

Standard heterosis estimation for quality protein maize hybrids over best released and commercialized hybrids

Abstract

Maize plays an indispensable role in meeting high food demand. It is globally one of the most widely adopted and cultivated crops. Hybrid development from fixed inbred lines is one of the *tacticsto boost*maize production. The national average maize yield in Ethiopia is low and thus, selection of promising germplasm, knowledge of combining ability, and heterotic grouping are prerequisites to developing high-yielding maize varieties. Forty-two Quality Protein Maize (QPM) crosses (21 inbred lines each crossed with two testers) along with three popular standard hybridchecks were evaluated in two replications using alpha lattice during the 2017 cropping season at Ambo, Arsi-Negele, and Kulumsa. The objective of this study was to estimate standard heterosis for grain yield, other agronomic and morphological characters. Significant difference among crosses was observed for 19 traits at Ambo, 14 traits at Arsi-Negele, and 19 traits at Kulumsa in the hybrid trial. For GY, at Ambo, almost all crosses showed negative heterosis against the best check (AMH853) At Arsi-Negele 14 crosses had positive standard heterosis, from these only three crosses: L8xT1(50.8%), L8xT2 (46.6%), and L7xT1 (33.9%) showed significant difference against Jibat but at Kulumsa, the difference for standard heterosis was positive but non-significant only by two crosses: (L7xT1 (6.6%) and L19xT1 (4.7%). Based on mean grain yield and standard heterosis, L8xT2, L7xT1, L8xT1, L19xT1, L6xT2, and L18xT1 are promising. The study of the results highlighted that the breeding program was successful in generating QPM hybrids. Based on the finding we suggest that it is better to use the parents of theses hybrids s potential source materials in the breeding program for future work in the breeding program through involving them in different crosses formation.

Keywords: cross, inbred lines, heterosis

1. Introduction

The phenomenon of heterosis was defined by Shull (1952) as “the interpretation of increased

36 vigor, size, fruitfulness, speed of development, resistance to disease and to insect pests, or to
37 climatic rigors of any kind manifested by crossbred organisms as compared with
38 corresponding inbreeds, as the specific results of unlikeness in the constitution of the uniting
39 parental gametes”. Falconer and Mackay (1996) defined as the difference between the hybrid
40 value for one trait and the mean value of the two parents for the same trait. According to
41 Miranda (1999), heterosis is the genetic potential expression of the superiority of a cross in
42 relation to its parents.

43 Three types of estimation of heterosis are explained in the literature; namely, mid-parent or
44 average heterosis, which is the increased vigor of the F1 over the mean of two parents; and
45 high-parent or better-parent heterosis, which is the increased vigor of the F1 over the better-
46 parent (Jinks, 1983) and standard heterosis (Berhanu,2009; Beyene, 2016 and Abiy, 2017).
47 Heterosis is usually considered to be similar with hybrid vigor (Stuber, 1994). Heterosis, or
48 hybrid vigor, refers to the phenomena in which the offspring of two inbred parents exhibit
49 phenotypic performance beyond the mid-parent or better-parent used to generate the hybrid
50 (Li *et al.*, 2018). Grain yield in maize is expected to exhibit heterosis as a consequence of
51 partial to complete dominance of genes controlling the trait (Miranda, 1999).

52 Maize breeders need also to determine the genetic diversity of inbreeds because it facilitates
53 the identification of those that would produce crosses possessing high levels of heterosis
54 (Badu-Apraku *et al.*, 2013). The information facilitates the development of high-yielding
55 hybrids without testing all possible hybrid combinations among the potential parents
56 available in a hybrid program. Three major dominance theories, such as dominance,
57 overdominance, and epistasis, as the main theories, to explain mechanisms underlying the
58 phenomena of heterosis. However, it is generally accepted that heterosis, to a large extent, is
59 due to over-dominance gene action (Singh, 2005). On the other hand, the expression of
60 heterosis also depends on the level of genetic divergence between parents; i.e., differences in
61 allele frequencies are necessary for the expression of heterosis. For that reason, expression of
62 heterosis is expected to be lower in crosses between broad base open-pollinated populations
63 (Miranda, 1999).

64 Heterosis is important in maize breeding and is dependent on the level of dominance and

65 differences in gene frequency (Falconer & Mackay,1996). The manifestation of heterosis
66 depends on the genetic divergence of the two parental varieties (Hallauer; Miranda, 1988).
67 Low grain yield heterosis is observed for crosses among genetically similar germplasm and
68 for crosses among broad genetic base germplasm (Vasalet *al.*, 1993). Higher levels of
69 heterosis were seen with increased divergence within a certain range, but that heterosis
70 declined in extremely divergent crosses (Prasad and Singh, 1986). Genetic divergence of the
71 parents is inferred from the heterotic patterns manifested in a series of crosses (Hallauer and
72 Miranda, 1988; Miranda, 1999).

73 Heterosis in maize has been investigated extensively. Hallauer and Miranda (1988) reported
74 the mid-parent heterosis ranged from -3.6% to 72.0% while high-parent heterosis ranged
75 from -9.9% to 43.0% for maize. Maize has attained the highest levels of production in the
76 temperate areas of the world employing modern agricultural techniques. Surprisingly, the
77 magnitude of heterosis has not been changed during the hybrid era in the tropical areas as
78 compared to with temperate because, in most of the tropical country's maize is grown as a
79 rainfed crop in the hot season, under varying conditions of moisture, generally subject to
80 periodic and erratic drought and/or excess of water at different stages of the growth cycle,
81 without effective weed and pest control, and usually under low-fertility conditions. In
82 general, it is grown as a subsistence crop, with very low levels of management and little
83 inputs (Duvick, 1999), even though mean commercial maize grain yield has substantially
84 increased during this time (Troyer, 1990). Berhanu (2009) reported estimate of heterosis
85 ranged from 28.95 to 202.34% over mid-parent and 16.97 to 175.46 % over the better-parent
86 for grain yield from crosses generated from LxT mating design.

