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Test Cross Mean Performance and Combining Ability Study of Elite Lowland Maize (*Zea mays L.*) Inbred Lines at Melkassa, Ethiopia

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Abstract

In Ethiopia, there are several maize production constraints, among which shortage of improved varieties is the major one. The objective of this study was to observe the mean performance of crosses and estimate combining abilities for grain yield and other agronomic traits in thirty six maize inbred lines using Line x Tester mating design. Seventy-two lines x test crosses (L1xT1, L1xT2, L2xT1, L2xT2… L36xT1 and L36xT2) and three standard checks were evaluated for 11 traits in alpha lattice design at Melkassa, Ethiopia. Analyses of variances showed significant mean squares due to crosses for all traits. Among the crosses, L34xT2, L36xT2, L30xT1, L19xT1 and L33xT2 crosses were the top five highest grain yield mean performance. While L35xT1, L23xT1, L13xT1, L24xT2 and L15xT1 crosses were lowest mean grain yield performance. GCA Mean squares were significant, but SCA mean squares were non-significant for all traits. The ratio of GCA/SCA mean square was high which exhibited the preponderance of additive gene effects in the inheritance of all traits. Furthermore, the GCA sum of square component was greater than the SCA sum of square for all traits, supported that variation among crosses was mainly due to additive rather than non-additive gene effect. Inbred lines L15, L25, L27, L33, L34 and L35 were the best general combiners for grain yield, and hence were promising parents for hybrids as well as for inclusion in breeding programmes for yield improvements. Inbred lines L2, L3, L4, L6, L10, L27, L30, L31 and L32 had negative and significant GCA effects for the days to anthesis, indicating that the lines had gene combinations that can enhance early maturity.

Keywords: Cross mean performance; SCA; GCA; Maize inbred lines; Ethiopia

Introduction

Maize [1] is one of the oldest food grains of the world and it is believed to be originated in Mexico [2]. It belongs to the grass family *Poaceae (Gramineae),* tribe *Maydeae* and is the only cultivated species in this genus [3]. Maize grain is recognized worldwide as a strategic food and feed crop that provides an enormous amount of protein and energy for humans and livestock, like Quality protein maize [4].

Several million people in the developing world consume maize as an important staple food and derive their protein and calorie requirements from it [5]. Maize is a potential source of protein for humans and animals [5]. It holds a great promise for increasing production [5]. Maize [1] was introduced to West Africa in the early 1500s by Portuguese traders and then to Ethiopia during the 1600s and 1700s [6]. Today, maize is becoming one of the most important food crops throughout Ethiopia. In terms of area, it is the second most important commodity next to tef (*Eragrostis tef*) [7]. In Ethiopia, maize is one of the top priority food crops selected to achieve food security. It is the staple food and one of the main sources of calorie, particularly in the major maize producing regions [7]. Overall, the area allocated and the productivity level of maize has been increasing since 1994. The area allocated in 1994 was about one million ha, which has increased to about 1.96 million ha of land in 2010/11 production season. Similarly, the average national productivity of maize has increased from about 1.5 t/ha in 1994 to about 2.54 t/ha in 2010/11 mainly due to the strong public push of improved seed and fertilizer [7].

Maize grows in different agro-ecological zones of Ethiopia ranging from sea level up to 2800 m a.s.l [8]. It is grown in areas with light to heavy soils, wide ranges of temperatures and rainfall, indicating that maize has good adaptability to different arrays of environmental variables. However, in spite of its wide adaptation and efforts made to develop improved maize technologies for different maize agro-ecological zones still many biotic (such as common leaf rust (CLR), maize streak virus (MSV), stalk borer, termite, etc.) and abiotic constraints (such as drought, low soil fertility, etc.) limit maize production and productivity in different maize producing agro-ecological zones [9]. Global coarse grains (such as maize) production in 2012 is expected to fall by 2.5 percent from 2011 2.5 percent. Severe droughts this year in the United States and across a large part of Europe and into central Asia have been the main cause of the reduced coarse grain crops [10].

Combining ability is an effective tool which gives useful genetic information for the choice of parents in terms of their performance in a series of crosses [11]. Line x tester [12] is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. It also provides information on genetic components and enables the breeder to choose appropriate breeding methods for hybrid variety or cultivar development programmes. Information on combining ability effects helps the breeder in choosing the parents with the high general combining ability and hybrids with high specific combining. In the maize breeding program, analysis of

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general combining ability (GCA), specific combining ability (SCA) and heterosis would help to identify best inbred lines for hybrid development and hybrid combinations for better specific combining ability. Combining ability analysis helps in identifying potential inbred lines for producing hybrids and synthetic varieties in maize breeding. Luchsinger and Violic (1972) examined eight characters in a maize diallel cross analysis and observed that additive effects were more important than non-additive ones for all the variables studied. Piovarci [13] Also determined combining ability and its components for maize grain yield in an eight inbred diallels and concluded that additive gene effects were more important than non-additive effects. Currently, large numbers of introduced elite maize inbred lines from CIMMYT-Zimbabwe are available in Ethiopian; Maize Improvement Project at the Melkassa Agricultural Research Center (MARC). Thirty-six lines selected for this study. These lines were highest resistance for drought and saline soils. Rift valley areas have drought and saline problems. MARC is one of the best maize growing areas in the Rift Valley of Ethiopia [14]. Therefore, the objectives of this study were to estimate crosses mean performance and combining abilities for grain yield and other agronomic traits in thirty six maize inbred lines using Line x Tester mating design.

Material and Methods

Experimental materials

The experimental material for the study consisted of seventy two lines by test crosses (L1xT1, L1xT2, L2xT1, L2xT2… L36xT1 and L36xT2) and three standard checks. The parents were crossed in Line x Tester mating design to generate 72 F_1 hybrids at Melkasa Agricultural Research Center, Ethiopia at main cropping season 2011/2012. The experiment was conducted during the main cropping season of 2012/13 at the Melkasa Agricultural Research Center (MARC) on F_1 (LineXTester crosses). This location is one of the best maize growing areas in the Rift Valley of Ethiopia [14]. The inbred lines were introduced from CIMMYT-Zimbabwe and were bred for resistance to various biotic and abiotic stresses of Africa. The two testers are single crosses of commercial CIMMYT inbred lines of known heterotic groups; CML312/CML442 (Tester A) and CML202/CML395 (Tester B). MHQ138 (check) is a three way hybrid, high yielding and tolerance /resistance to maize diseases. MH130 is also check which is a double top cross hybrid. Melkassa_2 is the 3rd check; it is early maturing and drought tolerant variety. All checks are released by the Melkassa Agriculture Research Center.

