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Full Length Research Paper

Genotype × environment interaction on sugar and biomass production in sweet sorghum (*Sorghum bicolor (*L). Moench) in western Kenya

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Genotype x environment interaction was determined from field experiments conducted to evaluate sweet sorghum genotypes in Western Kenya during the 2011, 2012 and 2013 rainy season from April to July at Alupe, Kibos, Homa Bay and Spectre International farm. The materials used in the study consisted of sixteen sweet sorghum genotypes and two sorghum genotypes sourced from ICRISAT and KARI. The treatments were laid out in a Randomized Complete Block Design (RCBD) and replicated three times. Data were collected on sorghum traits in accordance with the procedure outlined in the ICRISAT sorghum descriptor. The study revealed that genotype by environment interaction had significant influence on most of the traits. This indicates that selection for plant height, girth, brix juice, juice volume and stalks weigh cannot be carried out across the four environments, suggesting that selection for these traits have to be carried separately in each of the four environments.

Key words: Biomass, brix, environment, genotype, sweet sorghum.

INTRODUCTION

Genotype x Environment interaction can be defined as the differential response of varying genotypes under change(s) in the environment (Mather and Caligari, 1976). It refers to instances where the joint effects of genotype and environment are significantly greater or significantly reduced, than would be predicted from the sum of the separate effects (Andrew et al., 1998). In order to exploit the existing variability and develop new high yielding cultivars, sorghum improvement efforts under diverse environmental conditions are needed (Faisal and Aisha, 2011). There are many reports on G × E and stability studies in sorghum (Majisu and Dogget, 1972; Chapman et al., 2000; Haussmann et al., 2000; Kenga et al., 2004). Studying G × E for yield using 12 sorghum genotypes of diverse origin across 25 environments, Alagarswamy and Chandra (1998) found that 12% of the variation was due

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to genotypes, 61% due to environment while G × E accounted for 27%. Chapman et al. (2000) reported that most of the G × E in sorghum was a result of the genotype by location by year, but suggested breeders to deal with the genotype by location type over a fixed number of seasons.

The prevalence of environmental causes of variation over the genetic effects does not suggest that the importance of genotype should be minimized (Faisal and Aisha, 2011). However, global warming and climatic changes will reduce the productivity of many crops around the world. So that a considerable attention should be given to the effect of genotype x environment interaction in the plant breeding programs especially in the developed countries (Ghazy et al., 2012). Developing high yielding cultivars is mainly depending upon existing genetic variation among the germplasm under existing breeding programs. The relative performance of cultivars for quantitative traits such as yield and other characters, which influence yield, vary from an environment to another. Consequently, to develop a variety with high yielding ability and consistency, attention should be given to the importance of stability performance for the genotypes under different environments and their interactions (Ghazy et al., 2012). The interaction between genotype and environment has an important bearing on breeding for better varieties (Allard and Bradshaw, 1964). It is therefore important to conduct multi-location testing, quantify G × E and conduct stability analyses to select superior materials in sorghum.

The objective of the study was to investigate the influence of genotype by environment interaction on sugar and biomass yield of sweet sorghum in Western Kenya.

MATERIALS AND METHODS

Test materials

A total of sixteen varieties and two checks from ICRISAT (IESV 92038/2-SH, NTJ 2, IESV 92008 DL, IESV 93042-SH, IS 2331, IESV 91-018 LT, IESV 91104 DL, IESV 93046, Kenya Agricultural Research Institute (KARI) (KARI Mtama 2, GADAM,) Argentina (Malon, Paisano, Argensor 151 DP, Argensor 165 BIO) and United States of America (NK 5989-29005, NK 7829-29006, NK 8416-19075, NK 8830-29007) were evaluated in Randomized Complete Block Design with three replications during 2011, 2012 and 2013 for the 1st , 2nd and 3rd seasons respectively.

Each entry was raised in four rows of 3 m length with a spacing of 70 cm × 20 cm. Sowing was done manually by placing 3 seeds in holes spaced 20 cm apart. Data were obtained from plants harvested from the two inner rows of each plot. Care was taken to reduce border effects due to unequal competition of cultivars by the appropriate use of sorghum buffer rows. Nitrogen fertilizer was added at a rate of 70 kg N/ha. All the package of practices were followed to raise a good and healthy crop.

Study sites

Four study sites were used; Kibos, CYMMIT farm; altitude 1190 m above the sea level (masl), average daily temperature is 24°C, rainfall per annum is 1441 mm and the soils are planosol. Alupe; altitude is 1165 masl, average daily temperature is 22.2°C, rainfall per annum is 1550 mm and the soils are acrisol. Spectre International farm-Kisumu**,** The soil type is chromic vertisol described as poorly drained, very deep, very dark grey to black, very firm, cracking clay. The average daily temperature is 23.1°C. The annual average rainfall per annum is 1353 mm. The altitude is 1164 masl. Homa Bay; soil types are black cotton, cracking and swelling montmorillonite. The altitude is 1190 masl. The mean daily temperatures are 25.8°C. The annual rainfall per annum ranges from 900 to 1200 mm. The materials were evaluated for three seasons. Data collected included days to 50% flowering, plant height (cm), stem thickness (cm), cane weight (g), juice volume (ml), brix % at 90 and 120 days after planting, pol % juice, purity % juice, panicle height at harvest (cm), panicle diameter (cm) and 100-grain weight (g).

Sampling was done in the following manner: Flowering date was recorded when 50% of the plot had flowered. The length of the plant from the ground to the panicle tip was measured to estimate plant height. Stem diameter was measured 20 cm above ground. The juice volume measured by using measuring cylinder. The fresh main stalk was pressed and 2 to 3 droplets of juice were collected on a sucrose- sensitive refractometer to measure the brix. Pol analysis was done using polarimetric method. Six gram of basic lead acetate was added to 300 ml of juice in clarification process. The juice was filtered through a Whatman filter paper No. 91. The pol reading was then fitted in the formula below to obtain Pol at 20°C; POL20 = PT {1+ 0.000185(T-20) - 0.000003 (T-20)2}.

Data analyses

The data obtained on all the characters over four environments and three seasons was subjected to GenStat 14th edition to perform the analysis of variance (ANOVA). The analysis used the Linear Model for randomized completely block design.

$$Y_{ij} = \mu + r_i + g_j + e_{ij}$$

Where: Y_{ij}= Observed effect for ith replication and jth genotypes, μ = grand mean of the experiment, r_i= effect due to the ith replication, g_j= effect due to jth genotype, e_{ij} = effects due to the residual or random error of the experiment.

Other analysis done included additive main effect and multiplicative interaction (AMMI) and Interaction Principle Component Axes (IPCA).

RESULTS

Performance of genotypes based on brix and biomass

Higher brix value during the 1st season in 2011 (Table 1) was obtained from sweet sorghum cultivated in Kibos (13.9). Among the genotypes subjected to evaluation, IS 2331 recorded highest brix in Kibos (17.19). Pol percentage (Table 1) which is an indicator of sucrose percent varied from 5. 83 to 6.65 percent (environmental mean) across the two environments. Genotype IS 2331 showed the highest pol percent (10.8) while the lowest pol percentage was recorded by IESV 91018 LT (3.4%).

Table 1. Performance of genotypes for sugar and biomass related traits across two environments during the 1st season in 2011.

Location	Brix juice %		Girth (mm)		Height (cm)		Purity %		Pol % juice	
	Alupe	Kibos	Alupe	Kibos	Alupe	Kibos	Alupe	Kibos	Alupe	Kibos
GADAM	9.34	11.23	14.6	16.6	105.33	110.33	27.23	44.43	2.74	4.82
IESV 91018 LT	9.66	10.84	15.5	16.5	210.67	212.67	28.35	32.13	3.49	3.60
IESV 91104 DL	12.9	13.75	14.53	17.73	190.33	181.33	42.2	61.11	5.73	11.07
IESV 92008 DL	15.27	15.07	14.5	17.15	167.33	188.33	59.06	23.42	9.10	4.10
IESV 92038/2 SH	13.4	12.93	14.5	18.37	165..67	173.67	42.67	48.2	5.78	6.17
IESV 93042 SH	11.93	12.56	15.6	16.6	163.67	175.67	47.04	43.7	6.49	5.86
IESV 93046	13.06	14.43	13.87	17.87	270.00	278.20	51.07	57.99	6.78	8.34
IS 2331	15.86	17.19	15.47	17.47	261.00	272.33	62.56	61.97	9.91	10.84
KARI MTAMA 2	11.24	13.35	14.63	15.63	171.50	181.00	34.05	52.2	3.92	7.03
NTJ 2	11.44	14.21	13.97	16.97	200.24	237.67	38.18	30.47	4.41	4.63
Mean	12.41	13.956	14.717	17.08	193.34	201.12	43.24	45.56	5.83	6.65
LSD	4.707	2.356	1.728	1.604	15.75	14.65	29.2	31.03	5.03	5.30
CV%	22.11	9.84	6.84	5.76	11.35	11.15	39.36	39.71	50.23	46.53

The high coefficient of variation for purity percent and pol percent of 39 and 46% respectively in Kibos can be attributed to large variation among the genotypes with respect to the two attributes. For instance, the top performing genotype IS 2331 recorded purity percent of 61.9 and pol percent of 10.8 while the lowest performing genotype IESV 92008 DL registered purity percent and pol percent of 23.4 and 4.1 respectively under the same environment.

IESV 93046 and IS 2331 were the tallest varieties across the four locations (Table 2) registering mean height of 269.64 and 252.76 cm respectively. IESV 93046 was the best performing genotype in terms of juice volume (1199 ml) and brix % (14.2). Environment wise, Homa Bay was best performing registering highest genotypic mean of brix percent and pol percent of 14.8 and 8.8 respectively (Table 3).

Purity is important when sugar is to be produced from the juice. Alupe, Kibos, Homa Bay and Spectre environments varied for purity percent (Table 3) as evident from the varying environment mean (21 to 58.6%). Purity percent was at the maximum in Homa Bay (58.6) and the least was observed in Kibos (21). Among the genotypic means for purity IESV 93046 exhibited the highest value of 73.6% in Homa Bay.

From Table 3 Spectre environment registered the maximum environmental mean (590.2 ml) in terms of juice yield, whereas Alupe environment was the least favored (384 ml). Among the test genotypes, maximum juice yield was recorded by IESV 93046 (1550 ml) at Spectre International farm.