87 The development of hybrid varieties played a great role in improving food and feed supplies.
88 Food and feed supplies would unquestionably be greatly reduced if only non-hybrids were
89 available to the producer (Stuber, 1994). Hybrid varieties are the first filial generations (F1)
90 from crosses between two or more pure lines, inbreds, open-pollinated varieties, clones or
91 other populations that are genetically dissimilar (Singh, 2005). The development of maize
92 hybrid began in the early 1900s (Shull,1908; East, 1908; Hallaueret *al.*, 1988; Smith *et al.*,
93 2017). According to Singh (2005), most of the commercial hybrid varieties are F1's from two
94 or more inbreds. The success of hybrid maize development depends on the capacity of the

95 breeding program to rapidly develop lines that combine well and identify the superior
 96 heterotic combinations to maximize the vigor of the hybrid (Kim and Ajala, 1996). An
 97 inbred is a nearly homozygous line obtained through continuous inbreeding of cross-
 98 pollinated species with selection accompanying inbreeding (Singh, 2005).
 99 Similar to the CM, QPM hybrids proved to yield more grain than open-pollinated QPM
 100 cultivars, but mean grain yield does not differ for a single, three-way, and double-cross QPM
 101 hybrids (Pixley and Bjarnason, 2002). The broader genetic constitution of three-way and
 102 double-cross hybrids might have helped them to buffer the extreme environmental diversity
 103 of the environment better than single crosses (Pixley and Bjarnason, 2002). In a different
 104 trial, Pixley and Bjarnason (1993) also observed a QPM hybrid exceeding a normal
 105 endosperm hybrid check by an average of 14% for grain yield, 48% for Trp concentration in
 106 grain, and 60% for Trp concentration in protein. Berhanu (2009) evaluated tester crosses of
 107 white QPM and CM inbred lines and reported higher grain yield heterosis overall mid and
 108 better parents and some of the crosses over the standard checks. Similarly, Beyene (2016)
 109 reported higher heterosis from diallel crosses evaluated at Bako, Ethiopia. This study aimed
 110 to estimate the standard or economic heterosis of the crosses over the standard checks.

111 **2. Materials and methods**

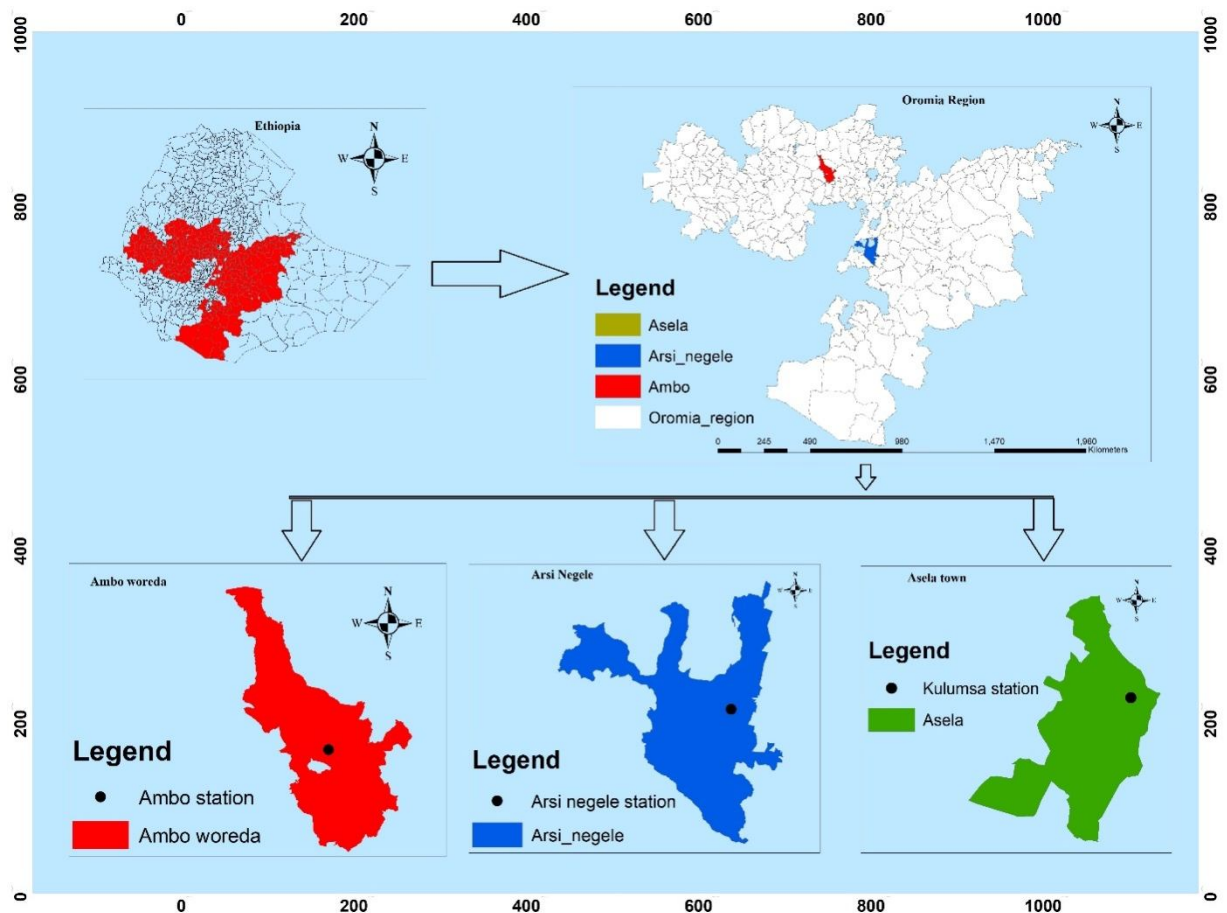
112 **2.1. Study sites**

113 [The study was conducted at three sites in the highland agroecology of Ethiopia including;](#)
 114 [Ambo, Arsi-Negele, and Kulumsa Agriculture Research Centers in the 2017 main cropping](#)
 115 [season.](#)

116
 117 Table 1. Latitude, longitude, altitude (masl), long-term annual rainfall (mm), maximum
 118 temperature (MaxT) (°C), minimum temperature (MinT) (°C), soil type, and soil pH of the
 119 study sites.

Site	Latitude	Longitude	Altitude	Annual rainfall	MaxT	MinT	Soil type	pH
Ambo	8° 57' N	38° 7' E	2225	1115	25.5	11.7	Heavy clay	7.8
A. Negele	7° 19' N	38° 39' E	1960	886	26.0	9.1	clay loam	6.5-7.5
Kulumsa	8° 02' N	39° 10' E	2200	830	23.2	10.0	luvisol	6.0

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121
122 *Figure 1 map of the study area*

123 **2.2. Experimental materials**

124 From the 21 inbred lines and the two testers 42 F1 hybrids were generated at Ambo Highland
 125 Maize Breeding Program (AHMBP). The 42 F1 hybrids along with three standard checks: one
 126 QPM (AMH852Q) and two CM (Jibat and AMH853), designated as hybrid check, were
 127 tested. Each new hybrids and standard check hybrids were planted in three replication and
 128 tested at three locations during 2017 main cropping season. Each cross planted in one row plot
 129 with 0.25 and 0.75 m spacing between plants and rows, respectively which consisted of 21
 130 plants per plot.

131 **2.3 Statistical Analysis**

132 Standard heterosis (STH) or economic heterosis in percent were calculated for those
 133 parameters that showed significant differences among crosses following the method
 134 suggested by Falconer and Mackay (1996).

135 Standard heterosis (SH), was estimated for traits that showed significant MS for cross vs best
136 check at individual locations. In order to consider traits for combined analysis, cross x
137 location for MPH and MPH whereas to estimate SH, genotype x location interaction should
138 be non-significant as additional criterion. For SH, the traits which had significant check x
139 location interaction, SH was conducted for each location.