Experimental design and field managements

The experiment was designed 7×15 alpha lattice design [15]. The experiment had two replications. Each plot consisted of one row of 5 m length with 75 cm and 25 cm spacing between rows and plants, respectively. As recommended by the center, 50 kg P_2O_5 ha^{-1} and 25 kg N ha^{-1} was applied at planting, followed by a side dressing of 25 kg N ha^{-1} 35 days later. Urea and Dominium phosphate (DAP) was used as sources of N and P_2O_5, respectively. Other crop management practices such as land preparation, weeding, disease and insect control were applied following research recommendations

Statistical analysis and procedures

Data collection and Analysis of variance (ANOVA): Data were recorded on eleven quantitative characters. Data related to days to 50% anthesis, 50% days to silking, 1000-kernel weight, grain yield and anthesis silking interval were recorded on the plot basis while data related to other characters were recorded on five randomly selected plants leaving border plants of each row. The mean values were subjected to line x tester analysis. Analyses of variances (ANOVA) were computed for grain yield and other agronomic traits by using SAS 9.2 software.

Combining ability analysis: Line x tester analysis was done for traits that showed statistically significant differences among the crosses using the adjusted means based on the method described by Kempthorne [12]. General combining ability (GCA) and specific combining ability (SCA) effects for grain yield and other agronomic traits were calculated using the line x tester model. The F-test of mean square due to lines, testers and their interactions were computed against mean square due to error [16]. Significances of GCA and SCA effects of the lines and hybrids were determined by an F - test using the standard errors of GCA and SCA effects.

Results and Discussion

Analysis of variance

Analysis of variance showed a highly significant difference ($P<0.01$) among the crosses for the anthesis data, plant height, ear height silking day and ear length. While the mean square due to crosses were significant ($P<0.05$) for the grain yield, anthesis silking interval, number of ears per plant, 1000 kernel weight, number of kernels per row and ear diameter (Table 1). Mean square due to check were highly significant for the anthesis day and the number of days to silking. Mean squares due to check and check Vs cross were significant for the anthesis day, plant height, and ear length. This indicated the presence of inherent variation among the lines, which makes selection possible. Similarly, several previously studied reported significant differences among crosses for grain yield and related trait in different sets of maize genotypes [17-22] (Table 1).

Mean performance of F_1 crosses (Line x Tester)

Mean values for the 11 characters are shown in Table 2. Forty-six of 72 crosses had a higher grain yield than the best hybrid check MHQ 138 (5.40t/ha). The overall mean grain yield of the crosses were 5.45 t/ha, ranging from 4.13 t/ha to 6.27 t/ha. Cross L34xT2 (6.27 t/ha), L25xT2l (6.24), and L18 xT2 (6.00 t/ha) had a higher grain yield, whereas crosses L23xT1 (4.856t/ha), L24xT2 (4.88t/ha) and L35xT1 (4.13t/ha) were lower grain yield. Cross L12xT1 (78.5) was the latest anthesis day while cross L2xT2 (70.2) was earliest athesis day.

The mean anthesis silking interval was ranging from 0.7 (L31xT2) to 1.7 (L26xT1, L26xT2, L28xT1) day (Table 2). Crosses L9xT2 (258.13 cm), L13xT2 (216.3 cm) and L33 x T2 (215.3 cm) had highest plant height while crosses L7 x T1 (173.3 cm), L17x T1 (175 cm) and L35xT21 (177.4 cm) showed lowest plant height. Crosses L11 x T2 (118.8 cm), L16 x T1 (117.0 cm) and L16 x T2 (115.5cm) had highest ear height while L31xLT2 (87.2 cm), L7xT1 (90.5 cm) and L10xT2 (92.5 cm) had lowest ear height. All crosses were showed less thousand kernels weight than check of MHQ 138 (242 gm).Overall means ear diameter of 45.3 mm with ranged from 41.2 mm (L11 x T1) to 48.6 mm (L13xT2). Cross L13xT2 (48.8 mm) followed by cross L5xT1 (48.1 mm) and L25xT2 (48.2 mm) (Table 2) had a highest ear diameter while crosses L11xT1 (41.2 mm), L21xT1 (42.6 mm) and L10xT1 (41.7 mm) showed a lowest ear diameter. MHQ 138 (35.88) standard check had a higher number of kernels per row than all crosses.

Crosses L17xT2, L29xT2 and L13xT1 had the lowest number of ears per plant while crosses L1xT1, L11xT2, and L16xT2 had showed the maximum number of ears per plant. Mean ear length was 16.6 cm

SoV	Df	GY(t/ha)	AD(days)	ASI(day)	PH(cm)	EH(cm)	ED(cm)	EL(cm)	EPP(#)	KPR(#)	SD(days)	TKWT(gm)
Rep	1	4.15*	2.4*	1.3	60.16*	218.4*	.0.92	1.02	0.13*	76.32*	3.8*	13949.1*
Entry	74	1.59*	10.9**	1.15*	435.6**	178.3**	12.12*	3.1**	0.04*	8.4*	11.1**	1741.8*
Crosses(Cr)	71	1.62*	9.51**	1.14*	440.7**	184.4**	12.42*	3.05**	0.04*	8.15*	10.78**	1680.9*
GCA line	16	1.82*	12.76**	1.33*	697.4**	306.8**	16.3*	4.11**	0.06**	11.4*	13.1**	2103.4*
GCA tester	1	4.71*	112**	5.84*	2425.5**	31.2	31.1*	14.95*	0.002	5.14	117.2**	9236.8*
SCA	35	1.33	3.33	0.82	127.3	66.3	8.04	1.6	0.02	4.9	4.36	1042.5
Ck	2	0.99	10.6**	0.5	460.6*	43.1	7.56	6.14*	0.018	0.04	11.5**	4303.0
Ck vs Cr	1	1.62	16.6*	1.147	440.7*	120.2	0.044	1680.9*	0.01	0.04	11.8	1680.0
Error	74	0.96	2.87	0.73	83.2	45.1	0.03	0.68	___	4.72	3.72	806.9
% contribution. GCA		60.87	82.79	65.02	85.79	82.64	68.12	73.49	76.4	73.36	85.2	72.62
% contribution. SCA		39.13	17.21	34.98	14.21	17.36	31.88	26.51	23.54	26.64	14.8	27.38
Ratio GCA/SCA		1.56	4.81	1.86	4.14	4.76	2.14	2.77	3.24	2.75	5.76	2.65

**=significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, GY= grain yield AD = anthesis, date, ASI=anthesis silking interval, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, KPR = number of kernels per row, SD=silking days, PH = plant height, Rep= replication, TKWT = thousand kernels weight.

