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Combining abilities and genetic parameters for grain yield and some agronomic traits in maize (*Zea mays* L.)

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Abstract

Background: The improvement of maize hybrids relies on significant genetic variability among the inbred lines used and the degree to which it is transferred to progeny. Understanding the genetic parameters and heritability of traits in every population is an essential precondition for selection program. This study was designed to estimate the magnitude of genetic parameters and heritability of traits in line \times tester mating design. Fifteen yellow maize inbred lines derived from different sources were crossed with two lines as tester i.e., Gm-1001 and Gm-1002 in 2019 summer season. During 2020 season, the resulted 30 crosses along with check hybrid SC-168 were evaluated in a yield trial at two locations: Gemmeiza and Sids Agric. Res. Station.

Results: The mean squares among two locations were highly significant for all studied traits except KR^{-1} . The L_1 and L_3 had the best general combiners for GY and fed^{-1} . In addition, the T_1 as a tester was a GCA effects good combiner for earliness, shorter plants and lower ear placement traits. While T_2 was good combiner for grain yield and some of attributes. Crosses $L_5 \times T_1$ and $L_7 \times T_2$ had positive and significant SCA effects for grain yield. The GCA variances were higher than SCA variances for all studied traits except for ED trait, indicating that additive genetic variance played the major role than non-additive genetic variance in the inheritance of these traits. Generally, phenotypic coefficient of variability was higher than genotypic coefficient of variability for all studied traits, suggesting that there was an influence by environments in the expression of these traits. Recorded heritability percentage in broad sense ranged from low for (ear position%, no. of ears/100 plants, ear diameter and grain yield) traits, medium for (days to 50% silking, plant height, ear height and no. of kernels/row) traits to moderate high for ear length trait.

Conclusion: Our investigation concluded that most of the studied lines exhibited highly general combiners and the superior crosses were as a result of a good \times good combiner for most of yield components traits.

Keywords: Maize, Line \times tester, Combining ability, Gene action and genetic parameters

1 Background

Maize (*Zea mays* L.) is playing main role in human and livestock nutrition worldwide and is used for several industrial purposes such as oil and starch [11]. Internationally, maize is known as queen of cereals because of

its highest genetic yield potential. The high yielding of maize hybrids influenced by inbred lines which had high general and specific combining abilities. Thus, maize breeders need to develop more maize inbred lines to produce more new hybrids. In breeding programs high yielding lines are often used as parents because the target is to increase grain yield. Line \times tester mating design assesses a set of lines as a female by crossing each to a common tester as a male [21]. Combining ability is crucial for selecting appropriate parents for hybridization and identifying superior crosses in breeding programs

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[25]. Combining ability analysis is suitable to assess the potential inbred lines and helps to identify the nature of gene action involved in different quantitative traits. This mating design helps in defining the ability of the parental lines to inherit traits to the progeny and built on the basics of a factorial experiment however the line is considering as one factor and the tester as the other one. Simultaneously, it is useful in assessing several types of gene action and permits the inference of effects attributed to lines, testers and their interaction [17]. Progress of several crop development depends on the genetic variability and heritability present in the plant materials. The range of variability is measured by genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) which offers information about relative extent of variation in altered traits. Hence, to have a thorough complete idea, it is necessary to an investigative valuation of yield components. Heritability gives the information on the magnitude of inheritance of quantitative traits [34]. Heritability is a heritable portion of phenotypic variance and helps the breeders to select out elite genotype from a diverse genetic component. GCV and PCV values were characterized as low when less than 10%, moderate 10–20% and high more than 20% [10]. While heritability was characterized as low when less than 40%, medium 40–59%, moderately high 60–79% and very high heritability 80% and above [31].

The objectives of this study were to determine general and specific combining abilities effects, identify the superior crosses to improve the yielding ability in maize breeding programs, identify the nature of gene action and genetic variability for yield and yield components traits.

2 Methods

2.1 Plant materials and its sources

The plant materials of this investigation were composed of fifteen new yellow maize inbred lines derived from different sources at two Agricultural Research Stations; [Gemmeiza (Gm) and Sids (Sd)] namely L_1 , L_2 to L_{15} along with two testers; Gm-1001 (T_1) and Gm-1021 (T_2).

2.2 Experimental sites and growing seasons

In 2019 season, the fifteen yellow maize inbred lines were crossed with the two testers in a line \times tester mating design at Gemmeiza Agric. Res. Sta., National Maize Research Program to obtain 30 single crosses. During 2020 growing season, the resulted 30 crosses along with yellow check hybrid SC-168 were evaluated in a yield trial at Gemmeiza and Sids, Agricultural Research Stations.