Analysis of variance

Across location and seasons analysis of variance (Table 4) showed that genotypes and seasons were significantly different (P<0.001) for all the major traits evaluated. Locations x seasons interactions were significantly different (P<0.001) for brix juice percent, juice volume and purity percent. Location x variety interactions were significantly different (P<0.001) for girth, stalk weight and juice volume. Higher interactions of location by season by variety was significant (P<0.05) for brix percent. For brix juice percent, genotypes, environments and interactions accounted for 8.9, 31 and 5.5% of the sum of squares treatment respectively (Table 4).

Analysis of variance for Additive Main Effect and Multiplicative Interaction (AMMI) model showed significant differences amongst treatments, genotypes, environments and interactions between genotypes and environments (P>0.001) (Table 5). For girth, genotypes, environments and interactions accounted for 60.8, 28.1 and 10.9% of the sum of squares treatment respectively. For brix juice percent, genotypes, environments and interactions accounted for 14.4, 69.6 and 16.0% of the sum of squares treatment respectively. For purity juice percent, genotypes, environments and interactions accounted for 19.1, 60.1 and 20.7% of the sum of squares treatment respectively. When the analysis was split into Interaction Principle Component Axes (IPCA), IPCA-1 and IPCA-2 showed significant different mean purity percent (P<0.01) and captured 58.5 and 37.3% of the sum of squares for interaction (Table 5).

Figure 1 presents AMMI biplot providing a visual expression of the relationships between the second interaction principal component axis (IPCA2) and means of genotypes and environments based on brix percent juice.

The AMMI biplot (Figure 1) showed four groupings of genotypes; IESV 91018 LT, generally low brix and stable; NK 7829-29006 and KS 5989-29005, low brix and

Table 2. Mean of agronomic and quality parameters of sweet sorghum genotypes across locations in 2012 season two at 120 days after planting.

Variety	Height (cm)	Girth (mm)	Brix (%)	Pol (%)	Juice volume (mm)	Purity (%)	Grain weight (g)	Stalk dry weight (g)
ARGENSOR 151 DP	139.49	18.3	9.45	4.01	452	37.68	203.6	346.9
ARGENSOR 165 BIO	217.49	19.5	11.11	4.78	796	39.44	302.4	659.4
GADAM	107.01	18.3	9.43	4.32	215	40.87	146	300.6
ICSV 91018 LT	220.53	22.5	7.56	2.34	1161	26.41	250	567.7
ICSV 9104 DL	196.71	20.3	12.7	6.74	607	46.76	269.6	402.3
ICSV 92008 DL	178.85	19.2	12.56	6.44	698	45.52	313.4	456.4
ICSV 92038/2 SH	166.55	20.5	11.56	5.72	536	43.38	286	532.8
ICSV 93042 SH	167.6	20	11.08	5.52	532	44.45	237.8	414.5
ICSV 93046	269.64	20.4	14.24	9.47	1199	57.30	290.7	448.2
IS 2331	252.76	19.2	13.32	7.72	694	53.00	251.7	587.8
KARI MTAMA 2	167.88	18.7	11.11	6.05	190	45.68	183.7	404.1
KS 5989-29005	120.18	21.2	9.77	4.73	232	43.64	219.1	420.6
MALON	117.06	20.5	8.91	3.87	279	37.33	220.6	417.4
NK 7829-29006	95.59	22	8.94	5.48	168	47.63	202.9	383.3
NK 8416-19075	114.9	18.3	9.04	4.64	111	44.91	192.3	295.6
NK 8830-29007	100.86	21.3	8.84	4.13	178	42.07	203.2	384.0
NTJ 2	202.47	20	10.12	4.07	731	36.09	273	453.4
PAISANO	115.18	21.3	9	4.22	411	42.51	252	555.4
P-values	0.016	<.001	<.001	<.001	0.035	<.001	<.001	<.001
Lsd	21.194	2.20	2.307	2.432	317.8	13.59	134.20	159.61
Sed	10.721	1.11	1.167	1.229	160.8	6.87	67.89	80.74
CV %	8.0	6.8	13.6	28.8	38.6	19.6	34.8	26.3

Lsd=Least significance difference, Sed= Standard error of difference, CV=Coefficient of variation.

unstable. The other two groups included NK 8830-29700 and NTJ 2 that had moderate brix yield and stable and IESV 93046 that had high brix yield but unstable. Homa Bay showed high brix yields and high stability while Kibos was low yielding and very unstable environment. However, Spectre was more stable than Alupe. Figure 2 presents AMMI biplot providing a visual expression of the relationships between the second interaction principal component axis (IPCA2) and means of genotypes and environments based on girth.

The AMMI biplot (Figure 2) showed four groupings of genotypes; NK 8416-19075 thin and unstable; ARGENSOR.151 DP thin and stable. The other two groups included IESV 93046 and NTJ 2 that had moderate girth and stable and NK 7829-29006 and KS 5989-29005 that were thick but unstable. Homa Bay and Alupe showed high stem girth and high stability while Spectre and Kibos were low girth and unstable environments.

Figure 3 presents AMMI biplot providing a visual expression of the relationships between the second interaction principal component axis (IPCA2) and means of genotypes and environments based on purity juice percent.

The AMMI biplot (Figure 3) showed three groupings of genotypes; IESV 91018 LT low purity percent and unstable; IS 2331 moderate purity percent and stable; IESV 93046 high purity and unstable. Homa Bay environment registered high purity percent but was unstable while Kibos recorded low purity percent and was equally unstable.

Results from AMMI analysis (Table 6) revealed that the best environment was Homa Bay recording the best overall mean for girth, brix juice percent and purity percent. The best four genotypes in terms of brix were IESV 93046, IESV 92008 DL, IS 2331 and IESV 91104 DL. IESV 93046 can be considered stable and adaptable to wider environments in terms of sugar quality. Kibos consistently registered the lowest genotypes means on the parameters evaluated.

DISCUSSION

High brix was recorded by some genotypes (Table 3), IESV 93046 registered brix of 17.2% in Alupe and IESV 92008 DL registered brix of 17.2% in Homa Bay. The results are closer to what was observed by Reddy et al., (2005) of 16 to 23% brix and slightly higher than that observed by Woods (2000) of 11.0 to 18.5% brix among

Table 3. Mean of quality parameters of sweet sorghum genotypes by locations in 2012 season two at 120 days after planting.

Variety	Brix (%)				Pol (%)				Juice Volume(ml)				Purity %			
	AL	HB	KB	SP	AL	HB	KB	SP	AL	HB	KB	SP	AL	HB	KB	SP
ARGENSOR 151 DP	7.37	14.21	8.97	7.24	2.57	8.46	2.84	2.15	147	372	867	422	35.1	59.5	27	29.5
ARGENSOR 165 BIO	10.02	14.77	10.13	9.52	3.97	8.24	3.49	3.43	537	923	843	880	32.3	55.1	34	36.1
GADAM	11.14	12.25	5.17	9.17	5.41	7.18	0.50	4.18	143	212	328	178	46.5	57.5	14	45.5
IESV 91018 LT	10.57	9.17	3.90	6.60	4.09	2.96	0.44	1.85	890	1293	1103	1357	38.4	31.1	8.9	27.2
IESV 9104 DL	17.11	16.35	6.11	11.24	11.52	9.34	1.23	4.89	718	680	390	640	67.1	57.1	20	43.4
IESV 92008 DL	13.10	17.25	7.45	12.45	6.91	10.91	1.52	6.42	555	688	640	908	52.4	62.3	16	51.6
IESV 92038/2 SH	13.99	16.22	6.06	9.97	7.78	9.86	1.01	4.23	463	635	468	577	55.7	60.7	15	42
IESV 93042 SH	14.37	14.23	5.43	10.27	8.83	7.59	1.10	4.54	463	650	299	717	59.6	53	21	44.1
IESV 93046	17.26	18.51	5.34	15.83	12.07	13.63	0.84	11.34	933	1423	890	1550	69.4	73.6	15	71.2
IS 2331	16.83	16.83	8.04	11.57	11.70	11.12	2.31	5.77	612	885	493	787	68.6	66	28	49.9
KARI MTAMA 2	11.46	18.56	5.62	8.78	6.71	12.50	1.46	3.51	90	157	228	283	51.6	67.4	24	39.4
KS 5989-29005	9.13	15.14	5.88	8.95	4.51	9.52	1.53	3.37	137	188	303	300	49	62.9	25	37.5
MALON	6.57	14.21	5.96	8.89	3.12	8.29	0.87	3.19	133	317	279	385	42.1	57.8	14	35.3
NK 7829-29006	5.44	14.46	6.32	9.52	6.48	9.14	1.89	4.39	85	183	193	210	54.6	63.2	28	44.7
NK 8416-19075	7.46	13.58	6.61	8.52	5.64	7.37	1.80	3.72	52	98	215	78	51.9	55.9	28	44.2
NK 8830-29007	6.91	14.13	5.72	8.61	3.03	8.45	1.38	3.64	103	227	200	183	43.2	59.4	23	42.3
NTJ 2	11.74	12.94	6.21	9.61	5.67	6.25	0.79	3.57	540	943	607	833	47.7	48.1	12	36.5
PAISANO	6.58	13.66	7.34	8.42	2.37	8.81	2.08	3.63	320	452	538	335	35.3	64.4	28	42
Location Means	**10.95**	**14.80**	**6.46**	**9.73**	**6.24**	**8.87**	**1.50**	**4.32**	**384.0**	**573.7**	**493.6**	**590.2**	**50.0**	**58.6**	**21**	**42.36**
P-values	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	0.004	<.001	<.001
Lsd	2.674	2.746	3.492	1.960	3.009	2.645	3.406	1.828	147.9	195.5	218.5	210.8	15.03	20.59	11.35	13.63
Sed	1.314	1.350	1.718	0.9645	1.467	1.454	1.674	0.8995	72.77	96.11	107.5	103.7	7.314	10.02	5.655	6.708
CV %	14.47	17.18	17.25	13.06	26.81	31.89	27.25	26.24	23.18	17.05	21.95	21.01	16.80	23.36	11.92	19.38

AL=Alupe, HB=Homa Bay, KB=Kibos and SP=Spectre International Farm, Lsd=Least significance difference, CV=Coefficient of variation.

genotypes evaluated. This variation could be attributed to stalk variety, different soils and climatic conditions.

