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Estimation of General and Specific Combining Ability of Maize Inbred Lines Using Single Cross Testers for Earliness

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Abstract Maize (*Zea mays* L.) is third most consumed crop worldwide after rice and wheat. Maize is the main staple food in sub-Saharan Africa and Kenya, however, production has continuously been low over the past years. A line by tester analysis was carried out for 30 inbred lines and two testers to evaluate the GCA and SCA effects for yield and associated traits at three locations in Kenya during the 2016/2017 growing season. There were significant GCA and SCA mean squares indicating that both additive and non-additive gene effects contributed to the inheritance of the traits studied. Sum of squares of GCA was more than of SCA hence additive main effects contributed more to the inheritance of the traits than non-additive gene effects. Lines 1, 17, 6, 29 and 30 were good general combiners for grain yield. Testcrosses L30×T2 (4.40 t ha^{-1}), L13×T1 (3.85 t ha^{-1}), L20×T1 (3.59 t ha^{-1}) and L9×T1 (3.52 t ha^{-1}) yielded higher than best check mean and had good specific combining ability for grain yield and earliness in anthesis and silking dates. These genotypes can be evaluated further for grain yield and earliness and commercially released for use in areas with short rains.

Keywords: *general combining ability, specific combining ability, line by tester, single cross testers, earliness*

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1. Introduction

Maize (*Zea mays* L.) is ranked third most consumed cereal crop in the world for food, feed, and fodder after rice and wheat [1]. The average yield of maize worldwide between 2004 and 2014 was 5.11 t ha^{-1} with world largest producers, USA, China and Brazil contributing an average of 7.24 t ha^{-1} while sub-Saharan Africa contributing 1.58 t ha^{-1} to world average yield [2]. In sub-Saharan Africa and Kenya, maize is depended by small-scale farmers as a major source of food and income [3]. Although maize is a staple food in Kenya and sub-Saharan Africa, its demand is higher than its production thus affecting food security [4,5]. Causes of low production have been the use of poor seed, overdependence in poor and unpredictable rains, small-scale farming and occurrence of pests and diseases [6]. Therefore, there is urgent requirement to increase maize production in Kenya and sub-Saharan Africa by introducing more improved hybrids [5].

Introduction of maize hybrids has effectively increased maize acreage and yield in the recent past because of hybrid vigour [7]. Combining ability studies are key in developing improved maize hybrids in maize breeding [3]. Combining ability is the capability of an inbred line to combine well with other inbred lines to form elite hybrids; it is the relative capability of a genotype to transfer its good traits to its offspring [8]. Combining ability studies help plant breeders in the identification of inbred lines that are best combiners and give high yield without making all possible crosses among potential parents which is costly and wastes time [9]. Combining ability is categorized into general combining ability (GCA) and specific combining ability (SCA) [10]. General combining ability (GCA) is average line performance in hybrid combinations while specific combining ability (SCA) refers to when some hybrid combinations are better or worse than the average performance of the parents [8].

Combining ability studies give information on additive and non-additive gene action in the expression of heterosis, improving the efficiency of selection of good hybrids for improvement [3]. GCA gives information on additive gene effects while SCA gives information on non-additive gene effects [11]. Lines with good GCA have elite genes originating from either testers or lines crossed to form good hybrids while lines with good SCA originate from the interaction effect of crossing the lines and the testers [8].

In plant breeding programs, the line by tester mating design discovered by Kemphthorne (1957) is extensively used in combining ability studies giving information on the general combining ability (GCA) of lines, testers and specific combining ability (SCA) of crosses [12]. The mating design gives information on type and amount of gene action, heritability, effects of combining ability, amount and type of heterosis for different traits [13].

Previous research has reported the use of the line by tester mating design in the estimation of combining ability and heterosis in quantitative genetic studies in maize [10].

In plant breeding, grain yield is the key trait for improvement expressed by many genes acting additively, thereby, affected by environmental changes hence making breeding for high grain yield hard [14]. Grain yield is genetically associated with other yield-related traits such that a change in expression of one trait affects the other. Therefore, selection for high grain yield requires prior knowledge of association with other related traits [15]. Prior knowledge is key to a breeder in guiding which traits to improve, ignore and make decisions on the best approach to improve yield without neglecting other vital traits [9]. Therefore, the objective of the study was to access the combining ability of maize inbred lines for grain yield and yield-related traits.

2. Materials and Methods

2.1. Germplasm

60 three-way cross maize hybrids were used as experimental materials in this study. The three-way cross maize hybrids were developed from crosses of 30 inbred lines (as female parents) and two single cross testers (as male parents) (CML539/CML442) and (CML78/P300C5). The 30 inbred lines were best selections for earliness from CIMMYT and KALRO maize breeding programs. Four commercial checks were included in the study together with the two single crosses CML539/CML442 and CML78/P300C5. The two single crosses were used as testers because they have been proven to be early maturing through previous breeding activities (Table 1).

2.2. Study Locations

In the current study, the three way cross maize hybrids were evaluated in three locations (Table 2).

2.3. Experimental Design and Crop Management

The 60 three-way cross hybrids together with four checks were planted in an incomplete block design (6×6 alpha lattice design) with two replications in Kakamega, Kiboko, and Kitui [18]. Each hybrid was sown in a two-row plot of 5.0 m. Two seeds were planted in each hill and thinning was later done to one plant per hill. Plant spacing was 0.75 m between rows and 0.25 m between hills. Phosphate fertilizer (60 kg P_2O_5) was applied during sowing and nitrogen fertilizer (60 kg N ha^{-1}) during topdressing and weeds controlled in the entire growth cycle of plants to ensure healthy plant growth.

2.4. Data Collection

Data collection was done for all locations following the standard protocols provided by CIMMYT [19];

Anthesis date: the date when 50% of the plants per plot have shed pollen, silking date: The date when 50% of the plants per plot have shown silks, plant height: determined by measuring 10 representative plants from the ground to the first tassel branch upon physiological maturity of each plant, ear height: determined by measuring 10 representative plants from the ground to the ear placement of each plant upon physiological maturity, plant number: number of plants counted before harvest after removing the plants of the first hill on each side of the row, ear aspect: refers to the quality of the ears and was done on a scale of 1-5 (1= nice and uniform cobs with the preferred texture in the area; 5= ugly cobs with undesirable texture in the area), field weight: refers to the weight of the ears per plot taken directly after harvest, and grain yield: refers to the weight of shelled grain per plot.

Table 1. List of maize genotypes used in the study

	Lines				
1	Entry 021	11	IRMA 52	21	RF 291-8-3-4-9
2	KIKAMBA 4-3-1	12	IRMA 35	22	RF 291-10-5-4-4
3	KATUMANI 4-3-11	13	IRMA 82	23	RF 295-2-1-1-4
4	KIKAMBA 4-4-3	14	IRMA 66	24	RF 291-1-1-7-2
5	ENTRY 65 P1P2	15	IRMA 95	25	Local 4-4-1
6	ENTRY 7 DH	16	IRMA 60	26	IRMA 33
7	KATUMANI 4-3-1	17	IRMA 87	27	Local 10-2-3
8	DH LINE ENTRY 1	18	IRMA 54	28	Kikamba 4-2-2
9	CML 205	19	RF 305-5-1-1-1	29	RF 291-3-10-15-2
10	P100C6	20	RF 291-3-10-15-1	30	CML 539
	Testers				
1	CML 539/CML 442	2	CML 78/P300C5		
	Checks				
1	SC DUMA 43	3	WE1101		
2	PAN 4M-19	4	DH 04		

Table 2. Geographical and Climatic data for three locations used in the study

Location	Geographic location			Mean annual Rainfall (mm)	Temperature (˚C)		Agro-ecology and soil type	Source
	Longitude	Latitude	Altitude		Min	Max		
Kakamega	34˚45˚E	0˚16˚N	1585	1995	13.0	28.6	Sub humid with basaltic loam soils	[16]
Kiboko	37˚75˚E	2˚15˚S	993	548	17.0	30.6	Semi-arid with ferrasols to ferric luvisol soils	[16]
Kitui	38˚1E	1˚22˚S	1115	775	14.0	34.0	Semi-arid with red sandy soils	[17]

2.5. Data Analysis

Analysis of variance for the data collected was carried out using the General Linear Model of the Genstat program [20]. The study was carried out across locations categorizing genotypes as fixed effects and locations as random effects using the linear model:

$$\begin{aligned} Y_{ijk} &= \mu + r(e_k) + e_k + I_i + t_j \\ &+ (l \times t)_{ij} + (l \times e)_{ik} \\ &+ (t \times e)_{jk} + (l \times t \times e)_{eijk} + \epsilon_{ijk} \end{aligned}$$

Where;

Y_{ijk} = observed genotype response of the i^{th} line crossed to j^{th} tester evaluated in r replications across k environments

μ = overall grand mean of trial

$r(e_k)$ = effect of replication in k environments

I_i = effect of the i^{th} line

t_j = effect of the j^{th} tester

$(l \times t)_{ij}$ = effect of interaction of the i^{th} line and j^{th} tester

$(l \times e)_{ik}$ = effect of interaction of the i^{th} line and k environments

$(t \times e)_{jk}$ = effect of interaction of the j^{th} tester and k environments

$(l \times t \times e)_{eijk}$ = effect of interaction of the i^{th} line, j^{th} tester and k environments

ϵ_{ijk} = random experimental error

The estimates of the GCA of lines (GCA) and testers (GCA) were estimated according to [8].

