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Mid-parent and Better Parent Heterosis Study on Highland Quality Protein Maize Hybrids in Ethiopia

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Determination of heterosis in maize hybrids is necessary for the identification of superior F1 hybrids for breeding programs. Therefore, this study was conducted to estimate the amount of mid parent (MPH) and better parent heterosis (BPH) for grain yield, yield-related, agronomic, and morphological traits. Hybrid development from fixed inbred lines is one of the strategies for the improvement of 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 hybrids were evaluated in two replications using alpha lattice during the 2017 cropping season at Ambo and, Arsi-Negele. Parental line trials consisting of 21 lines, two testers, and one conventional maize (CM) parent check (FS67) were established in two replications laid out using RCBD side by side with the hybrid trials at Ambo and Arsi-Negele. At Ambo, almost all crosses showed positive and significant BPH except three crosses (L1xT1, L4xT1, and L13xT1). The maximum BPH (276.2%) was obtained from L17xT2. Similarly, at Arsi-Negele, most of the crosses had positive and significant BPH except for five crosses for BPH which are showing negative heterosis. The highest BPH was obtained from L10xT2 at Arsi-Negele. Generally, the high yielding crosses had reasonable BPH. Based on the result promising crosses and lines were identified. Some of the crosses showed good performance in terms of heterosis against the mid parent and better parent:

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L17xT2 (329.88% MPH, 276.18% BPH), L3xT2(320.05% MPH, 273.91%BPH), and L19xT2(2802.57% MPH, 247.31% BPH) at Ambo, whereas at Arsi-Negele L10xT2 (128.38% MPH, 111.27%BPH) and L11xT2(115.33% MPH, 98.00% BPH) showed the higher heterosis compared with the mid parent and better parent. Crosses that showed best yield performance were: L8xT2, L7xT1, L8xT1, L19xT1, L6xT2, and L18xT1. These crosses should be reconsidered for further evaluation and possible release.

Keywords: Better parent heterosis; mid parent heterosis; quality protein maize.

1. INTRODUCTION

Maize breeders need to determine the genetic diversity of inbreeds because it facilitates the identification of those that would produce crosses possessing high levels of heterosis [1]. The information facilitates the development of high-yielding hybrids without testing all possible hybrid combinations among the potential parents available in a hybrid program. The phenomenon of heterosis was defined by Shull [2] as "the interpretation of increased vigor, size, fruitfulness, speed of development, resistance to disease and insect pests, or climatic rigor of any kind manifested by crossbred organisms as compared with corresponding inbreeds, as the specific results of unlikeness in the constitution of the uniting parental gametes". Falconer and Mackay [3] defined it as the difference between the hybrid value for one trait and the mean value of the two parents for the same trait. According to Miranda [4], heterosis is the genetic expression of the superiority of a hybrid over its parents. Three types of estimation of heterosis are reported in the literature; namely, mid-parent or average heterosis, which is the increased vigor of the F1 over the mean of two parents; and high-parent or better-parent heterosis, which is the increased vigor of F1 over the better-parent [5] and standard heterosis [6-8]. Heterosis is usually considered synonymous with hybrid vigor [9]. Heterosis, or hybrid vigor, refers to the phenomenon in which the offspring of two inbred parents exhibit phenotypic performance beyond the mid-parent or better parent used to generate the hybrid [10]. Grain yield in maize is expected to exhibit heterosis as a consequence of partial to complete dominance of genes controlling the trait [4]. Three major theories, *viz*. dominance, overdominance, and epistasis, have been put forward to explain the mechanisms underlying the phenomena of heterosis. However, it is generally accepted that heterosis, to a large extent, is due to overdominance gene action [11]. On the other hand, the expression of heterosis also depends on the level of genetic divergence between parents; i.e., differences in allele frequencies are necessary for the expression of heterosis. For that reason, the expression of heterosis is expected to be lower in crosses between broad base open-pollinated populations [4].

Heterosis is important in maize breeding and depends on the level of dominance and differences in gene frequency [3]. The manifestation of heterosis depends on the genetic divergence of the two parental varieties [12]. Low grain yield heterosis were observed for crosses among genetically similar germplasms and for crosses among broad genetic base germplasms [13]. Higher levels of heterosis were seen with increased divergence within a certain range, but that heterosis declined in extremely divergent crosses [14]. Genetic divergence of the parents is inferred from the heterotic patterns manifested in a series of crosses [4,12].