Purity is important when sugar is to be produced from the juice. Alupe, Kibos, Homa Bay and Spectre environments varied for purity percent (Table 3) as evident from the varying environment mean (21 to 58.6). Mean purity percent was at the maximum in Homa Bay (58.6) and the least was observed in Kibos (21). Among the genotypic means for purity IESV 93046 exhibited the highest value of 73.6% in Homa Bay. Similar report was given earlier by Woods (2000) where the apparent purity for the sweet sorghum varieties considered varied from 48.2 to 69.7% whereas that of sugarcane juice was 83.6%. Sucrose purity is used to calculate the ease with which sucrose can be extracted and crystallized and 75% is required as the minimum (Woods, 2001). Among the genotypes evaluated IESV 93056 has potential of being exploited for sucrose extraction and crystallization.

Superior performance of genotypes in Homa Bay (Table 3) can be attributed to montmorillonite soils in this environment which are very efficient in nutrient uptake. Genotypes performed better in Spectre International farm than Kibos despite the fact that these environments have similar average

Table 4. General ANOVA for sugar and biomass traits across location and seasons.

Source of variation	d.f.	Girth	Explained percentage	Stalk weight	Explained percentage	Brix juice %	Explained percentage	Juice volume	Explained percentage	Purity juice %	Explained percentage
Location	3	2308.77***	19.59	1.29**	1.65	817.70***	31.02	310314.00*	1.92	4101.40*	4.62
Season	1	16494.31***	46.65	27.40***	11.67	495.85**	6.27	7617835.00***	15.72	7617.20**	2.86
Location x Season	3	7.89ns	0.07	3.06ns	3.91	104.58***	3.97	607658.00***	3.76	12516.30***	14.10
Location/season/rep	16	4.02**	0.18	0.17ns	1.16	42.26***	8.55	42435.94ns	1.40	622.97*	3.74
Variety	17	19.00***	0.91	5.48**	39.67	41.61***	8.94	992040***	34.80	2120.90***	13.53
Location x Variety	51	2.01***	0.29	0.23ns	4.99	8.53ns	5.50	47190ns	4.97	451.70ns	8.65
Season x Variety	17	4.85***	0.23	1.72***	12.45	12.36ns	2.66	396022***	13.89	776.60ns	4.96
Location x Season x Variety	51	0.45ns	0.06	0.30***	6.51	10.54*	6.80	55770***	5.87	482.20	9.23
Residual	284	1.80	1.45	0.14	16.93	7.32	26.29	27732	16.25	358.50	38.22
Total	427	82.81		0.55		18.52		113491		623.88	

ns=not significant *Significant at 0.05, ** significant at 0.01, *** significant at 0.001.

Table 5. AMMI ANOVA for sugar and biomass traits across locations.

Source of variation	df	Girth	Explained percentage	Brix Juice %	Explained percentage	Purity juice %	Explained percentage
Treatments	71	9.99***		40.59***		1011***	
Genotypes	17	25.41***	60.88	24.40***	14.40	809***	19.16
Environments	3	66.66***	28.19	668.50***	69.60	14382***	60.11
Block	8	4.19ns		59.36***		1288***	
Interactions	51	1.52ns	10.92	9.05**	16.00	292***	20.73
IPCA I	19	3.28ns	80.39	15.09***	62.26	458***	58.50
IPCA II	17	0.80ns	17.55	6.81ns	25.16	327**	37.36
Residuals	15	0.11ns	2.19	3.93ns	12.80	41ns	4.13
Error	136	2.24		5.23		139	
Total	215	4.87		18.92		470	

ns=not significant *Significant at 0.05, ** significant at 0.01, *** significant at 0.001.

daily temperatures and rainfall per annum. Very deep and firm clay soils at Spectre International farm might have contributed to better performance under this environment. Woods (2000) reported that sweet sorghum performance variation could be attributed to different soil conditions.

Combined analysis of variance (Table 4) revealed highly significant (P≤0.001) variations among environments, genotypes, seasons, genotype x

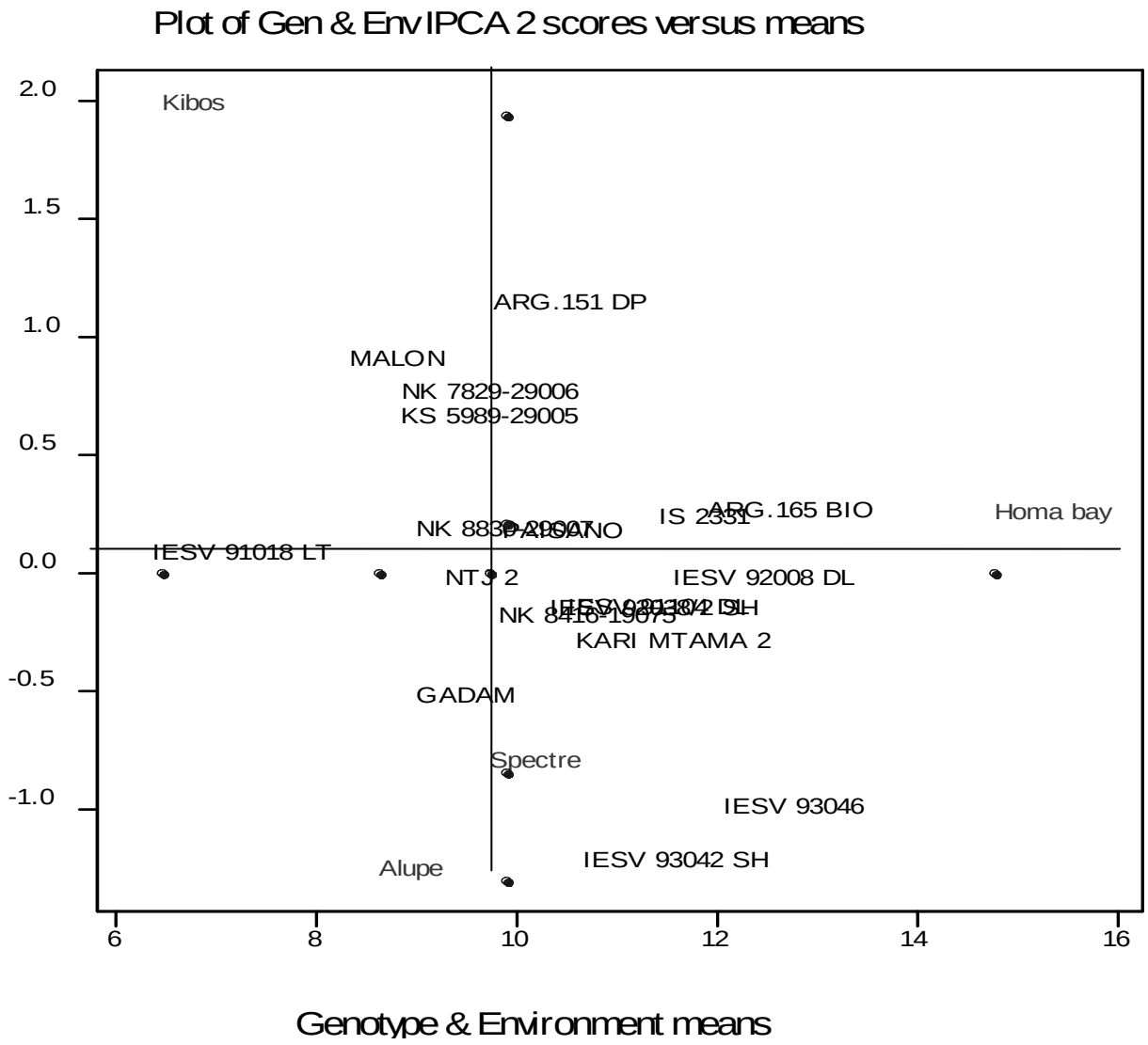

Figure 1. AMMI biplot of interaction principal component axis-2 (IPCA-2) against mean brix % juice of 18 genotypes and four environments.

environment and environment x variety x season interaction.

This result revealed that there was a differential yield performance among the sweet sorghum genotypes across testing environments and seasons. Maarouf and Moataz (2009) reported variation between sorghum genotypes with respect to fodder production. This indicate that, simultaneous selection for girth, brix% , stalk weight and purity percent is not possible across the four environments and that selection for each location have to be carried out separately. This limit their wider utilization, as reported by Pham and Kang (1988) who stated that, significant G x E for a quantitative trait is known to reduce the usefulness of the genotype means over all locations or environments for selecting and advancing superior genotypes to the next stage of selection.

Across location and seasons analysis of variance (Table 4) showed that genotypes and seasons were significantly different (P<0.001) for all sugar related traits. Seasons x variety interactions were significantly different (P<0.001) for girth, stalk weight and juice volume. Chapman et al., (2000) reported that most of the G × E in sorghum was a result of the genotype by location by year, but suggested breeders to deal with the genotype by location type over a fixed number of seasons. This difference among seasons can be attributed to heavy rains received in 2012.

When the interaction between environments and genotypes was significant further analysis was done using Additive Main Effects and Multiplicative Interaction (AMMI) model to determine adaptive response of specific

