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Yield stability of stem borer resistant maize hybrids evaluated in regional trials in East Africa

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Twenty-seven stem borer-resistant maize hybrids and three checks were evaluated in 14 locations in Kenya and Ethiopia to study the genotype x environment interaction (GEI) and yield stability. An analysis of variance was conducted for grain yield, number of days to silking, plant height, ear height and grain moisture content, and reaction to turicum leaf blight, gray leaf spot, maize streak virus diseases and common rust. The yield stability and adaptation pattern of genotypes were examined with genotype plus genotype x environment (GGE) interaction biplot. Variations due to location, genotype and GEI effects were highly significant for all traits. Location variance among the hybrids was the most important source of variation for all traits, accounting for 58 to 90% of the total variance. The genotypic variance was higher than the GEI variance for turicum leaf blight, plant height and silking date. The GEI variance was higher than the genotypic variance for grain yield, ear height, gray leaf spot, common rust and grain moisture content. The GGE biplot showed that 50% of the entries had positive PC1 scores suggesting above average performance, and 50% of them had negative PC1 scores indicating below average performance. Based on the mean grain yield and stability parameters, hybrid CKIR07003 (5.5 t/ha), CKIR07004 (5.5 t/ha) and CKIR07005 (5.6 t /ha) were identified as high-yielding and stable genotypes, and could be nominated for national performance trials for commercial release in various countries.

Key words: G x E interaction, genotype plus genotype x environment (GGE) biplot, stem borer resistance, yield stability.

INTRODUCTION

Maize is an important food crop in sub-Saharan Africa providing 50% of the calories in diets in southern Africa, 30% in Eastern Africa and 15% in West and Central Africa (Pingali and Pandey, 2000). Improving grain yield and resistance to major stem borer and leaf diseases are the major objectives of maize improvement programs in sub-Saharan Africa (Vivek et al., 2009) where the livelihood of millions of resource-poor farmers depends on successful maize production.

Among insect pests in maize production, stem borers

are the biggest cause of reduced maize yield in Africa from damage to leaves, stems, ears, to kernels. As examples, the spotted stem borer *Chilo partellus* Swinhoe (Crambidae) and the African stem borer *Busseola fusca* Fuller (Noctuidae) are the chief lepidopteran stem borer species causing significant annual loss of maize estimated at 13.5%, and worth US \$91 million in Kenya (De Groote et al., 2002).

The application of chemical insecticides has been recommended in order to protect plants against the stem borers. However, in addition to posing health problems, insecticides are frequently unavailable or too expensive for subsistence farmers in Africa. Therefore, an environmentally safe and economically feasible stem borer control practice is needed. Host plant resistance is

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a practical, easy to adopt and use method of stem borer control. Developing high-yielding maize varieties that are stem borer resistant will minimize the overall cost of production.

Newly-developed maize cultivars need to be tested in many locations for several years to determine their performance and adaptability before commercial release. Inconsistent genotypic responses to environmental factors such as temperature, soil moisture, soil type or fertility level from location to location and year to year are a result of genotype x environment interaction (GEI). GEI has been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988). Large GEI variation impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Nachit et al., 1992).

In sub-Saharan Africa, GEI has been reported in maize (Beyene et al., 2011; Pixely and Bjarnason, 2002; Vivek et al., 2009). When GEI is present, one of the options available to the breeder is to use stability analyses to identify the most high-yielding and stable cultivar. The sites regression (SREG) (Crossa and Cornelius, 1997) has been suggested as the appropriate model for analyzing multi-environment trials when large yield variation is due to different environments (Yan et al., 2000). The SREG method uses a graphical display known as the 'genotype plus genotype x environment interaction (GGE) biplot' which identifies cultivars which are superior in different environments.

International Maize and Wheat Improvement Center (CIMMYT) is involved in strengthening and expanding plant-breeding efforts of national programs and the private sector by regularly exchanging improved germplasm through regional and international trials where national partners can identify adapted and high-yielding genotypes suitable for their specific locations. In 1999, CIMMYT and the Kenya Agricultural Research Institute (KARI) initiated the Insect Resistant Maize for Africa (IRMA) project with the aim of developing and deploying maize varieties that are resistant to key field and storage insect pests. Since its inception, maize germplasm including inbred lines, hybrids and open-pollinated varieties has been evaluated and new varieties released for various maize-growing ecologies of Kenya. The objectives of this study were, therefore, to determine the yield stability of stem borer-resistant experimental maize hybrids, their agronomic performance and their reaction to foliar diseases evaluated across 14 locations in Kenya and Ethiopia.