140 Standard heterosis (SH) = $\frac{F1-STV}{STV} \times 100$ according to Berhanu (2009).

141 Where, *F1* = mean value of the cross, *STV* = value of the highest yielding standard variety

142 Test of significance of heterosis (the numerator in each equation before multiplying by 100)
143 was determined using the t-test. The critical difference (CD) for testing the significance of
144 SH was calculated using the following formulas:

145 Critical difference for heterosis over standard heterosis (SH)

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$$CD \text{ for SH} = \sqrt{2MSe/r} \times t$$

147 Where *MSe* is error MS, *r* is the number of replication and *t* is the Table value at 0.05,

148 0.01 and 0.001, *CD* is Critical Difference, *SH* is standard heterosis, *t* -value in the formula is
149 not included in square root. The absolute values of the relevant heterosis were tested against
150 this critical difference.

151 **3. Result and discussion**

152 Analysis of Variance (ANOVA) for the hybrid trial showed a significant genotypic
153 difference for Grain Yield (GY), Days to Tasseling (DT), Day to Silking, (DS) Plant Height
154 (PH), Ear Height (EH), Ear Per Plant (EPP), Ear Length (EL), Kernel Per Row (KPR), Ear
155 Diameter (ED), Thousand Seed Weight (TSW) and Biomass yield (BIOM) at each of the
156 three locations (Table 2, 3 and 4). A similar result was also reported by (Berhanu, 2009). The
157 genotypic difference for Gray Leaf Spot (GLS) and Leaf above uppermost Ear (LFAE) was
158 not significant in any of the three locations. Variances due to genotype were significant only
159 at Kulumsa for Common Leaf Rust (CLR), Leaf Angle (LANG), and Leaf Area (LFAR),
160 while for Turicum Leaf Blight (TLB) and Harvest Index (HI) these differences were
161 significant only at Arsi-Negele. For Anthesis Silking Interval (ASI), Kernel Modification
162 (MOD), Plant Aspect (PAS), and Number of Kernel Rows ear⁻¹ (NKR) difference between
163 the crosses was significant only at Ambo (Table 2). For days to maturity (MD), leaves per
164 plant (LFPP) and leaves below the uppermost ear (LFBE) these differences were significant
165 at two of the three locations.

166 *Table 2. General ANOVA for grain yield and other agronomic traits of maize hybrids and lines evaluated at Ambo Agricultural*
 167 *Research Center, 2017.*

Ambo	Mean Square										
Source of Variation	DF	GY	DT	DS	ASI	MD	PH	EH	Mod	GLS	CLR
Rep with cross	1.00	7.72**	0.43	0.19	0.05	3.86	786.29**	340.01**	1.86**	0.00	0.00
Genotype	44	5.36***	28.67***	24.38***	0.008***	3.48*	1324.9***	614.86***	0.61***	0.00	0.00
Cross	41.00	4.90***	22.97***	15.98***	4.94***	3.60*	1276.53***	606.06***	0.48*	0.00	0.00
Cross vs Checks	1.00	14.54***	201.60***	254.25***	3.05	0.26	18.57	200.80*	9.52***	0.00	0.00
Cross vs best check	1.00	20.15***	188.89***	191.64***	0.01	0.59	1978.12***	1285.72***	2.16**	0.00	0.00
Error Cross	41.00	0.71	2.92	3.17	1.44	1.83	72.40	40.84	0.24	0.00	0.00
Source of Variation	DF	TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW	
Rep with cross	1.00	0.00	1.31**	0.76**	0.31*	9.56	1.19	26.86	0.03	8893.28**	
Genotype	44	0.04	0.40***	0.33***	0.16**	10.37***	2.43*	34.44***	0.23***	6119.3***	
Cross	41.00	0.05	0.40***	0.34***	0.16***	9.59***	2.19	35.77**	0.24***	6373.16***	
Cross vs Checks	1.00	0.03	0.69 *	0.81**	0.278*	5.46	31.11***	35.50	0.35**	18679.10***	
Cross vs best check	1.00	0.01	0.91**	0.28	0.07	11.04	2.05	14.88	0.00	1699.22	
Error Cross	41.00	0.05	0.11	0.07	0.07	3.20	1.39	13.33	0.04	1168.31	
Source of Variation	DF	BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE	
Rep with cross	1.00	73.90*	2682.96***	28.58	10.71	1.11	12033.58	31.77***	0.11	38.67***	
Genotype	44	24.06*	196.57	12.45	70.53	0.60	9910.92	2.78***	0.46	1.82***	
Cross	41.00	21.75**	209.51	12.73	71.28**	0.59	9848.86	2.92***	0.47*	1.84***	
Cross vs Checks	1.00	94.74**	105.55	114.00**	1264.0***	0.01	96670.47***	0.00	7.36***	9.26***	
Cross vs best check	1.00	126.39**	43.23	11.56	1.44	0.02	562.60	0.11	0.82	0.40	
Error Cross	41.00	14.17	192.14	10.98	41.54	0.72	11302.14	1.01	0.37	0.59	

168 *= significant at 0.05 probability level, **= significant at 0.01 probability level and *** = significant at 0.001 probability level, DF = Degree of freedom, GxL= Genotype by
 169 location interaction, GY = Grain yield (t/ha), DT = Days to tasseling (days), DS = Days to silking (days), ASI = Anthesis Silking Interval (days), MD = Days to Maturity
 170 (days), PH = Plant Height (cm), EH = Ear Height (cm), MOD = Kernel Modification (1-5 scoring), GLS = Gray Leaf Spot (1-5 scoring), CLR = Common Leaf Rust (1-5
 171 scoring), TLB = Turicum Leaf Blight (1-5 scoring), EAS = Ear Aspect (1-5 scoring), PAS = Plant Aspect (1-5 scoring), EPP = Ear Per Plant (number), EL= Ear Length
 172 (cm), NKR = Number of Kernel Rows (number), KPR = Kernel Per Row (number), ED = Ear Diameter (cm), TSW = Thousand Seed Weight (gram), BIOM = Biomass yield
 173 (t/ha), HI = Harvest Index (%), LANG = Leaf Angle (degree), LL = Leaf Length (cm), LW = Leaf Width (cm), LFAR = Leaf Area (cm²), LFPP = Leaf Per Plant (number),
 174 LFAE = Leaf above upper most ear (number), LFBE = Leaf below upper most ear (number).

