZMI 102/CML312
X9	CML373/CML204	X33	TZMI 102/CML384
X10	CML373/CML312	X34	TZMI 102/TZMI 711
X11	CML373/CML384	X35	TZMI 102/TZMI 712
X12	CML373/TZMI 102	X37	TZMI 711/CML204
X13	CML373/TZMI 711	X38	TZMI 711/CML373
X14	CML373/TZMI 712	X39	TZMI 711/CML312
X16	CML312/CML204	X40	TZMI 711/CML384
X17	CML312/CML373	X41	TZMI 711/TZMI 102
X18	CML312/CML384	X43	TZMI 711/TZMI 712
X19	CML312/TZMI 102	X44	TZMI 712/CML204
X20	CML312/TZMI 711	X45	TZMI 712/CML373
X21	CML312/TZMI 712	X46	TZMI 712/CML312
X23	CML384/CML204	X47	TZMI 712/CML384
X24	CML384/CML373	X48	TZMI 712/TZMI 102
X25	CML384/CML312	X49	TZMI 712/TZMI 711

*Parentage implies the inbred lines involved in the single cross hybrids.

The genotypes were also grouped into either high yielding or low yielding by the average ordinate environment (AOE) (Figure 2, Table 4) (Mohammadi & Amri, 2009). The dotted line is a performance line which passes through the origin of the biplot and helps to determine mean