GCA of lines (GCA_l) = ((xi…)/mr)+((x…)/mfr)

Where;

(xi…)/mr = the total of i^{th} female parent divided by all male (m) parents and replications (r)

(x…)/mfr = grand total of all the genotypes divided by all male parents (m), female parents (f) and replications (r);

GCA of testers (GCA_t) = (xj…)/(fr)+ (x…)/mfr

Where;

(xj…)/(fr) = The total of the j^{th} male parent divided by all female (f) parents and replications (r)

The GCA effect standard errors for lines (SE_{Line}) and testers (SE_{Tester}) were also estimated using the following formulae [21];

Standard error for line (SE_{Line}) = $\sqrt{}$(MSE/(S×T))

Standard errors for tester (SE_{Tester}) =$\sqrt{}$(MSE/(S×L))

Where;

MSE, S, L, and T = mean square error, number of sites, number of lines and number of testers respectively.

Determination of significance of lines and testers was carried out using the t-test as follows;

$$t_x = GCA_x / SE_x$$

Where t_x, GCA_x, and SE_x represent t-statistic, general combining ability and standard error of line or tester respectively.

The SCA effect of the lines and testers was carried out as follows [21].

$$SCA = xi_j / r - \left((xi\ldots)/mr\right) - \left(xj/fr\right) + \left((x\ldots)/mfr\right)$$

Where;

xi_j/r = ji^{th} combination total divided by all replications (r)

The SCA standard error (SE) for line by tester effect was estimated using the following formula [21].

$$\text{SCA standard error } (SE) = (MSE / S)$$

The significance of the line by tester interaction was determined using the t-test as shown below:

$$t_x = SCA_x / SE_x$$

Heritability estimate (H^2) in a broad sense was calculated as the ratio of the genotype variance to the phenotype variance and expressed in percentage using the following formulae [22].

Heritability estimate across environments (H^2) = $(\sigma^2 g)/(\sigma^2+(\sigma^2\ e)/rl)\times 100$

Heritability estimate within environments $(H^2)=(\sigma^2 g)/(\sigma^2+(\sigma^2 e)/r)\times 100$

Where;

$\sigma^2 g$ = genotype variance, σ^2 e = environmental variance, r = replication and l = location

3. Results and Discussions

3.1. Results

Analysis of variance showed significant genotype by environment interactions for Kakamega, Kiboko and Kitui therefore, the three test locations were considered to be representative environments. The results are therefore presented for each location.

3.2. Analysis of variance

Combined mean square analysis across environments showed highly significant differences ($p \le 0.01$) for all the measured traits thereby indicating that the environments were highly variable (Table 3). The mean squares of genotypes (testcrosses) showed highly significant differences ($p \le 0.01$) for all the traits measured hence suggesting that the genotypes responded differently in different environments (Table 3). The mean squares of the interaction effect of genotypes and environments were highly significant ($p \le 0.01$) for all traits except days to silking thereby showing different responses of genotypes in different environments (Table 3). Mean squares of lines were highly significant ($p \le 0.01$) for all traits and mean squares of testers were highly significant ($p \le 0.01$) for all traits except days to tasselling and ear height (Table 3). The mean squares of the interaction effect between lines and testers were highly significant ($p \le 0.01$) for all traits except days to silking which showed no significant differences (Table 3). Environment by line interaction showed highly significant differences for all the traits except days to silking which showed no significant difference and ear aspect which showed significance at ($p \le 0.05$) (Table 3). Environment by tester interaction showed highly significant differences

($p \le 0.01$) for all the measured traits. Mean squares of the interaction effect of environments, lines and testers were highly significant ($p \le 0.01$) for grain yield, days to tasselling and number of plants harvested while significant at ($p \le 0.05$) for plant height and ear aspect (Table 3). Days to silking and ear height mean squares showed no significant differences for the interaction effect of environments, lines, and testers (Table 3).

Table 3. Mean squares of testcrosses for grain yield (t ha^{-1}) and selected agronomic traits evaluated in Kakamega, Kiboko and Kitui during the 2016/2017 growing season

Source	df	GY	DTS	DTT	PH	EH	EA	NP
Rep(Env)	6	2.93**	14.36	14.62*	375.46*	259.49**	0.35	41.03*
Env	5	313.90**	5210.66**	5264.47**	92971.83**	39578.02**	51.06**	8646.36**
Genotypes	59	4.25**	54.35**	62.76**	756.32**	355.48**	1.34**	247.33**
GCA Line	29	5.03**	82.29**	108.78**	1118.52**	528.01**	1.48**	331.46**
GCA Tester	1	22.87**	374.16**	10.72	2358.70**	258.33	14.92**	523.69**
SCA (Line x Tester)	29	2.83**	15.39	18.54**	339.60**	186.51**	0.74**	153.40**
Genotype x Env	295	1.49**	16.05	11.48**	252.56**	104.26**	0.48**	56.95**
Env x Line	145	1.82**	15.49	11.62**	249.24**	110.31**	0.41*	71.95**
Env x Tester	5	8.55**	129.34**	75.63**	2173.64**	443.53**	4.48**	110.46**
Env x Line x Tester	145	0.90**	12.7	9.14**	189.63*	86.5	0.42*	40.11**
Error	282	0.47	13.42	5.83	147.71	72.70	0.31	15.33
S.E.D (Mean)		**0.71**	**3.80**	**2.51**	**13.07**	**8.90**	**0.56**	**4.00**
L.S.D (0.05)		**1.40**	**7.48**	**4.94**	**25.70**	**17.50**	**1.10**	**7.86**
CV%		**23.2**	**6.00**	**4.10**	**7.60**	**11.10**	**19.80**	**13.80**
Mean		**3.02**	**62.91**	**61.09**	**171.7**	**79.93**	**2.82**	**29.06**

df = degrees of freedom, GY=grain yield (t ha^{-1}), DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested, ** and * = significance at ($p \le 0.01$) and ($p \le 0.05$)

3.3. Mean Performance

3.3.1. Combined Mean Performance of Testcrosses in Kakamega, Kiboko and Kitui

Combined mean performance of the best and last 15 testcrosses evaluated in Kakamega, Kiboko, and Kitui for grain yield and associated agronomic traits averaged over two seasons are presented in Table 4. 11 Out of the best 15 selections of testcrosses originated from crosses with tester 1 (CML539/CML442) and four testcrosses originated from tester 2 (CML78/P300C5) (Table 4 and Appendix 1).

The grain yield trial mean across locations was 3.05 t ha^{-1}, with a range of 0.05 t ha^{-1} to 9.22 t ha^{-1}. The mean from the best 15 selections was 3.80 t ha^{-1}, having a higher mean than the checks mean (2.63 t ha^{-1}) and the trial mean. The minimum and maximum yield ranged from 0.05 t ha^{-1} to 9.22 t ha^{-1}. The top-performing testcrosses from the 15 best selections across locations were L1×T1 (4.42 t ha^{-1}), L30×T2 (4.40 t ha^{-1}), L17×T1 (4.09 t ha^{-1}), L1×T2 (3.91 t ha^{-1}) and L6×T2 (3.87 t ha^{-1}) which outperformed the best check hybrid with 2.86 t ha^{-1}. The least performing testcrosses were L11×T1 (3.48 t ha^{-1}), L12×T1 (3.51 t ha^{-1}) and L9×T1 (3.52 t ha^{-1}) (Table 4 and Appendix 1).

Days to silking across locations trial mean, checks mean and mean from the 15 best selections were 63.06 days, 65.52 days and 63.59 respectively. The minimum and maximum days to silking ranged from 49 days to 89 days. Testcrosses with the least days to silking from the best 15 selections were L1×T2 (62.58 days), L17×T2 (62.58 days), L20×T1 (60.92 days) and L8×T1 (61.25 days). Best selections of testcrosses with the highest days to silking were L1×T1 (65.17 days), L9×T1 (65.50 days) and L12×T1 (65.50 days). Testcrosses L22×T2 (57.96 days), L23×T2 (57.92 days), L24×T2 (57.50 days) and L10×T1 (66.50 days), L30×T1 (68.75 days) had the lowest and highest average number of days to silking for all testcrosses evaluated respectively (Table 4 and Appendix 1).