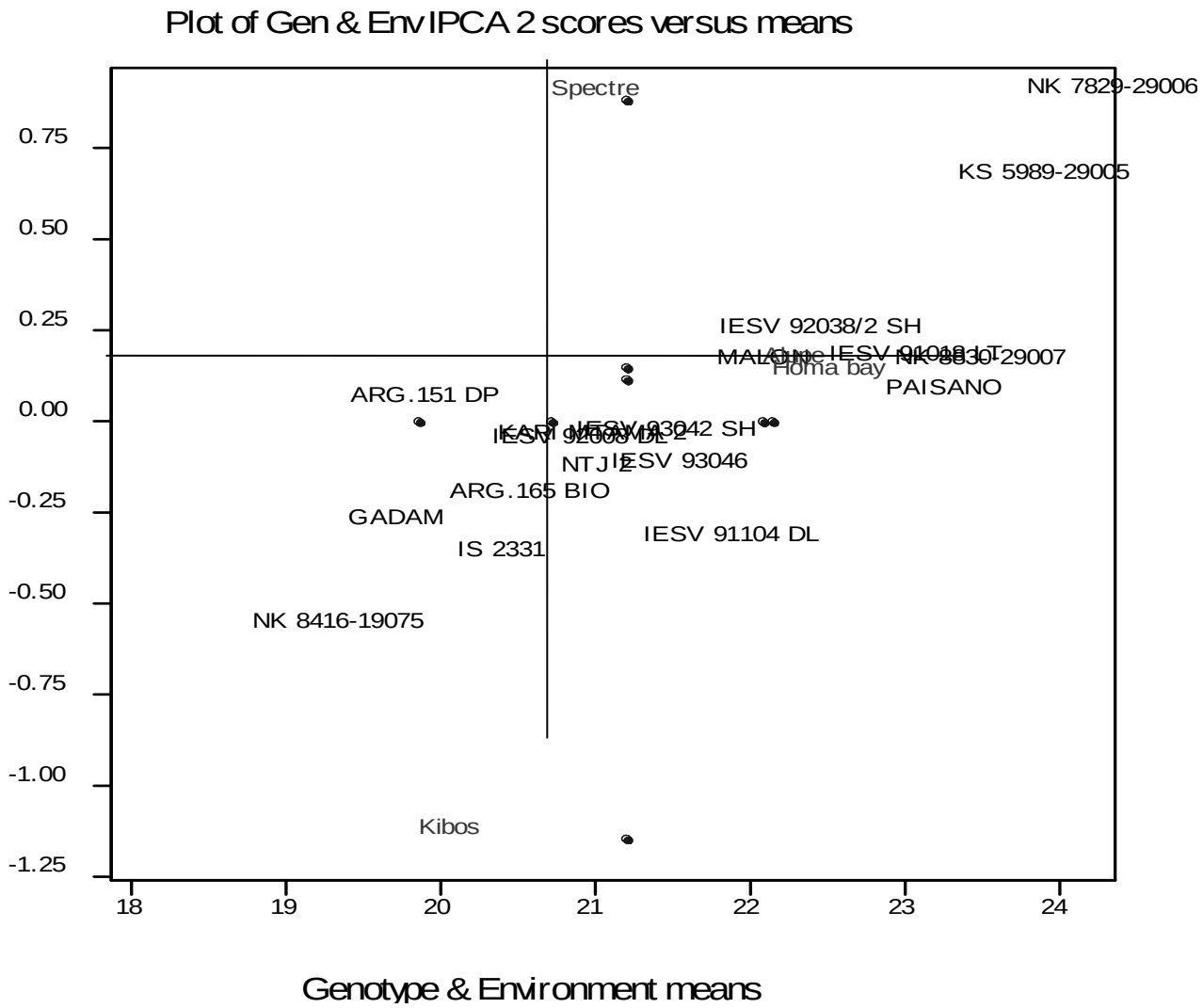

Figure 2. AMMI biplot of interaction principal component axis-1 (IPCA-1) against mean girth of 18 genotypes and four environments.

genotypes to specific locations (Annicchiarico, 2002; Egesi and Asiedu, 2002).

Analysis of variance for Additive Main Effect and Multiplicative Interaction (AMMI) model showed significant differences amongst treatments, genotypes, environments and interactions between genotypes and environments ($P<0.001$) (Table 5). For brix percent, genotypes, environments and interactions accounted for 14.4, 69.6 and 16.0% of the sum of squares treatment respectively. These variations are closer to the ones reported by Alagarswamy and Chandra (1998) while studying G × E for yield using 12 sorghum genotypes of diverse origin across 25 environments. He found that 12% of the variation was due to genotypes, 61% due to environment while G × E accounted for 27%.

Interaction principal component axis (IPCA1) based on brix percent was significant ($P<0.001$) while Interaction principal component axis (IPCAII) on the same parameter was not significant (Table 5). Van Euwijik (1995) noted that the first axis represents the hypothetical environmental variable which describes interaction as much as possible and therefore is best suited to discriminate between genotypes.

Conclusions

High performance demonstrated by genotypes IESV 93046 and IS 2331 for stem brix and stem biomass shows their potential for exploitation for ethanol production. Homa Bay is the best environment for sweet sorghum production. The study indicated that selection for girth, brix percent juice, purity percent and stalks weigh cannot be carried out across the four environments, suggesting that selection for these traits have to be carried separately in each of the four environments.

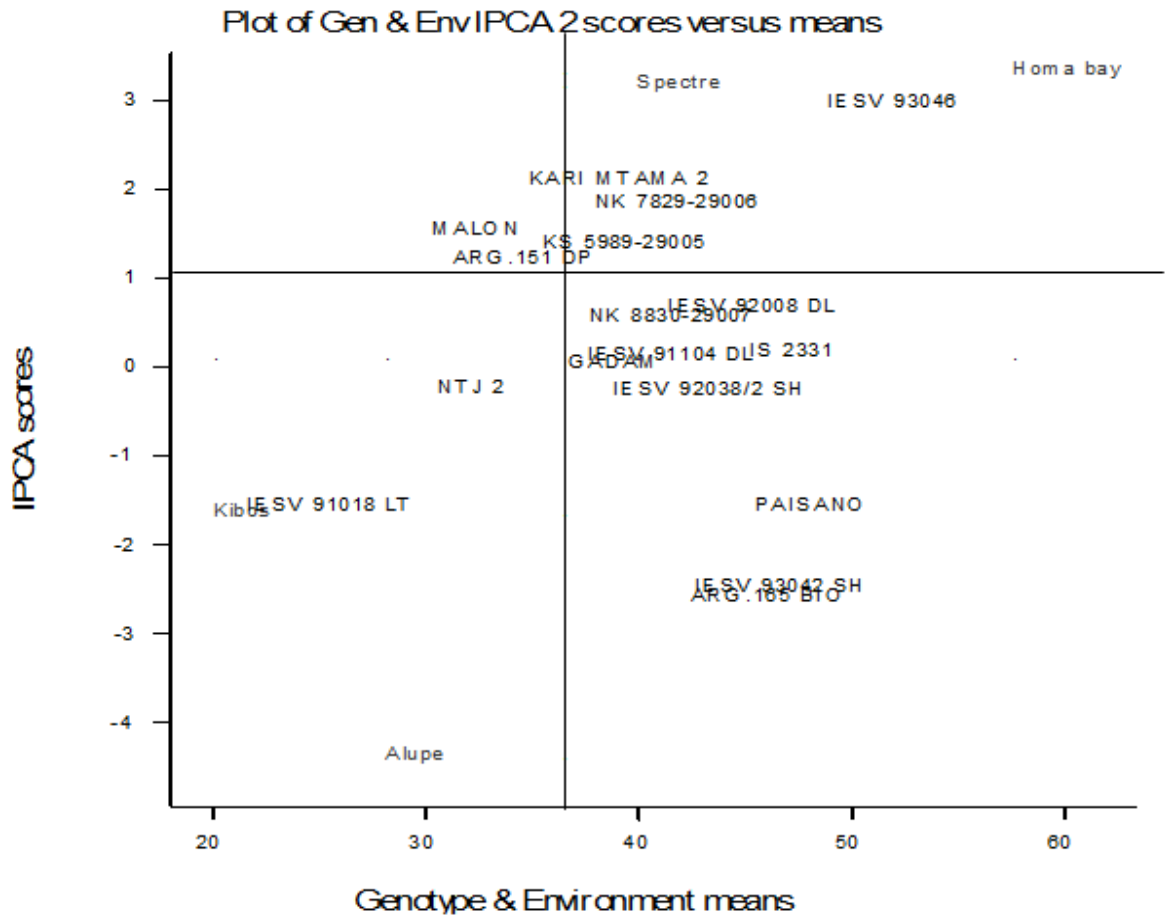

Figure 3. AMMI biplot of interaction principal component axis-1 (IPCA-1) against mean purity % of 18 genotypes and four environments.

Table 6. First four AMMI selections per environment on the basis of girth, brix % and purity %.

S/N	Girth (mm)					
	Environment	**Mean**	**1**	**2**	**3**	**4**
1	Homa bay	22.14	NK 8830-29007	PAISANO	KS 5989-29005	MALON
2	Alupe	22.08	NK 8830-29007	PAISANO	KS 5989-29005	MALON
3	Spectre	20.71	NK 7829-29006	KS 5989-29005	PAISANO	NK 8830-29007
4	Kibos	19.86	NK 7829-29006	KS 5989-29005	PAISANO	NK 8830-29007
				Brix%		
1	Homa bay	14.763	IESV 93046	IESV 92008 DL	IS 2331	IESV 91104 DL
2	Spectre	9.731	IESV 93046	IESV 92008 DL	IS 2331	IESV 91104 DL
3	Alupe	8.626	ARG.165 BIO	IESV 93042 SH	NK 8416-19075	PAISANO
4	Kibos	6.46	ARG.165 BIO	ARG.151 DP	IS 2331	IESV 92008 DL
				Purity %		
1	Homa bay	57.6	IESV 93046	NK 7829-29006	IS 2331	KARI MTAMA 2
2	Spectre	39.9	IESV 93046	IESV 92008 DL	IS 2331	GADAM
3	Alupe	28.12	IESV 93042 SH	PAISANO	ARG.165 BIO	GADAM
4	Kibos	20.01	ARG.165 BIO	PAISANO	NK 8416-19075	IS 2331

Conflict of Interests

The authors have not declared any conflict of interests.

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Full Length Research Paper

Evaluation of tropical maize inbred lines for resistance to two stem borer species, *Busseola fusca* and *Chilo partellus*

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Stem borers, *Busseola fusca* (Fuller) Noctuidae*, Lepidoptera* and *Chilo partellus* (Swinhoe) Pyralidae*, Lepidoptera*, are serious insect pests of maize. However, genotypes showing exclusive resistance to each of these borers and with resistance to both species have not been identified in Kenya. The objective of this study was to evaluate tropical maize inbred lines for resistance to the two species. 112 maize inbred lines were artificially infested with the stem borers at three sites in Kenya. Each row of each line received three different treatments in different parts, namely infestation with *B. fusca* larvae, infestation with *C. partellus* larvae, and protection with beta 25 g/L cyfluthrin pesticide. Data was collected on leaf feeding damage rating, cumulative stem tunnel length, number of exit holes, number of dead-hearts, stalk strength and selected agronomic traits. There were significant differences among the test genotypes, ($p<0.01$) for resistance to *B. fusca* and *C. partellus,* for all the traits measured. The results also showed that most of the test genotypes were susceptible to *B. fusca* and less so to *C. partellus*. Twenty one (21) lines showed resistance to both *B. fusca and C. partellus* in at least two sites, and only four lines showed resistance to both species across the locations. Among all the test genotypes, 26 lines showed resistance to *C. partellus* only, while five entries had resistance to *B. fusca* only. Furthermore, 84 and 28 entries showed susceptibility to *B. fusca* and *C. partellus,* respectively. The others were categorized as either moderately resistant or moderately susceptible to either species. The identified inbred lines variously resistant to *B. fusca* and *C. partellus* may be used as parents in hybrid breeding programmes that emphasize stem borer resistance or as sources of resistance in breeding programs.

Key words: *Busseola fusca*, *Chilo partellus*, combined resistance, tropical maize inbred lines.