performance of a genotype with the arrow on the performance line showing increasing mean grain yield performance. The highest nominal yield was attributed to genotypes X16, X24, X27, X40 and was identified as the best performers. The poorest performers included X49, X42, X17 and X14 (Figure 2 and Table 4). These genotypes are referred to as vertex genotypes characterised by having the longest distance from the origin of the biplot in their directions. From this study, genotype X27, X16 and X24 showed the best performance in KARI Kakamega, Kabete and KARI Kiboko respectively. They were also the most responsive genotypes which also showed specific adaptation (Abay et al., 2009). They show lower or decreased stability (Sharma et al., 2010).
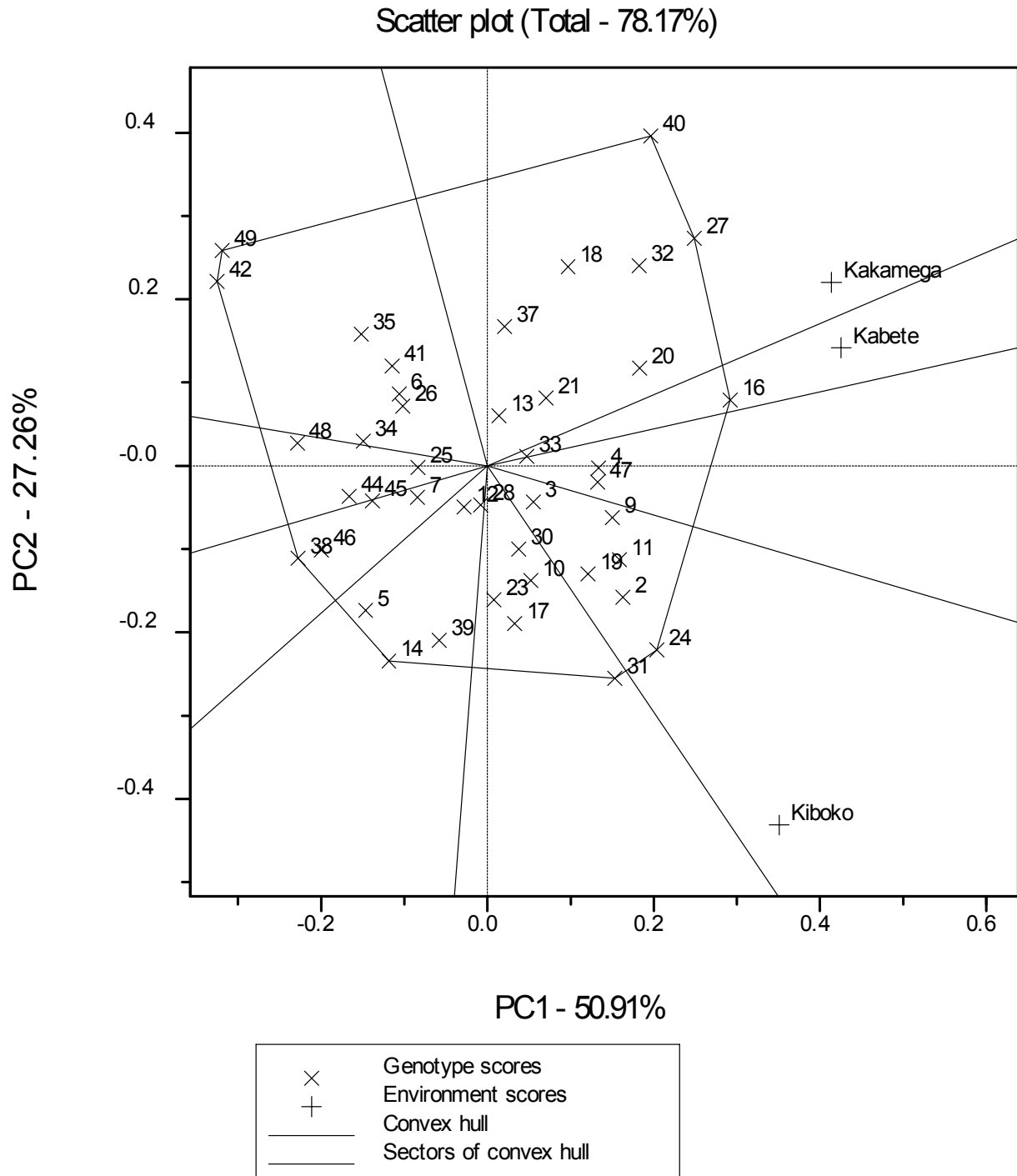
Figure 2. Polygon view of the GGE-biplot showing the mega-environments and their respective highest yielding and stable. The parentage of the genotypes is listed on Table 4