The trial mean, checks mean and mean from the best selections of days to tasselling across locations was 61.24 days, 63.60 days and 61.67 days respectively. The minimum and maximum days to tasselling ranged from 49 days to 87 days. Testcrosses with the least mean days to tasselling from the 15 best selections were L20×T1 (58.67 days), L8×T1 (58.58 days) and L6×T1 (61.08 days). Testcrosses with the highest days to tasselling were L1×T1 (63.00 days), L30×T2 (63.00 days) and L9×T1 (63.75 days). Testcrosses L22×T2 (56.72 days), L23×T2 (56.42 days), L20×T2 (57.33 days) and L30×T1 (66.17 days), L9×T2 (66.25 days) had the lowest and highest average number of days to silking for all testcrosses respectively (Table 4 and Appendix 1).

Across locations plant height trial mean, check mean and mean of the best 15 selections were 172.52 cm, 183.17 cm, and 175.25 cm respectively. The minimum and maximum plant height ranged from 68.75 cm to 282.50 cm. Testcrosses from best selections with the highest plant height were L13×T1 (185.70 cm), L9×T1 (185.30 cm) and L11×T1 (181.10 cm). Testcrosses with the lowest average plant height from the best selections were L30×T1 (168.30 cm), L17×T1 (166.20 cm) and L17×T2 (166.70 cm). Testcrosses that had the highest and lowest average plant height from all testcrosses were L13×T1 (185.70 cm), L9×T1 (185.30 cm), L24×T1 (184.70 cm) and L19×T2 (152.70 cm), L30×T1 (153.00 cm), L19×T1 (155.50 cm) respectively (Table 4 and Appendix 1).

The ear height trial mean, check mean and the mean from best selections were 80.33 cm, 85.33 cm, and 82.38 cm. Minimum and maximum ear height ranged from 24 cm to 148 cm. Testcrosses with the highest ear height from the best selections were L6×T2 (87.12 cm), L9×T1 (90.01 cm) and L12×T1 (86.95 cm). Testcrosses with the lowest ear height from best selections were L1×T1 (69.90 cm), L26×T1 (67.47 cm) and L25×T1 (69.02 cm). Testcrosses L19×T1 (66.92 cm), L19×T2 (67.52 cm) and L30×T1

(67.92 cm) had the lowest ear height from all 60 testcrosses while L24×T1 (92.77 cm), L12×T2 (87.49 cm) and L13×T2 (87.77 cm) had the highest ear height (Table 4 and Appendix 1).

Table 4. Mean comparison for the best and last 15 genotypes of the 60 testcrosses and 4 checks evaluated for grain yield (t ha^{-1}) and associated agronomic traits in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

L×T	GY	RNK	DTS	RNK	DTT	RNK	PH	RNK	EH	RNK	EA	RNK	NP	RNK
L1×T1	4.42	**1**	65.17	**40**	63.00	**42**	180.40	**44**	84.22	**49**	2.38	**8**	33.67	**5**
L30×T2	4.40	**2**	63.67	**32**	63.00	**42**	168.30	**19**	78.22	**20**	2.08	**2**	34.08	**4**
L17×T1	4.09	**3**	64.17	**35**	62.25	**36**	166.20	**13**	78.35	**22**	2.33	**6**	32.33	**13**
L1×T2	3.91	**4**	62.58	**21**	61.67	**32**	178.10	**41**	84.88	**51**	2.38	**8**	31.92	**16**
L6×T2	3.87	**5**	62.92	**25**	61.50	**30**	175.50	**36**	87.12	**58**	1.88	**1**	33.33	**8**
L13×T1	3.85	**6**	63.50	**30**	61.75	**33**	185.70	**56**	82.97	**45**	2.42	**9**	32.00	**15**
L6×T1	3.79	**7**	63.33	**29**	61.08	**25**	170.00	**23**	82.17	**39**	2.75	**21**	32.50	**11**
L29×T1	3.76	**8**	64.08	**34**	61.17	**26**	169.90	**22**	77.87	**19**	2.71	**20**	29.42	**32**
L17×T2	3.72	**9**	62.58	**21**	63.25	**45**	166.70	**15**	81.99	**38**	2.50	**12**	34.50	**1**
L20×T1	3.59	**10**	60.92	**10**	58.67	**12**	171.60	**27**	80.16	**29**	3.17	**31**	34.17	**3**
L8×T1	3.56	**11**	61.25	**11**	58.58	**10**	172.20	**29**	74.87	**12**	3.21	**32**	32.08	**14**
L27×T1	3.56	**11**	63.67	**32**	61.42	**29**	177.50	**40**	83.37	**48**	3.21	**32**	32.75	**9**
L9×T1	3.52	**12**	65.50	**41**	63.75	**46**	185.30	**55**	90.01	**63**	2.42	**9**	27.00	**40**
L12×T1	3.51	**13**	65.50	**41**	62.75	**40**	180.20	**43**	86.95	**57**	2.96	**27**	33.50	**7**
L11×T1	3.48	**14**	65.00	**38**	61.17	**26**	181.10	**47**	82.48	**43**	2.92	**26**	33.58	**6**
L20×T2	2.74	**39**	62.08	**17**	57.33	**3**	159.90	**5**	77.27	**17**	2.79	**22**	30.08	**24**
L28×T2	2.72	**40**	60.17	**6**	59.00	**14**	159.90	**5**	81.44	**33**	2.71	**20**	28.92	**34**
L25×T2	2.69	**42**	60.33	**7**	57.75	**6**	170.50	**24**	82.27	**41**	2.79	**22**	29.83	**28**
L7×T2	2.67	**43**	61.50	**12**	59.92	**19**	166.90	**17**	84.41	**50**	2.79	**22**	27.83	**37**
L22×T2	2.42	**45**	57.96	**3**	56.72	**2**	157.90	**4**	73.72	**7**	2.51	**14**	28.07	**36**
L30×T1	2.41	**46**	68.75	**48**	66.17	**52**	153.00	**2**	67.92	**3**	3.37	**34**	28.67	**35**
L18×T2	2.39	**47**	63.00	**26**	61.35	**28**	162.50	**7**	72.99	**6**	2.75	**21**	23.17	**49**
L22×T1	2.36	**48**	60.92	**10**	58.42	**8**	170.50	**24**	79.82	**26**	2.67	**19**	20.25	**53**
L7×T1	2.22	**49**	61.83	**15**	58.75	**13**	163.20	**8**	74.78	**11**	2.96	**27**	21.42	**51**
L24×T2	2.22	**49**	57.50	**1**	57.67	**5**	163.30	**9**	79.22	**24**	2.96	**27**	19.58	**55**
L19×T2	2.22	**49**	60.92	**10**	59.42	**15**	152.70	**1**	67.52	**2**	3.13	**30**	21.92	**50**
L10×T2	2.17	**50**	65.00	**38**	64.67	**49**	180.20	**43**	76.62	**16**	2.21	**4**	15.83	**57**
L23×T2	1.95	**51**	57.92	**2**	56.42	**1**	162.40	**6**	74.25	**9**	3.25	**33**	21.25	**52**
L9×T2	1.73	**52**	65.50	**41**	66.25	**53**	176.30	**37**	86.88	**56**	3.21	**32**	17.67	**56**
L19×T1	1.69	**53**	62.50	**20**	59.58	**17**	155.50	**3**	66.92	**1**	3.38	**35**	19.92	**54**
Check 1	2.86	**35**	62.91	**24**	61.20	**27**	190.40	**57**	85.58	**52**	2.47	**11**	29.08	**33**
Check 2	2.41	**46**	65.13	**39**	62.92	**41**	174.95	**35**	81.00	**32**	2.67	**19**	26.84	**41**
Check 3	2.71	**41**	68.21	**47**	66.50	**54**	184.15	**53**	87.34	**59**	2.52	**15**	25.67	**45**
Check 4	2.54	**44**	65.84	**43**	63.80	**47**	183.30	**52**	87.39	**60**	2.71	**20**	26.09	**42**
SE	**0.97**		**3.06**		**2.30**		**20.60**		**11.44**		**0.47**		**4.48**	
Checks mean	**2.63**		**65.52**		**63.60**		**183.17**		**85.33**		**2.59**		**26.92**	
Trial mean	**3.05**		**63.06**		**61.24**		**172.52**		**80.33**		**2.74**		**28.94**	
min	**0.05**		**49.00**		**49.00**		**68.75**		**24.00**		**1.00**		**1.00**	
max	**9.22**		**89.00**		**87.00**		**282.50**		**148.00**		**5.00**		**49.00**	
L.S.D (0.05)	**2.69**		**8.49**		**6.38**		**57.19**		**31.77**		**1.31**		**12.44**	
CV	**23.00**		**9.70**		**7.50**		**23.80**		**24.00**		**22.00**		**21.10**	

L=line, T=tester, GY=grain yield (t ha^{-1}), RNK= rank, DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested, SE= standard error

The ear aspect trial mean was 2.74, checks mean was 2.59 and mean from best selections was 2.62. The minimum and maximum ear aspect ranged from 1 to 5. The testcrosses with the best scores were L6×T2 (1.88), L30×T2 (2.08) and L15×T2 (2.17) while L30×T1 (3.37), L23×T2 (3.25) and L19×T1 (3.38) had the poorest ear aspect scores respectively (Table 4 and Appendix 1).