2.3 Experimental design and its management

A randomized Complete Blocks Design (RCBD) with four replications was used at each location. Plot size was

one row, 6 m long and 0.8 m a part. Seeds were planted in hills evenly spaced at 0.25 m along the row at the rate of two kernels hill⁻¹, which thinned to one plant hill⁻¹ after 21 days from planting date. The field trails were kept clean of weeds throughout the growing season, whereas all cultural practices for maize production were applied as recommended at the proper time.

2.4 Data recorded

The collected data were days to 50% silking (DTS day), plant height (PHT cm), ear height (EHT cm), ear position% (Epos %), no. of ears/100 plants (E100P), ear length (EL cm), ear diameter (ED cm), no. of kernels/row (KR⁻¹) and grain yield (GY ard fed⁻¹) adjusted to 15.5% moisture content, one ardab = 140 kg and one feddan = 4200 m².

2.5 Statistical analysis

Data were analyzed using general linear model (GLM) procedures in SAS [29]. Means for all maize combinations adjusted for block effects through sites were analyzed according to Sendecore and Cochran [32]. Combining ability analysis was performed for traits that showed statistical differences among crosses. Kempthorne [18] was employed to determine general and specific combining abilities and their interaction effects with two locations.

3 Results

3.1 Analysis of variance

Analyses of variance across two locations for all studied traits are presented in Table 1. The results showed that the magnitude of mean squares among two locations were highly significant ($P \leq 0.001$) for all studied traits except KR⁻¹. Moreover, highly significant differences were detected among crosses for all studied traits. Significant or highly significant mean squares were observed for lines (L), testers (T) and ($L \times T$) interaction for all studied traits, except (T) for ED and $L \times T$ for EHT and Epos%. Significant or highly significant differences were observed between lines \times location interaction for DTS, PHT, EHT and GY ard fed⁻¹, testers \times location interaction for EL, ED and KR⁻¹. Meanwhile, Mean squares due to $L \times T \times \text{Loc}$ interactions were significant for E100P and ED traits.

3.2 Mean performance

For all traits studied, the mean performance of the 30 crosses and one check hybrid SC-168 over two locations are presented in Table 2. Mean values of crosses for DTS ranged from 55.13 days for $L_1 \times T_2$ to 61.63 days for $L_{13} \times T_1$. Furthermore, all crosses were significantly earlier than the check hybrid SC-168 (64.89 days). Regarding PHT, crosses ranged from 241.75 cm for cross $L_8 \times T_2$ to 302.13 cm for cross $L_{14} \times T_1$. Four crosses; $L_8 \times T_2$, $L_{10} \times$

Table 1 Analysis of variances for nine traits combined across two locations

sov	df	DTS	PHT	EHT	EPOS%	E100P	EL	ED	KR ⁻¹	GY ard fed ⁻¹
Locations (Loc.)	1	589.07**	37,550.02**	24,804.39**	381.35*	2252.16**	199.84**	5.37**	17.60	646.50**
Reps/Loc	6	2.26	1239.96	747.66	34.84	147.10	0.61	0.19	11.88	18.71
Crosses (C)	29	16.45**	1516.70**	1516.01**	77.10**	265.20**	13.93**	0.13**	64.87**	42.33**
Lines (L)	14	25.48**	1726.74**	1570.48**	91.55**	207.89**	11.38**	0.20**	56.10**	29.86*
Testers (T)	1	70.42**	15,584.82**	18,972.82**	585.03**	3146.50**	177.16**	0.06	656.70**	454.37**
Lines × Testers	14	3.56*	301.81*	214.64	26.37	116.71*	4.83**	0.07**	31.37**	55.37**
C × Loc	58	1.69	145.18	72.58	16.10	55.55	1.19	0.03	3.73	9.39
Lines × Loc	14	5.30**	408.95**	143.55	34.99	92.83	1.37	0.05*	5.77	27.12*
Testers × Loc	1	2.40	5.40	17.13	16.28	45.41	31.83**	0.32**	36.04*	39.04
L × T × Loc	14	1.53	192.12	155.93	30.54	134.08*	1.28	0.05*	7.09	9.01
Pooled error	174	2.048	174.679	153.088	26.961	65.468	1.076	0.032	7.026	15.875