175 *Table 3 General ANOVA for grain yield and other agronomic traits of maize hybrids and lines evaluated at Arsi-Negele Agricultural Research Center, 2017.*

Arsi-Negele											
Mean Square											
Source of Variation	DF	GY	DT	DS	ASI	MD	PH	EH	Mod	GLS	CLR
Rep with cross	1	9.51**	36.01*	33.44	0.05	20.01***	2690.53***	762.01***	0.19	0.24	1.44*
Genotype	44	3.30***	29.92***	20.08**	0.01	3.55**	543.56***	307.03***	0.83	0.12	0.40
Cross	41	3.53***	27.13***	17.12*	4.88	3.49***	542.65***	308.64***	0.80	0.12	0.38
Cross vs Check	1	0.66	150.17***	174.57***	0.92	8.42	16.59	49.21	0.04	0.08	0.11
Cross vs Best Check	1	0.33	105.39***	84.66**	1.13	0.61	907.60***	607.24***	2.66	0.17	1.03
Error Cross	41	0.95	7.52	9.49	2.93	1.26	71.92	41.99	1.15	0.12	0.29
Source of Variation	DF	TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW	
Rep with cross	1	2.67***	3.44**	0.05	0.07*	14.58**	40.04***	14.86	1.66***	133.21	
Genotype	44	0.32*	0.41	0.28	0.05***	5.94***	3.11	33.12***	0.18***	5956.59***	
Cross	41	0.32*	0.43	0.30	0.04***	5.42***	2.78	29.31***	0.20***	5928.86***	
Cross vs Check	1	0.28	0.00	0.01	0.05	10.13*	31.11***	41.26	0.31*	8495.98*	
Cross vs best Check	1	0.72*	0.02	0.16	0.00	28.05***	8.00	173.95***	0.02	4992.84	
Error Cross	41	0.17	0.28	0.22	0.02	1.70	2.19	11.67	0.06	1912.74	
Source of Variation	DF	BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE	
rep with cross	1	9.51*	70.59	16.01	838.11**	9.33**	114635.53**	1.81	0.08	2.56	
Genotype	44	3.61**	200.01*	29.53	71.26	0.50	6890.64	0.80	0.20	0.50	
Cross	41	3.84*	208.77*	31.37	67.88	0.47	6518.12	0.80	0.20	0.52	
Cross vs Check	1	1.75	372.59	499.51**	195.25	1.17	20534.05	4.62*	1.88**	0.36	
Cross vs Best Check	1	0.50	188.04	1.36	307.17	1.50	31116.96	0.35	0.13	0.07	
Error Crosses	41	1.70	105.09	59.64	85.94	0.86	9657.96	1.01	0.20	0.64	

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Table 4. General ANOVA for grain yield and other agronomic traits of maize hybrids evaluated at Kulumsa Agricultural Research Center, 2017.

Kulumsa	Mean Square										
Source of Variation	DF	GY	DT	DS	ASI	MD	PH	EH	Mod	GLS	CLR
Rep	1	7.92**	8.05	15.42*	1.19	5.25	520.01	5.25	2.50*	0.00	2.33**
Genotype	44	4.79***	41.32***	40.60***	0.00	14.40	466.46**	342.48***	0.47	0.00	0.80**
Cross	41	4.86***	28.41***	29.35***	1.25	14.99	469.42**	339.43***	0.45	0.00	0.82***
Cross vs Check	1	0.79	623.01***	552.02***	2.14	2.95	1122.00*	983.15**	0.12	0.00	1.46*
Cross vs best check	1	9.86**	367.42***	326.52***	1.21	16.35	163.72	84.66	0.19	0.00	0.23
Error cross	41	0.95	2.34	2.72	1.19	13.32	195.33	82.98	0.53	0.00	0.30
Source of Variation	DF	TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW	
Rep	1	0.03	0.01	0.15	0.01	13.22*	0.43	7.54	0.02	1505.53	
Genotype	44	0.05	0.37**	0.19	0.18*	7.93***	1.96	23.50*	0.20***	4558.27***	
Cross	41	0.06	0.38**	0.19	0.18*	8.06***	1.96	24.18*	0.21***	4301.81***	
Cross vs Check	1	0.03	0.31	0.64*	0.01	14.96*	4.82	15.66	0.01	22678.24***	
Cross vs best check	1	0.05	0.00	0.50	0.11	11.90*	4.97	32.22	0.18	7899.42**	
Error cross	41	0.06	0.16	0.13	0.10	2.13	1.70	13.04	0.07	971.44	
Source of Variation	DF	BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE	
Rep	1	35.52*	3.16	4.76	0.53	0.10	130.42	12.44***	0.03	11.19***	
Genotype	44	20.38***	134.46	50.43***	55.44***	0.93***	9290.79***	0.91**	0.25	0.52**	
Cross	41	21.41***	139.08	31.24***	54.18***	0.88**	8835.74**	0.91**	0.25*	0.54**	
Cross vs Check	1	1.90	73.25	931.43***	205.88**	0.50	26672.33**	2.11*	0.35	0.84	
Cross vs best check	1	3.42	173.46	339.06***	34.96	0.00	2370.29	1.76*	0.54	0.30	
Error cross	41	7.22	100.52	6.32	19.61	0.34	3629.30	0.40	0.14	0.24	

186 *= significant at 0.05 probability level, **= significant at 0.01 probability level and *** = significant at 0.001 probability level, DF = Degree of freedom,
 187 GxL= Genotype by location interaction, GY = Grain yield (t/ha), DT = Days to tasseling (days), DS = Days to silking (days), ASI = Anthesis Silking Interval
 188 (days), MD = Days to Maturity (days), PH = Plant Height (cm), EH = Ear Height (cm), MOD = Kernel Modification (1-5 scoring), GLS = Gray Leaf Spot
 189 (1-5 scoring), CLR = Common Leaf Rust (1-5 scoring), TLB = Turcicum Leaf Blight (1-5 scoring), EAS = Ear Aspect (1-5 scoring), PAS = Plant Aspect (1-5
 190 scoring), EPP = Ear Per Plant (number), EL= Ear Length (cm), NKR = Number of Kernel Rows (number), KPR = Kernel Per Row (number), ED = Ear
 191 Diameter (cm), TSW = Thousand Seed Weight (gram), BIOM = Biomass yield (t/ha), HI = Harvest Index (%), LANG = Leaf Angle (degree), LL = Leaf
 192 Length (cm), LW = Leaf Width (cm), LFAR = Leaf Area (cm²), LFPP = Leaf Per Plant (number), LFAE = Leaf above upper most ear (number), LFBE = Leaf
 193 below upper most ear (number).
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Source of Variation	DF	Mean Square							
		GY	DT	DS	PH	EH	EPP	EL	KPR
Location	2	329.73**	2278.14**	1159.35**	123422.80**	60676.02**	4.61**	294.57*	669.62**
Genotype	44	9.34***	87.93***	71.47***	1817.37***	1067.41***	0.27***	18.31***	59.84***
Cross	41	9.67***	68.49***	50.82***	1793.51***	1068.88***	0.29***	16.89***	57.99***
Check	2	0.38	5.06	11.56	337.17	197.17	0.04	9.82*	21.86
Cross vs Check	1	13.59***	1050.80***	1038.19***	5756.21***	2748.07***	0.00	93.55***	211.59***
Cross vs best check	1	6.62**	326.52***	233.01***	3425.59***	2105.9***	0.07	24.50**	35.90
Genotype x Location	88	2.05***	6.00*	6.79	258.82***	98.48**	0.05	2.97	15.61
Cross x Location	82	1.81***	5.01	5.82	247.55***	92.63**	0.05	3.09	15.64
Check x Location	4	4.85*	13.06	12.81	510.58	243.33	0.11*	0.65	8.26
pooled error crosses	123	0.87	4.26	5.13	113.21	55.27	0.06	2.34	12.68
pooled error genotypes	132	0.93	4.22	5.05	118.95	62.94	0.05	2.42	12.81
pooled error checks	6	0.67	4.39	3.61	278.89	182.28	0.02	4.70	18.93