The trial mean of the number of plants harvested was 28.96, checks mean was 26.92 and best 15 selection mean was 32.46. The minimum and maximum ranged from 1 to 49 plants. Testcrosses with the highest mean number of plants were L17×T2 (34.50), L12×T2 (34.50) and L20×T1 (34.17) while L24×T2 (19.58), L10×T2 (15.83) and L9×T2 (17.67) had the lowest mean number of plants (Table 4 and Appendix 1).

3.4. The General Combining Ability (GCA) Effects

3.4.1. The General Combining Ability (GCA) Effects of Inbred Lines in Kakamega, Kiboko and Kitui

Across location evaluation of GCA for grain yield showed 16 lines had a positive GCA while 14 lines had a negative GCA for grain yield. The best general combiners for grain yield with positive GCA were lines 1, 17, 6, 29 and 30 with GCA values of 1.08, 0.83, 0.75, 0.53 and 0.32

respectively. Line 1 showed a positive and significant ($p\leq0.05$) GCA for grain yield. Lines 7 (-0.64), 22 (-0.69) and 19 (-1.13) were the poorest general combiners for grain yield. Tester 1 (CML539/CML 442) showed positive GCA (0.18) while tester 2 (CML78/P300C5) showed negative GCA (-0.18) for grain yield (Table 5).

17 lines had a positive GCA while 13 lines had a negative GCA for days to silking. Lines 23, 22, 4 and 24 had the least days to silking with negative GCA of -3.51, -3.43, -2.85 and -2.35 respectively. The lines having the most days to silking were 30, 12 and 10 with positive GCA of 3.32, 2.94 and 2.86 respectively. Tester 1 showed positive GCA (0.74) while tester 2 showed negative GCA (-0.72) for days to silking (Table 5).

17 lines showed positive, and 13 lines showed negative GCA for days to anthesis. Lines 23, 22, 4 and 20 with GCA values of -3.60, -3.46, -3.14 and -3.06 respectively took the least days to anthesis. Lines 9, 30 and 10 with positive GCA of 3.94, 3.53 and 3.73 respectively took the most days to anthesis. Tester 1 showed positive GCA (0.17) while tester 2 showed negative GCA (-0.11) for days to anthesis (Table 5).

Plant height had 15 lines with positive GCA and 15 lines with negative GCA. Lines 19 (significant at ($p\leq0.01$)), 30, 22 and 28 with negative GCA of -17.71, -11.10, -7.61 and -8.30 respectively had the shortest plant height. Lines 13, 16 and 14 with GCA of 12.31, 9.38 and 10.65 had the highest plant height. Tester 1 had a GCA of 1.74 and tester 2 had a GCA of -1.70 (Table 5).

Ear height had 18 lines with positive GCA and 12 lines with negative GCA. Lines 19 (significant at ($p\leq0.05$)), 30, 8 and 18 with negative GCA of -12.78, -6.92, -6.81 and -6.44 respectively had the shortest ear height. Lines 9, 12, 24 and 9 had the highest ear height with GCA of 8.45, 7.23, 6.00 and 8.45 respectively. Tester 1 and 2 had GCA values of -0.65 and 0.65 respectively (Table 5).

Ear aspect had 14 lines with positive GCA while 16 lines had negative GCA. The best combiners for ear aspect were lines 6, 1, 17 and 16 with GCA of -0.46, -0.40, -0.36 and -0.38 while the poorest combiner was line 19 with a GCA of 0.48. Tester 1 and 2 had GCA values of 0.06 and -0.11 respectively (Table 5).

18 lines had positive GCA while 12 lines had negative GCA for number of plants harvested. Lines 12, 17 and 4 had the highest number of plants harvested with GCA of 4.90, 4.32 and 3.90 respectively while lines 19 and 9 had the lowest number of plants harvested with GCA values of -6.76 and -8.18 respectively. Tester 1 and tester 2 had GCA values of 0.80 and -0.85 respectively (Table 5).

Table 5. General Combining Ability (GCA) effects of 30 inbred lines evaluated for grain yield (t ha^{-1}) and associated agronomic traits in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

Line	RANK	GY	DTS	DTT	PH	EH	EA	NP
1	1	1.08*	0.99	1.28	7.45	4.56	-0.40	3.69
17	2	0.83	0.49	1.69	-5.36	0.18	-0.36	4.32
6	3	0.75	0.24	0.23	0.92	4.65	-0.46	3.82
29	4	0.53	0.69	0.44	-1.98	1.82	-0.19	0.40
30	5	0.32	3.32	3.53	-11.10	-6.92	-0.04	2.28
13	6	0.31	0.61	1.15	12.31	5.38	-0.29	2.28
12	7	0.25	2.94	3.07	7.36	7.23	0.11	4.90
16	8	0.23	2.19	2.53	9.38	0.43	-0.38	0.86
8	9	0.18	-1.97	-2.42	-2.55	-6.81	0.16	1.95
27	10	0.16	0.78	0.69	1.61	2.58	0.35	2.40
4	11	0.08	-2.85	-3.14	-3.73	0.70	0.22	3.90
14	12	0.08	0.94	0.98	10.65	0.46	-0.29	1.53
20	13	0.08	-1.39	-3.06	-6.06	-1.28	0.22	3.03
21	14	0.08	-0.51	-0.77	4.59	1.22	-0.17	3.03
11	15	0.07	0.74	-0.10	4.13	2.87	0.10	3.19
15	16	0.00	1.28	0.94	4.93	-7.40	-0.25	-0.18
3	17	-0.07	-2.22	-2.31	-3.43	1.27	0.25	-0.22
25	18	-0.07	-1.64	-2.43	-3.78	-1.68	0.04	2.11
5	19	-0.08	1.94	1.78	0.38	-0.38	0.19	-0.76
2	20	-0.12	-1.01	0.03	7.59	4.03	-0.14	-4.22
26	21	-0.21	0.82	0.53	-1.76	-1.99	0.23	1.53
28	22	-0.24	-1.43	-1.43	-8.30	1.52	-0.05	0.82
10	23	-0.26	2.86	3.73	4.43	-4.09	-0.26	-6.31
18	24	-0.30	1.57	0.94	-4.20	-6.44	-0.21	-2.81
24	25	-0.33	-2.35	-0.68	2.22	6.00	-0.04	-6.31
9	26	-0.46	2.61	3.94	9.03	8.45	0.05	-6.76
23	27	-0.46	-3.51	-3.60	-2.03	0.08	0.40	-1.64
7	28	-0.64	-1.22	-1.72	-6.72	-0.40	0.10	-4.47
22	29	-0.69	-3.43	-3.46	-7.61	-3.22	-0.18	-4.96
19	30	-1.13*	-1.18	-1.56	-17.71**	-12.78**	0.48	-8.18*
Testers								
CML 539/CML 442		**0.18**	**0.74**	**0.17**	**1.74**	**-0.65**	**0.06**	**0.80**
CML 78/P300C5		**-0.18**	**-0.72**	**-0.11**	**-1.70**	**0.65**	**-0.11**	**-0.85**
S.E		**2.69**	**8.49**	**6.38**	**57.19**	**31.77**	**1.31**	**12.44**
L.S.D (0.05)		**23.00**	**9.70**	**7.50**	**23.80**	**24.00**	**22.00**	**21.10**
CV%		**0.97**	**3.06**	**2.30**	**20.60**	**11.44**	**0.47**	**4.48**

GY=grain yield (t ha^{-1}), DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested, SE= standard error, ** and * = significance at ($p\leq0.01$) and ($p\leq0.05$)

3.5. The Specific Combining Ability (SCA) effects

3.5.1. The Specific Combining Ability (SCA) Effects in Kakamega, Kiboko and Kitui

A combined analysis indicated 14 testcrosses crossed to tester 1 and six crossed to tester two of the 20 best selections. L30×T2 (1.18) (significant at ($p \le 0.01$)), L9×T1 (0.71) (significant at ($p \le 0.05$)), L6×T2 (0.22), L13×T1 (0.28), L20×T1 (0.25) and L10×T1 (0.47) were testcrosses with good specific combining ability for grain yield from combined analysis across locations. L6×T1 (-0.22) and L5×T1 (-0.38) were poor specific combiners (Table 6 and Appendix 2).