INTRODUCTION

New maize varieties with tolerance to biotic and abiotic stresses and with better agronomic traits have been developed in Africa maize breeding programs. The spotted stem borer (*Chilo partellus* Swinhoe) Pyralidae and African stem borer (*Busseola fusca* Fuller) Noctuidae, Lepidoptera are among the most damaging insect pests that greatly reduce maize grain yield in east African environments (Citation). Tropical environments are favourable for insect development and lead to the formation of several generations of the pests in the same

season leading to severe crop yield losses (Mailafiya et al., 2011). For example, in Kenya, grain yield loss due to stem borers in maize is estimated annually at about 400,000 metric tons or about $72 million (De Groote et al., 2003; De Groote et al., 2005). This amount represents an average of 13.5% of the farmers' total annual harvest of maize.

There is, however, limited germplasm with resistance to these pests in most maize breeding programs. There are seldom those identified with combined resistance to both insect pests if they occur. Several options for managing maize stem borers have potential to mitigate their damaging effects, but each option has its own limitations. Host plant resistance forms an important part of integrated pest management as it provides inherent control without environmental issues and is compatible with other pest management approaches (Singh et al., 2012). Effective breeding methods for resistance to borer damage could, therefore, be designed by plant breeders using both improved and new sources of stem borer resistance.

Development of effective methods requires a better understanding of the genetic basis of the resistances among the germplasm used. Suitable maize germplasm should have resistance to both *B. fusca* and *C. partellus*. Recent reports indicate that climate change has led to *C. partellus* increasingly displacing *B. fusca* from the high altitude areas in Kenya (Mailafiya et al., 2011; Tefera et al., 2011; Mwimali et al., 2015). Furthermore, farmers exchange maize germplasm across agro-ecologies, therefore, the need to investigate the reaction of these tropical maize inbred lines for resistance to these borers becomes paramount. The aim of this study was to evaluate the responses of tropical maize inbred lines for resistance to *B. fusca* and *C. partellus* the two major stem borer species in Eastern Africa.

MATERIALS AND METHODS

Germplasm

One hundred and twelve (112) maize inbred lines used in the study were sourced from the International Maize and Wheat Improvement Center (CIMMYT), Mexico and the Kenya Agricultural and Livestock Research Organization (KALRO) breeding programmes (Table 1). Two elite, but stem borer resistant and susceptible maize lines from CIMMYT and KALRO were included as checks. The lines were developed from the CIMMYT multiple borer resistance (MBR) population. The MBR population was developed through a recurrent selection method under artificial infestation with southern corn borer (SWCB), sugarcane borer (SCB) *Diatrae sacharalis*, European corn borer (ECB) *Ostrinia nubilalis*, and fall armyworm (FAW) *Spodoptera* species in various locations globally (Smith et al., 1989).

Testing locations

Experiments were established at KALRO Kakamega, KALRO Kiboko, and KALRO Embu sites in Kenya. KALRO Kakamega (37°75'E 2° 15'S, 1585 m asl) centre is located in the moist transitional mid altitude agro-ecological zone of Western Kenya and experiences mean annual temperatures of 25°C. Kakamega lies within a high potential agro-ecological zone and receives a bimodal mean annual rainfall of approximately 1850 to 1916 mm. The soils in Kakamega are well drained, moderately deep to very deep, red to dark in colour and in some places shallow over petroplinthite (Jaetzold and Schmidt, 1982).

KALRO-Kiboko (2°15'S 37°75' E, 975 m asl) is located in the dry mid altitude agro-ecological zone of Eastern Kenya and experiences mean annual temperature ranges of 28 to 37°C, with February and October being the hottest months. Kiboko receives a mean annual rainfall of approximately 530 mm. The soils are well drained, Fluvisols, Ferralsols, and Luvisols with soil pH of about 7.9 (Jaetzold and Schmidt, 1982; KARI Land Resources and Analytical Services, 2007).

KALRO-Embu centre (03°56' 44'S and 39°46' 00'E, 1510 m asl) is located in the moist transitional mid altitude agro-ecological zone of eastern slopes of Mt. Kenya and experiences mean annual temperature ranges of 14 to 25°C. Embu lies within a high potential agro-ecological zone. Rainfall received is bi-modal ranging between 800 and 1400 mm annually. The soils are deep (about 2 m); well weathered Humic Nitisols with moderate to high inherent fertility (Jaetzold and Schmidt,1982).

Experimental design and treatments

The maize inbred lines were evaluated in a 28 × 4 α-lattice design with three replications in each location. Each inbred line was sown to one row plot of 6.75 m each per replication. Two seeds were sown per hill and later thinned to one. Each plot consisted of one row with inter-row spacing of 0.75 m and inter-hills spacing of 0.25 m within the rows.

Fertilizers were applied to give 60 kg N and 60 kg P_2O_5 ha^{-1} as recommended for each location. Nitrogen was applied in two splits, while supplementary irrigation was applied when needed. The fields were kept free of weeds by hand weeding throughout the growth cycle.

Artificial infestation with insects

Each 6.75 m plot was divided into three parts, namely, *B. fusca* and *C. partellus* infested on either side of the plot at Embu and Kakamega, while the middle part was protected using insecticide Bulldock® (active ingredient, beta cyfluthrin 25 g/L). At Kiboko, 5 m row plots were used, and were infested with *C. partellus* on one half of the plot while the remaining part was protected using the insecticide. Insect larvae were obtained from the International Centre for Insect Physiology and Ecology (ICIPE) and the KALRO Katumani centres' stem borer insect pests mass rearing facilities (Tefera et al., 2010, 2011). Plants were artificially infested in a controlled and uniform manner with the respective stem borer species by placing 10 first instar larvae in the maize whorl using a camel brush 21 days after planting.

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Table 1. Scale for scoring stem borer leaf damage from seedling to whorl-stage in maize (CIMMYT, 1989).

Numerical scores	Visual ratings of plant damage	Reaction to resistance
0	No damage	Probable escape
1	Few pin holes	Highly resistant
2	Few shot holes on a few leaves	Resistant
3	Several shot holes on leaves (<50%)	Resistant
4	Several shot holes on leaves (>50%) or small lesions (<2 cm long)	Moderately resistant
5	Elongated lesions (>2 cm long) on a few leaves	Moderately resistant
6	Elongated lesions on several leaves	Susceptible
7	Several leaves with long lesions with leaf tattering	Susceptible
8	Several leaves with long lesions with severe leaf tattering	Highly susceptible
9	Plant dying due to death of growing points (dead-hearts)	Extensively sensitive to damage

Data collection and analysis

Plants were evaluated for leaf damage scores using a scale of 1 (resistant) to 9 (susceptible) (Table 1) (CIMMYT, 1989) at the V3 stage of maize growth.

Other plant damage parameters were measured at harvest, namely, cumulative tunnel length (measured as the total length of tunneling along the maize stalk), tunnel length to plant height ratio, number of exit holes, number of dead-hearts, stalk strength, and number of larvae recovered per plant. Agronomic traits were measured following standard protocols used at CIMMYT (CIMMYT, 1989). The traits measured were number of days to anthesis and to silking, plant height (cm), ear height (cm), ear position (ratio of plant height to ear placement), number of ears harvested, stem and root lodging, grain weight (kg) and moisture content (%) at harvest, plant stand (number of plants per row at harvest), number of rotten ears, plant and ear aspect (where 1=good and uniform plants/ears with the stature, colour and strength preferred in the area, 5=ugly plants/ears with the undesirable features in the area), stem diameter (measurement across the stalk) (cm), internode length (four below the upper-most ear), and leaf damage.

A rank summation index (RSI) was constructed to determine the ranking of each line within the population for suitable response. The index was obtained by the sum of the means of each of the leaf feeding damage score, number of dead-hearts, number of exit holes, and cumulative stem tunnel length for each line, to get its mean performance when compared with other lines within the same population. An entry with the least value was ranked higher for the resistance traits. The rank selection index (Mulamba and Mock et al., 1978; Mutinda et al., 2013) was determined as follows:

$RSI=\sum Ri's$

where Ri is the rank of mean of each of the desired traits. Rank summation index is the mean performance of each of the desired traits of each genotype using the ranking of leaf feeding damage score, number of dead-hearts, number of exit holes, and cumulative stem tunnel length.

Least square means for insect damage parameters and agronomic traits were calculated using plot data for each location separately. All analysis of variance using PROC GLM of SAS was performed for individual as well as for combined environments, considering environments as random effects and genotypes as fixed effects (SAS Institute Inc., 2012). Genotypic and phenotypic correlation coefficients were determined using variance-covariance matrix and estimates of genotypic and phenotypic variances (Falconer and Mackay, 1996).

Genotypic correlation was calculated as follows:

$$r_G = \sigma_{G\,(X,\,Y)} / \sqrt{\sigma^2_{G(X)}, \sigma^2_{G(Y)}}$$

where r_G is the genetic correlation between traits X and Y, $\sigma_{G\,(X,\,Y)}$ is the genotypic covariance between trait X and Y, and $\sigma^2_{G(X)}$ is the genotypic variance of trait X and the $\sigma^2_{G(Y)}$ is the genotypic variance of trait Y.

Phenotypic correlation was calculated as follows:

$$r_P = \sigma_{P\,(X,\,Y)} / \sqrt{\sigma^2_{P(X)}, \sigma^2_{P(Y)}}$$

where r_P is the phenotypic correlation between traits X and Y, $\sigma_{P\,(X,\,Y)}$ is the phenotypic covariance between trait X and Y, and $\sigma_{P\,(X)}$ is the genotypic variance of trait X and the $\sigma^2_{P(Y)}$ is the phenotypic variance of trait Y.

Correlation coefficients based on plant damage and some agronomic traits for *B. fusca* and *C. partellus* were also computed. In broad-sense heritability, H^2 was estimated using the following formulae:

$H^2=Vg/Vp,$

where Vg is the genotypic variance, while the Vp is the phenotypic variance.

RESULTS

Mean performance of maize inbred lines

There were highly significant differences for resistance to both *B. fusca* and *C. partellus* ($p\leq0.01$) (Tables 2 and 3). At Embu and Kakamega, significant differences were observed for leaf feeding damage ($p\leq0.01$), number of exit holes ($p\leq0.03$ to 0.04), and number of dead hearts ($p\leq0.01$) for *B. fusca* and *C. partellus*, except for cumulative stem tunnel length for both sites.