Table 1: Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 36 lines and two testers evaluated at Melkassa 2012

Crosses	GY (t/ha)	AD (Days)	ASI	PH (cm)	EH (cm)	TKWT (gm)	ED (mm)	SD (days)	KPR	EL (cm)	EPP
L1xT2	5.71ab	71.9 u-y	1.2ab	204.2c-o	95.6i-v	221.1a-g	45.4a-k	73.1j-o	35.9a-e	17.2a-g	1.33a-i
L2xT2	5.45ab	70.2xy	0.9ab	195.4j-u	97.1g-v	227.4a-e	46.2a-i	71.1no	36.7a-e	17a-h	1.08i-r
L3xT2	5.75ab	72.8o-w	0.7b	198.7h-s	95.9i-v	188.5g	46.9a-g	73.5i-o	36.7a-e	17.1a-h	1.4a-f
L4xT2	5.19abc	72.3s-y	0.7b	190.8n-v	91r-v	210.1a-g	43.8f-m	73k-o	35.8a-e	16.9a-i	1.25b-l
L5xT2	5.57ab	75c-r	1.5ab	192.2m-v	94.1k-v	214.9ab-g	43.9e-m	76.5b-k	34.5de	16.9a-i	1.07i-r
L6xT2	5.02bc	73.6k-v	0.7b	200.6f-r	100e-s	197.9d-g	44.5d-m	74.3f-o	35.2a-e	16.8a-j	1.22c-n
L7xT2	5.14abc	74.6e-s	0.8ab	187.6p-x	93.5m-v	204.9b-g	44.9b-l	75.4c-l	35.4a-e	17a-h	1.22c-n
L8xT2	5.37ab	75.2b-p	1ab	201.8e-q	101.3d-s	212.2a-g	45.1a-l	76.2b-k	37.7b	17.3a-f	1.23b-m
L9xT2	5.52ab	75.1b-q	1.4ab	235.6a	111.2a-d	208.2a-g	44.6c-m	76.5b-k	36.8a-e	17.2a-g	1.4a-f
L10xT2	5bc	72.7p-x	1.1ab	202.6c-p	92.5o-v	202.1b-g	43.1h-m	73.8i-o	36a-e	16.2d-l	1.13g-q
L11xT2	5.61ab	73.9i-u	1.3ab	220.1b	118.8a	195.5e-g	42.3k-m	75.2c-l	35.9a-e	16.9a-i	1.49ab
L12xT2	5.51ab	74.5e-t	1.4ab	214.4b-g	96.4h-v	204.7b-g	44.8b-l	75.9b-k	35.8a-e	17.4a-f	1.27a-k
L13xT2	5.95ab	75.4b-n	1.2ab	216.3b-e	108.1a-g	223.3a-g	48.6a	76.6a-j	36.7a-e	16.9a-i	1.13g-q
L14xT2	5.74ab	74.1g-u	0.8ab	207.4b-m	101.4d-s	221.6a-g	44.5d-m	74.9c-l	36.2a-e	17.2a-g	1.25b-l
L15xT2	4.99bc	76.2a-j	1.6ab	200.2f-r	98.2g-v	220.9a-g	44.9b-l	77.8a-f	35.6a-e	16.3c-l	1.1h-r
L16xT2	5.65ab	75.6b-l	1ab	215.1b-f	115.2a-c	208.8a-g	47.3a-f	76.6a-j	35.8a-e	15.8f-l	1.18d-o
L17xT2	5.19abc	73.7j-v	1.1ab	197.8h-t	102.6d-p	224.2a-g	44.2d-m	74.8d-m	35b-e	16e-l	0.91p-r
L18xT2	6ab	73.7j-v	0.8ab	201.4e-r	99.2e-t	233.5a-d	46.5a-h	74.5e-n	36.6a-e	16.1e-l	1.01k-r
L19xT2	4.9bc	74.7d-s	1.3ab	205.9b-n	102.8d-p	220.2a-g	46.4a-h	76b-k	36.2a-e	17.9a-c	1.03j-r
L20xT2	5.83ab	76.1a-k	0.9ab	197i-u	96.4h-v	226.9a-e	46.7a-g	77a-i	36.6a-e	17.9a-c	1.09i-r
L21xT2	5.65ab	74.9d-r	1.5ab	209.3b-k	105.1c-k	225.4a-f	45.3a-k	76.4b-k	36.3a-e	17.1a-h	1.11g-r
L22xT2	5.68ab	72.3s-y	1.4ab	212.9b-h	104.7c-l	218.9a-g	45.8a-k	73.7i-o	36.9a-e	16.9a-i	1.19c-o
L23xT2	5.72ab	73.3l-v	0.8ab	213b-h	107.3b-h	217.8a-g	46.2a-i	74.1g-o	35.2a-e	16.6b-k	1.21c-n
L24xT2	4.88bc	73m-v	0.9ab	202.3d-p	99.4e-t	213a-g	45.2a-l	73.9i-o	35.9a-e	16.7a-k	1.11g-r
L25xT2	6.24a	73.8j-v	1.1ab	206.4b-n	104.8c-l	237.9ab	48.2ab	74.9c-l	36a-e	17.2a-g	1.01k-r
L26xT2	5.23abc	75.3b-o	1.7a	208.3b-l	104.4c-m	199.2c-g	47.4a-e	77a-i	36.3a-e	15.3i-l	1.07i-r
L27xT2	5.66ab	72t-y	1.3ab	184.3s-x	96.2i-v	202.3b-g	47.1a-f	73.3j-o	36a-e	17a-h	1.13g-q
L28xT2	5.91ab	72.8o-w	1.1ab	182.4t-x	95.4i-v	225.4a-f	44.4d-m	73.9i-o	37.2a-d	16e-l	1.27a-k
L29xT2	5.66ab	73.8j-v	1ab	186.4q-x	88.1uv	226.6a-e	46.8a-g	74.8d-m	36.5a-e	17.4a-f	0.96n-r