Testcrosses that showed earliness in days to silking included L30×T2 (-1.82) (significant at ($p \le 0.01$)), L24×T2 (-2.32) (significant at ($p \le 0.01$)), L20×T1 (-1.33) and L12×T1 (-1.08) while testcrosses L30×T1 (1.80) (significant at ($p \le 0.05$)), L24×T1 (2.30) (significant at ($p \le 0.01$)), L20×T2 (1.31) and L12×T2 (1.06) showed lateness. Testcrosses that showed earliness in days to anthesis included L24×T2 (-2.60) (significant at ($p \le 0.01$)), L30×T2 (-1.47), L9×T1 (-1.42), L2×T1 (-1.67) and L12×T1 (-1.54) while (L12×T2) (1.49), L24×T1 (2.54), L2×T2 (1.61), L30×T1 (1.42) and (L9×T2) (1.36) showed lateness (Table 6 and Appendix 2).

Testcrosses that showed a reduced plant height included L6×T1 (-4.50), L15×T1 (-5.56), L30×T1 (-9.39) (significant at ($p \le 0.05$)), L24×T2 (-8.97) (significant at ($p \le 0.05$)), L23×T2 (-5.67) and L10×T1 (-5.75) while L29×T1 (-3.29), L25×T1 (-3.32), L15×T1 (-3.22), L22×T2 (-3.70), L30×T1 (-4.50), L24×T2 (-7.42) (significant at ($p \le 0.01$)), L7×T1 (-3.58) and L23×T2 (-6.49) (significant at ($p \le 0.05$)), had a reduced ear height. Testcrosses L24×T1 (8.92) (significant at ($p \le 0.05$)), L30×T2 (9.34) (significant at ($p \le 0.05$)), L23×T1 (5.62) and L10×T2 (5.71) recorded a high plant height while L24×T1 (7.42) (significant at ($p \le 0.01$)), L30×T2 (4.50), L23×T1 (6.48) (significant at ($p \le 0.05$)) and L7×T2 (4.16) had a reduced ear height (Table 6 and Appendix 2).

Testcrosses that were good specific combiners for ear aspect were L30×T2 (-0.53) (significant at ($p \le 0.01$)), L6×T2 (-0.32) and L9×T1 (-0.45) (significant at ($p \le 0.05$)). Testcrosses L6×T1 (0.38) (significant at ($p \le 0.05$)) and L10×T1 (0.23) had poor specific combining ability for ear aspect. Testcrosses that had a high number of plants harvested included L30×T2 (3.56), L9×T1 (3.86) and L10×T1 (6.16) (significant at ($p \le 0.05$)). L17×T1 (-1.89) and L12×T1 (-1.30) had a low number of plants harvested (Table 6 and Appendix 2).

3.6. Relative standard heterosis of testcrosses

Standard heterosis was estimated in comparison to tester 1 (CML539/CML442), tester 2 (CML78/P300C5), trial mean, check mean and best check mean.

A combined analysis for heterosis of grain yield across all locations indicated a total of 29 testcrosses with positive heterosis and 32 testcrosses with negative heterosis (Figure 1). There was a range of -66.74 to 30.28 for heterosis of grain yield relative to both testers (Figure 1). Lines that showed a positive heterosis for grain yield of both testers included 1, 17, 6, 29, 30, 13, 12, 16 and 8, therefore, recommended as best across locations. Lines 27, 14, 4, 20, 21, 11, 15, 3, 25, 5 and 2 showed positive heterosis only with tester 2 for grain yield (Table 7). The heterosis range relative to trial mean, check mean and the best check was -55.97 to 26.78, -34.49 to 36.86 and -46.25 to 31.34 respectively (Table 7).

Table 6. Specific Combining Ability (SCA) effects of testcrosses evaluated for grain yield (t ha^{-1}) and associated agronomic traits in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

L×T	GY	DTS	DTS	PH	EH	EA	NP
L1×T1	0.08	0.55	0.50	-0.62	0.32	-0.06	0.07
L30×T2	1.18**	-1.82*	-1.47	9.34*	4.50	-0.53**	3.56
L17×T1	0.01	0.05	-0.67	-2.01	-1.17	-0.14	-1.89
L1×T2	-0.08	-0.57	-0.55	0.57	-0.32	0.11	-0.02
L6×T2	0.22	0.52	0.32	4.45	1.83	-0.32	1.27
L13×T1	0.28	-0.74	-0.62	-0.18	-1.75	-0.12	-0.18
L6×T1	-0.22	-0.54	-0.37	-4.50	-1.83	0.38*	-1.22
L29×T1	-0.03	-0.24	-0.50	-1.61	-3.29	0.07	-0.89
L17×T2	-0.01	-0.07	0.61	1.96	1.17	0.19	1.94
L20×T1	0.25	-1.33	0.50	4.09	2.1	0.13	1.24
L27×T1	0.14	-0.74	-0.50	2.32	1.46	0.03	0.45
L8×T1	0.12	-0.41	-0.22	1.19	2.34	0.22	0.23
L9×T1	0.71*	-0.74	-1.42	2.74	2.21	-0.45*	3.86
L12×T1	-0.002	-1.08	-1.54	-0.73	0.38	0.02	-1.30
L11×T1	0.15	0.63	0.04	3.44	0.28	-0.02	0.49
L10×T1	0.47	0.01	-0.04	-5.75	-0.07	0.23	6.16*
L29×T2	0.03	0.22	0.45	1.57	3.29	-0.01	0.94
L14×T1	0.03	-0.41	-0.62	-1.75	-1.44	0.17	2.07
L16×T2	0.21	0.06	-0.30	1.41	-0.27	-0.07	0.81
L25×T1	0.14	0.17	0.71	-4.21	-3.32	-0.04	0.57
SE	**0.34**	**0.79**	**0.88**	**3.82**	**2.72**	**0.17**	**2.51**

L=line, T=tester, GY=grain yield (t ha^{-1}), DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested, SE= standard error, ** and * = significance at ($p \le 0.01$) and ($p \le 0.05$)

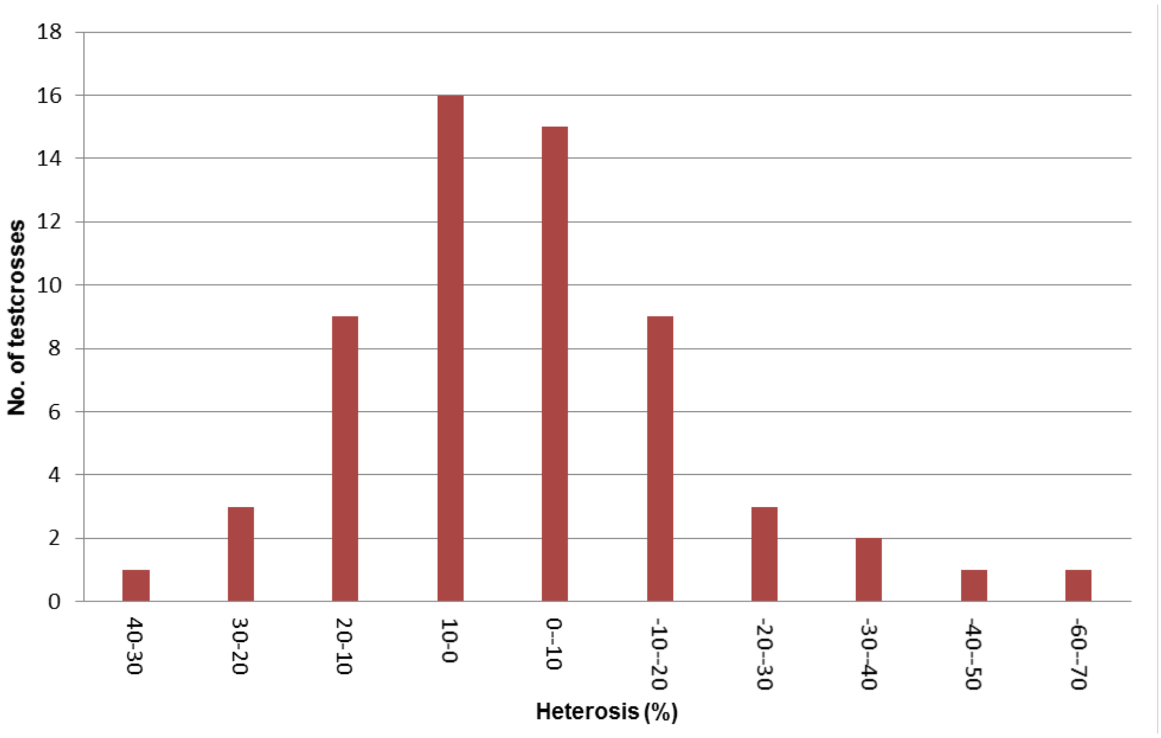

Figure 1. Distribution of heterosis (%) for grain yield (t ha^{-1}) relative to both testers among 60 testcrosses in Kakamega, Kiboko and Kitui during the 2016/2017 growing season