Source of Variation	DF	Mean Square			DF	Mean Square				
		ED	TSW	BIOM		ASI [†]	MD [†]	EAS [†]	LFPP [†]	LFBE [†]
Location	2	8.57*	235157.73**	1475.99**	1	352.80***	22826.27***	8.45	1.04	73.69
Genotype	44	0.50***	13595.74***	26.23***	44	7.08***	4.30***	0.57***	1.70	1.18
Cross	41	0.53***	13699.93***	27.02***	41	7.27***	4.34	0.57**	1.75	1.23
Check	2	0.06	1039.38	8.17	2	6.33*	2.25	0.19	1.15	0.77
Cross vs Check	1	0.08	34436.88***	29.82*	1	0.63	7.23*	1.27**	0.48	0.06
Cross vs Best Check	1	0.00	15592.55***	42.01*	1	4.69	9.43*	1.34**	0.72	0.00
Genotype x Location	88	0.06	1519.21	10.91*	44	2.64	2.73*	0.21*	1.99***	1.17***
Cross x Location	82	0.07	1451.95	9.99	41	2.54	2.76**	0.22*	2.09***	1.16***
Check x Location	4	0.03	2948.70*	12.96	2	0.33	3.25	0.06	0.26	0.77
pooled error crosses	123	0.05	1350.83	7.7D	82	2.18	1.54	0.13	0.70	0.41
pooled error genotypes	132	0.05	1320.95	7.35	88	2.11	1.58	0.13	0.69	0.41
pooled error checks	6	0.07	630.48	3.49	4	1.33	0.92	0.04	0.78	0.41

197 **3.1 Standard Heterosis**

198 Tables 6,7, and 8 presents Standard heterosis (SH) for five traits (GY, PH, EH, MOD and
199 EAS) at Ambo, four traits (GY, PH, EH, and TLB) at Arsi-Negele, and three traits (GY,
200 LFANG, and LFPP) at Kulumsa. For the combined data, the standard heterosis is presented in
201 Table 5. The traits that had non-significant MS for cross vs best check were not included in
202 estimating standard heterosis. The best checks used for calculating SH were Jibat at Arsi-
203 Negele and Kulumsa and AMH853 at Ambo.

204 **3.1.1 Standard heterosis at an individual location**

205 At Ambo, all crosses did not show any SH over the best check (AMH853) for GY (Table 6).
206 At Arsi-Negele, 13 crosses showed positive SH and three of them showed significant
207 differences. SH ranged from -46.25% (L2xT2) to 50.81% (L8xT1) (Table 7). At Kulumsa,
208 only two crosses (L7xT1 and L19xT1) had positive SH over Jibat but were not statistically
209 significant. At this location, SH ranged from -55.52% (L13xT1) to 6.57% (L7xT1) (Table 8)
210 which is in line with the result of Abiy (2017). He reported SH ranged -30.42% to 10.10%
211 from highland maize hybrids tested at Ambo and Kulumsa but none of the crosses had
212 significantly different SH.

213 AT Ambo, all crosses had negative and significant SH, except three crosses (L7xT1, L8xT1,
214 and L8xT2) which had positive and non-significant SH over CM best check (AMH853), for
215 PH and EH. These three crosses were the highest grain yielder next to the standard check.
216 SH ranged from -38.54% (L1xT1) to 2.89% (L8xT1) for PH and from -42.91% (L2xT2) to
217 3.72% (L8xT1) for EH (Table 6). Similarly, at Arsi-Negele, two crosses (L7xT1) and
218 L8xT1) showed positive and non-significant SH for PH. The crosses showed positive SH but
219 only SH from L7xT1 showed statistically significant. At Arsi-Negele SH ranged from -
220 31.64% (L2xT2) to 8.76% (L7xT1) for PH and from -44.38 (L3xT1) to 16.85 (L7xT1) for
221 EH (Table 7). The result of this study is in line with the negative SH reported by Berhanu
222 (2009) and Patilet *al.* (2017). At Kulumsa, the orthogonal contrast of cross-vs- check was
223 non-significant due to this, the estimation of SH was not done.

224 All crosses had positive SH for MOD except, L2xT1 at Ambo. This cross had zero SH for
225 MOD indicating, its ability to produce well-modified endosperm than other crosses. Out of

226 42 crosses, 24 showed significant SH over AMH853 (Table 6). The highest (150.0%) SH
227 was recorded by L20xT2 indicates this cross was the poorest for MOD. A lower magnitude
228 of SH is desirable with regard to this trait.

229 At Arsi-Negele, most of the crosses manifested by negative heterosis over the best check
230 (Jibat) except, three crosses of which one had positive SH and the other zero SH for TLB.
231 Ten crosses showed significant negative SH for TLB which indicates that these crosses
232 tolerate TLB better than the standard check

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Table 6. Standard heterosis (SH) for traits that were not included in the across location heterosis determination of the 42 F1hybrids obtained by LxT and evaluated at Ambo in 2017 (best check was AMH853).