L30xT2	5.66ab	72.7p-x	0.8ab	201.3e-r	98.7f-v	204.3b-g	46.9a-g	73.5i-o	36.4a-e	17.8a-d	0.96n-r
L31xT2	5.51ab	71.3v-y	0.7b	186.2r-x	87.2v	222.3a-g	46.4a-h	72l-o	36.3a-e	17.3a-f	1l-r
L32xT2	5.1abc	73.1l-v	1.2ab	196.4j-u	96i-v	219.6a-g	44.5d-m	74.3f-o	36.7a-e	17.3a-f	1.1h-r
L33xT2	5.87ab	75.5b-m	1.1ab	215.4b-f	107.4b-h	227.7a-e	47.5a-d	76.6a-j	36.2a-e	16.7a-k	1.23b-m
L34xT2	6.27a	77a-e	1.1ab	207.9b-l	100.4e-s	225.3a-f	45.6a-k	78.1a-d	36.1a-e	16.1e-l	1.13g-q
L35xT2	5.13abc	75.1b-q	0.9ab	192.1m-v	100e-s	208.4a-g	46.3a-h	76b-k	36a-e	15.8f-l	1.03j-r
L36xT2	5.99ab	74.7d-s	1.5ab	208.9b-k	104.3c-m	216.1a-g	44.7b-m	76.2b-k	35.5a-e	16.3c-l	1.13g-q
L1xT1	5.18abc	76.6a-g	1ab	195.6j-u	92.4o-v	214.5a-g	45.2a-l	77.6a-g	36.3a-e	17.1a-h	1.53a
L2xT1	5.3abc	72.6q-x	1.1ab	186r-x	97.8g-v	215.1a-g	46.2a-i	73.7i-o	36.9a-e	17.3a-f	1.05j-r
L3xT1	5.49ab	73m-v	1.3ab	189.4o-w	92.8o-v	208.8a-g	44.1d-m	74.3f-o	36a-e	15.5h-l	1.42abcd
L4xT1	5.48ab	73.6k-v	1.1ab	192.9l-v	94.5k-v	213a-g	42.7i-m	74.7d-m	34.6de	16e-l	1.36a-h
L5xT1	4.97bc	77.5a-c	0.9ab	200.8e-r	99.7e-s	193.3e-g	48.1a-c	78.4a-c	34.5de	15.6g-l	1.27a-k
L6xT1	5.22abc	72.9n-v	0.9ab	191.4n-v	99.1e-u	219.5a-g	43.4g-m	73.8i-o	35.6a-e	16.7a-k	1.16d-p
L7xT1	5.36ab	74.5e-t	1.5ab	173.3x	90.5s-v	213.2a-g	44.6c-m	76b-k	34.8de	15.1kl	1.04j-r
L8xT1	5.51ab	75c-r	1.3ab	205.7b-n	98.1g-v	197.9d-g	44.1d-m	76.3b-k	35.5a-e	16.5b-l	1.41a-e
L9xT1	5.17abc	75.2b-p	1.1ab	220.8ab	105.9c-i	214.2a-g	43.9e-m	76.3b-k	35.6a-e	16e-l	1.25b-l
L10xT1	5.76ab	73.7j-v	0.8ab	188.3p-x	92.1o-v	193.5e-g	41.7lm	74.5e-n	35.6a-e	15.6g-l	1.28a-j
L11xT1	5.61ab	74.3f-u	1.4ab	217.5b-d	107.5b-g	203.9b-g	41.2m	75.7b-k	36.6a-e	16.8a-j	1.37a-g
L12xT1	4.98bc	78.5a	1.6ab	214.9b-f	104.6c-l	197.2d-g	46.5a-h	80.1a	36.8a-e	17.5a-e	1.01k-r
L13xT1	4.88bc	77.6ab	1.6ab	198.2h-s	104.8c-l	214.4a-g	43.9e-m	79.2ab	35.6a-e	15.5h-l	0.93op-r
L14xT1	5.66ab	75.2b-p	0.9ab	218.4bc	111.8a-d	207.2a-g	46.5a-h	76.1b-k	35.9a-e	17a-h	1.15e-p
L15xT1	4.91bc	77a-e	1.2ab	181.6u-x	94.1k-v	201.6b-g	45.3a-k	78.2a-d	34.3e	15.3i-l	1.01k-r
L16xT1	5.55ab	78.1a	1.1ab	200.6f-r	117ab	189.2fg	46.9a-g	79.2ab	35.3a-e	14.9l	1.45a-c
L17xT1	5.2abc	76.5a-h	1.3ab	175wx	97.3g-v	197e-g	44.2d-m	77.8a-f	34.8de	16.1e-l	0.88qr
L18xT1	5.79ab	74.6e-s	1.1ab	195j-u	102.3d-q	234.8a-c	44.9b-l	75.7b-k	37.6a-c	18.3a	1.06j-r
L19xT1	5.9ab	77.2a-d	1.2ab	194k-u	100.9d-s	203.6bc-g	45.5a-k	78.4a-c	37.1a-d	16.9a-i	1.09i-r
L20xT1	5.56ab	75.4b-n	1.5ab	201.9d-q	103.1d-o	199.6c-g	45.4a-k	76.9a-i	37.1a-d	17.2a-g	1.27a-k
L21xT1	5.44ab	76.7a-f	1.2ab	198.8g-s	103d-o	202.8b-g	42.6j-m	77.9a-e	37.9a	16.9a-i	0.97m-r
L22xT1	4.98bc	76.8a-f	1.1ab	210.1b-j	109.1a-f	206.3a-g	44.3d-m	77.9a-e	35.6a-e	16.6b-k	1.26b-l
L23xT1	4.85bc	75.5b-m	1ab	209.4b-k	107.4b-h	210.6a-g	44.6c-m	76.5b-k	35.7a-e	16.8a-j	1.23b-m
L24xT1	5.56ab	75.9b-k	1.1ab	196.3j-u	103.9d-n	209.8a-g	45.2a-l	77a-i	37a-e	17.3a-f	1.25b-l
L25xT1	5.65ab	72.5r-x	1.5ab	195.5j-u	101.7d-r	207.9a-g	44.8b-l	74h-o	35.8a-e	17.3a-f	1.13g-q
L26xT1	5.66ab	77.5a-c	1.7a	200.4fg-r	105.6c-j	200.1c-g	46.4a-h	79.2ab	35b-e	14.9l	1.24b-l
L27xT1	5.79ab	74h-u	1.4ab	189.3o-w	96i-v	205.2b-g	45.8a-k	75.4c-l	37a-e	16.4c-l	1.25b-l
L28xT1	5.49ab	74.5e-t	1.7a	189.2o-w	93n-v	219.3a-g	46.7a-g	76.2b-k	35.9a-e	16.5b-l	1.02j-r
L29xT1	5.58ab	75.2b-p	1.3ab	194.2k-u	96.4h-v	224.8a-g	46.3a-h	76.5b-k	36.9a-e	16.1e-l	1.07i-r
L30xT1	5.96ab	73.3l-v	1.1ab	203c-p	91.5q-v	222.4a-g	45.8a-k	74.4e-n	36.6a-e	18.1ab	1.1h-r
L31xT1	5.04bc	72.9n-v	1.5ab	182.1u-x	92.1o-v	213.9a-g	45.1a-l	74.4e-n	36.5a-e	15.2j-l	1.2c-n
L32xT1	5.87ab	73m-v	1ab	184.2s-x	88.4t-v	222.3a-g	44.5d-m	74h-o	37.2a-d	17.4a-f	1.14f-q
L33xT1	5.67ab	76.4a-i	1.3ab	188.1p-x	91.9p-v	220.8a-g	47.3a-f	77.7a-f	35.3a-e	15.8f-l	1.24b-l
L34xT1	5.52ab	74.8d-s	1.4ab	205.7b-n	100.9d-s	225.6a-e	46.6a-h	76.2b-k	35.1b-e	16e-l	0.93o-r
L35xT1	4.13c	76.5a-h	1.6ab	177.4v-x	94.1k-v	207.6a-g	45b-l	78.1a-d	34.9c-e	15.2j-l	0.86r
L36xT1	5.36ab	76.4a-i	1.1ab	200.7e-r	110a-e	208.1a-g	45.4a-k	77.5a-h	37a-e	16.4c-l	0.93o-r
MH 130	5.18abc	69.9y	0.9ab	206.1b-n	102.3d-q	210.3a-g	46.1a-j	70.8o	35.6a-e	16.5b-l	1.02j-r
Melkassa 2	5.23abc	73.9i-u	1.1ab	212.3b-i	98.4g-v	202.3b-g	44.2d-m	75c-l	36a-e	15.3i-l	1.2c-n
MHQ138	5.4ab	70.5w-y	0.8ab	185.9r-x	93.8l-v	242a	45.4a-k	71.3m-o	37.9a	17.4a-f	1.02j-r