At Embu and Kakamega, the genotypic variances ranged from 0.01 to 0.36 for all sites under *B. fusca* and *C. partellus* infestation (Table 3). Mean performance of entries at Embu under *B. fusca* infestation showed a wide range for dead hearts (0 to 3.05), leaf feeding damage (1 to 6.76), number of exit holes (0 to 11.40), and cumulative tunnel length (0.08 to 5.48 cm). There was a

Table 2. Mean performance of top 19 maize inbred lines for selected stem borer resistance traits under *B. fusca* infestation at Embu (averaged over two seasons).

Entry	Genotype	No. of dead hearts	No. of exit holes	Stem borer leaf Damage scores (1-9)	Cumulative tunnel length (cm)	Rank selection index	Rank
91	CKSBL10040	0.01	1.20	1.69	0.11	0.75	1
90	CKSBL10045	0.01	0.80	2.20	0.08	0.77	2
85	CKSBL10039	0.03	3.50	1.67	0.98	1.55	3
82	CKSBL10042	0.02	2.40	2.32	0.44	1.30	4
81	CKSBL10038	0.02	6.90	1.44	0.87	2.31	5
16	CKSBL10206	0.02	4.70	2.52	0.16	1.85	6
10	CKSBL10026	0.28	8.80	2.25	0.12	2.86	7
61	CKSPL10090	0.03	8.10	1.63	1.00	2.69	8
73	CKSBL10016	0.19	6.50	2.11	0.92	2.43	9
75	CKSBL10028	0.08	3.10	2.46	0.82	1.62	10
41	CKSBL10157	0.00	5.10	2.02	1.12	2.06	11
13	CKSBL10203	0.00	0.00	2.31	0.79	0.78	12
70	CKSBL10013	0.02	7.90	1.80	1.23	2.74	13
24	CKSBL10165	0.03	3.50	1.96	1.32	1.70	14
95	CML312	0.02	11.40	2.33	0.60	3.59	15
21	CKSBL10213	0.00	10.40	2.13	0.86	3.35	16
65	CKSPL10229	0.07	5.10	2.12	1.22	2.13	17
49	CKSPL10028	0.02	8.30	2.50	0.76	2.90	18
63	CKSPL10146	0.75	6.90	1.97	0.66	2.57	19
96	CML395 (sus. check)	3.05	8.71	6.76	5.48	6.00	92
	Genotype variance	0.01	0.05	0.18	0.22	-	-
	Residual variance	0.06	0.31	0.39	3.06	-	-
	Grand mean	0.21	4.90	2.55	2.08	-	-
	LSD	0.42	0.99	1.13	3.12	-	-
	CV	23.65	28.69	22.43	25.75	-	-
	Heritability	0.21	0.32	0.58	0.18	-	-
	P-value	0.01	0.03	<0.0001	0.16	-	-

sus. check: Susceptible check.

varied range for heritability estimates (0.18 to 0.58) for all traits among the top 19 entries under *B. fusca* infestation (Table 2).

In Kakamega, the mean performance of entries under *B. fusca* infestation showed a wide range for dead hearts (0 to 3.31), leaf feeding damage (0.96 to 4.03), number of exit holes (2.15 to 9.08), and cumulative tunnel length (0.02 to 2.27 cm). There was a diverse range for heritability estimates (0.28 to 0.58) for all traits among the top 19 entries under *B. fusca* infestation (Table 3).

Mean performance of entries at Embu under *C. partellus* infestation showed a wide range for dead hearts (0.00 to 1.33), leaf feeding damage (1.72 to 6.65), number of exit holes (0.30 to 6.93), and cumulative tunnel length (0.02 to 0.52). There was a varied range for heritability estimates (0.31 to 0.74) for all traits among the top 19 entries under *B. fusca* infestation (Table 4).

In Kakamega, the mean performance of entries under *C. partellus* infestation revealed a widespread range for dead hearts (0.00 to 1.32), leaf feeding damage (1.80 to 3.47), number of exit holes (0.17 to 1.79), and cumulative tunnel length (0.00 to 2.18). There was a varied range for heritability estimates (0.11 to 0.78) for all traits among the top entries under *C. partellus* infestation (Table 5). Similarly, in Kiboko, the mean performance of entries under *C. partellus* infestation revealed a wide range for dead hearts (0.00 to 1.02), leaf feeding damage (1.40 to 6.65), number of exit holes (0.10 to 6.21), and cumulative tunnel length (0.08 to 2.29). There was a diverse range for heritability estimates (0.11 to 0.78) for all traits among the top entries under *C. partellus* infestation (Table 6).

There were *C. partellus* only resistant entries at Embu (8), Kiboko (9), and Kakamega (4) and 6 each for *B. fusca* only resistant entries at Embu and Kakamega. Twenty one entries showed combined resistance to both *B. fusca* and *C. partellus* in at least two sites: entries

Table 3. Mean performance of top 18 maize inbred lines for selected stem borer resistance traits under *B. fusca* infestation at Kakamega (averaged over two seasons).

Entry	Genotype	No. of dead hearts	No. of exit holes	Stem borer leaf Damage scores (1-9)	Cumulative tunnel length (cm)	Rank selection index	Rank
22	CKSBL10250	0.07	2.22	1.53	0.57	1.10	1
79	CKSBL10043	0.87	2.15	2.38	0.5	1.48	2
90	CKSBL10045	0.24	2.55	2.24	0.42	1.36	3
80	CKSBL10035	0.01	3.39	1.91	0.06	1.34	4
25	CKSBL10169	0.02	2.91	3.12	0.55	1.65	5
75	CKSBL10028	0.08	3.51	1.83	0.15	1.39	6
91	CKSBL10040	0.01	4.18	1.26	0.05	1.38	7
85	CKSBL10039	0.05	5.13	1.13	0.04	1.59	8
49	CKSPL10028	0.01	5.33	1.53	0.03	1.73	9
56	CKSPL10081	0.02	5.53	1.82	0.04	1.85	10
100	CKSBL10026	0.28	5.68	0.96	0.2	1.78	11
29	CKSBL10286	0.03	5.61	2.02	0.02	1.92	12
7	CKSBL10194	0.03	5.61	2.08	0.45	2.04	13
38	CKSBL10321	0.00	5.15	2.35	2.27	2.44	14
92	CML264	0.01	5.8	1.93	0.78	2.13	15
111	CML489	0.07	7.05	1.16	0.23	2.13	16
95	CML312	0.02	7.03	1.52	0.4	2.24	17
60	CKSPL10089	0.25	6.96	2.14	0.64	2.50	18
102	CML334	0.33	9.08	1.38	0.13	2.73	89
96	CML395 (susceptible check)	3.31	8.3	4.03	0.21	3.96	102
	Genotypic variance	0.01	0.27	0.06	0.36	-	-
	Residual variance	0.06	33.14	0.26	1.52	-	-
	Grand mean	0.07	6.73	2.55	2.08	-	-
	LSD	0.42	0.99	1.13	3.12	-	-
	CV	25.65	23.69	22.43	25.73	-	-
	Heritability	0.41	0.35	0.58	0.28	-	-
	P-value	0.009	0.04	<0.0001	0.36	-	-

sus. check: Susceptible check.

CKSBL10026 and CKSBL10028.

DISCUSSION

The analysis of variance revealed significant variation among the genotypes for all characters examined. The partitioning of the phenotypic variance and genotypic variance provided a better understanding of the variation patterns among *B. fusca* and *C. partellus* and their response to the test genotypes across different environments. For example, the number of dead hearts exhibited the least genotypic variance (0.01), while the number of exit holes had the highest (0.27) in Kakamega for *B. fusca*, compared to Embu which had 0.01 and 0.05, respectively. Kiboko had the least genotypic variance for all traits measured for *C. partellus*.

Observations on the number of dead hearts and Number of exit holes may imply that trait variations for borer resistance are not completely under genetic control. The higher genotypic variances than the environmental variances suggest that selection for particular stem borer resistance trait can be carried out and that progress can be made.

The suggestions may apply to observations on the moderate to high broad sense heritability values for borer resistance traits. In both maize and sorghum, the role of leaf resistance and other traits in conferring resistance to stem borers *C. partellus* (Swinhoe), *O. nubilalis* (Hubner), *Sesamia nonagrioides*, and *Diatreae* species is well documented (Butrón et al., 2009; Singh et al., 2012). Even though heritability estimates indicate the relative values of selection based on the phenotypic expression, it is not definitive unless genetic gain under selection is considered together with heritability (Akinwale et al., 2011). The low to moderate broad sense heritability

Table 4. Mean performance of top maize inbred lines for selected stem borer resistance traits under *C. partellus* infestation at Embu (averaged over two seasons).

Entry	Genotype	No. of dead hearts	No. of exit holes	Stem borer leaf Damage scores (1-9)	Cumulative tunnel length (cm)	Rank selection index	Rank
100	CKSBL10026	1.33	1.98	1.72	0.20	0.45	1
91	CKSBL10040	0.00	0.30	1.72	0.05	0.47	2
49	CKSPL10028	1.32	1.65	1.80	0.04	0.48	3
73	CKSBL10016	0.02	0.93	2.16	0.25	0.48	4
90	CKSBL10045	0.33	0.57	2.17	0.39	0.68	5
97	CKSBL10001	0.01	1.02	2.19	0.27	0.68	6
79	CKSBL10043	1.28	3.66	2.20	0.50	0.7	7
41	CKSBL10157	0.21	2.04	2.21	0.02	0.74	8
82	CKSBL10042	0.01	1.20	2.39	0.27	0.75	9
25	CKSBL10169	0.03	2.52	2.46	0.09	0.76	10
80	CKSBL10035	0.07	2.25	2.54	0.1	0.78	11
109	LPSC7-F86-3-1-1-1-BB-#-B-B	0.34	2.28	2.58	0.02	0.81	12
70	CKSBL10013	0.03	4.86	2.59	0.23	0.83	13
9	CKSBL10197	0.03	6.12	2.60	0.07	0.84	14
13	CKSBL10203	0.01	2.61	2.60	0.52	0.85	15
81	CKSBL10038	0.38	6.84	2.78	0.10	0.86	16
101	CML444	0.01	6.93	2.97	0.02	0.88	17
53	CKSPL10070	0.01	5.22	3.23	0.03	0.89	18
93	CML202	0.36	4.50	6.51	0.09	0.89	19
96	CML395 (susceptible check)	1.02	6.21	6.65	0.23	3.75	90
	Genotype variance	0.05	0.08	0.29	0.36	-	-
	Residual variance	0.25	0.50	0.31	1.52	-	-
	Grand mean	0.26	1.09	3.23	0.79	-	-
	LSD	0.85	1.27	1.1	2.07	-	-
	CV	24.14	28.58	17.17	23.14	-	-
	Heritability	0.38	0.31	0.74	0.41	-	-
	P-value	0.49	0.001	<0.0001	0.01	-	-

sus. check: Susceptible check.

estimates (H^2<0.50) for characters, such as number of dead hearts, number of exit holes, leaf feeding damage and cumulative stem tunneling may be due to environmental influence on the traits.