Heterosis in maize has been investigated extensively. Two main ways of expressing hybrid advantage have been used. First, it has been expressed as mid-parent advantage, the increase in yield or other character of the hybrid compared to the mean of the parents, and is an estimate of the mean directional dominance (potence) of the alleles for a given character. Second, it has been expressed as heterobeltiosis (better parent heterosis), the increase in yield or other character of the hybrid compared to that of the better-parent for the character. Heterobeltiosis implies that there is dispersion for dominant alleles between the parents which may increase or decrease the character (Lakshmikant et al., 2011). Hallauer and Miranda [12] reported that mid-parent heterosis ranged from -3.6% to 72.0%, while high-parent heterosis ranged from -9.9% to 43.0% for maize. Maize has attained the highest levels of production in the temperate areas of the world employing modern agricultural techniques. Surprisingly, the magnitude of heterosis has not been changed during the hybrid era in tropical areas compared to temperate because, in most tropical countries, maize is grown as a rainfed crop in the hot

season, under varying conditions of moisture, generally subject to periodic and erratic drought and/or excess of water at different stages of the growth cycle, without effective weed and pest control, and usually under low-fertility conditions. In general, it is grown as a subsistence crop, with very low levels of management and little input [15], even though mean commercial maize grain yield has substantially increased during this time [16]. Birhanu [6] reported an estimate of heterosis ranging from 28.95 to 202.34% over mid-parent and 16.97 to 175.46 % over the better parent grain yield from crosses generated from LxT mating design.

The development of hybrid varieties has played a great role in improving food and feed supplies. Food and feed supplies would unquestionably be greatly reduced if only nonhybrids were available to the producer [9]. Hybrid varieties are the first filial generations (F1) from crosses between two or more pure lines, inbreeds, open-pollinated varieties, clones, or other populations that are genetically dissimilar [11]. The development of the maize hybrids began in the early 1900s [12,17-19]. According to Singh [11], most of the commercial hybrid varieties are F1's from two or more inbreeds. The success of hybrid maize development depends on the capacity of the breeding program to rapidly develop lines that combine well and identify superior heterotic combinations to maximize the vigor of the hybrid [20]. An inbred line is a nearly homozygous line obtained through continuous inbreeding of cross-pollinated species with selection accompanying inbreeding [11].

Similar to the CM, QPM hybrids proved to yield more grains than open-pollinated QPM cultivars, but the mean grain yield does not differ for a single, three-way, and double-cross QPM hybrid [21]. The broader genetic constitution of three-way and double-cross hybrids might have helped them to buffer the extreme environmental diversity of the environment better than single crosses [21]. In a different trial, Pixley and Bjarnason [21] also observed a QPM hybrid exceeding a normal endosperm hybrid check by an average of 14% for grain yield, and 48% for tryptophan (Trp) concentration in grains, and 60% for Trp concentration in protein. Birhanu [6] evaluated tester crosses of white QPM and CM inbred lines and reported higher grain yield, heterosis overall, mid and better parents, and some of the crosses over the standard checks. Similarly, Beyene [7] reported higher heterosis in diallel crosses evaluated at Bako, Ethiopia. In this study, the aim was to estimate better parent and mid-parent heterosis of the crosses.

2. MATERIALS AND METHODS

2.1 Study Sites

The study was conducted at two locations in the highland agroecology of Ethiopia, including; Ambo and Arsi-Negele Agriculture Research Centers during the 2017 main cropping season.

2.2 Experimental Materials

From the 21 inbred lines and two testers, 42 F1 hybrids were generated at Ambo Highland Maize Breeding Program (AHMBP). The 42 F1 hybrids along with three standard checks: one QPM (AMH852Q) and two CM (Jibat and AMH853), designated as hybrid checks, were tested.