Code	%GY	%PH	%EH	%MOD	%EAS	Code	%GY	%PH	%EH	%MOD	%EAS
L1xT1	-78.18***	-38.54***	-35.47***	83.33*	77.78***	L13xT1	-76.64***	-33.33***	-37.16***	83.33*	77.78***
L1xT2	-30.59**	-17.15***	-22.64***	50.00	0.00	L13xT2	-49.12***	-23.12***	-34.79***	66.67*	11.11
L2xT1	-49.56***	-21.19***	-29.39***	0.00	11.11	L14xT1	-44.85***	-10.41**	-14.53**	50.00	11.11
L2xT2	-72.15***	-36.61***	-42.91***	50.00	66.67***	L14xT2	-28.51**	-7.32*	-14.86**	116.67***	22.22
L3xT1	-45.50***	-17.73***	-24.32***	33.33	44.44**	L15xT1	-25.22**	-11.95**	-15.20**	100.00**	44.44**
L3xT2	-11.84	-12.72**	-17.23***	33.33	11.11	L15xT2	-41.67***	-7.51*	-16.89***	100.00**	22.22
L4xT1	-70.83***	-35.65***	-38.51***	83.33*	66.67***	L16xT1	-40.90***	-14.45***	-23.65***	33.33	22.22
L4xT2	-45.83***	-18.69***	-29.39***	50.00	22.22	L16xT2	-37.83***	-18.67***	-34.79***	50.00	22.22
L5xT1	-36.18***	-9.83**	-15.54**	83.33*	55.56***	L17xT1	-26.53**	-5.20	-4.73	16.67	33.33*
L5xT2	-28.84**	-17.15***	-24.66***	116.67***	22.22	L17xT2	-7.79	-10.79**	-19.26***	100.00**	11.11
L6xT1	-26.64**	-2.12	1.01	66.67*	22.22	L18xT1	-14.14	-0.39	-1.01	83.33*	22.22
L6xT2	-18.86*	-6.55	-5.41	83.33*	33.33*	L18xT2	-48.03***	-9.63*	-18.92***	100.00**	22.22
L7xT1	-23.25*	2.50	2.03	66.67*	44.44**	L19xT1	-43.31***	-7.51*	-18.24***	33.33	44.44**
L7xT2	-19.52*	-8.29*	-13.51**	50.00	22.22	L19xT2	-36.07***	-9.25*	-24.66***	100.00**	22.22
L8xT1	-22.37*	2.89	3.72	116.67***	33.33*	L20xT1	-36.18***	-3.28	-6.08	116.67***	22.22
L8xT2	-3.40	1.16	2.03	100.00**	22.22	L20xT2	-38.16***	-11.56**	-18.24***	150.00***	44.44**
L9xT1	-12.50	-10.21**	-13.51**	83.33*	0.00	L21xT1	-33.66***	-8.67*	-5.41	33.33	33.33*
L9xT2	-22.59*	-7.32*	-12.50*	16.67	22.22	L21xT2	-29.38**	-9.44*	-19.93***	66.67*	22.22
L10xT1	-36.51***	-9.25*	-12.50*	83.33*	55.56***	Minimum	-78.18	-38.54	-42.91	0.00	0.00
L10xT2	-25.33**	-8.09*	-10.14*	83.33*	44.44**	Maximum	-3.40	2.89	3.72	150.00	77.78
L11xT1	-39.47***	-12.52**	-14.86**	83.33*	55.56***	CD,0.05	1.65	18.99	13.85	0.97	0.66
L11xT2	-26.65**	-11.37**	-17.57***	33.33	22.22	CD,0.01	2.20	25.36	18.51	1.29	0.88
L12xT1	-34.65***	-7.72*	-5.07	50.00	11.11	CD,0.001	2.89	33.22	24.24	1.69	1.15
L12xT2	-40.24***	-10.41**	-23.31***	50.00	0.00						

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Table7. Standard heterosis (SH) for traits that were not included in the across location heterosis determination of the 42 F1hybrids obtained by LxT and evaluated at Arsi-Negele in 2017 (best check was Jibat).

Code	%GY	%PH	%EH	%TLB	Code	%GY	%PH	%EH	%TLB
L1xT1	-40.22*	-30.79***	-40.45***	16.67	L13xT1	-32.25*	-31.36***	-44.38***	-25.00
L1xT2	-9.77	-17.23***	-29.21***	-25.00	L13xT2	-17.10	-21.47***	-40.45***	-8.33
L2xT1	-22.48	-25.99***	-41.01***	0.00	L14xT1	1.95	-1.41	-5.62	-8.33
L2xT2	-46.25**	-31.64***	-39.88***	8.33	L14xT2	-23.45	-15.25**	-21.91**	-16.67
L3xT1	-11.40	-15.54**	-25.28***	8.33	L15xT1	-26.22	-16.67**	-28.65***	-8.33
L3xT2	-15.31	-10.73*	-19.10*	-16.67	L15xT2	-1.14	-11.86*	-21.91**	-16.67
L4xT1	-31.76*	-25.99***	-34.83***	-25.00	L16xT1	1.95	-7.34	-11.24	0.00
L4xT2	-8.96	-24.58***	-41.57***	-33.33*	L16xT2	-20.36	-25.42***	-42.13***	-16.67
L5xT1	25.90	-8.76	-17.42*	-16.67	L17xT1	-10.59	-9.60	-8.43	-16.67
L5xT2	5.70	-11.86*	-24.16**	-25.00	L17xT2	-14.33	-20.05***	-27.52***	-16.67
L6xT1	-18.57	-1.41	-5.62	-8.33	L18xT1	14.50	-5.93	-9.55	-33.33*
L6xT2	1.79	-10.45*	-10.11	-25.00	L18xT2	-1.63	-13.56**	-28.09***	-25.00
L7xT1	33.88*	8.76	16.85*	-33.33*	L19xT1	26.38	-3.95	-6.18	-25.00
L7xT2	1.47	-9.60	-16.29*	-33.33*	L19xT2	-4.07	-5.08	-17.98*	-25.00
L8xT1	50.81**	5.93	5.06	-41.67**	L20xT1	5.54	-1.98	-2.81	-16.67
L8xT2	46.58**	-1.69	-0.56	-33.33*	L20xT2	-23.62	-12.59*	-24.719**	-25.00
L9xT1	-16.29	-6.21	-7.87	-16.67	L21xT1	-18.73	-10.73*	-15.17*	-25.00
L9xT2	-7.82	-7.91	-14.60*	-16.67	L21xT2	-14.98	-12.15*	-23.03**	-41.67**
L10xT1	-15.47	-9.60	-21.35**	-33.33*	Minimum	-46.25	-31.64	-44.38	-41.67
L10xT2	12.21	-8.47	-15.73*	-25.00	Maximum	50.81	8.76	16.85	16.67
L11xT1	-44.46**	-12.99**	-20.22**	-25.00	CD,0.05	1.93	17.16	12.79	0.85
L11xT2	5.05	-11.58*	-18.54*	-33.33*	CD,0.01	2.57	22.93	17.09	1.14
L12xT1	-3.75	-7.63	-5.06	-25.00	CD,0.001	3.37	30.02	22.38	1.49
L12xT2	-13.84	-9.04	-25.28***	-41.67**					

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241 **Table 8. Standard heterosis (SH) for traits that were not included in the across location heterosis**
 242 **determination of the 42 F1hybrids obtained by LxT and evaluated at Kulumsa in 2017 (best**
 243 **check was Jibat).**