Table 7. Percent grain yield of testcrosses relative to testers, trial mean, check mean and best check mean evaluated in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

Line	(%) yield relative to CML539/CML442	(%) yield relative to CML78/P300C5	(%) yield relative to trial mean	(%) yield relative to check mean	(%) yield relative to best check mean
1	21.73	30.28	26.78	36.86	31.34
17	16.57	25.69	21.95	32.70	26.82
6	14.95	24.24	20.44	31.39	25.39
29	9.77	19.63	15.59	27.22	20.85
30	4.28	14.75	10.47	22.79	16.04
13	3.75	14.27	9.96	22.36	15.57
12	2.22	12.91	8.53	21.13	14.23
16	1.61	12.37	7.97	20.64	13.70
8	0.11	11.03	6.56	19.42	12.38
27	-0.53	10.46	5.97	18.91	11.82
14	-2.99	8.27	3.66	16.93	9.67
4	-3.02	8.24	3.63	16.90	9.64
20	-3.07	8.20	3.59	16.86	9.59
21	-3.10	8.17	3.56	16.84	9.57
11	-3.30	8.00	3.37	16.68	9.39
15	-5.93	5.65	0.91	14.55	7.08
3	-8.13	3.70	-1.14	12.78	5.16
25	-8.31	3.54	-1.31	12.64	5.00
5	-8.56	3.31	-1.55	12.44	4.78
2	-10.06	1.97	-2.95	11.22	3.46
26	-13.47	-1.06	-6.14	8.47	0.47
28	-14.57	-2.04	-7.17	7.59	-0.49
10	-15.58	-2.94	-8.12	6.77	-1.38
18	-17.16	-4.35	-9.59	5.50	-2.77
24	-18.31	-5.37	-10.67	4.57	-3.77
9	-24.16	-10.59	-16.15	-0.15	-8.91
23	-24.52	-10.91	-16.48	-0.44	-9.22
7	-33.27	-18.70	-24.67	-7.50	-16.90
22	-36.54	-21.61	-27.72	-10.13	-19.77
19	-66.74	-48.51	-55.97	-34.49	-46.25
CML539/CML442	**3.26**				
CML78/P300C5		**2.90**			
Trial mean			**3.05**		
Check mean				**2.63**	
Best check mean					**2.86**

SE for heterosis of grain yield = 0.97

4. Discussions

4.1. Analysis of variance

The presence of highly significant mean squares ($p \leq 0.01$) of environments for grain yield and yield-related traits indicated that the genotypes responded differently in different environments [3]. Significant mean squares ($p \leq 0.01$) of the genotypes (testcrosses) for grain yield and the yield-related traits indicated that the genotypes had high genetic variability and had a high potential of making good-yielding hybrids [12]. The high line and tester mean squares in comparison to the line by tester mean square interaction effects for the measured traits indicated that additive gene effects were of more importance in the inheritance of traits. These findings are in agreement with previous research in maize [25,32].

4.2. Mean performance of testcrosses

Evaluation of the mean performance of the testcrosses indicated that most of them yielded better than the commercial checks. Some testcrosses had better performance for more than one attribute. Testcrosses that showed high grain yield could be used in breeding programs as materials that provide source genes to improve on other materials that might have other desirable traits but low in grain yield. Testcrosses that had earliness in anthesis and silking, with medium plant and ear height and good performance in ear aspect could be used to provide genes for developing high yielding and early maturing genotypes. These results and findings are in agreement with other researchers on maize who reported that experimental genotypes performed better than best checks for most yield and yield-related traits [12,25,33].

4.3. General and specific combining ability studies

The mean squares of the GCA of lines and GCA of testers were higher than the mean squares of the SCA of testcrosses (line by tester interaction) for all the traits studied, therefore, indicated that additive gene effect had the greatest contribution to the genetic variation of the traits than non-additive genetic. Several researchers reported the same results on evaluation of different maize genotypes [11,23,24].

Highly significant mean squares of the GCA of lines, testers, and SCA of testcrosses showed that additive and non-additive gene effects were substantial in the expression of grain yield. The same findings were also reported in previous research [25,26].

Number of days to silking showed significant mean squares for GCA of lines and GCA of testers, but there was no significant difference for SCA of testcrosses hence indicating that additive gene action was of more importance in the expression of days to silking. Other researchers also reported the same findings [23,27].

Number of days to taselling had significant mean squares for both the effect of GCA of lines and SCA of testcrosses hence indicating that both the additive and non-additive gene effects were vital in the expression of days to silking. The same findings were also reported previously [28].

Plant height and ear height mean squares for GCA of lines and SCA of testcrosses were highly significant. Mean squares of GCA of testers were significant only for plant height and non-significant for ear height hence indicating that both additive and non-additive genetic effects were of importance in the expression of plant height and ear height. Previous research also reported the same results [23,29].

Ear aspect and number of plants harvested mean squares were highly significant for the GCA of lines, GCA of testers and SCA of testcrosses hence showing that additive and non-additive gene actions contributed in the expression of ear aspect and number of plants harvested. A study on quality protein maize inbred lines also reported the incidence of additive and non-additive gene effect controlling the expression of ear aspect [30]. Contrary to the current findings, Seyoum et al. [12] reported that additive gene effect controls number of plants trait expression.

4.4. Heterosis

Grain yield and other associated traits had significant mean squares for genotypes, thereby, indicating that there was a significant amount of heterosis [10]. The heterosis of genotypes was estimated relative to grain yield (t ha^{-1}) of testers, trial mean, checks mean and best check mean.

Lines 1, 17, 6, 29, 30, 13, 12, 16 and 8 showed positive heterosis for grain yield to both testers and therefore could be used to develop new high yielding genotypes as reported by [3].

The heterosis for grain yield of best check mean across environments ranged from 31.34 to -46.25 with all lines with positive heterosis for both testers performing better than the best check mean. The results conform to previous research in maize breeding whereby testcrosses perform better than commercial check hybrids [13,31].

5. Conclusion and Recommendations

Line GCA mean squares from analysis of variance was highly significant for all the traits studied. Tester GCA was equally significant for all traits except for days to anthesis and ear height. Significant GCA and SCA mean squares indicated that additive gene action and non-additive gene action contributed to the inheritance of the traits studied. The sum of squares of GCA was higher than the sum of squares of SCA for all the traits studied, hence indicating that testcross variation was primarily due to additive main effects rather than non-additive effects. Therefore, showing the possibility of breeding using recurrent selection and backcrossing to transfer candidate genes to other genotypes that need to be improved for yield and yield-associated traits.

GCA analysis showed that lines 1, 17, 6, 29 and 30 were good general combiners for grain yield across locations and therefore could be utilized to develop new varieties. Lines 23, 22, 4, 24 and 23, 22, 4, 20 had the best general combining ability for days to anthesis and days to silking respectively and therefore could be used as sources of genes for earliness. Lines 19, 30, 8, 18 and 19, 30, 22, 28 were the best combiners for reduced ear and plant height respectively which could be used to develop lodging resistant varieties. Lines 13, 16, 14 and 12, 24, 9 were top general combiners for increased plant and ear height respectively. Lines 6, 1, 17 and 16 were top general combiners for good ear aspect while lines 17, 12 and 4 were good combiners for number of plants harvested.

SCA analysis and evaluation of mean performance showed that testcrosses L30×T2 (4.40 t ha^{-1}), L13×T1 (3.85 t ha^{-1}), L20×T1 (3.59 t ha^{-1}) and L9×T1 (3.52 t ha^{-1}) were higher yielding than best check mean. They had good specific combining ability for grain yield and good specific combining ability for earliness in anthesis and silking dates. These testcross hybrids can be investigated further for grain yield and earliness and after that commercially released.

From the present findings, good testcrosses and inbred lines for grain yield and other related traits were identified successfully. These genotypes comprise a source of useful genetic materials that can be utilized for future maize improvement programs. Future studies need to separate the inbred lines used in this study into different heterotic groups by using divergent testers.