2.3 Experimental Design and Crop Husbandry

The hybrid trial was laid out using an alpha lattice design consisting of one-row plots replicated twice. Randomized complete block design (RCBD) was used for testing the performance of the parental lines. For the hybrid trial, each plot consisted of a 5.25 m long row with 0.75 and 0.25 cm interrow, and intra-row spacing. For the inbred line trial, each plot consisted of a 3.75 m long row with 0.75 and 0.25 cm interrow, and intra-row spacing. The plot was hand-planted with two seeds per hill and later was thinned to one plant per hill to attain the

Table 1. Latitude, longitude, altitude (m), long-term annual rainfall (mm), maximum temperature (MaxT) (^{o}C), minimum temperature (MinT) (^{o}C), soil type, and soil pH of the study sites

Site	Latitude	Longitude	Altitude (m)	Annual rainfall (mm)	MaxT ^{o}C	MinT ^{o}C	Soil type	pH
Ambo	8˚ 57ˈ N	38˚ 7ˈ E	2225	1115	25.5	11.7	Heavy clay	7.8
A.Negele	7˚19ˈ N	38˚ 39ˈ E	1960	886	26.0	9.1	clay loam	6.5-7.5

final plant density of 53,333 plants per hectare. Diammonium phosphate (DAP) fertilizer was applied at planting at the rate of 150 kg ha^{-1} while 200 kg ha^{-1} of urea was applied in partition 1/3 at planting, 1/3 at knee height, and 1/3 at flowering at Ambo. At Arsi-Negele, 100 kg ha^{-1} DAP and 150 kg ha^{-1} urea fertilizer were applied based on the site recommendation following the same time of application mentioned for Ambo above. The rest of the field management practices are applied based on recommendations for each site.

2.4 Data Collected

Data on morphological, phenological, yield and related yield traits were recorded and presented as follows. Days to tasseling (DT), Days to silking (DS), Anthesis, silking interval (ASI), Days to maturity (MD), Plant aspect (PAS), Disease score: turcicum leaf blight (TLB), and common leaf rust (CLR), Ear aspect (EAS), Number of ears per plant (EPP), Kernel Modification (MOD) Grain yield (GY), Number of leaves per plant (LFPP), Number of leaves above upper most ear per plant (LFAE), Number of leaves bellow upper most ear per plant (LFBE), Leaf angle (LANG), Leaf length (LL), Leaf width (LW), Leaf area (LFAR), Plant height (PH), ear height (EH), ear length (EL), Ear diameter (ED), Number of kernel rows (NKR), Number of kernels per row (KPR), Thousand seed weight (TSW), Biomass (BIOM) and Harvest index (HI) and Grain Yield (GY). For the following traits; 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 scoring), and MOD= kernel modification (1-5 scoring), the lower value (e.g., the value 1) indicates good performance of the genotype whereas the higher value (e.g., 5) indicates that the specific genotype performs poor for that trait.

Table 2. List of QPM parental inbred lines used to generate single-cross hybrids using line x tester mating design and standard checks

Cod	Pedigree	Tryptophan (%)
L1	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-1-B-B-B-#	0.056
L2	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-2-6-B-B-#	0.062
L3	(CLQRCWQ50/CML312SR)-2-2-1-BB-1-B-B-B-#	0.077
L4	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-1-B-B-B-#	0.077
L5	([NAW5867/P49SR(S2#)//NAW5867] F#-48-2-2-B*/CML511) F2)-B-B-39-1-B-#	0.066
L6	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-9-1-B-#	0.063
L7	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-35-2-B-#	0.063
L8	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-44-2-B-#	0.069
L9	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-18-2-B-#	0.086
L10	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-30-1-B-#	0.080
L11	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-35-2-B-#	0.109
L12	(CML395/(CML395/[NAW5867/P49SR(S2#)//NAW5867] F#-48-2-2-B*4) F2)-B-B-30-1-B-#	0.076
L13	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-2-6-B-B-#	0.060
L14	(CML395/(CML395/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2)-B-B-46-1-B-#	0.063
L15	(CML395/(CML395/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2)-B-B-50-1-B-#	0.062
L16	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-10-3-B-#	0.061
L17	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-14-1-B-#	0.073
L18	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-29-1-B-#	0.060
L19	(CML395/(CML395/CML511) F2)-B-B-7-2-B-#	0.060
L20	(CML395/(CML395/CML511) F2)-B-B-11-2-B-#	0.066
L21	(CML395/(CML395/CML511) F2)-B-B-37-1-B-#	0.061
T1	CML144	
T2	CML159	