*, ** significant at 0.05 and 0.01 levels of probability, respectively

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

T_2 , $L_7 \times T_2$ and $L_{15} \times T_2$ were significantly shorter than the shortest check hybrid SC.168. For EHT, the lowest ear height was desirable trait for loading resistance. Thus, 9 out of 30 crosses had significantly lower ear height compared with the best check hybrid SC-168 (144.75 cm) and the crosses ranged from 106.39 cm for cross $L_{11} \times T_2$ to 164.00 cm for cross $L_{14} \times T_1$. For Epos%, 12 out of 30 crosses were significantly toward lower ear placement than the check hybrid SC-168 (54.32%). For E100p, mean values of crosses ranged from 96.20 for $L_9 \times T_1$ to 117.90 for $L_{11} \times T_2$ and four crosses; $L_3 \times T_2$, $L_5 \times T_2$, $L_{11} \times T_2$ and $L_{12} \times T_2$ were significantly higher than the check hybrid SC-168. Concerning EL, nine crosses involving T_1 as a tester (parent) had significantly compared with the best check hybrid SC-168. ED trait ranged from 4.31 cm for cross $L_{15} \times T_2$ to 5.05 cm for crosses $L_1 \times T_1$ and $L_{13} \times T_1$ and most of crosses did not vary significantly from the check hybrid SC-168. For KR⁻¹, the crosses ranged from 31.20 for cross $L_{13} \times T_2$ to 39.18 for cross $L_2 \times T_1$ and seven crosses differed significantly compared with the check hybrid. Concerning GY ard fed⁻¹, results revealed that the cross $L_5 \times T_2$ had the highest grain yield (32.03) that was different significantly than the check hybrid followed by cross $L_1 \times T_2$ (31.45 ard fed⁻¹). Furthermore, 14 crosses out of 30 crosses did not vary significantly compared with the check hybrid (27.53 ard fed⁻¹).

3.3 General combining ability effects

General combining ability (g_i) effects for fifteen inbred lines and two testers for all studied traits across two locations are shown in Table 3. The parents L_1 , L_4 , L_6 , L_7 , L_8 and L_{11} had negative significant or highly significant (desirable) toward earliness. With respect to PHT and EHT, the inbred lines L_6 , L_7 , L_8 , L_{10} and L_{11} showed

negative and significant or highly significant GCA effects. For Epos%, the inbred lines L_1 , L_{11} and L_{15} had negative and significant GCA effects for lowest ear position. Concerning E100p, the lines L_5 and L_{11} showed positive and highly significant GCA effects. For EL, six inbred lines (L_2 , L_3 , L_5 , L_9 , L_{12} and L_{14}) exhibited positive and highly significant GCA effects. The inbred lines L_1 , L_6 , L_8 , L_9 and L_{13} showed positive estimates of GCA effects for ear diameter. For KR⁻¹, L_2 , L_3 and L_5 expressed significant positively and seemed to be the best combiner for GCA effects. The best general combiners for GY ard fed⁻¹ were L_1 and L_3 . These inbred lines which possessed high GCA effects for grain yield showed the same effect for one or more of the traits contributing to grain yield. Results showed that, T_1 as a tester has good combiner GCA effects for earliness, shorter plants and lower ear placement traits. While T_2 as a tester has good combiner GCA effects for grain yield and some of its attributes.

3.4 Specific combining ability

Specific combining ability effects of 30 crosses for all studied traits combined across two locations are illustrated in Table 4. Results revealed that, crosses $L_7 \times T_2$ and $L_9 \times T_2$ showed the negative and significant SCA (desirable) effects for DTS toward earliness; $L_{12} \times T_1$ for PHT and EHT toward shorter plants. For ear position, $L_{15} \times T_2$ showed negative and significant SCA effects toward lower ear placement. Concerning E100p, cross $L_4 \times T_2$ showed positive and significant SCA effect. Regarding to EL, five crosses out of 30 crosses exhibited positive and significant SCA effect and the cross $L_5 \times T_1$ was the best one. The crosses $L_1 \times T_1$ and $L_{15} \times T_1$ were the best combiners for ED. Four crosses; $L_1 \times T_2$, $L_4 \times T_1$, $L_7 \times T_2$ and $L_{12} \times T_2$ had positive significantly SCA effect for

Table 2 Mean performances of 30 single crosses and check for all the studied traits combined across two locations