Since selection indices for stem borer resistance traits provide efficiency in the improvement of quantitatively inherited traits, such as stem borer resistance in maize (Mulamba and Mock, 1978; Mutinda et al., 2013), a rank selection index was used to identify genotypes with resistance for both *B. fusca* and *C. partellus*. In response to tropical maize inbred lines for resistance to two *B. fusca* and *C. partellus*, stem borers showed that resistance may be exclusive for *B. fusca* only or *C. partellus* only or for both borers where they exist. It was observed that five entries had resistance to *B. fusca* only, 26 entries showed resistance to *C. partellus* only, and 21 entries showed combined resistance to both *B. fusca* and *C. partellus* in at least two sites. Four entries CKSBL10025, CKSBL10039, CKSBL10040, and CKSBL10028 showed resistance to both species across the sites. Eighty four and 28 entries, respectively showed susceptibility to *B. fusca* and *C. partellus* in all test genotypes (Table 7). Most of the genotypes were found to be susceptible to *B. fusca* and less so for *C. partellus.* These may be attributed to its (*B. fusca*) fitness and adaptation in Africa, because it is indigenous unlike *C. partellus*. These findings suggest that genotypes with the specific borer resistance can be deployed directly as parent lines in the formation of hybrids with resistance to *B. fusca* and *C. partellus* to areas where these borers occur in league or exclusively.

The knowledge on genetic correlations between borer resistance traits is important in creating selection criteria (Sujiprihati et al., 2003). Since grain yield is a result of interrelationships of yield components (Schnable and Springer, 2013; Udaykumar et al., 2013), to maintain grain

Table 5. Mean performance of top maize inbred lines for selected stem borer resistance traits under *C. partellus* infestation at Kakamega (averaged over two seasons).

Entry	Genotype	No. of dead hearts	No. of exit holes	Stem borer leaf Damage scores (1-9)	Cumulative tunnel length (cm)	Rank selection index	Rank
100	CKSBL10026	0.07	0.17	2.75	0.59	3.58	1
91	CKSBL10040	0.03	0.31	3.26	0.14	3.74	2
80	CKSBL10035	0.01	1.09	2.46	0.24	3.80	3
79	CKSBL10043	0.31	1.34	2.16	0.14	3.95	4
4	CKSBL10073	0.31	1.38	2.16	0.14	3.99	5
12	CKSBL10200	0.23	1.29	2.03	0.67	4.22	6
47	CKSPL10280	0.04	1.25	3.03	0.06	4.38	7
49	CKSPL10028	0.01	0.74	3.00	0.85	4.60	8
45	CKSPL10256	0.70	1.52	2.57	0.00	4.79	9
38	CKSBL10321	1.32	1.79	1.80	0.04	4.95	10
37	CKSBL10155	0.03	1.16	3.31	0.47	4.97	11
56	CKSPL10081	0.30	1.32	2.98	0.43	5.03	12
5	CKSBL10107	0.74	1.61	2.61	0.14	5.10	13
83	CKSBL10008	1.04	1.65	2.41	0.03	5.13	14
60	CKSPL10089	0.34	1.40	2.37	1.07	5.18	15
15	CKSBL10205	0.68	1.50	3.02	0.00	5.20	16
6	CKSBL10195	0.66	1.42	2.00	1.23	5.31	17
92	CML264	1.28	1.71	2.85	0.19	6.03	18
48	CKSPL10309	0.68	1.43	2.66	2.18	6.95	19
96	CML395 (susceptible check)	0.99	1.62	3.47	1.04	7.12	86
	Genotype variance	0.05	0.09	0.05	0.05	-	-
	Residual variance	0.25	17.72	0.38	1.19	-	-
	Grand mean	0.26	4.54	2.3	0.77	-	-
	LSD	0.85	8.72	1.12	1.85	-	-
	CV	19.14	19.53	24.58	20.67	-	-
	Heritability	0.58	0.78	0.65	0.11	-	-
	P-value	0.50	<0.0001	<0.0001	0.27	-	-

sus. check: Susceptible check.

yield, breeding for stem borer resistance should be based on multi-trait selection. To do this, several correlations for stem borer resistance traits for *B. fusca* and *C. partellus* were examined to understand their relationships. There were highly significant differences for correlations among the lines for resistance to both *B. fusca* and *C. partellus* and agronomic traits in all sites. The correlation coefficients were positive and significant for the number of exit holes and stem diameter for *B. fusca* r=0.83, (p≤0.01) while that for *C. partellus* was r=0.39, (p≤0.01).

The findings from the current study, corroborate with previous studies that have shown that most cultivated grass species have large stem diameters that support a higher larval survival and more larvae have been recovered per plant unlike wild grass species (Akinwale et al., 2011; Hosseini et al., 2011). However, there were no significant correlations between leaf feeding damage and the number of exit holes for *B. fusca,* but a negative significant correlations r=-0.45, (p≤0.01) for *C. partellus*. For both borers, besides the length of the life cycles for the two borers, morphological characteristics such as trichome density, leaf pubescence, leaf glossiness, thorns, spines, cuticles, and waxes may hinder insect development (Munyiri et al., 2013; Santamaria et al., 2013). These may in turn affect the observed differences in resistance traits due to leaf feeding and larval survival on hosts.

Similarly, both *B. fusca* and *C. partellus* had negative significant correlations for number of exit holes r=0.68 (p≤0.01) and plant aspect r=-0.62 (p≤0.01), plant height r=-0.22 (p≤0.01) and leaf feeding damage r=-0.49 (p≤0.01) respectively. In addition, both *B. fusca* and *C. partellus* showed negative significant correlation for plant height r=-0.53 (p≤0.01) and plant aspect r=-0.53 (p≤0.01), respectively. Leaf feeding damage relative to the cumulative tunneling for both stem borers indicated no

Table 6. Mean performance of top maize inbred lines for selected stem borer resistance traits under *C. partellus* infestation at Kiboko (averaged over two seasons).

Entry	Genotype	No. of dead hearts	No. of exit holes	Stem borer leaf Damage scores (1-9)	Cumulative tunnel length (cm)	Rank selection index	Rank
91	CKSBL10040	0.00	0.10	2.00	0.11	0.55	1
82	CKSBL10042	0.01	0.29	2.08	0.79	0.79	2
90	CKSBL10045	0.01	0.40	1.40	0.44	0.56	3
49	CKSPL10028	0.01	0.58	1.52	1.88	1.00	4
79	CKSBL10043	0.01	0.77	1.79	1.48	1.01	5
4	CKSBL10073	0.02	0.31	1.76	0.92	0.75	6
13	CKSBL10203	0.02	0.90	2.12	0.89	0.98	7
81	CKSBL10038	0.03	0.54	2.01	1.23	0.95	8
85	CKSBL10039	0.03	0.65	2.31	1.00	1.00	9
80	CKSBL10035	0.03	0.84	1.49	1.27	0.91	10
99	CKSBL10004	0.04	0.49	1.97	1.32	0.96	11
70	CKSBL10013	0.05	0.84	1.49	1.22	0.90	12
24	CKSBL10165	0.06	0.55	1.68	0.66	0.74	13
32	CKSBL10178	0.06	0.86	1.54	1.56	1.01	14
53	CKSPL10070	0.21	0.33	1.99	0.16	0.67	15
7	CKSBL10194	0.31	0.53	1.73	0.98	0.89	16
111	CML489	0.33	0.19	1.87	0.08	0.62	17
103	CML254	0.38	0.76	1.49	0.87	0.88	18
61	CKSPL10090	0.89	1.46	2.69	2.29	1.83	19
96	CML395 (susceptible check)	1.02	6.21	6.65	0.23	3.53	95
	Genotype variance	0.05	0.08	0.24	0.22	-	-
	Residual variance	0.25	0.5	0.33	3.06	-	-
	Grand mean	0.26	1.09	2.29	2.08	-	-
	LSD	0.85	1.27	1.01	3.12	-	-
	CV	27.14	28.35	20.16	35.73	-	-
	Heritability	0.38	0.34	0.69	0.18	-	-
	P-value	0.16	0.05	0.01	0.02	-	-

significant correlations (Table 8). Based on stem borer resistance trait rank selection indices leaf feeding damage, cumulative stem tunneling and number of exit holes were found to be reliable parameters that may be used in discriminating genotypes for resistance to the two borers. The findings may imply that both *B. fusca* and *C. partellus* affect plants negatively in a similar manner. For example, stem tunneling disrupts nutrients and water uptake, leaf feeding damage reduces the photosynthetic area, exit holes may cause weakened stems which may result in susceptible to stem lodging and other plant deformities, thus result in increased losses to grain yield.

Previous studies showed that stem tunneling damage had a significant influence on maize plant growth, and that the direct effect of stem tunneling on loss in maize grain yield was greater than the effect of leaf feeding (Kumar, 1997; Singh et al., 2012).

The results from the current study agree with the findings of Ajala et al., (2010), Akinwale et al. (2011), and Mailafiya et al., (2011) reported that leaf damage and cumulative tunneling were positively correlated. These may show differences among *B. fusca* and *C. partellus* nature of feeding, stem tunneling, oviposition, and exit from host plants. Other studies found that *B. fusca* and *C. partellus* stem borer damage reduced the number of ears harvested per plant and plant height (Sujiprihati et al., 2003; Sharma et al., 2007; Akinwale et al., 2011).

Further trait correlations between *B. fusca* and *C. partellus* revealed positive and significant correlations for for both borers for number of exit holes ($r=0.75$, $p\leq0.01$), leaf feeding damage score ($r=0.55$, $p\leq0.05$), cumulative stem tunneling ($r=0.26$, $p\leq0.01$), number of rotten ears ($r=0.47$, $p\leq0.05$), number of ears harvested ($r=0.72$, $p\leq0.05$), number of plants per plot ($r=0.73$, $p\leq0.05$), plant aspect ($r=0.99$, $p\leq0.05$), plant height ($r=0.81$, $p\leq0.01$), root lodging ($r=0.50$, $p\leq0.05$), and stem lodging ($r=0.56$, $p\leq0.05$). However, no significant differences were observed for trait correlations between *B. fusca* and *C. partellus* for number of dead hearts, stem diameter and internode length across the sites (Table 9).