Cr mean	5.46	74.6	1.2	199.5	100	212.4	45.3	75.8	36.1	16.6	1.15
Ck mean	5.27	71.3	0.9	120.9	98.2	218.2	45.22	72.2	36.5	16.4	1.08
Grand Mean	5.45	74.5	1.2	199.6	100	212.7	45.3	75.7	36.1	16.6	1.15
LS (5%)	1.2	2.6	1	15.7	11.1	36.4	3.6	3.6	2.8	1.7	0.27
CV (%^)	18.12	2.2	2.9	4.6	7	14.4	5.4	5.1	6.2	6.4	11.8
Min	4.13	69.9	0.7	173.3	87.2	188.5	41.2	71.1	34.3	18.3	0.9
Max	6.27	78.5	1.7	235.6	118.8	242	48.6	80.2	37.9	14.9	1.53

GY=grain yield AD=anthesis date, ASI=anthesis silking interval, Df=degrees of freedom, ED=ear diameter, EH=ear height, EL=ear length, EPP=number of ears per plant, , KPR=number of kernels per row, PH=plant height, Rep=replication, SD=silking day ,TKWT=thousand kernels weight . Numbers within the same column with different letter/s are significantly difference from each other according to LSD test. Some letters represent as interval e.g. Cross L6xT2 had K-v in anthesis date; it included from k to v letters alphabetically.

Table 2: Estimates of mean values for grain yield and related traits with LSD comparisons.

ranged from 14.9 cm (L26xT1) to 18.3 cm (L18xT1). Crosses L18xT1, L19xT2 and L20xT2 had a higher ear length while crosses L26xT1, L16xT1 and L7xT1 had showed lower ear length. Among the 72 crosses, L34xT2 (6.27t/ha), L36xT2 (5.99t/ha), L30xT1 (5.96t/ha), L19xT1 (6.27t/ha), and L33xT2 (5.87/ha) were shown best yield (Table 2). The least yield was obtained from the crosses L35xT1 (4.13t/ha), L23xT1 (4.85t/ha), L13xT1 (4.88t/ha), L24xT2 (4.88t/ha), and L15xT1 (4.91t/ha). The overall yield mean was 5.45t/ha. High grain yield was founded 45 out of 72 crosses than the best hybrid MHQ138 which yielded 5.40t/ha (Table 2). However, they are non-significant when compared to check MHQ138 (Table 2). Cross combination that had a high grain yield could be used in the breeding program to improve the grain yield.

A number of crosses showed mean performance for more than one trait as compared to the best hybrid check (Table 3). Cross combinations that were earliest in anthesis date, shorter in the ear and plant height could be used as source of gene for the development of early maturing and shorter statures variety. Similar, Dagne et al. and Gudeta [22,23] identified experiment variety performing better than the best check for most yield and related traits. Most of the crosses had a comparable grain yield to checks. Table 3 showed top 5 crosses which showed good and poor grain yield performance compared to checks. Statistically, the top five crosses didn't show significant differences from the check, but they were comparable (Table 2).

Combining ability analysis

A GCA Significant difference was observed among crosses for all traits while non-significant difference for SCA (Table 1). This indicated that additive gene action was more important than non-additive gene action. The ratio of GCA/SCA mean square further exhibited the preponderance of additive gene effects in the inheritance of all traits (Table 1).