3.3 Mean Performance and Stability of the Maize Genotypes

Through the genotype ranking, the genotype which had the highest grain yield and absolutely stable in performance across test environments was also identified (Figure 3). The ideal genotype basically has the highest average value of all genotypes and is absolutely stable (PCA scores near zero) in that it does not exhibit any genotype by environment interaction hence broad adaptation (Yan & Kang, 2003; Sharma et al., 2010; Akcura et al., 2011). In view of this, hybrid X20 was the most ideal genotype with large PC1 scores (high mean yield) and

small (absolute) PC2 scores (high stability). The genotype X20 could be used as a reference for genotype evaluation (Kaya et al., 2006). It could also have the greatest commercial success because it showed the highest stability. Other desirable genotypes included X16, X32 and X27 (Figure 3 and Table 4) and this could be included in further testing in both early and later stages of selection (Mitrović et al., 2012).
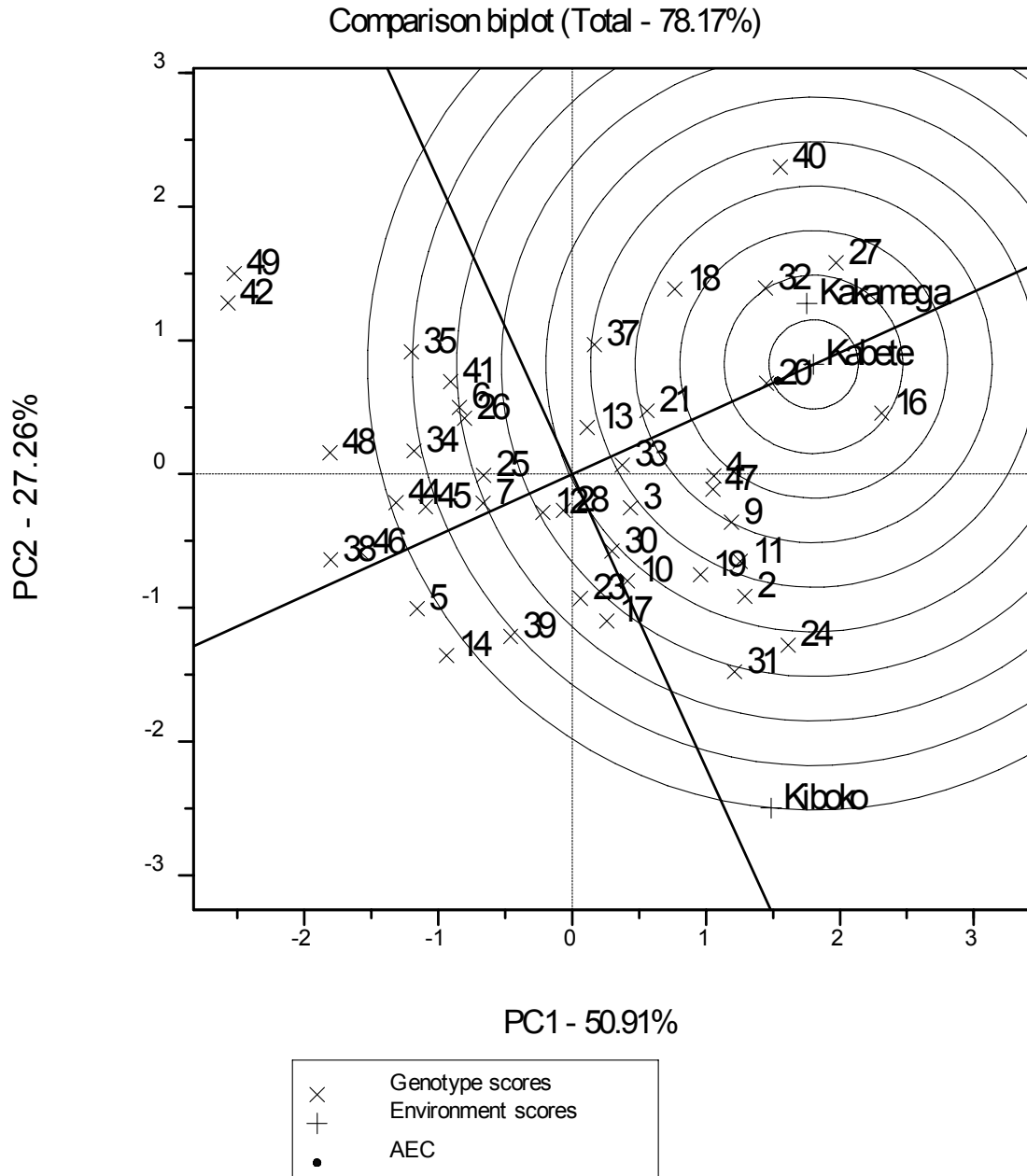

Figure 3. GGE-biplot based on genotype and environment focused scaling for comparison genotype and environments. Ranking of entries is based on both mean and stability

3.4 Discriminating Ability and Representativeness of Test Environments

The PC1 and PC2 were also used to obtain the ideal test environments whereby such an environment is characterised by large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments) (Yan and Rajcan, 2002). The ideal location should also have the capacity to differentiate the genotypes and representative of the target location. In this study, representativeness referred to as the average location which was used as a reference or a benchmark.