Better-parent heterosis (BPH) and mid-parent heterosis (MPH) in percent were calculated for those parameters that showed significant differences among crosses following the method suggested by Falconer and Mackay [3]. In addition, MPH and BPH were done only for those traits that had significant MS for cross vs parents and significant MS between crosses as criteria of selection. To consider traits for combined analysis for MPH and BPH, the cross -x- location for interaction should be nonsignificant as an additional criterion. For traits that had significant

cross-x-location interaction, the traits were considered for MPH and BPH for each location.

$$\text{Mid-parent heterosis (MPH)} = \frac{\text{F1}-\text{MPV}}{\text{MPV}}\ x\ 100$$

$$\text{Better parent heterosis (BPH)} = \frac{\text{F1}-\text{BPV}}{\text{BPV}}\ \text{x}\ 100$$

Where F1= mean value of the cross, MPV = the mean value of the two parents (lines and tester), BPV = the mean value of the better parent

The test of significance of heterosis (the numerator in each equation before multiplying by 100) was determined using the t-test. The critical differences (CD) for testing the significance of MPH, and BPH were calculated using the following formulas:

Critical differences for heterosis over MPH:

$$\text{CD (MPH)} = \sqrt{3MSe/2r}\ \text{x t}$$

Critical difference for heterosis over better parent heterosis

$$\text{CD (BPH)} = \sqrt{2MSe/r}\ \text{x t}$$

Where MSe is the error MS, r is the number of replications, and t is the table value at 0.05, 0.01and 0.001, CD is Critical Difference, MP is mid-parent, BP is the better parent, t -value in the formula is not included in the square root. The absolute values of the relevant heterosis were tested against this critical difference.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The combined analysis of variance (ANOVA) for the hybrid showed highly significant differences among crosses for Grain Yield (GY), Days to Tasseling (DT), Day to Silking, (DS) Plant Height (PH), Anthesis Silking Interval (ASI), Days to Maturity (DM), Plant Height (PH, Ear Height (EH), Ear Aspect (EA). Plant Aspect (PA), Ear Per Plant (EPP), Ear Length (EL), Kernel Per Row (KPR), Number of Kernel Row per plant (NKR), Ear Diameter (ED), Thousand Seed Weight (TSW), Biomass yield (BIOM), Number of Leaves Per Plant (LFPP), and Number of Leaf Bellow Ear (LFBE) in combined analysis whereas, the difference between crosses was non-significant for Kernel modification (MOD), Common Leaf Rust (CLR), Turcicum Leaf Blight (TLB), Harvest Index (HI), Leaf Angle (LANG), Leaf Length (LL), Leaf Width (LW), Leaf Area (LEAR), and Number of Leaf above Ear (LFAE) (Table 4). A similar result was also reported by (Birhanu, 2009). The cross-mean squares were highly significant (P< 0.01) for all traits except GY and LFPP (Table 4). The cross*location effect was highly significant for GY, MD, PH, EH, TLB, and PAS, also significant at p< 0.05 level for LFPP and LFBE but non- significant for the rest of the traits (Table 4).

At both locations the mean square of the cross was significant for GY, DT, ASI, MD, PH, EH, EPP, EL, KPR, ED, TSW, and BIOM but again at both locations the difference was nonsignificant for CLR, NKR, LANG, LW, and LEAR (Table 3). The mean square was significant for DS, MOD, EAS, PAS, LL, LFPP, LFAE, and LFBE whereas, the difference was nonsignificant for TLB and HI only at Ambo. The mean square of the cross for TLB and HI, the difference among crosses was significant only for Arsi-Negele and nonsignificant for DS, MOD, EAS, PAS, LL, LFPP, LFAE and LFBE (Table 3).

3.2 Mid-parent and Better-parent Heterosis

The mid-parent and better-parent heterosis were computed for individual locations for traits showing significant mean square between crosses. Values of mid-parent heterosis (MPH) and better-parent heterosis (BPH) were estimated for 18 traits at Ambo and 14 traits at Arsi-Negele. The results of MPH and BPH is presented in Tables 5 and 6 for individual locations.