MATERIALS AND METHODS

Germplasm

Twenty-seven stem borer-resistant three-way hybrids developed through the IRMA project and three checks were used in this study. The hybrids were developed as follows: three stem borer-susceptible elite inbred lines, CML254, CML334 and CML444 were

crossed with 10 stem borer-resistant advanced lines to obtain 30 single crosses (SC). Based on seed availability, 27 SC served as parents, and crossed either with CML312, CML395 or Pop. 390 MIRT C5 Bco S2 Comp to obtain 27 three-way cross hybrids (Table 1). The 10 selected lines were elite or advanced lines in the CIMMYT breeding program, having above-average resistance to stem borers in previous experiments (Beyene et al., 2011). The CIMMYT multiple borer-resistant (MBR) maize population was developed by compositing global maize germplasm reputed to be resistant with a number of stem borer species (Smith et al., 1989). Initially, the multiple borer-resistant population was developed by recombination followed by recurrent selection under infestation with Southern corn borer *Diatraea crambidoides*, sugarcane borer *Diatraea sacharalis*, European corn borer *Ostrinia nubilalis* and fall armyworm *Spodoptera frugiperda*. Resistant lines were then developed from these populations following recurrent selection under artificial infestation with *Chilo partellus* and *B. fusca* (Beyene et al., 2011; Mugo et al., 2001, 2007).

Field evaluations

Twenty-seven test hybrids and three checks were evaluated in a 6 x 5 alpha lattice design with three replications per location during the 2010 the main maize planting seasons (March-September). The hybrids were grown in 14 different environments in target ecologies (Table 2). Each entry was planted in two-row plots of 5 m length. The rows were spaced 0.75 m apart and the hills spaced 0.25 m apart. Two seeds per hill were sown and later thinned at three weeks post-emergence to one plant per hill to give a plant population of 53,333 plants per hectare. Data recorded from each plot included number of days to 50% pollen shed, number of days to 50% silking, plant height, ear height and grain moisture (%). Grain yield in tons per hectare (t/ha) adjusted to 12.5% moisture content was calculated using unshelled grain weight. Disease severity ratings for gray leaf spot caused by *Cercospora zeae maydis* (GLS), leaf blight caused by *Exerohilium turcicum* (ET), common rust caused by *Puccinia sorghi* (PS) and maize streak virus caused by maize streak *geminivirus* (MSV) were recorded on a plot basis using a 1-5 scale where 1 = no symptoms on leaves, 2 = light disease symptoms on 20 to 40% leaf area, 3 = moderate symptoms on 40 to 60% leaf area, 4 = severe symptoms on 60% of leaf area, 5 = severe symptoms on 75% or more of the leaf area. For all the diseases, using the visual scale, a plant showing <1-1.0 was considered highly resistant; 1.1-2.0 resistant; 2.1-3.0 moderately resistant; 3.1-4.0 susceptible; 4.1-5.0 highly susceptible.

Data analysis

Analysis of variance (ANOVA) was conducted for each location individually. A multi-location combined analysis was conducted using the PROC MIXED procedure of SAS (SAS, 2003). Genotypes were considered as fixed effects, and replications and blocks within replications as random effects. Broad sense heritability was calculated as the proportion of genetic variance relative to the total phenotypic variance. For the combined multi-location analysis, variances were partitioned into relevant sources of variation to test for differences among genotypes and the presence of G x E interaction. The effect of maturity on G x E was excluded by adjusting grain yield in each trial according to the anthesis date.

To determine stability and identify superior hybrids across environments the sites regression (SREG) model was used (Cornelius et al., 1996; Crossa and Cornelius, 1997). A two-dimensional GGE biplot of the two principal components (PCs) was plotted (Yan et al., 2000). Genotypes and environments were displayed in the same plot. Each genotype and environment was

Table 1. List of hybrids and pedigree used in the study.