Grain yield

GCA means squares were significantly difference, whereas SCA mean squares were non-significant for grain yield (Table 1). Pswararyi and Vivek [24] Carried out diallel analysis, among cimmyt's early maturing maize germplasm and reported significant GCA mean square and non-significant SCA for grain yield. This study was indicated that the importance of both additive and non-additive gene action for this trait. Piovarci [25] Analyzed a diallel cross and noted that GCA was more important than SCA for yield. In the line with this study Pswararyi and Vivek, Dange et al., [17,24] previously reported dominate the role SCA gene action in grain yield and Strube [26] reported that SCA effects were greater than GCA effects for yield.

Line GCA effects for grain yield ranged between -0.98 t/ ha (L6) to 1.88 t/ ha (L35) (Table 4). Even though a total of 18 of the inbred lines showed positive GCA effects for grain yield, only 6 inbred lines (L15, L25, L27, L33.L34 and L35) were found to be the best general combiner for grain yield as these lines had positive and significant GCA effect. Inbred lines with positive and significant GCA are desirable parents for hybrid development as well as for inclusion in the breeding program, as the lines may contribute favorable alleles in the synthesis of new varieties. Inbred lines with negative and significant GCA effect were L6 and L17, indicating that these were poor general combining ability for grain yield (Table 4). Similarly, Teshale [18] recorded significant positive and negative GCA effects for grain yield and Mandefro [17] also found significant positive GCA effects for grain yield. The results of this study are also in agreement with the findings of Amiruzzaman et al., Legesse et al. Gudeta, Hadji and Dagne et al. [17,20-22,27,28] who reported significant positive and negative GCA effects for grain yield in maize germplasm.

Number of days to tasseling and silking

For a number of days to anthesis and silking, mean squares due to line GCA were highly significant (p<0.01) (Table 1) but SCA were not significant. Shewangizaw and Leta et al. [28,29] Reported GCA is more important than SCA for days to anthesis and silking. Ahmad and Saleem (2003) [30] also reported that the preponderance of additive gene action in inheritance of days to anthesis days and silking. Further Leggess et al. [28] reported a predominance of additive gene action in inheritance of days to tussling and silking.

Line GCA effect for days to anthesis ranged between - 4.20 (L2) to 2.79 (L13) (Table 4). Among 17 inbred lines with negative GCA effects, eight inbred lines had a significant GCA effect for a number of days to tasseling. These inbred lines had gene combinations that enhance early maturity. Ten inbred lines exhibited positive and significant GCA effect for number of days to tasseling, indicating that these lines were undesirable as they showed a tendency to increase late maturity. Seventeen of the inbred lines showed negative GCA effects for number of days to Silking, out of which L2, L3, L6, L23, and L30 were highly significant (p<0.01) and L4, L10 and L32 was significant (P<0.05). On the other hand, inbred lines L5, L6, L12, L13, L15, L19, L26 and L31and L35 expressed positive and significant GCA (Table 4). This result is in agreement with Demissew et al. and Gudeta [22,23] who reported significant positive and negative GCA effect for a number of days to tasseling and silking. Similar finding were also reported by Teshale Dagne et al. [1,18].

Good performing genotype for grain yield		poor performing genotype for grain yield	
Genotype	GY t/ha	Genotype	*GY t/ha*
L34 XT2	6.27	L35 XT1	4.13
L36 XT2	5.99	L23 XT1	4.85
L30 XT1	5.96	L13XT1	4.88
L19XT1	5.90	L24 XT2	4.88
L33 XT2	5.87	L15 XT1	4.91

Table 3: Summary of five good and poor performing crosses for grain yield evaluated at Melkassa in 2012/2013

line	GY(t/ha)	AD(days)	SI(days)	PH(cm)	EH(cm)	ED(cm)	EL(cm)	EPP	KPR(#)	SD(days)	TKWT(gm)
L1	0.39	-0.45	-0.43	1.38	-8.52*	0.65	0.74	0.26**	-0.03	-0.88	19.94
L2	-0.54	-4.20**	-0.68	-11.36*	-3.52	1	1.24*	-0.09	2.16*	-4.88**	21.94
L3	0.20	-2.45**	-0.43	-6.61	-8.02*	0.05	-0.45	0.24**	0.56	-2.88**	-43.05**
L4	-0.27	-1.70*	-0.68	-9.76*	-12.0**	-3.47**	-0.3	0.15*	-2.23*	-2.38*	01.94
L5	-0.63	2.79**	0.06	-5.86	-4.27	0.6	-0.55	0.01	-3.83	2.85**	-27.80
L6	-0.98*	-1.95*	-0.93*	-5.11	1.22	-2.58*	0.29	0.03	-1.43	-2.85**	-13.05
L7	-0.51	2.54**	0.06	-23.3**	-10.0**	-0.77	-0.85	-0.02	-2.53*	2.6	-01.30
L8	-0.18	-0.20	0.06	17.13**	-1.02	-1.09	0.29	0.16*	1.26	-0.14	-11.80
L9	-0.04	0.29	0.31	34.88**	12.72**	-1.62	-0.1	0.17**	0.26	0.6	-03.90
L10	-0.41	-1.70*	-0.68	-5.61	-12.0**	-4.82**	-0.8	0.05	-0.53	-2.38*	-33.05*
L11	0.53	-0.95	0.65	23.38**	17.47**	-5.67**	0.29	0.27**	0.46	-0.3	-22.80
L12	-0.45	1.79*	1.16**	16.63**	0.72	0.22	1.29*	-0.02	0.56	2.95**	-49.3**
L13	-0.17	2.79**	0.82	12.13**	11.22**	1.4	-0.65	-0.13*	0.06	3.61**	02.99
L14	0.48	0.04	-0.94*	4.88	11.72**	-0.09	0.84	0.05	-0.08	-0.9	-15.30
L15	1.2**	2.54**	0.81	-11.36*	-6.27	-0.42	-1.35*	-0.09	-2.73*	3.35**	15.69
L16	0.35	2.29**	-0.19	11.63*	22.2**	3.22*	-2.05**	0.17**	-1.38	2.1*	-27.30
L17	-0.97*	0.54	0.06	-14.8**	1.22	-1.59	-1	-0.27**	-2.98**	0.6	-10.55
L18	0.77	-0.2	-0.68	-0.36	-0.52	0.82	0.94	-0.13*	2.66*	-0.88	56.19**
L19	-0.27	1.79*	0.31	-1.11	5.97	1.07	1.24*	-0.09	1.61	2.1*	-03.05
L20	0.75	1.04	0.06	-0.61	-0.52	1.07	1.34*	0.02	1.86	1.1	-05.05
L21	0.21	1.04	0.31	3.88	3.72	-2.64*	0.54	-0.13*	2.51*	1.35	15.19
L22	-0.43	0.29	0.06	15.63**	10.72**	-0.92	0.44	0.05	0.66	0.35	-05.80
L23	-0.25	-0.2	-0.94*	12.38**	8.72*	-0.32	-0.008	0.05	-1.38	-1.1	13.94
L24	-0.32	0.04	-0.44	-0.36	1.47	0.55	0.59	0.03	0.86	-0.4	-02.10
L25	1.21**	-1.2	0.31	2.13	1.97	2.56*	0.99	-0.08	-0.23	-0.89	39.44**
L26	-0.12	2.29**	0.56	7.13	3.97	2.32	-2.40**	-0.02	-1.18	2.89**	-19.65
L27	0.95*	-2.28*	1.31**	-16.1**	-5.77	2.05	-0.05	0.05	2.46*	-0.97	-10.75
L28	0.64	-0.7	0.56	-16.8**	-8.02*	0.7	-0.7	-0.03	0.21	-0.14	20.84
L29	0.50	1.79*	0.06	-9.51*	-9.52**	1.27	0.29	-0.14*	1.21	1.85	29.44*
L30	0.73	-2.28**	-0.68	3.88	-6.27	1.5	2.14**	-0.11	1.16	-2.96**	-3.05
L31	-0.44	-3.2**	-0.19	-19.1**	13.52**	0.8	-0.55	-0.05	1.41	3.39**	5.44
L32	-0.07	-1.95*	-0.43	-9.86*	-9.27**	-1.09	1.19*	-0.06	1.66	-2.38*	10.69
L33	1.00*	1.04	0.06	2.88	-0.77	3.55**	-0.6	0.09	-0.93	1.1	29.94*
L34	0.98*	1.04	0.31	10.63*	1.22	1.0	-0.45	-0.11	-1.08	1.35	29.54*
L35	1.88**	2.04*	0.31	7.38	8.47*	0.62	-1.5	-0.2	-2.18*	2.35*	-12.97