crosses	DTS	PHT	EHT	Epos%	E100P	EL	ED	KR ⁻¹	GY ard ed ⁻¹
L ₁ × T ₁	59.25	290.25	140.63	48.34	100.13	14.60	4.05	30.98	27.96
L ₁ × T ₂	55.13	263.38	122.75	46.60	106.13	15.13	4.78	36.40	31.45
L ₂ × T ₁	60.75	298.13	151.88	50.89	107.21	18.83	4.99	39.18	29.82
L ₂ × T ₂	58.00	257.38	124.63	48.51	103.50	16.25	4.53	36.78	25.02
L ₃ × T ₁	60.25	290.13	156.63	54.05	101.58	17.83	4.86	37.13	27.58
L ₃ × T ₂	57.63	266.50	136.50	51.06	113.39	16.10	4.60	36.86	30.90
L ₄ × T ₁	58.63	287.50	161.13	55.85	101.98	17.18	4.86	36.95	26.13
L ₄ × T ₂	55.25	256.38	134.00	52.26	107.85	14.88	4.48	35.03	31.01
L ₅ × T ₁	60.75	281.88	144.13	51.09	104.98	17.75	4.76	37.10	25.15
L ₅ × T ₂	56.13	255.88	126.50	49.32	114.93	16.53	4.36	37.60	32.03
L ₆ × T ₁	58.88	274.13	136.63	49.80	98.15	16.08	4.96	35.00	24.06
L ₆ × T ₂	54.63	254.50	119.75	47.07	102.89	15.15	4.75	34.95	29.93
L ₇ × T ₁	58.38	276.25	134.00	48.39	101.93	16.28	4.80	33.85	26.25
L ₇ × T ₂	55.25	248.00	120.63	48.68	105.00	14.45	4.54	33.68	28.77
L ₈ × T ₁	56.25	275.88	134.50	48.73	96.44	15.63	5.03	32.15	25.37
L ₈ × T ₂	56.13	241.75	115.50	47.74	103.89	14.23	4.68	31.53	29.63
L ₉ × T ₁	59.88	289.50	143.38	49.50	99.20	17.63	4.90	35.68	26.85
L ₉ × T ₂	57.38	260.63	128.50	49.26	103.41	16.18	4.79	35.95	28.85
L ₁₀ × T ₁	60.75	269.13	141.00	52.53	97.35	16.93	4.85	33.38	22.78
L ₁₀ × T ₂	56.63	246.75	120.88	48.95	102.30	14.95	4.61	32.45	27.59
L ₁₁ × T ₁	59.25	278.88	142.13	50.92	102.95	17.18	4.78	35.00	25.99
L ₁₁ × T ₂	55.63	253.88	106.39	41.45	117.90	15.83	4.58	33.70	28.02
L ₁₂ × T ₁	61.00	283.50	154.38	54.52	101.74	17.80	4.86	34.23	26.85
L ₁₂ × T ₂	57.13	282.88	139.00	48.93	113.79	16.40	4.76	35.68	30.54
L ₁₃ × T ₁	61.63	293.50	158.88	54.10	100.10	16.05	5.05	32.80	25.70
L ₁₃ × T ₂	58.00	279.88	138.75	49.60	108.84	13.60	4.60	31.20	28.95
L ₁₄ × T ₁	61.25	302.13	164.00	54.26	103.09	18.03	4.84	35.53	24.70
L ₁₄ × T ₂	58.88	286.38	148.75	51.79	107.20	15.70	4.49	35.25	28.18
L ₁₅ × T ₁	60.50	288.38	145.38	44.57	98.76	17.35	4.74	34.28	23.00
L ₁₅ × T ₂	58.63	249.75	121.13	48.51	99.46	14.38	4.31	32.04	26.59
X ⁻	58.26	272.77	137.08	49.91	104.30	16.23	4.74	34.88	27.53
SC.168	64.89	266.47	144.75	54.32	102.30	15.99	4.81	34.05	27.53
LSD 0.05	1.40	12.95	12.13	5.09	7.93	1.02	0.18	2.60	3.90
0.01	1.84	17.02	15.94	6.69	10.42	1.34	0.23	3.41	5.13

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

KR⁻¹. The most desirable inter and intra allelic interactions were represented by crosses L₅ × T₁ and L₇ × T₂ for GY. In addition, that, these crosses showing desirable value of SCA effect.

Genetic parameters and their interactions with locations for all studied traits combined across two locations are shown in Table 5. Results revealed that the GCA variances were higher than SCA variances for all studied traits Except for ED trait. Furthermore, results reported that interaction of SCA × Loc was higher than GCA × Loc for all studied traits except DTS, EL, KR⁻¹ and GY ard fed⁻¹.

Estimation of correlation coefficients between all studied traits across two locations are presented in Table 6. Results showed that EHT had highest positive and significant correlation with DTS and PHT (0.802 and 0.902), respectively. EL gave positive and significant correlation coefficients with DTS, PHT, EHT and Epos%. Grain yield has positive and significant correlations with E100p (0.703).