At Ambo, for GY, MPH and BPH ranged from -34.13% (L1xT1) to 329.89% (L17xT2) and -41.26% (L1xT1) to 276.18% (L17xT2), respectively. Most of the crosses except L2xT2 had a positive and significant difference for MPH. Similarly, for BPH, most of the crosses except L2xT1, L2xT2, L3xT1 and L14xT1 had positive values and significant differences for GY. Some crosses had negative heterosis for both MPH and BPH (Table 5). At Arsi-Negele, from 42 crosses, 39 of them had positive heterosis. Out of the 39 crosses that had positive MPH, 25 of them showed significant differences. For BPH, 37 crosses had a positive value of heterosis and out of these crosses, the difference was significant for 17 crosses. The magnitude ranged from -10.36% (L15xT1) to 128.38% (L10xT2) and from -25.87% (L11xT1) to 111.27% (L10xT2) respectively for MPH and BPH.

Table 3. Mean square of a table for crosses tested at each location in 2017

Location			Mean Square								
Ambo	**SV**	**DF**	**GY**	**DT**	**DS**	**ASI**	**MD**	**PH**	**EH**	**Mod**	**CLR**
	rep	1	7.72**	0.43	0.19	0.05	3.86	786.29**	340.01**	1.86**	0.00
	Cross	41	4.90***	22.97***	15.98***	4.94***	3.60*	1276.53***	606.06***	0.48*	0.00
	Error	41	0.71	2.92	3.17	1.44	1.83	72.40	40.84	0.24	0.00
			TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW
	rep	1	0.00	1.31**	0.76**	0.31*	9.56	1.19	26.86	0.03	8893.28**
	Cross	41	0.05	0.40***	0.34***	0.16***	9.59***	2.19	35.77**	0.24***	6373.16***
	Error	41	0.05	0.11	0.07	0.07	3.20	1.39	13.33	0.04	1168.31
			BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE
	rep	1	73.90*	2682.96***	28.58	10.71	1.11	12033.58	31.77***	0.11	38.67***
	Cross	41	21.75**	209.51	12.73	71.28***	0.59	9848.86	2.92***	0.47*	1.84***
	Error	41	14.17	192.14	10.98	41.54	0.72	11302.14	1.01	0.37	0.59
Arsi-Negele	**SV**		**GY**	**DT**	**DS**	**ASI**	**MD**	**PH**	**EH**	**Mod**	**CLR**
	rep	1	9.51**	36.01*	33.44	0.05	20.01***	2690.53***	762.01***	0.19	1.44*
	Cross	41	3.53***	27.13***	17.12*	4.88	3.49***	542.65***	308.64***	0.80	0.38
	Error	41	0.95	7.52	9.49	2.93	1.26	71.92	41.99	1.15	0.29
			TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW
	rep	1	2.67***	3.44**	0.05	0.07*	14.58**	40.04***	14.86	1.66***	133.21
	Cross	41	0.32*	0.43	0.30	0.04***	5.42***	2.78	29.31***	0.20***	5928.86***
	Error	41	0.17	0.28	0.22	0.02	1.70	2.19	11.67	0.06	1912.74
			BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE
	rep	1	9.51*	70.59	16.01	838.11**	9.33**	114635.53**	1.81	0.08	2.56
	Cross	41	3.84*	208.77*	31.37	67.88	0.47	6518.12	0.80	0.20	0.52
	Error	41	1.70	105.09	59.64	85.94	0.86	9657.96	1.01	0.20	0.64

= significant at 0.05 probability level, **= significant at 0.01probabilty level and * = significant at 0.001probabilty level, DF = Degree of freedom, GY = Grain yield (t/ha), DT = Days to tasseling (days), DS = Days to silking (days), ASI = Anthesis Silking Interval (days), MD = Days to Maturity (days), PH = Plant Height (cm), EH = Ear Height (cm), MOD = Kernel Modification (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 scoring), EPP = Ear Per Plant (number), EL= Ear Length (cm), NKR = Number of Kernel Rows (number), KPR = Kernel Per Row (number), ED = Ear Diameter (cm), TSW = Thousand Seed Weight (gram), BIOM = Biomass yield (t/ha), HI = Harvest Index (%), LFANG = Leaf Angle (degree), LL = Leaf Length (cm), LW = Leaf Width (cm), LFAR = Leaf Area (cm2), LFPP =Leaf Per Plant (number), LFAE = Leaf above upper most ear (number), LFBE = Leaf bellow upper most ear (number)*