Entry	Hybrid code	Pedigree
1	CKIR07010	(CML334/MBR C5 Bc F114-1-1-3-B-8-2-B-B-B-B)//CML312
2	CKIR07011	(MBR C5 Bc F8-1-1-1-B-2-2-B-B-B-B/CML444)//CML312
3	CKIR07012	(CML254/MBR C5 Bc F108-2-3-1-B-4-2-B-B-B-B)//CML312
4	CKIR07013	(CML334/MBR C5 Bc F108-2-3-1-B-5-2-B-B-B-B)//CML312
5	CKIR07017	(MBR C5 Bc F13-3-2-1-B-4-2-B-#-#//CML444)//CML312
6	CKIR07018	(EMAP1A-233-B-6-1-B-B-B-B-#-#//MBR C5 Bc F114-1-2-3-B-4-2-B-B-B-B)//CML312
7	CKIR07001	(CML334/MBR C5 Bc F114-1-1-3-B-8-2-B-B-B-B)//CML395
8	CKIR07002	(MBR C5 Bc F8-1-1-1-B-2-2-B-B-B-B/CML444)//CML395
9	CKIR07003	(CML254/MBR C5 Bc F108-2-3-1-B-4-2-B-B-B-B)//CML395
10	CKIR07004	(CML334/MBR C5 Bc F108-2-3-1-B-5-2-B-B-B-B)//CML395
11	CKIR07005	(Pool B -36-B-4-3-B-#-#//MBR C5 Bc F108-2-3-1-B-5-2-B-B-B-B)//CML395
12	CKIR07008	(MBR C5 Bc F13-3-2-1-B-4-2-B-#-#//CML444)//CML395
13	CKIR07009	(EMAP1A-233-B-6-1-B-B-B-B-#-#//MBR C5 Bc F114-1-2-3-B-4-2-B-B-B-B)//CML395
14	CKIR09001	(CML334/MBR C5 Bc F114-1-1-3-B-8-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
15	CKIR09002	(MBR C5 Bc F8-1-1-1-B-2-2-B-B-B-B/CML444)//Pop. 390 MIRT C5 Bco S2 Comp.
16	CKIR09003	(CML254/MBR C5 Bc F108-2-3-1-B-4-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
17	CKIR09004	(CML334/MBR C5 Bc F108-2-3-1-B-5-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
18	CKIR09005	(Pool B -36-B-4-3-B-#-#//MBR C5 Bc F108-2-3-1-B-5-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
19	CKIR09006	(MBR C5 Bc F4-1-2-1-B-1-2-B-B-B-B/MBR/MDR C3 Bc F1-1-1-1-B-3-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
20	CKIR09007	(MBR C5 Bc F13-3-2-1-B-4-2-B-#-#//CML444)//Pop. 390 MIRT C5 Bco S2 Comp.
21	CKIR09008	(EMAP1A-233-B-6-1-B-B-B-B-#-#//MBR C5 Bc F114-1-2-3-B-4-2-B-B-B-B)//Pop. 390 MIRT C5 Bco S2 Comp.
22	CKIR06001	(MBR C5 Bc F8-1-1-1-B-2-2-B/CML444)//Pop. 390 MIRT C5 Bco S2 Comp.
23	CKIR06004	(CML202/MBR C5 Bc F4-1-2-1-B-1-2-B)//Pop. 390 MIRT C5 Bco S2 Comp.
24	CKIR06006	(CML334/MBR C5 Bc F108-2-3-1-B-5-2-B)//Pop. 390 MIRT C5 Bco S2 Comp.
25	CKIR06007	(MBR C5 Bc F4-1-2-1-B-1-2-B/MBR/MDR C3 Bc F1-1-1-1-B-3-2-B)//Pop. 390 MIRT C5 Bco S2 Comp.
26	CKIR06008	(EMAP1A-233-B-6-1-B-B-B-B/MBR C5 Bc F114-1-2-3-B-4-2-B)//Pop. 390 MIRT C5 Bco S2 Comp.
27	CKIR06009	(MBR C5 Bc F13-3-2-1-B-4-2-B/CML444)//Pop. 390 MIRT C5 Bco S2 Comp.
28	WH505	Commercial check
29	Local Check 1	
30	Local Check 2	

defined by their respective scores on the two PCs. Angles between environment vectors were used to judge correlations (similarities/dissimilarities) between pairs of environments (Yan and Kang, 2003).