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Appendices

Appendix 1. Mean comparison for the 60 testcrosses and 4 checks evaluated for grain yield (t ha^{-1}) and associated agronomic traits in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

L×T	GY	RNK	DTS	RNK	DTT	RNK	PH	RNK	EH	RNK	EA	RNK	NP	RNK
L1×T1	4.42	**1**	65.17	**40**	63.00	**42**	180.40	**44**	84.22	**49**	2.38	**8**	33.67	**5**
L30×T2	4.40	**2**	63.67	**32**	63.00	**42**	168.30	**19**	78.22	**20**	2.08	**2**	34.08	**4**
L17×T1	4.09	**3**	64.17	**35**	62.25	**36**	166.20	**13**	78.35	**22**	2.33	**6**	32.33	**13**
L1×T2	3.91	**4**	62.58	**21**	61.67	**32**	178.10	**41**	84.88	**51**	2.38	**8**	31.92	**16**
L6×T2	3.87	**5**	62.92	**25**	61.50	**30**	175.50	**36**	87.12	**58**	1.88	**1**	33.33	**8**
L13×T1	3.85	**6**	63.50	**30**	61.75	**33**	185.70	**56**	82.97	**45**	2.42	**9**	32.00	**15**
L6×T1	3.79	**7**	63.33	**29**	61.08	**25**	170.00	**23**	82.17	**39**	2.75	**21**	32.50	**11**
L29×T1	3.76	**8**	64.08	**34**	61.17	**26**	169.90	**22**	77.87	**19**	2.71	**20**	29.42	**32**
L17×T2	3.72	**9**	62.58	**21**	63.25	**45**	166.70	**15**	81.99	**38**	2.50	**12**	34.50	**1**
L20×T1	3.59	**10**	60.92	**10**	58.67	**12**	171.60	**27**	80.16	**29**	3.17	**31**	34.17	**3**
L8×T1	3.56	**11**	61.25	**11**	58.58	**10**	172.20	**29**	74.87	**12**	3.21	**32**	32.08	**14**
L27×T1	3.56	**11**	63.67	**32**	61.42	**29**	177.50	**40**	83.37	**48**	3.21	**32**	32.75	**9**
L9×T1	3.52	**12**	65.50	**41**	63.75	**46**	185.30	**55**	90.01	**63**	2.42	**9**	27.00	**40**
L12×T1	3.51	**13**	65.50	**41**	62.75	**40**	180.20	**43**	86.95	**57**	2.96	**27**	33.50	**7**
L11×T1	3.48	**14**	65.00	**38**	61.17	**26**	181.10	**47**	82.48	**43**	2.92	**26**	33.58	**6**
L10×T1	3.47	**15**	66.50	**46**	64.92	**50**	172.20	**29**	75.18	**13**	2.79	**22**	29.75	**29**
L29×T2	3.46	**16**	63.08	**27**	61.83	**34**	169.70	**21**	85.76	**53**	2.46	**10**	29.58	**31**
L14×T1	3.38	**17**	64.17	**35**	61.58	**31**	182.40	**50**	78.36	**23**	2.71	**20**	33.50	**7**
L16×T2	3.34	**18**	64.42	**36**	63.17	**44**	180.90	**46**	80.80	**31**	2.21	**4**	29.92	**27**
L25×T1	3.33	**19**	62.17	**18**	59.50	**16**	165.50	**12**	74.34	**10**	2.83	**24**	32.58	**10**
L21×T1	3.30	**20**	63.25	**28**	60.00	**20**	179.80	**42**	80.74	**30**	2.67	**19**	32.42	**12**
L24×T1	3.29	**21**	63.58	**31**	63.08	**43**	184.70	**54**	92.77	**64**	2.50	**13**	26.00	**43**
L23×T1	3.29	**21**	60.83	**9**	58.50	**9**	177.10	**38**	85.90	**55**	3.08	**29**	33.67	**5**
L16×T1	3.29	**21**	65.75	**42**	64.00	**48**	181.50	**49**	80.04	**27**	2.58	**17**	30.00	**26**
L15×T1	3.29	**21**	65.50	**41**	62.50	**37**	172.90	**32**	68.72	**4**	2.88	**25**	32.75	**9**
L4×T1	3.23	**22**	60.33	**7**	58.25	**7**	171.70	**28**	79.68	**25**	3.17	**31**	33.50	**7**
L5×T2	3.20	**23**	64.50	**37**	62.58	**38**	171.20	**26**	83.22	**46**	2.88	**25**	30.92	**20**
L18×T1	3.18	**24**	65.92	**44**	62.58	**38**	172.70	**31**	74.12	**8**	2.35	**7**	29.42	**32**
L12×T2	3.16	**25**	66.17	**45**	65.50	**51**	178.10	**41**	87.49	**61**	2.79	**22**	34.50	**2**
L3×T1	3.11	**26**	61.67	**13**	59.83	**18**	172.50	**30**	80.07	**28**	3.08	**29**	27.08	**39**
L4×T2	3.10	**27**	59.75	**5**	57.58	**4**	164.40	**11**	81.69	**36**	2.82	**23**	32.50	**11**
L2×T1	3.08	**28**	61.75	**14**	59.58	**17**	177.40	**39**	82.18	**40**	2.50	**12**	24.83	**48**
L21×T2	3.03	**29**	61.50	**12**	60.58	**23**	172.90	**32**	81.67	**35**	2.54	**16**	31.83	**17**
L26×T1	3.00	**30**	63.58	**31**	60.50	**22**	173.20	**34**	77.70	**18**	3.08	**29**	31.58	**18**
L8×T2	2.97	**31**	60.54	**8**	58.63	**11**	166.60	**14**	71.65	**5**	2.64	**18**	30.07	**25**
L28×T1	2.97	**31**	62.75	**22**	60.25	**21**	167.00	**18**	81.57	**34**	2.75	**21**	30.92	**20**
L14×T2	2.96	**32**	63.50	**30**	62.50	**37**	182.50	**51**	82.55	**44**	2.25	**5**	27.75	**38**
L3×T2	2.93	**33**	59.67	**4**	57.67	**5**	164.20	**10**	82.47	**42**	2.96	**27**	30.67	**22**
L13×T2	2.93	**33**	63.50	**30**	62.67	**39**	182.50	**51**	87.77	**62**	2.54	**16**	30.75	**21**
L27×T2	2.92	**34**	63.67	**32**	62.08	**35**	169.30	**20**	81.76	**37**	3.04	**28**	30.25	**23**
L15×T2	2.86	**35**	62.83	**23**	61.50	**30**	180.50	**45**	76.46	**15**	2.17	**3**	25.08	**46**
L2×T2	2.85	**36**	62.00	**16**	62.58	**38**	181.30	**48**	85.83	**54**	2.75	**21**	24.92	**47**
L11×T2	2.83	**37**	62.25	**19**	60.75	**24**	170.70	**25**	83.23	**47**	2.83	**24**	31.00	**19**
L5×T1	2.80	**38**	65.17	**40**	63.08	**43**	173.10	**33**	76.01	**14**	3.04	**28**	25.75	**44**
L26×T2	2.74	**39**	63.83	**33**	62.67	**39**	166.80	**16**	78.30	**21**	2.92	**26**	29.67	**30**
L20×T2	2.74	**39**	62.08	**17**	57.33	**3**	159.90	**5**	77.27	**17**	2.79	**22**	30.08	**24**
L28×T2	2.72	**40**	60.17	**6**	59.00	**14**	159.90	**5**	81.44	**33**	2.71	**20**	28.92	**34**
L25×T2	2.69	**42**	60.33	**7**	57.75	**6**	170.50	**24**	82.27	**41**	2.79	**22**	29.83	**28**
L7×T2	2.67	**43**	61.50	**12**	59.92	**19**	166.90	**17**	84.41	**50**	2.79	**22**	27.83	**37**
L22×T2	2.42	**45**	57.96	**3**	56.72	**2**	157.90	**4**	73.72	**7**	2.51	**14**	28.07	**36**
L30×T1	2.41	**46**	68.75	**48**	66.17	**52**	153.00	**2**	67.92	**3**	3.37	**34**	28.67	**35**
L18×T2	2.39	**47**	63.00	**26**	61.35	**28**	162.50	**7**	72.99	**6**	2.75	**21**	23.17	**49**
L22×T1	2.36	**48**	60.92	**10**	58.42	**8**	170.50	**24**	79.82	**26**	2.67	**19**	20.25	**53**
L7×T1	2.22	**49**	61.83	**15**	58.75	**13**	163.20	**8**	74.78	**11**	2.96	**27**	21.42	**51**
L24×T2	2.22	**49**	57.50	**1**	57.67	**5**	163.30	**9**	79.22	**24**	2.96	**27**	19.58	**55**
L19×T2	2.22	**49**	60.92	**10**	59.42	**15**	152.70	**1**	67.52	**2**	3.13	**30**	21.92	**50**
L10×T2	2.17	**50**	65.00	**38**	64.67	**49**	180.20	**43**	76.62	**16**	2.21	**4**	15.83	**57**
L23×T2	1.95	**51**	57.92	**2**	56.42	**1**	162.40	**6**	74.25	**9**	3.25	**33**	21.25	**52**
L9×T2	1.73	**52**	65.50	**41**	66.25	**53**	176.30	**37**	86.88	**56**	3.21	**32**	17.67	**56**
L19×T1	1.69	**53**	62.50	**20**	59.58	**17**	155.50	**3**	66.92	**1**	3.38	**35**	19.92	**54**
Check 1	2.86	**35**	62.91	**24**	61.20	**27**	190.40	**57**	85.58	**52**	2.47	**11**	29.08	**33**
Check 2	2.41	**46**	65.13	**39**	62.92	**41**	174.95	**35**	81.00	**32**	2.67	**19**	26.84	**41**
Check 3	2.71	**41**	68.21	**47**	66.50	**54**	184.15	**53**	87.34	**59**	2.52	**15**	25.67	**45**
Check 4	2.54	**44**	65.84	**43**	63.80	**47**	183.30	**52**	87.39	**60**	2.71	**20**	26.09	**42**
SE	**0.97**		**3.06**		**2.30**		**20.60**		**11.44**		**0.47**		**4.48**	
Checks mean	**2.63**		**65.52**		**63.60**		**183.17**		**85.33**		**2.59**		**26.92**	
Trial mean	**3.05**		**63.06**		**61.24**		**172.52**		**80.33**		**2.74**		**28.94**	
min	**0.05**		**49.00**		**49.00**		**68.75**		**24.00**		**1.00**		**1.00**	
max	**9.22**		**89.00**		**87.00**		**282.50**		**148.00**		**5.00**		**49.00**	
L.S.D (0.05)	**2.69**		**8.49**		**6.38**		**57.19**		**31.77**		**1.31**		**12.44**	
CV	**23.00**		**9.70**		**7.50**		**23.80**		**24.00**		**22.00**		**21.10**	