L36	0.33	-0.2	0.31	-21.8**	-5.02	0.05	-0.2	-0.13*	1.06	0.11	8.44
SE	0.48	0.84	0.42	4.56	3.35	1.27	0.54	0.06	1.08	0.97	14.2
SED	0.69	1.19	0.6	6.45	4.75	1.8	0.76	0.09	1.53	1.37	20.08

GY=grain yield AD=anthesis, date, ASI=anthesis silking interval, DF=degrees of freedom, ED=ear diameter, EH=ear height, EL=ear length, EPP=number of ears per plant, KPR=number of kernels per row, PH=plant height, Rep=replication, SD=silking day, TKWT=thousand kernels weight.

Table 4: Estimates of general combining ability effects for eleven traits of 36 maize inbred lines used in a Line by tester study at Melkassa, Ethiopia during 2012 cropping season

Ear length

Line GCA mean squares were highly significant (P<0.01) while non-significant difference for SCA (Table 1). Similarly Dagne et al. [17] reported significant mean square due to GCA for ear length. Mandefro [27] reported no importance of non- additive gene action for ear length.

Eighteen inbred lines showed a positive GCA effect for ear length. Among which five inbred lines (L2, L12, L19, L20 and L32) had positive and significant (P<0.05) and one inbred line (L30) had positive and highly significant (P<0.01) GCA effect. These inbred lines had a tendency to increase ear length. Nineteen inbred lines showed a negative GCA effect for ear length, among which two inbred lines (L16 and L26) had negative and highly significant GCA effect. These two inbred lines found to be poor general combiners as they showed negative and significant GCA effect. Similarly, [17,20,31] Amiruzzaman et al., Jumbo and Carena and Dagne et al. reported positive and negative significant GCA effect for ear length. The positive GCA effect is desirable as to indicate the tendency to increase ear length, which directly contributes to increase grain yield maize.

Ear diameter

Line GCA means squares were significant difference in ear diameter (Table 1). Both additive and non-additive gene effects were important as reported by Dagne, Hadji and Gudeta [1,21,22]. Line GCA effects were ranged from -5.67 (L11) to 3.55 (L33). Twenty-one inbred lines showed positive GCA effects. Three inbred lines (L16, L25 and L33) showed significant and positive GCA effects (Table 4). These lines were the best general combiners for ear diameter as they had significant and positive GCA effects. L33 (3.55) had highest positive GCA effects. On the other hand, five inbred lines had highly significant and negative GCA effects were poor general combiners for this trait. The present study is in agreement with Amiruzzman et al., Jumbo and Carena, Dagne et al. and Gudeta [17,20,22,31] who reported significant positive and negative GCA effects for ear diameter.

Anthesis silking interval

Anthesis silking interval, lines GCA were significant difference (P<0.05). Line GCA effects ranged from -0.94 (L14 and L23) to 1.31 (L27) (Table 4). Fourteen inbred lines expressed negative GCA effects in the desired direction, among these L6, L14 and L23 showed negative and significant (p<0.05) GCA effects. On the other hand, L12 and L27 expressed positive GCA effects and highly significant in the undesired direction. Similar to this result Mwambula [32] reported that anthesis-silking interval was one of the most useful secondary traits for selecting for better yields under drought stress condition.