RESULTS

Analysis of variance

There were significant differences between the genotypes and the locations for grain yield, agronomic traits and reaction to leaf diseases (Table 3). Genotype x location interaction was significant for all traits, indicating the importance of genotype x environment interaction in affecting the traits. Location variance was the most important source of variation accounting for 58 to 90% of the total variance for all the traits (Table 3). The genetic variance for the traits ranged from 1 to 12%. For turicum leaf blight, plant height and silking date, the genotypic

variance was higher than that of the genotype x location interaction. For grain yield, ear height, GLS, common rust and grain moisture content, genotype x location interaction variance was higher than the genotypic variance (Table 3). Although the experiments were carried out in 14 different locations, the sources of variation for different traits in the analysis of variance, excluding error, explained 77 to 96% of the total variance (Table 3), showing good experimental accuracy.

Mean performance

There were significant differences among the hybrids for grain yield, agronomic traits and reaction to leaf diseases (Table 3). Mean grain yields ranged from 4.0 t/ha for CKIR06008 and CKIR09003 to 5.7 t/ha for CKIR07013 and CKIR07011. Thirteen experimental hybrids had an above average grain yield, while eight hybrids had an

Table 2. Characteristics of 14 trial sites used in the evaluation of stem borer-resistant (SBR) hybrids.

Site	Name	Longitude	Latitude	Elevation (masl)	Rainfall (mm)	Temp max (°C)	Temp (min)	Soil texture
1	Alupe	34° 7' E	0°30' N	1150	1688	29	16	Clay loamy
2	Bako*	36° 46' E	9° 6' N	1088	1210	28	14	Nitosols
3	Bukura	34° 36' E	0° 15' N	1397	1800	20	22	Orthic ferralsol
4	Elgon Downs	35° 16' E	0° 30' N	2080	1280	17	20	Loamy Clay
5	Emali	37° 28' E	2° 5' S	960	600	30	14	Loamy Clay
6	Kakamega	34° 44' E	0° 16' N	1530	1916	29	13	Sandy loam
7	Katumani	37° 25' E	1° 6' S	1580	528	25	14	Loamy sand
8	Kiboko	37° 75' E	2° 15' S	975	530	35	14	Sandy clay
9	Kibos	34° 49' E	0° 03' S	1170	865	29	15	Black heavy clay
10	Mpeketoni	40° 41' E	2° 23' S	12	980	32	23	Sandy loam
11	Msabaha	40° 2' E	3° 16' S	91	1157	40	13	Sandy loam
12	Mtwapa	39° 219 E	4° 347 S	30	965	29	22	Sandy soils
13	Sang'alo	34° 37' E	0° 30' N	1459	1553	25	13	Sandy Clay loam
14	Thika	37° 5' E	1° 2' S	1483	900	27	15	Sandy Clay loam

*=In Ethiopia, all other in Kenya.

Table 3. Means for grain yield in each environment and agronomic traits averaged across 14 environments of 30 maize hybrids evaluated in Kenya and Ethiopia in 2010.