Estimates of genetic variability; phenotypic and genotypic variances, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) and heritability in broad sense for grain yield and its attributes

Table 3 General combining abilities effects for fifteen inbred lines and two testers for all the studied traits combined across two locations

Crosses	DTS	PHT	EHT	Epos%	E100P	EL	ED	KR ⁻¹	GY ard fed ⁻¹
L ₁	-1.07**	4.05	-5.39	-2.44*	0.32	-0.36	0.17**	0.81	2.17*
L ₂	1.12**	4.98	1.18	-0.21	1.06	1.31**	0.02	3.10**	-0.10
L ₃	0.68*	5.55	9.49**	2.65*	3.18	0.73**	-0.01	2.12**	1.97*
L ₄	-1.32**	-0.83	10.49**	4.15**	0.61	-0.20	-0.07	1.11	1.05
L ₅	0.18	-3.89	-1.76	0.29	5.65**	0.91**	-0.18**	2.47**	1.07
L ₆	-1.51**	-8.45**	-8.89**	-1.47	-3.78	-0.61*	0.12**	0.10	-0.53
L ₇	-1.45**	-10.64**	-9.76**	-1.38	-0.84	-0.86**	-0.07	-1.11	-0.01
L ₈	-2.07**	-13.95**	-12.08**	-1.68	-4.14*	-1.30**	0.11**	-3.04**	-0.02
L ₉	0.37	2.30	-1.14	-0.53	-2.99	0.67**	0.11**	0.94	0.33
L ₁₀	0.43	-14.83**	-6.14*	0.83	-4.48*	-0.29	-0.01	-1.96**	-2.34*
L ₁₁	-0.82*	-6.39*	-12.82**	-3.72**	6.12**	0.27	-0.06	-0.53	-0.55
L ₁₂	0.80*	10.42**	9.61**	1.82	3.46	0.87**	0.07	0.07	1.17
L ₁₃	1.55**	13.92**	11.74**	1.94	0.17	-1.40**	0.09*	-2.88**	-0.40
L ₁₄	1.80**	21.48**	19.30**	3.12**	0.84	0.63*	-0.08*	0.51	-1.09
L ₁₅	1.30**	-3.70	-3.83	-3.37**	-5.19**	-0.36	-0.21**	-1.72**	-2.73**
SE gi (L)	0.36	3.30	3.09	1.30	2.02	0.26	0.05	0.66	0.99
LSD 0.05	0.70	6.48	6.06	2.54	3.97	0.51	0.09	1.30	1.95
0.01	0.92	8.51	7.97	3.34	5.21	0.67	0.12	1.71	2.57
T ₁	-0.54**	-8.06**	-8.891**	-1.56**	-3.62**	-0.86**	0.02	-1.65**	-1.38**
T ₂	0.54**	8.06**	8.891**	1.56**	3.62**	0.86**	-0.02	1.65**	1.38**
S.E. gi (T)	0.13	1.21	1.13	0.47	0.74	0.09	0.02	0.24	0.36
LSD 0.05	0.26	2.37	2.21	0.93	1.45	0.19	0.03	0.47	0.71
0.01	0.34	3.11	2.91	1.22	1.90	0.24	0.04	0.62	0.94

*, ** significant at 0.05 and 0.01 levels of probability, respectively

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

traits are presented in Table 7. Results showed that high phenotypic and genotypic variance values were recorded for PHT, EHT and E100p traits. Generally, phenotypic variance was higher than genotypic variance for all studied traits, suggesting that there was a minimal environment influence in the expression of these traits. PCV and GCV values differed and ranged rate for all studied traits; low PCV and GCA values were recorded for DTS, PHT, E100p and ED; moderate PCV values for EHT, Epos%, EL, KR⁻¹ and GY traits and the GCV receded low values for the same traits. Heritability percentage in broad sense recorded ranged from low, medium to moderate high; low heritability values for Epos%, E100p, ED and GY traits; medium for DTS, PHT, EHT and KR⁻¹ traits and moderately high heritability for EL trait.

4 Discussion

The magnitude of mean squares among two locations were highly significant ($P \leq 0.001$) for all studied traits except KR⁻¹, indicating the existence of a clear variation between the two locations for these traits. These results agree with those reported by several researchers among

of them; Mutimaamba et al. [24] and Mousa et al. [23]. Moreover, highly significant differences were detected among crosses for all studied traits, indicating that crosses had an extensive genetic diversity between themselves providing chance for selection among them. In literature, many works have found significant differences between crosses producing from maize, Aly [5], Darshan and Marker [9], Mutimaamba et al. [24], Mousa et al. [23] and Aly et al. [4]. Significant or highly significant mean squares were observed for lines (L), testers (T) and (L × T) interaction for all studied traits, except (T) for ED and L × T for EHT and Epos%. These results mean that extreme diversity exists among inbred lines and among testers and the inbred lines performed differently in their respective crosses depending on the type of testers used for these traits. These results agree with what was obtained by Abd El-Moula et al. [2], Aly and Khalil [6], Darshan and Marker [9] and Mousa et al. [23]. Significant or highly significant differences were observed between lines × location interaction for DTS, PHT, EHT and GY ard fed⁻¹, testers × location interaction for EL, ED and KR⁻¹. These results mean that lines and testers varied