Thousand-kernel weight

For thousand kernels weight means squares due to line GCA were significant difference (P<0.05). But mean squares due to SCA were not significant 0(Table 1). Similarly, Gudeta [22] reported non-significant SCA mean square. In contrast, Dagne et al. [17] reported that the importance of both additive and non-additive gene action for the trait. Line GCA effects of thousand-kernel weight was ranged from -49.3 g (L12) to 56.19 (L18) (Table 4). Sixteen lines expressed positive GCA effects for thousand-kernel weight, out of which L18 and L25 showed positive and highly significant (p<0.01) GCA effects in the desired direction. Alternatively, L3, L10 and L12 expressed a negative and significant difference of GCA effects in the undesired direction. The present result is in agreement with the findings of several researchers who reported significant positive and negative GCA effects for thousand-kernel weight. [17,18,20,22,33]

Number of kernel per rows

Numbers of kernels per row mean square due to SCA were not significant while significant difference due to GCA. This result is similar to the report of Dagne and Gudeta [1,22] on maize. Line GCA effects for number of kernels per rows were ranged from -2.98 (L17) to 2.66 (L18) (Table 8). A total of 20 inbred lines showed positive GCA effects for number of kernels per rows, only three inbred lines (L2, L18, L21 and L27) showed positive and significant (P<0.05) GCA effects for number of kernels per rows. Five inbred lines (L4, L7, and L15and L35) exhibited significant negative GCA effects for number of kernels per rows. Significantly positive and negative GCA effects were obtained for number of kernels per row. Inbred lines with significant difference and positive GCA effect, suggesting the presence of divergence to improve this trait. This result is in agreement with the finding of Dagne et al., Gudeta and Amiruzzaman et al.,[17,20,22] who reported both positive and negative significant GCA effects for number of kernels per row.

Plant height

Mean squares due to line GCA were highly significant difference (p<0.01), Whereas, Mean squares due to SCA was not significant (Table 1). Line GCA effects of plant height was ranged from -23.36 (L7) to 34.88 (L9). Seventeen inbred lines expressed positively and the remaining 19 expressed negative GCA effects. Among these, L8, L9, L11, L12, L13, L22 and L23 expressed positive and highly significant (p<0.01) GCA effects for increased plant height while six of the inbred lines L7, L17, L27, L28, L31 and L36 had negative and highly significant (p<0.01) GCA effects for reduced plant height (Table 4). L7 was the most general combiner for reduced plant height; whereas L9 and L11 were the best general combiners for increased plant height. Significantly positive and negative GCA effects were obtained for plant height, suggesting the presence of divergence to improve this trait. Teshale, Dagne and Hadji [1,18,21] recorded significant positive and negative GCA effects for plant height.

Ear height

Mean squares due to line GCA were highly significant (p<0.01) for and plant ear height, whereas, mean squares due to SCA was not significant (Table 1). Line GCA effects for ear height ranged from 12.02 (L4 and L10) to 22.22 cm (L16) (Table 4).Among a total of 18 of the inbred lines that showed the positive GCA effect for ear height, only six inbred lines (L9, L13, L14, L16, L22 and L31) showed positive and highly significant (p<0.01) GCA effects. On the other hand, six (L4, L7, L10, L11, L29 and L32) showed negative and highly significant (p<0.01) GCA effects for ear height. Dagne [1] Recorded significant positive and negative GCA effects for ear height. Further, Gudeta [22] found significant positive and negative GCA effects for ear height.

Number of ear per plant

For number ear per plant (EPP), mean squares due to line GCA were highly significant (p<0.01) while mean squares due to SCA were not significant (Table 1). Seventeen inbred lines showed positive GCA effects among which 5 inbred lines (L1, L3, L9, L11 and L16) had positive and highly significant (p<0.01) GCA effects. On the other hand, five inbred lines (L17, L13, L18, L21, L29 and L36) showed negative and significant (p<0.05). Similarly, Manda and Mwambula [32] reported that ears per plant were the most useful secondary traits for selecting for better yields under drought stress conditions. Additionally, Dagne et al. [17] who reported significant positive and negative GCA effect for number of ears per plant.

Conclusion and recommendation

The present study consisted of 72 crosses and 3 checks which were evaluated at the Melkassa Agricultural Research Centre; Ethiopia with the objectives of observing of mean crosses performance and estimating combining abilities maize elites for 11 characters. The analysis of variance revealed that the crosses were significantly different from most of the characters. Further, significant differences were also recorded among the checks and checks vs crosses for anthesis day, Plant height and ear length. Results of Line Tester analysis showed that the lines GCA mean squares were significant for all studied traits. The Testers GCA mean squares were significant for all traits except ear height, number of ears per plant and kernels per row. SCA mean squares were non-significant for all traits. Significant lines in terms of GCA mean squares for all traits indicated the predominant role of additive gene actions in determining the inheritance of these traits. In this study, the GCA sum of squares component was greater than the SCA sum of squares for the studied traits, suggesting that variations among crosses were mainly due to additive rather than non-additive gene effects; and hence, the selection would be effective in improving grain yield and other agronomic traits.

Based on combining ability analysis L15, L25, L27, L33, L34 and L35 were the top general combiners for grain yield and these inbred lines can be used for variety development in the future lowland maize improvement program. Inbred lines L2, L3, L4, L6, L10, L27, L30, L31 and L32 were the best general combiners for days to anthesis, indicating these lines had a favorable allele frequency for earliness and can be used to develop early maturing varieties. Inbred lines L2, L4, L7, L15, L17, L27, L28, L29, L31, L32 and L36 were best general combiners for shorter plant height, which are desirable for lodging resistance. Inbred lines L2, L18, L21 and L27 were the best general combiners for kernels per row. These lines had favorable allele to improve the number of seeds per cob.

For ear diameter L16, L25and L33 lines were good general combiners, indicating these lines had the tendency to increase ear diameter. For ear length L2, L12, L19, L20 and L30 lines were good general combiner indicating these lines had the tendency to increase ear length. For thousand-kernel weight L18, L25, L29, L33 and L34 were the top general combiners as such line had the tendency to increase thousand kernel weights. Among the crosses, L34xT2 (6.27 t/ha), L36xT2 (5.99t/ha) and L30xT1 (5.96 t/ha) crosses were highest grain yield (t/ha). These hybrids could be included in further investigation for grain yield and related traits and could be possible candidates of future releases.

From these finding better performing test crosses, inbred lines with desirable GCA effects for grain yield and other grain yield related traits were successfully identified. These germplasm constitute a source of valuable genetic material that could be successively used for future breeding work. In general, the results of this study could be useful for researchers who need to develop high yielding varieties of maize, particularly adapted to the rift valley areas of Ethiopia as well as sub-Saharan Africa. However, the present study was conducted at one location and the result is only an indication and we cannot reach at a definite conclusion. Therefore, it is advisable to continue with this study over many years and locations.

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