Entry	Hybrid code	GY	AD	PH	EH	MCI	ET	GLS	MSV	PS
1	CKIR07010	5.4	69.6	213.6	104.1	16.8	2.0	1.2	3.8	1.6
2	CKIR07011	5.7	68.4	209.4	100.2	16.8	2.1	1.2	3.5	1.7
3	CKIR07012	5.6	70.4	207.3	105.0	16.7	1.9	1.2	3.5	1.5
4	CKIR07013	5.7	71.0	214.2	107.1	18.0	1.9	1.2	3.5	1.5
5	CKIR07017	5.2	68.4	208.6	99.8	17.1	2.0	1.2	3.7	1.7
6	CKIR07018	5.1	67.5	206.9	100.2	15.8	2.1	1.2	3.9	1.5
7	CKIR07001	5.4	72.1	215.3	113.7	17.9	2.1	1.2	1.4	1.6
8	CKIR07002	5.1	70.0	203.7	106.8	17.5	2.2	1.2	1.5	1.6
9	CKIR07003	5.5	72.8	208.9	112.2	17.5	2.1	1.2	2.2	1.4
10	CKIR07004	5.5	71.7	210.7	110.8	17.8	2.2	1.2	2.2	1.5
11	CKIR07005	5.2	70.0	213.0	115.4	17.4	2.2	1.2	0.9	1.5
12	CKIR07008	5.6	69.7	202.3	103.3	17.4	2.1	1.2	2.0	1.6
13	CKIR07009	5.0	70.0	204.8	106.9	16.7	2.2	1.2	2.0	1.5
14	CKIR09001	4.4	68.0	201.3	105.2	16.6	2.4	1.4	2.9	1.7
15	CKIR09002	4.4	67.8	191.7	99.5	16.1	2.5	1.4	2.4	1.7
16	CKIR09003	4.0	65.4	195.9	101.2	15.9	2.4	1.4	3.6	1.8
17	CKIR09004	4.6	68.6	199.8	105.8	16.1	2.2	1.3	2.7	1.7
18	CKIR09005	4.5	67.5	198.1	107.8	16.0	2.4	1.3	2.2	1.6
19	CKIR09006	4.3	66.0	193.5	99.1	15.7	2.6	1.3	3.1	1.7
20	CKIR09007	4.4	67.6	191.0	98.1	16.0	2.5	1.4	3.4	1.9
21	CKIR09008	4.3	66.6	193.8	99.0	16.0	2.5	1.3	3.4	1.7
22	CKIR06001	4.7	67.1	192.9	102.6	16.1	2.5	1.4	3.0	1.8
23	CKIR06004	4.6	68.8	204.0	101.3	16.1	2.3	1.4	2.2	1.5
24	CKIR06006	4.5	69.2	198.8	104.1	16.6	2.3	1.3	3.2	1.5
25	CKIR06007	4.8	65.9	194.4	99.9	16.3	2.5	1.4	3.3	1.7
26	CKIR06008	4.0	65.8	193.3	95.8	15.6	2.9	1.3	2.8	1.8
27	CKIR06009	4.3	67.4	195.3	98.4	16.0	2.4	1.3	3.5	1.8
28	WH505	5.3	70.9	201.5	98.8	17.4	1.9	1.2	2.1	1.4

Table 3. Contd

29	Local Check 1	4.4	69.9	207.7	108.2	16.1	2.2	1.3	2.7	1.6
30	Local Check 2	4.1	67.0	193.0	104.6	16.0	2.1	1.4	3.3	1.6
	Nlocs	14.0	11.0	11.0	12.0	14.0	9.0	9.0	8.0	10.0
	Var_Loc	3.0	87.7	1965.4	814.9	10.4	0.2	0.3	20.5	0.2
	Entry_Variance	0.2	3.4	49.4	19.9	0.4	0.030	0.010	1.228	0.022
	LocxEntry_Variance	0.3	3.0	42.3	35.6	1.3	0.084	0.050	3.312	0.053
	Residual_Variance	0.8	3.9	131.2	47.0	2.5	0.1	0.1	3.3	0.1
	Gmean	4.8	68.7	202.2	103.8	16.6	2.3	1.3	2.8	1.6
	LSD	0.7	1.7	8.1	5.9	1.1	0.2	0.2	1.5	0.2
	CV	7.0	1.3	2.0	2.9	3.4	5.2	6.0	27.6	5.7
	Heritability	0.8	0.9	0.9	0.8	0.7	0.9	0.5	0.5	0.7

GY= Grain yield t/ha; AD = Number of days to anthesis PH = Plant height (cm); EH = Ear height (cm); MC= Kernel moisture content in %; ET= turcicum leaf blight (1-5); GLS= gray leaf spot (1-5); MSV= Maize streak virus (1-5); PS-Common rust (1-5).

equal or higher grain yield than the commercial check, WH505 (Table 3). The top six high-yielding hybrids were CKIR07013 (5.7 t/ha), CKIR07011 (5.7 t/ha), CKIR07008 (5.6 t /ha), CKIR07012 (5.6 t/ha), CKIR07003 (5.5 t/ha) and CKIR07004 (5.5 t/ha). These hybrids were comparable with the best commercial check hybrid in terms of number of days to silking and reaction to turcicum leaf blight and gray leaf spot, but were slightly higher in plant and ear heights. All the hybrids were resistant to gray leaf spot and common rust with a disease score of below 2. About 50% of the hybrids were susceptible to maize streak virus with a disease score of above 3; however, the most resistant hybrids were CKIR07005, CKIR07001 and CKIR07002 (Table 3). Medium to high estimates of heritability were found in different traits (Table 3). The highest heritability ($h^2 = 0.9$) was recorded for number of days to silking, plant height and turcicum leaf blight score, while the lowest was for gray leaf spot and maize streak virus score ($h^2 = 0.5$). Grain yield and ear height had a heritability of 0.8.