L=line, T=tester, RNK=rank, GY=grain yield (t ha^{-1}), SE= standard error, DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested

Appendix 2. Specific Combining Ability (SCA) effects of testcrosses evaluated for grain yield (t ha^{-1}) and associated agronomic traits in Kakamega, Kiboko and Kitui during the 2016/2017 growing season (averaged over 2 seasons)

L×T	GY	DTS	DTT	PH	EH	EA	NP
L1×T1	0.08	0.55	0.50	-0.62	0.32	-0.06	0.07
L30×T2	1.18**	-1.82*	-1.47	9.34*	4.50	-0.53**	3.56
L17×T1	0.01	0.05	-0.67	-2.01	-1.17	-0.14	-1.89
L1×T2	-0.08	-0.57	-0.55	0.57	-0.32	0.11	-0.02
L6×T2	0.22	0.52	0.32	4.45	1.83	-0.32	1.27
L13×T1	0.28	-0.74	-0.62	-0.18	-1.75	-0.12	-0.18
L6×T1	-0.22	-0.54	-0.37	-4.50	-1.83	0.38*	-1.22
L29×T1	-0.03	-0.24	-0.5	-1.61	-3.29	0.07	-0.89
L17×T2	-0.01	-0.07	0.61	1.96	1.17	0.19	1.94
L20×T1	0.25	-1.33	0.50	4.09	2.10	0.13	1.24
L27×T1	0.14	-0.74	-0.50	2.32	1.46	0.03	0.45
L8×T1	0.12	-0.41	-0.22	1.19	2.34	0.22	0.23
L9×T1	0.71*	-0.74	-1.42	2.74	2.21	-0.45*	3.86
L12×T1	-0.002	-1.08	-1.54	-0.73	0.38	0.02	-1.3
L11×T1	0.15	0.63	0.04	3.44	0.28	-0.02	0.49
L10×T1	0.47	0.01	-0.04	-5.75	-0.07	0.23	6.16*
L29×T2	0.03	0.22	0.45	1.57	3.29	-0.01	0.94
L14×T1	0.03	-0.41	-0.62	-1.75	-1.44	0.17	2.07
L16×T2	0.21	0.06	-0.3	1.41	-0.27	-0.07	0.81
L25×T1	0.14	0.17	0.71	-4.21	-3.32	-0.04	0.57
L21×T1	-0.04	0.13	-0.46	1.70	0.18	0.01	-0.51
L15×T1	0.04	0.59	0.33	-5.56	-3.22	0.30	3.03
L24×T1	0.35	2.30**	2.54**	8.92*	7.42**	-0.29	2.41
L23×T1	0.49	0.71	0.88	5.62	6.48*	-0.14	5.41*
L16×T1	-0.21	-0.08	0.25	-1.45	0.27	0.13	-0.76
L4×T1	-0.11	-0.45	0.17	1.92	-0.35	0.11	-0.3
L5×T2	0.38	0.39	-0.14	0.74	2.96	0.02	3.44
L18×T1	0.22	0.71	0.42	3.38	1.21	-0.26	2.32
L12×T2	0.002	1.06	1.49	0.69	-0.38	0.03	1.35
L3×T1	-0.09	0.26	0.92	2.38	-0.55	0.00	-2.59
L4×T2	0.11	0.43	-0.22	-1.96	0.35	-0.05	0.35
L2×T1	-0.06	-0.87	-1.67	-3.71	-1.19	-0.18	-0.84
L21×T2	0.04	-0.15	0.40	-1.74	-0.19	0.05	0.56
L26×T1	-0.05	-0.87	-1.25	1.44	0.35	0.02	0.16
L28×T1	-0.05	0.55	0.46	1.81	0.72	-0.04	0.20
L8×T2	-0.12	0.39	0.16	-1.23	-2.34	-0.17	-0.18
L14×T2	-0.03	0.39	0.57	1.71	1.44	-0.11	-2.02
L13×T2	-0.28	0.72	0.57	0.14	1.75	0.17	0.23
L3×T2	0.09	-0.28	-0.97	-2.42	0.55	0.05	2.65
L27×T2	-0.14	0.72	0.45	-2.36	-1.46	0.03	-0.40
L15×T2	-0.04	-0.61	-0.39	5.51	3.22	-0.24	-2.98
L2×T2	0.06	0.85	1.61	3.67	1.18	0.24	0.90
L11×T2	-0.15	-0.65	-0.10	-3.48	-0.28	0.07	-0.44
L5×T1	-0.38	-0.41	0.08	-0.78	-2.96	0.03	-3.39
L26×T2	0.05	0.85	1.20	-1.49	-0.35	0.03	-0.10
L20×T2	-0.25	1.31	-0.55	-4.14	-2.10	-0.07	-1.19
L28×T2	0.05	-0.57	-0.51	-1.86	-0.72	0.09	-0.15
L25×T2	-0.14	-0.19	-0.76	4.17	3.31	0.09	-0.52
L7×T2	0.41	0.56	0.7	3.53	4.16	0.02	4.06
L22×T2	0.21	-0.73	-0.71	-4.60	-3.70	0.04	4.74
L30×T1	-1.18**	1.80*	1.42	-9.39*	-4.50	0.59**	-3.51
L18×T2	-0.22	-0.73	-0.48	-3.43	-1.22	0.31	-2.27
L22×T1	-0.21	0.71	0.66	4.55	3.70	0.02	-4.69
L24×T2	-0.35	-2.32**	-2.60**	-8.97*	-7.42**	0.34*	-2.35
L7×T1	-0.41	-0.58	-0.75	-3.58	-4.16	0.03	-4.01
L19×T2	0.44	-0.07	0.03	0.3	-0.35	-0.01	1.85
L10×T2	-0.47	-0.03	-0.01	5.71	0.07	-0.18	-6.10*
L23×T2	-0.49	-0.73	-0.93	-5.67	-6.49*	0.2	-5.35*
L9×T2	-0.71*	0.72	1.36	-2.79	-2.22	0.50**	-3.81
L19×T1	-0.44	0.05	-0.08	-0.34	0.35	0.06	-1.8
SE	**0.34**	**0.79**	**0.88**	**3.82**	**2.72**	**0.17**	**2.51**

L=line, T=tester, GY=grain yield (t ha^{-1}), SE= standard error, DTS= days to silking, DTT= days to tasselling, PH = plant height, EH = ear height, EA = ear aspect, NP = number of plants harvested, ** and * = significance at ($p \leq 0.01$) and ($p \leq 0.05$).