Code	%GY	%LFANG	%LFPP	Code	%GY	%LFANG	%LFPP
L1xT1	-47.11***	-33.33***	1.13	L13xT1	-55.52***	-21.05**	-3.53
L1xT2	-21.19*	-29.83***	2.33	L13xT2	-19.78*	-36.84***	3.53
L2xT1	-17.86	-29.83***	-3.53	L14xT1	-18.04	-31.58***	11.71**
L2xT2	-48.34***	-22.80***	5.86	L14xT2	-16.73	-14.04*	3.53
L3xT1	-43.78***	-40.36***	9.38*	L15xT1	-14.62	-24.57***	8.19
L3xT2	-23.99*	-40.36***	9.38*	L15xT2	-5.78	-19.31**	5.86
L4xT1	-50.08***	-21.05**	2.33	L16xT1	-20.05*	-26.32***	8.19
L4xT2	-21.28*	-35.09***	1.13	L16xT2	-24.34*	-22.80***	-1.20
L5xT1	-13.92	-49.12***	7.06	L17xT1	-15.41	-26.32***	11.71**
L5xT2	-19.44*	-43.85***	12.91**	L17xT2	-32.49**	-22.80***	7.06
L6xT1	-13.05	-17.54**	10.58*	L18xT1	-16.64	-21.05**	15.24***
L6xT2	-4.20	-33.33***	5.86	L18xT2	-12.43	-29.83***	4.66
L7xT1	6.57	-21.05**	8.19	L19xT1	4.73	-24.57***	9.38*
L7xT2	-23.38*	-38.59***	-2.40	L19xT2	-17.43	-24.57***	8.19
L8xT1	-4.38	-24.57***	15.24***	L20xT1	-21.19*	-24.57***	10.58*
L8xT2	-2.01	-31.58***	4.66	L20xT2	-26.97**	-29.83***	8.19
L9xT1	-22.85*	-17.54**	9.38*	L21xT1	-12.43	-17.54**	7.06
L9xT2	-8.32	-31.58***	10.58*	L21xT2	-5.52	-8.78	9.38*
L10xT1	-23.21*	-33.33***	5.86	Minimum	-55.52	-49.12	-3.53
L10xT2	-18.56	-31.58***	3.53	Maximum	6.57	-8.78	15.24
L11xT1	-24.43*	-21.05**	11.71**	CD,0.05	2.22	5.91	1.23
L11xT2	-22.42*	-24.57***	1.13	CD,0.01	2.96	7.90	1.64
L12xT1	-17.78	-29.83***	5.86	CD,0.001	3.88	10.35	2.14
L12xT2	-9.81	-36.84***	14.11				

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245 The other crosses with zero value of SH are also good for TLB providing their stability and
 246 other agronomic traits are better than the standard check. The high yielder crosses (L8xT1
 247 and L8xT2) showed significant tolerance to TLB than the standard check. The highest
 248 (16.67%) and lowest (-41.67%) SH for TLB was scored by L1xT1 and L21xT2, respectively
 249 (Table 7). In contrast to this result, Beyene (2016) reported positive and significant heterosis
 250 over the standard check. Berhanu (2009) also reported positive and negative SH over the
 251 check.

252 At Ambo, positive SH was obtained from all crosses for EAS. There were also crosses
 253 (L1xT2, L9xT1, and L12xT2) with zero SH for EAS which indicates these crosses were

254 good for EAS compared with the rest of the crosses. Positive and significant SH was
255 obtained from 16 crosses which shows that about 38% of the crosses had poor EAS. Most
256 crosses with significant SH were crossed that have T1 as one of their parents implying that
257 T1 was a poor EAS combined towards improving EAS than T2 (Table 6). The result of EAS
258 in this study was in line with the report of Beyene (2016). He reported positive and
259 significant heterosis over the best check.

260 At Kulumsa, all crosses had negative with highly significant SH for LFANG. This implies
261 that all crosses had a narrow-leaf angle compared to the standard check (Jibat). Duvick
262 (2005) also reported as leaves became more upright in the 1970s era in a comparison of
263 single crosses representing U.S. corn belt hybrids of three eras: 1930s, 1950s, and 1970s. The
264 narrowest (-49.12%) was recorded by L5xT1 but L21xT2, which manifested the highest SH
265 to the negative direction with the value of -8.78% for LFANG had relatively wider LFANG
266 (Table 8). Varieties with narrow leaves can help to economize the space and to exposed
267 leaves found at the lower side of the plant and due to this greater number of leaves can
268 access solar radiation. Due to LFANG reduction, leaf area can be increased and the higher
269 leaf area ultimately can increase photosynthesis which is the heart of efficient utilization of
270 resources by the plant (Huanga *et al.*, 2017). Almost all crosses showed positive SH for
271 LFPP except, for four crosses with negative but non-significant SH. Fourteen crosses showed
272 positive and significant heterosis. The highest (15.24%) and lowest (-3.53%) SH were shown
273 by L18xT1 and L2xT1, respectively (Table 8). Similarly, Berhanu (2009) reported positive
274 and negative SH over the check.

275 **3.1.2 Standard heterosis across locations**

276 In the combined analysis, SH estimation was computed for five traits which showed
277 significant MS for cross vs best check (AMH853). The estimated SH is presented in Table 9.

278 The highest SH of 20.8 % (1.67 t ha⁻¹ grain yield advantage over AMH853) for GY was
279 obtained from L8xT2, even though the difference was not significant (Table 9). This cross
280 can be released after carrying out further evaluation across locations. SH standard heterosis
281 ranged from -52.6% (L13xT1) to 20.8% (L8xT2) for GY. The five high-yielding crosses
282 across the three locations were L6xT2 (8.20), L7xT1 (9.13), L8xT1 (9.09), L8xT2 (9.67), and
283 L19xT1 (8.30) (data not shown). Similarly, Beyene (2016) and Abiy 2017 reported non-

284 significant SH. The two authors reported SH THAT ranged from -44.07% to -9.72% and
285 from -30.42 to 10.1, respectively. Berhanu (2009) obtained SH ranging between -28.17% to
286 20.33% and was able to identify one cross with significant SH.

287 For DT, almost all crosses had positive and significant SH except, L16xT2 (-0.19%) which
288 recorded negative SH. Similarly, most crosses had positive and significant SH for DS which
289 indicates the crosses were late in flowering compared with standard check variety for both
290 DS and DT. The value of SH ranged from -0.19% (L16xT2) to 16.10% (L1xT1) DT and
291 from 0.71% (L16xT2) to 13.57% (L1xT1) for DS (Table 9). In contrast to the current
292 finding, Berhanu (2009), Abiy (2017) and Patilet *al.* (2017) reported negative and significant
293 SH for DT and DS.

294 Only four crosses had positive SH for EL but none of them were significantly different.
295 These crosses were, L6xT1 (3.06%), L7xT1 (1.36%), L9xT1 (0.34%) and L9xT2 (6.80%).
296 The value of SH for EL ranged from -35.4% (L1xT1) to 6.8% (L9xT2). The other crosses
297 showed negative SH and a few of them showed significant differences. The result agrees
298 with the previous works of Berhanu (2009) and Beyene (2016). These authors reported SH
299 that ranged from -26.4% to 1.47% and from -16.76% -6.8%, respectively.