Table 7. Distribution of maize inbred lines for resistance to under *B. fusca* and *C. partellus* infestation at Embu, Kiboko and Kakamega.

Entry	Genotype	Species and location				
		Chilo partellus			*Busseola fusca*	
		Embu	Kakamega	Kiboko	Embu	Kakamega
13	CKSBL10203	+	-	+	-	-
49	CKSPL10028	+	+	+	+	+
53	CKSPL10070	+	-	+	-	-
75	CKSBL10028	-	+	-	+	+
79	CKSBL10043	+	+	+	-	-
80	CKSBL10035	-	-	+	-	-
81	CKSBL10038	+	-	+	-	-
85	CKSBL10039	-	-	-	+	+
91	CKSBL10040	+	+	+	+	+
95	CML312	+	-	-	+	+
100	CKSBL10026	+	-	-	+	+
101	CML444	-	-	+	-	-
96	CML395 (susceptible check)	+	+	+	+	+
Total		9	9	9	7	7

+ = Present; - = Absent.

Table 8. Correlation coefficients for selected stem borer resistance traits under *B. fusca* and *C. partellus* infestation at Kakamega, Kiboko, and Embu.

Correlation		*Chilo partellus*					
		EXHL	LD	NE	PA	PH	TL
	DIAM	0.39**	0.22	0.17	0.24	0.40*	0.03
	EXHL	1	-0.46**	0.61**	-0.62**	0.89**	0.14
	LD	0.83**	1	-0.45**	0.29*	-0.49**	-0.06
Busseola fusca	NE	0.14	-0.17	1	-0.61**	0.65**	0.11
	PA	0.38**	0.54**	-0.20*	1	-0.53**	-0.23
	PH	0.69**	-0.68**	0.06	-0.50**	1	0.11
	TL	0.68**	0.89**	-0.22*	0.51**	-0.53**	1
-	-	0.34**	0.46**	0.26	0.12	-0.30**	0.47**

DIAM: Plant diameter; EXHL: number of exit holes; LD: leaf damage scores; NE: number of ears harvested; PA: plant aspect; PH: plant height; TL: cumulative stem tunneling; and *,**Significant (p≤0.05), highly significant (p≤0.01), ns: non-significant.

For successful selection of useful genotypes, an understanding of the genotypic and phenotypic inter-trait correlations is essential. The magnitude of genotypic and phenotypic correlations and their use in selection has been reported in literature (Ali et al., 2008; Al Tabbal and Al-Fraihat, 2012). For example, in this study, genotypic correlations were greater for most of the traits than the phenotypic correlation coefficient values (Table 9).

Grain yield showed significant and high positive genotypic (1.13) and phenotypic (0.83) correlation coefficients and high heritability values for both *B. fusca* (0.68) and *C. partellus* (0.80). Similarly, high genotypic correlations were observed for number of exit holes (1.01), leaf feeding damage (1.06), and cumulative stem tunneling (1.56) for both *B. fusca* and *C. partellus*. These may indicate a heritable correlation of these traits (Sahoo et al., 2011; Al Tabbal and Al-Fraihat, 2012). However, stem borer resistance traits had low heritability for number of dead hearts (0.21), leaf feeding damage (0.47), and cumulative stem tunneling (0.25), except for the number of exit holes (0.71); and correspondingly low phenotypic correlation values of less than 0.60.

Most agronomic traits had high phenotypic and genotypic correlations (0.58 to 1.68) and a wide range for heritability estimates for both *B. fusca* (0.18 to 0.86) and *C. partellus* (0.19 to 0.87). Despite the high genotypic variability revealed by the genetic coefficients of variation for the various stem borer resistance and agronomic

Table 9. Correlation coefficients for selected stem borer resistance traits between *B. fusca* and *C. partellus* infestation at Embu, Kakamega and Kiboko.

Parameter	Correlation coefficient (r)
Number of dead hearts	0.09**
Number of exit holes	0.75**
Leaf feeding damage score	0.55*
Cumulative stem tunneling	0.26*
Number of rotten ears	0.47*
Number of ears harvested	0.72*
Plant aspect	1.00*
Root lodging	0.50*
Stem lodging	0.56*
Plant height	0.81**
Stem diameter	0.40
Internode length[§]	0.70

[§]Four internodes below the uppermost ear.

traits, it may not provide information on the heritable variation that is useful for genetic improvement (Akinwale et al., 2011; Singh et al., 2012).

Expected genetic advance may be achieved through phenotypic selection when the genotypic coefficients of variation are coupled with heritable estimates (Sahoo et al., 2011; Al Tabbal and Al-Fraihat, 2012). Correlation coefficients may be useful as indicators of trait association among the borers, for example, the high number of exit holes and cumulative tunnel length shows the probability that either may be a useful selection criterion for resistance to *B. fusca* and *C. partellus* in maize.

Similar results have been reported indicating that selection based on these traits may lead to improvement in stem borer resistance (Munyiri et al., 2013). Low to moderate heritability values were observed for stem. *B.* fusca and *C. partellus* stem borers' resistance traits in the test germplasm suggest that those traits are under genetic control.

Previous studies have shown low heritability for various stem borer resistance traits due to compromised experimental procedures, low frequency for resistance genes in the reference populations (Singh et al., 2012; Chaudhary, 2013), or due to environmental influence or due to few sites used for evaluations (Falconer and Mackay, 1996).

Conclusions

The overall results suggest that a high variability of germplasm for resistance to *B. fusca* and *C. partellus* stem borers exists. Since both *B. fusca* and *C. partellus* stem borers are serious insect pests of maize, the identification of germplasm with resistance to these pests is key. The high heritability, genotypic and phenotypic correlations values showed the presence of inherent association between some stem borer resistance traits for both borers. Further genetic improvement may be explored for number of exit holes, cumulative stem tunneling alongside the agronomic traits in selection for the resistance to either or both *B. fusca* and *C. partellus* in maize. Leaf feeding damage scores, cumulative stem tunnel length and number of exit holes were the most effective parameters in discriminating the test genotypes for resistance to the two borers.

Genotypes identified for resistance to *C. partellus* only may be deployed in breeding programmes in zones where *C. partellus* exclusively occurs and likewise for regions with *B. fusca* only. Genotypes that showed combined resistance to both borers may be deployed to areas where these borers exist in league. However, breeding for resistance to these borers should continue besides deployment of these stem borer resistant hybrids.

The observed responses to either or both *B. fusca* and *C. partellus*, stem borers where they occur exclusively or in league helped to identify resistant maize inbred lines, and showed their possible use in hybrid breeding programmes in tropical maize that emphasize stem-borer resistance especially in Eastern and Southern Africa.

Conflict of Interests

The authors have not declared any conflict of interests.

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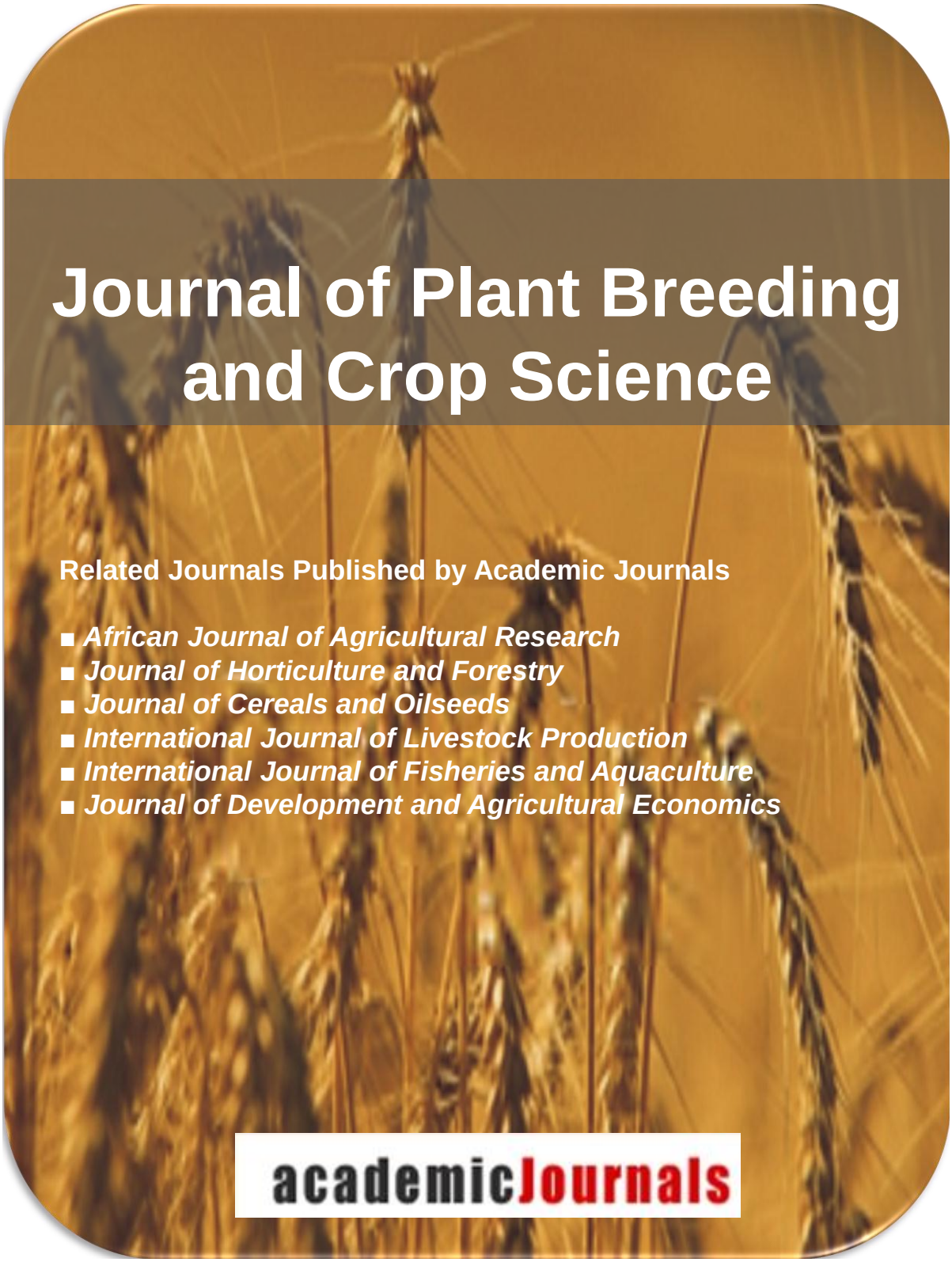

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