Table 4 Specific combining abilities effects for fifteen single crosses for all the studied traits combined across two locations

Crosses	DTS	PHT	EHT	Epos%	E100P	EL	ED	KR ⁻¹	GY ard fed ⁻¹
L ₁ × T ₁	0.35	0.12	-0.80	-0.52	0.28	-0.20	0.11*	-1.408*	-1.90
L ₁ × T ₂	-0.35	-0.12	0.80	0.52	-0.28	0.20	-0.109*	1.41*	1.90
L ₂ × T ₁	-0.21	4.56	4.39	0.59	-0.69	-0.38	-0.06	0.29	-0.45
L ₂ × T ₂	0.21	-4.56	-4.39	-0.59	0.69	0.38	0.06	-0.29	0.45
L ₃ × T ₁	0.23	0.25	0.45	0.07	3.65	0.07	-0.06	1.14	0.13
L ₃ × T ₂	-0.23	-0.25	-0.45	-0.07	-3.65	-0.07	0.06	-1.14	-0.13
L ₄ × T ₁	-0.15	-0.25	0.45	0.17	-5.217*	0.51	-0.07	2.54**	-1.55
L ₄ × T ₂	0.15	0.25	-0.45	-0.17	5.22*	-0.51	0.07	-2.542**	1.55
L ₅ × T ₁	0.10	-1.57	-1.05	-0.35	-2.10	0.95**	0.01	1.55	2.68*
L ₅ × T ₂	-0.10	1.57	1.05	0.35	2.10	-0.947**	-0.01	-1.55	-2.678*
L ₆ × T ₁	-0.33	1.25	2.08	0.27	0.12	-0.18	-0.04	-0.22	0.37
L ₆ × T ₂	0.33	-1.25	-2.08	-0.27	-0.12	0.18	0.04	0.22	-0.37
L ₇ × T ₁	0.854*	-3.19	0.33	0.45	0.30	-0.853*	-0.06	-2.108*	-2.088*
L ₇ × T ₂	-0.85*	3.19	-0.33	-0.45	-0.30	0.85*	0.06	2.11*	2.09*
L ₈ × T ₁	-0.02	0.37	0.14	-0.33	0.90	-0.22	-0.04	-0.51	-0.62
L ₈ × T ₂	0.02	-0.37	-0.14	0.33	-0.90	0.22	0.04	0.51	0.62
L ₉ × T ₁	0.917*	0.50	1.70	0.38	2.53	0.76*	0.02	1.49	-0.24
L ₉ × T ₂	-0.92*	-0.50	-1.70	-0.38	-2.53	-0.759*	-0.02	-1.49	0.24
L ₁₀ × T ₁	-0.65	-5.50	-1.67	0.19	2.77	-0.803*	-0.07	-1.21	0.90
L ₁₀ × T ₂	0.65	5.50	1.67	-0.19	-2.77	0.80*	0.07	1.21	-0.90
L ₁₁ × T ₁	-0.77	0.93	-4.98	-2.67	-2.35	-0.54	0.07	0.08	0.78
L ₁₁ × T ₂	0.77	-0.93	4.98	2.67	2.35	0.54	-0.07	-0.08	-0.78
L ₁₂ × T ₁	-0.27	-10.25*	-8.42*	-1.13	-4.37	-0.12	0.00	-2.096*	0.41
L ₁₂ × T ₂	0.27	10.254*	8.421*	1.13	4.37	0.12	0.00	2.10*	-0.41
L ₁₃ × T ₁	0.10	7.37	4.83	0.26	1.72	0.23	0.03	0.35	1.45
L ₁₃ × T ₂	-0.10	-7.37	-4.83	-0.26	-1.72	-0.23	-0.03	-0.35	-1.45
L ₁₄ × T ₁	-0.27	-0.69	-2.86	-0.89	-1.11	0.07	0.03	-1.01	-0.20
L ₁₄ × T ₂	0.27	0.69	2.86	0.89	1.11	-0.07	-0.03	1.01	0.20
L ₁₅ × T ₁	0.10	6.12	5.39	3.529*	3.58	0.70*	0.13*	1.11	0.34
L ₁₅ × T ₂	-0.10	-6.12	-5.39	-3.53*	-3.58	-0.697*	-0.134*	-1.11	-0.34
SE Sij	0.506	4.673	4.374	1.836	2.861	0.367	0.064	0.937	1.409
LSD 0.05	0.992	9.159	8.574	3.598	5.607	0.719	0.125	1.837	2.761
0.01	1.303	12.037	11.269	4.729	7.369	0.945	0.164	2.414	3.629