Genotypic performance and stability

The GGE biplot explained 67.44% of the genotype main effect; the G x E interaction with the PC1 score explained 59.17% and with the PC2 score explained 8.27% (Figure 1). Kakamega, Bako, Thika and Elgon Downs had longer vectors than other locations indicating that they were the best locations for genetic differentiation of cultivars. The most non-discriminatory locations were Kibos, Bukura and Msabaha as they had short environment vectors. If resources are limited, the least discriminatory test locations could be discarded as they provided little information. The obtuse angle between vectors for Msabaha and Bukura, Msabaha and Elgon Downs, and Msabaha and Sangalo, indicates a negative correlation between these locations in ranking these hybrids. The two-dimensional biplot showed that almost half of the

entries had either positive or negative PC1 scores suggesting above or below average performance. Five hybrids (entries 2, 3, 9, 10 and 12) had long environmental vectors, indicating that they were good performers under favorable locations such as Bako, Alupe, Sangalo and Elgon Downs. Three hybrids (entries 9, 10 and 12) were high-yielding and stable because they showed large PC1 scores and near-zero PC2 scores. On the other hand, two hybrids (16 and 26) were very poor in yield (having a high negative PC1 score but a stable (near-zero) PC2 score).

DISCUSSION

The occurrence of a significant G x E interaction effect indicated inconsistent phenotypic performance of the tested genotypes across locations, which may cause selections made in one environment to perform poorly in another environment. Location variance among the hybrids was the most important source of variation accounting for 58 to 90% of the total variance for all traits (Table 3). The 14 locations were distinct agro-ecologies with different annual rainfall, growing seasons and elevation (Table 2). Epinat-Le et al. (2001) provided biological interpretations of GEI. They found earliness of flowering, water balance, and mean temperature in the second part of the cycle contributed to GEI in maize yield.

The G x E interaction variance for grain yield and most other agronomic traits was higher than the genotypic variance (Table 3) indicating that it is essential to evaluate genotypes for such traits in different environments. A higher G x E interaction variance than genotypic variance for grain yield has been reported in a previous study with early maize hybrids tested in 30 locations in northern France (Epinat-Le et al., 2001). However, Beyene et al. (2011) reported that variation due to genotype was higher than the G x E interaction in a study of 30 stem borer-resistant hybrids tested across

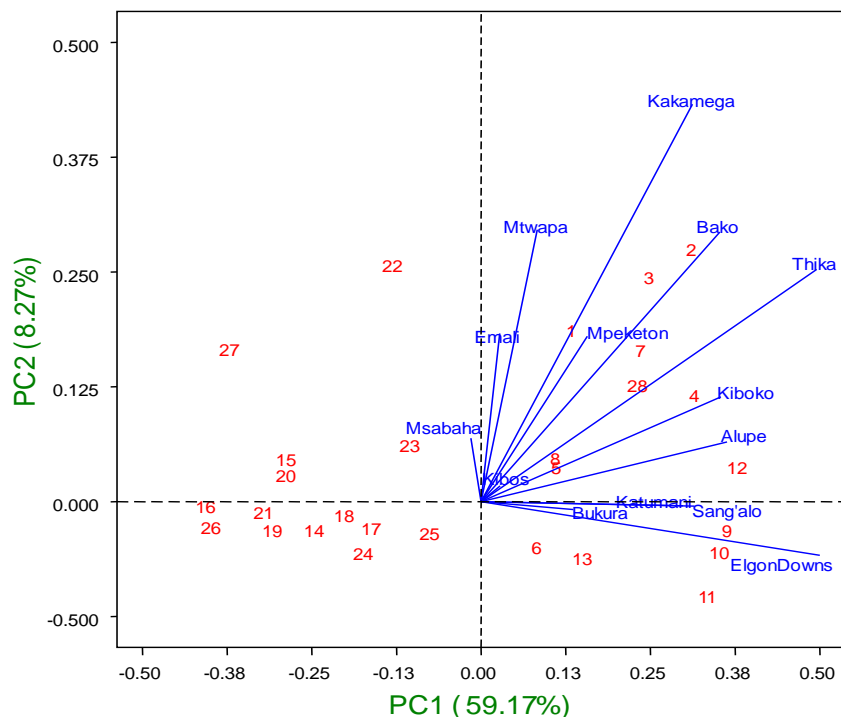


Figure 1. Graph of the SREG GGE biplot analysis based on the grain yield of 30 maize hybrids evaluated across 14 environments in Kenya and Ethiopia.