Kabete was the most ideal environment as identified from the GGE biplot (Figure 4). The AMMI analysis also identified the best environment as Kabete which had the highest PCA1 and the best 1PCA2 values of 3.5 and -0.9 respectively (Table 5). However, high PCAs show unstable yields which could be used in the selection site for genotypes to be grown in specific environments (Akcura et al., 2011). Thus, this study identified the locations which optimized genotype selection on the basis of their discriminating ability and representativeness.
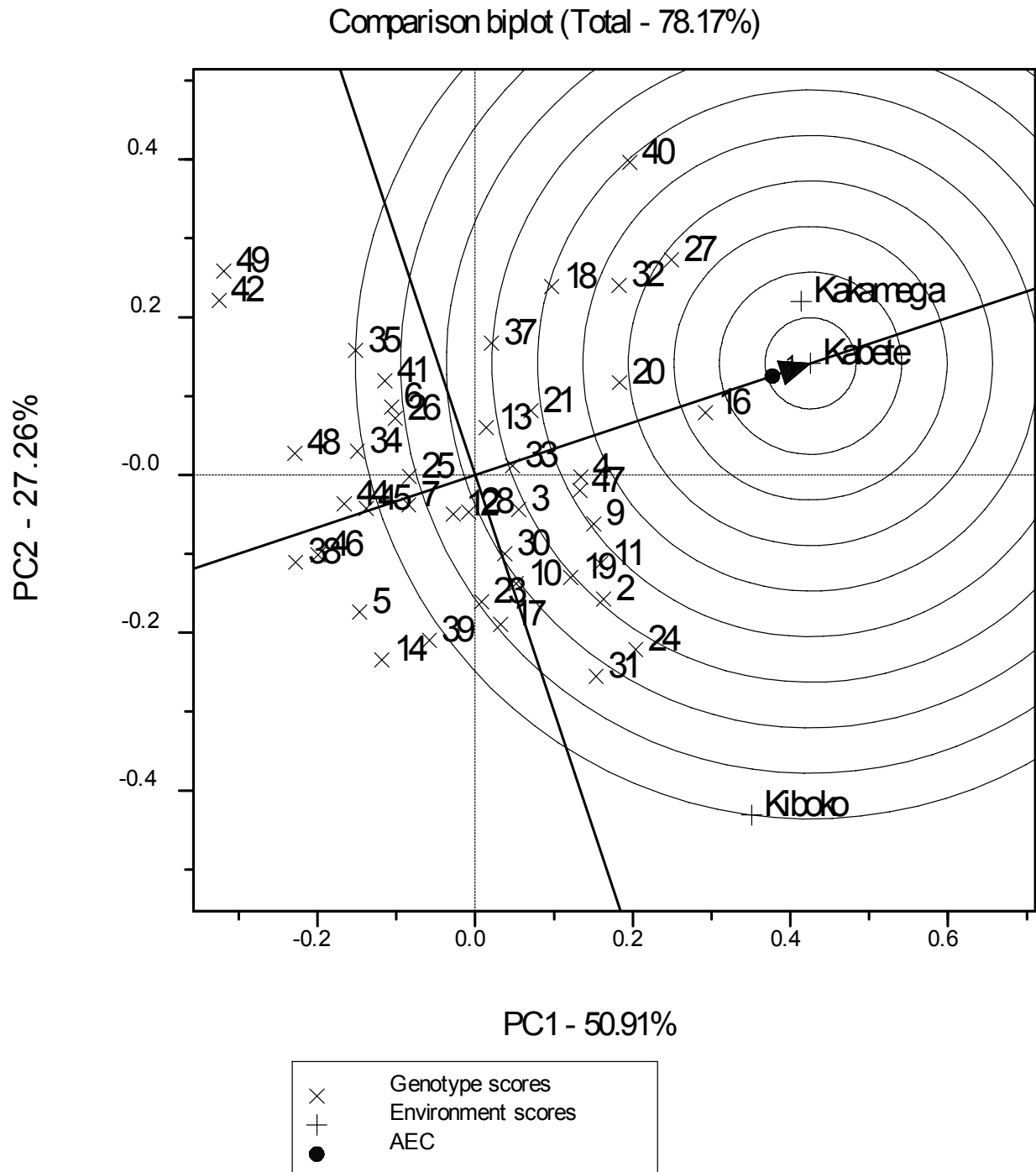

Figure 4. GGE-biplot based on genotype and environment focused scaling for comparison genotype and environments. Their parentage of the genotypes is listed on Table 4

From the AMMI analysis, genotypes X40 and X24 performed well in two of these environments (Table 4 and Table 5). However, the differences in ranking of these genotypes in the different environments implied differential yield performance among the maize genotypes as a result of the significant genotype by environment interaction. This is also referred to as crossover GEI (Frashadfar et al., 2012). The GGE biplot and the AMMI biplot ensured environment stratification while defining cultivars which optimized performance in the environments (Miranda et al., 2009).

Table 5. Environments ranked on IPCA scores including the first four recommended genotypes for each environment based on AMMI the estimates

Environment	NE	Environmental Mean	IPCAe[1]	IPCAe[2]	1st	2nd	3rd	4rd
Kabete	1	14.3	3.5	-0.9	X40	X16	X24	X2
KARI Kakamega	2	2.8	-3	-1.4	X8	X32	X27	X40
KARI Kiboko	3	7.4	-0.5	2.3	X31	X24	X10	X12

The parentage of the genotypes is listed on Table 4.

4. Conclusions and Implications

The results of this study indicated that the maize grain yield performance was greatly influenced by the environment while the GEI contributed the least phenotypic variation. Further testing of these maize hybrids in more seasons could enhance breeding efficiency with reference to cultivar stability and adaptation across environments. Genotype X20 was the most ideal genotype followed by X16, X32 and X27. Further tests of these hybrids for commercial use could be done to enable their release given the need for increased maize production and productivity in Kenya to avert recurrent food shortages.

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