300 Only four crosses (L15xT2, L16xT2, L17xT2, and L21xT2) showed positive SH for TSW
301 across locations but all were not statistically significant. SH ranged from -40.82 % (L3xT1)
302 to 17.46 % (L17xT2) (Table 9). In contrast to the current finding, Berhanu (2009) and Patilet
303 *al.* (2017) reported crosses with a positive and significant difference. Berhanu reported SH
304 ranging from -29.32% to 10.87%. Patilet *al.* (2017) also reported SH ranging from 30.24% to
305 64.15% for 100 seed weight.

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Table 9. Standard heterosis (SH) for traits that were included in the across location heterosis determination of the 42 F1hybrids obtained by LxT and evaluated at Ambo, Arsi-Negele, and Kulumsa in 2017 (best check was AMH853).

Code	%GY	%DT	%DS	%EL	%TSW	Code	%GY	%DT	%DS	%EL	%TSW
L1xT1	-51.25***	16.10***	13.57***	-35.4***	-38.9***	L13xT1	-52.6***	14.98***	12.32***	-28.57**	-38.9***
L1xT2	-13.06	8.61***	6.60**	-17.01	-9.70	L13xT2	-21.29	6.92**	5.00*	-15.99	-10.39
L2xT1	-21.94**	7.11**	6.42**	-15.99	-12.37	L14xT1	-13.94	12.17***	9.64***	-20.40*	-20.6*
L2xT2	-51.08***	13.85***	11.96***	-26.70**	-38.4***	L14xT2	-13.61	7.11**	6.96**	-19.72*	-0.80
L3xT1	-29.84*	11.61***	8.92***	-21.08*	-40.82***	L15xT1	-12.07	9.92***	7.85***	-28.6**	-18.38
L3xT2	-8.68	6.74**	4.82*	-6.63	-16.12	L15xT2	-7.67	5.99*	4.64	-7.82	5.02
L4xT1	-47.73***	13.85***	11.96***	-33.3***	-37.8***	L16xT1	-13.42	4.86*	3.93	-14.96	-10.25
L4xT2	-18.67	6.36**	5.17*	-20.40*	-10.19	L16xT2	-20.04	-0.19	0.71	-13.61	3.34
L5xT1	-2.57	12.73***	11.07***	-15.99	-28.13**	L17xT1	-8.97	10.30***	7.32**	-11.90	-14.08
L5xT2	-7.58	8.05***	6.60**	-8.84	-11.07	L17xT2	-10.93	4.12**	3.04	-7.99	17.46
L6xT1	-9.93	9.55***	6.78**	3.06	-20.20*	L18xT1	1.59	6.17**	4.64	-13.61	-15.18
L6xT2	2.46	6.36**	5.71*	-3.40	-7.56	L18xT2	-13.42	5.24*	5.17***	-17.69	-8.72
L7xT1	14.11	8.98***	6.78**	1.36	-26.70**	L19xT1	3.71	8.05***	5.89***	-7.82	-11.73
L7xT2	-7.00	3.93	1.97	-8.16	-4.71	L19xT2	-11.90	2.06	1.79	5.44	-0.62
L8xT1	13.60	9.73***	7.14**	-9.52	-18.99	L20xT1	-11.28	10.48***	10.35***	-12.41	-8.83
L8xT2	20.82	4.87*	3.57*	0.00	-3.25	L20xT2	-22.18	6.74**	7.67**	-7.31	-1.19
L9xT1	-8.62	10.67***	7.67**	0.34	-25.44*	L21xT1	-12.37	11.98***	7.67**	-21.76*	-21.8*
L9xT2	-3.38	4.86*	4.82*	6.80	-8.77	L21xT2	-6.44	7.30**	6.25*	-4.76	5.89
L10xT1	-17.72	10.86***	8.57***	-0.34	-22.85*	Minimum	-52.62	-0.19	0.71	-35.37	-40.82
L10xT2	-4.19	3.93	2.68	-5.27	-8.81	Maximum	20.82	16.10	13.57	6.80	17.46
L11xT1	-26.86*	9.55***	7.50**	-15.99	-19.76	CD=0.05	1.91	4.06	4.45	3.08	71.89
L11xT2	-8.33	2.62	1.79	-2.38	-3.27	CD=0.01	2.52	5.37	5.87	4.07	94.99
L12xT1	-11.39	15.73***	11.78***	-23.29*	-24.58*	CD=0.001	3.13	6.67	7.29	5.05	117.97
L12xT2	-12.33	11.23***	8.92***	-18.19	-10.54						

310 **4. Conclusion**

311 The analysis of variance showed significant difference among tested genotypes for grain yield, yield
312 related, phenological, agronomic and morphological traits at individual locations. In combined
313 analysis across location, the result showed very highly significant difference among genotypes for
314 most of the traits considered in the study. The highly significant difference observed for genotype by
315 location and cross by location interaction highlights that the performance of the genotypes is
316 inconsistent across location. This indicates that these new hybrids which performed good but with
317 unstable performance across location should be considered for their suitability for specific location by
318 doing further investigation. Based on the mean grain yield pooled over the three locations six
319 crosses: L8xT2, L7xT1, L8xT1, L19xT1, L6xT2, and L18xT1 were found to be superior to
320 the best check (AMH853) by 20.82, 13.60, 14.11, 3.71, 2.46, and 1.59 %, respectively.
321 Generally, this study identified crosses that have a noticeable level of heterosis above the
322 recently released standard variety (AMH853). This study indicates the existence of better
323 newly developed crosses that are nutritionally balanced compared with the standard
324 commercialized check varieties. We recommend these well-performed crosses to be
325 considered for release following the remain steps need to be followed for varieties release.

326

327 **Authors' contributions**

328 GMM collected the data, performed the analysis, and developed the manuscript. ATC reviewed and
329 made editorial comments on the draft manuscript.

330

331 **Authors' information**

332 GMM is a plant breeder with more than 10 years of experience who has been involved in the
333 development of maize germplasm development with the national maize breeding program.
334 ATC(Ph.D.) is a senior scientist currently working in CIMMYT-Ethiopia and taking over the leading
335 research works that have been planned and implemented on maize improvement. He was a crop
336 process leader at the Ethiopian Institute of Agriculture Research.
337 YMS is one of maize breeder in the national research system. Currently he continues working as
338 maize breeder in the system.

339

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343

344 **Availability of data and materials**

345 Availability of data and materials – data can be requested from the first author.

346 **Declarations**

347 **Ethics approval and consent to participate**

348 The researchers have obtained permission from funding institutions CIMMYT and EIAR.
349 Accordingly, the information under this article had been developed in collaboration with CIMMY,
350 Ethiopian Institute of agriculture research investigators, and university instructors.

351 Competing interests – authors declare no competing interests.

352 **Consent for publication**

353 Consent for publication – all authors have read and approved the publication of this paper.

354 **Competing interests**

355 The authors declare that they have no competing interests.
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