locations in Kenya. Van Eeuwijk (1995b) reported that variation due to the G x E interaction was small in relation to the genotypic variation of 18 Dutch maize varieties for silage dry matter content. There were variations among genotypes for their resistance to foliar diseases. Furthermore, the genotypic variance for all diseases was higher than the genotype x location interaction variance indicating that most of the variations for reaction to these diseases were genetic.

The 30 genotypes tested presented a range of variability for grain yield and other agronomic characteristics, with opportunities for selecting maize genotypes for high yield and acceptable agronomic traits. Eight hybrids had an equal or higher grain yield than the commercial check. These hybrids were comparable with the check hybrid, WH505, in grain yield, kernel moisture content, and reaction to gray leaf spot, maize streak virus and common rust, indicating that they could be suitable for growing in a wide range of environments. These results were in agreement with Beyene et al. (2011) who reported that some of the newly developed stem borer-resistant hybrids were as stable as and as high-yielding as the commercial check. These hybrids could be commercialized in Kenya and Ethiopia where there are efforts to develop high-yielding, stem borer and disease-resistant maize varieties.

All hybrids including the check were resistant to GLS and common rust. However, 14 of the 30 hybrids were

susceptible to MSV. The fact that the present hybrids possess genes for resistance to stem borers and are also resistant to attack by foliar diseases (GLS, rust, MSV) makes them suitable for growing across a wide range of agro-ecologies in east Africa. The correlation of stem borer-resistant hybrids to disease resistance in maize needs further study. However, Tefera et al. (2011) also reported that some maize hybrids resistant to stem borers were also partly resistant to foliar diseases. Gray leaf spot and leaf blight are cosmopolitan fungal diseases, occurring world-wide (Pratt and Gordon, 2006) and maize streak virus infects maize throughout sub-Saharan Africa (Bosque-Perez, 2000). These diseases may occur simultaneously, and recurrent epidemics are common when favored by weather conditions, the planting of susceptible cultivars and continuous maize cropping (Bigirwa et al., 2001; Pratt and Gordon, 2006).

The GGE biplot software helped in identifying the least and the most discriminatory locations. Thus, the GGE biplot methodology is a useful tool for identifying locations that optimize cultivar performance and for making better use of the limited resources available to the testing program. In the GGE biplot, the cosine of the angle between two vectors represents the correlation between them, and the vector length corresponds to discriminatory ability (Yan and Kang, 2003). The acute angle between Kakamega (in Kenya) and Bako (in Ethiopia) indicates a positive correlation between them, implying that hybrids

which performed well in one location also performed well in the other location. Kakamaga and Bako are at a mid-altitude elevation, receive annual rainfall > 980 mm and are considered areas with a high potential for maize production. Yan et al. (2000) indicated that the ideal environments for testing should have a high PC1 value and be of the same sign (for better hybrid discrimination) and a PC2 score near zero (more closely representative of the environment mean). In our study, Sangalo, Alupe and Elgon Downs were close to the ideal location as they had a high PC1 score and a near-zero PC2 score.

An ideal goal for any crop improvement program is to get stable and high-yielding cultivars. Thus, the GGE biplot is recommended where the location portion in multi-location trials is known to be the largest among all sources of variation (Yan and Kang, 2003) as seen in the present study where location variance accounted for 58 to 90% of the total variance for all traits studied (Table 3). Crossa et al. (2002) and Yan et al. (2000) reported that in the two-dimensional biplot, a genotype with a larger PC1 score has a greater average yield, and its performance varies across environments in direct proportion to the PC1 score of its environment. Three hybrids (9, 10 and 12) were close to the ideal genotype described by Yan and Tinker (2006) because they had a high yield (a large PC1 score) and were stable across environments (a PC2 score near zero). This might be due to the fact that two of the parents used in the hybrid formation were well-adapted CIMMYT released lines (CML395, CML312, and CML444). These lines proved useful in hybrid formation for subtropical and mid-altitude environments and have been used in many hybrids in CIMMYT and SSA national maize-breeding programs.

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