*, ** significant at 0.05 and 0.01 levels of probability, respectively

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

Table 5 Genetic parameters and their interactions with locations for all the studied traits combined across two locations

Genetic parameters	DTS	PHT	EHT	Epos%	E100P	EL	ED	KR ⁻¹	GY ard fed ⁻¹
σ ² GCA	0.65	124.24	149.87	4.60	23.65	1.142	-0.001 [®]	4.93	3.07
σ ² SCA	0.25	13.71	7.34	-0.52 [®]	-2.17 [®]	0.44	0.002	3.04	2.05
σ ² GCA × Loc	0.05	0.96	-2.14 [®]	-0.04 [®]	0.11	0.46	0.004	0.41	0.51
σ ² SCA × Loc	-0.13	4.36	0.71	0.89	17.15	0.05	0.005	0.02	-1.72 [®]

[®] Variance estimates preceded by negative sign is considered zero, Robinson et al. [28]

Table 6 Simple correlation coefficient between all the studied traits across two locations

	DTS	PHT	EHT	EPOS%	E100P	EL	ED	KR ⁻¹	GY ard fed ⁻¹
DTS	–	0.775**	0.802**	0.540**	–0.421*	0.707**	0.474**	0.165	–0.634**
PHT		–	0.902**	0.487**	–0.214	0.712**	0.648**	0.332	–0.358
EHT			–	0.786**	–0.305	0.677**	0.532**	0.323	–0.369*
EPOS%				–	–0.274	0.388*	0.268	0.242	–0.163
E/100P					–	–0.139	–0.483**	0.294	0.703**
EL						–	0.515**	0.658**	–0.356
ED							–	0.101	–0.370*
KR ⁻¹								–	0.235
GY ard fed ⁻¹									–

*, ** significant at 0.05 and 0.01 levels of probability, respectively

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

Table 7 Genetic variability, genotypic coefficient and phenotypic coefficient of variability and heritability in broad sense for all studied traits of maize across two locations

Genetic parameter						
Traits	σ^2_g	σ^2_e	σ^2_p	GCV %	PCV %	h ² b %
DTS	1.80	2.05	3.85	2.30	3.37	46.77
PHT	167.75	174.68	342.43	4.75	6.78	48.99
EHT	170.37	153.09	323.45	9.52	13.12	52.67
EPOS%	6.27	26.96	33.23	5.02	11.55	18.86
E/100P	24.97	65.47	90.44	4.79	9.12	27.61
EL	1.61	1.08	2.68	7.81	10.09	59.89
ED	0.01	0.03	0.05	2.38	4.48	28.23
KR ⁻¹	7.23	7.03	14.26	7.71	10.83	50.72
GY ard fed ⁻¹	3.31	15.88	19.18	6.61	15.91	17.24

DTS days to 50% silking (days), PHT plant height, cm, EHT ear height, cm, Epos% ear position %, E100P ears/100plant, EL Ear Length, cm, ED Ear Diameter, cm, KR⁻¹ no of Kernels Row, GY Grain Yield ard fed⁻¹

in their performance from location to another. Therefore, it would be useful to evaluate these lines and testers under multi- environmental conditions, especially for GY. Meanwhile, mean squares due to $L \times T \times Loc$ interactions were significant for E100P and ED traits. Many studies reported that the interaction of line \times tester \times locations was highly significant for GY as Aly et al. [7], Aly and Khalil [6], El-Gazzar et al. [12] and Gamea et al. [15].

Mean values of all crosses were significantly earlier than the check hybrid SC-168 (64.89 days). Four crosses; $L_8 \times T_2$, $L_{10} \times T_2$, $L_7 \times T_2$ and $L_{15} \times T_2$ were significantly shorter than the shortest check hybrid SC-168. In this respect, EL-Hosary and El-Gammal [13] and Kamara et al. [16] reported that the shortest plants in maize reduce lodging ratio and so increased yield potential. For EHT, the lowest ear height was desirable trait for lodging resistance. Thus, 9 out of 30 crosses had significantly lower ear height compared with the

best check hybrid SC-168. Concerning GY ard fed⁻¹, the cross $L_5 \times T_2$ had the highest grain yield and was different significantly than the check hybrid followed by cross $L_1 \times T_2$. Hence, these crosses can be used for improving maize grain yield [14] and [3].

High positive values of g_i effects would be favorite for all studied traits except DTS, PHT, EHT and Epos% (desirable) where high negative would be useful from the plant breeder's point of view. The parental lines L_1 , L_4 , L_6 , L_7 , L_8 and L_{11} had desirable values toward earliness. With respect to PHT and EHT, the inbred lines L_6 , L_7 , L_8 , L_{10} and L_{11} were the best general combiners toward shorter plant and lower ear placement, implying the tendency of this line to reduce plant height, which is very important for development of genotypes resistant to lodging [1] and [4]. The best general combiners for GY ard fed⁻¹ were L_1 and L_3 . These inbred lines which possessed high GCA effects for grain yield

showed the same effect for one or more of the traits contributing to grain yield, indicating that these lines could be considered as good combiners for improving grain yield which may contribute favorable alleles in the synthesis of new crosses.

The crosses $L_7 \times T_2$ and $L_9 \times T_2$ had desirable SCA effects for DTS toward earliness, $L_{12} \times T_1$ for PHT and EHT toward shorter plants. For ear position, $L_{15} \times T_2$ toward lower ear placement. Concerning E100p, cross $L_4 \times T_2$ showed positive and significant SCA effect. Regarding to EL, the cross $L_5 \times T_1$ was the best one. The crosses $L_1 \times T_1$ and $L_{15} \times T_1$ were the best combiners for ED. Four crosses; $L_1 \times T_2$, $L_4 \times T_1$, $L_7 \times T_2$ and $L_{12} \times T_2$ had positive significantly SCA effect for KR^{-1} . The most desirable inter and intra allelic interactions were represented by crosses $L_5 \times T_1$ and $L_7 \times T_2$ for GY.

The GCA variances were higher than SCA variances for all studied traits except for ED trait, indicating that additive genetic variance played the major role than non-additive genetic variance in the inheritance of these traits. Similar results were reported by Tessema et al. [36], Mosa [20], Mousa et al. [23] and Rachman et al. [26]. Furthermore, the SCA \times Loc interaction was higher than GCA \times Loc for all studied traits except DTS, EL, KR^{-1} and GY ard fed^{-1} , indicating that additive gene action was more stable than non-additive gene action under different environmental conditions for these traits. These results are in accordance with those obtained by Mousa and Aly [22], El-Gazzar et al. [12], Mousa et al. [23] and Aly et al. [4].

The high PCV and GCV variance values were recorded for PHT, EHT and E100p traits. Generally, phenotypic variance was higher than genotypic variance for all studied traits, suggesting that there was a minimal environmental influence on the expression of these traits. These results are in harmony with the results by Langade et al. [19], Sesay et al. [30], Wedwessen and Zeleke [37], Tesfaye et al. [35] and Aly et al. [4]. PCV and GCV values differed and ranged rate for all studied traits, low PCV and GCA values were recorded for DTS, PHT, E100p and ED, moderate PCV values for EHT, Epos%, EL, KR^{-1} and GY traits and the GCV receded low values for the same traits. Similar results were obtained by Reddy and Jabeen [27] for DTS, Sesay et al. [30] for EHT, EL and GY traits. Heritability percentage in broad sense were low for Epos%, E100p, ED and GY traits, medium for DTS, PHT, EHT and KR^{-1} traits and moderately for EL trait. Similar results were obtained by Sesay et al. [30], Sravanti et al. [33], Bartaula et al. [8] and Aly et al. [4].

5 Conclusion

Finally, it could be concluded that most of studied lines exhibited highly general combiners and the superior crosses were as a results of a good \times good combiner for

most of yield components traits. Thus, the results suggested that the production of F1 hybrids at commercial level could be dependent on the combination between the good combiner lines.

Abbreviations

DTS: Days to 50% silking (days); PHT: Plant height (cm.); EHT: Ear height (cm); Epos%: Ear position %; E100P: Ears/100plant; EL: Ear length (cm); ED: Ear diameter (cm); KR^{-1} : No. of kernels row; GY: Grain yield ard fed^{-1} ; GCA: General combining ability; SCA: Specific combining ability; PCV: Phenotypic coefficient of variability; GCV: Genotypic coefficient of variability.

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Author contributions

Conceptualization and methodology, RSHA, RSHA; application of the field trial at two location, RSHA, RMMH; made the statistical analysis of data, RMMH, MZ, RSHA; writing—original draft preparation, RMMH; review and editing, RMMH, MZ, RSHA; All authors have read and agreed to the published version of the manuscript.

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Declarations

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Competing interests

The authors declare no competing interest.

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