Table 4. Mean square of a table for combined across three locations for tested crosses in 2017

Source of variation	Mean Square									
	DF	**GY**	**DT**	**DS**	**ASI**	**MD**	**PH**	**EH**	**MOD**	**CLR**
Rep(location)	2	8.62***	18.22*	16.82	0.05	11.94***	1736.16***	551.01***	1.03	0.72**
Location	1	1.35	4190.01***	2251.34***	298.67***	21240.0***	219170.38***	109140.03***	6.29**	63.15***
Cross	41	6.37***	43.74***	27.34***	7.28***	4.34***	1647.61***	837.71***	0.84	0.19
Cross*location	41	2.07***	6.36	5.77	2.54	2.76**	171.59***	76.99**	0.45	0.19
Error	82	0.83	5.22	6.33	2.18	1.54	72.26	41.41	0.69	0.14
	DF	TLB	EAS	PAS	EPP	EL	NKR	KPR	ED	TSW
Rep (location)	2	1.34***	2.38***	0.40	0.19*	12.07**	20.62***	20.86	0.85***	4513.25
Location	1	73.34***	11.79***	14.88***	2.00***	181.60***	168.00***	517.44***	2.16***	395968.30***
Cross	41	0.16	0.58***	0.33***	0.17***	12.57***	3.71**	49.26***	0.39***	10680.30***
Cross*location	41	0.21**	0.25	0.32***	0.04	2.44	1.27	15.82	0.07	1621.71
Error	82	0.11	0.19	0.15	0.041	2.45	1.79	12.50	0.05	1540.52
	DF	BIOM	HI	LANG	LL	LW	LFAR	LFPP	LFAE	LFBE
Rep (location)	2	41.71**	1376.78***	22.29	424.41***	5.22**	63334.47**	16.79***	0.10	20.62***
Location	1	1184.13***	23457.31***	1904.60***	66853.73***	509.85***	11163485.6***	0.001	63.96***	66.88***
Cross	41	15.65**	208.82	20.82	78.29	0.69	10073.23	2.15**	0.35	1.28**
Cross*location	41	9.95	209.48	23.27	60.86	0.38	6293.77	1.58*	0.33	1.08*
Error	82	7.94	148.61	35.31	63.74	0.79	10480.04	1.01	0.29	0.61

= significant at 0.05 probability level, **= significant at 0.01probabilty level and * = significant at 0.001probabilty level, DF = Degree of freedom, GY = Grain yield (t/ha), DT = Days to tasseling (days), DS = Days to silking (days), ASI = Anthesis Silking Interval (days), MD = Days to Maturity (days), PH = Plant Height (cm), EH = Ear Height (cm), MOD = Kernel Modification (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 scoring), EPP = Ear Per Plant (number), EL= Ear Length (cm), NKR = Number of Kernel Rows (number), KPR = Kernel Per Row (number), ED = Ear Diameter (cm), TSW = Thousand Seed Weight (gram), BIOM = Biomass yield (t/ha), HI = Harvest Index (%), LFANG = Leaf Angle (degree), LL = Leaf Length (cm), LW = Leaf Width (cm), LFAR = Leaf Area (cm2), LFPP =Leaf Per Plant (number), LFAE = Leaf above upper most ear (number), LFBE = Leaf bellow upper most ear (number)*

This result is in line with the findings of Birhanu (2009) and Beyene (2016). They reported positive MPH and BPH with significant differences in grain yield in most of the crosses. However, the maximum MPH and HPH heterosis with a respective magnitude of 329.89% and 276.18% recorded in this study was lower than that of 508% and 473% reported by Beyene (2016) for crosses formed from fixed line of different origins mated using the diallel mating design. Whereas the maximum value obtained in the current experiment was higher than the maximum magnitude of MPH and BPH reported (MPH, 202.34% and BPH,175.46%) by Birhanu, [6] from test crosses. The high level of heterosis observed in the study is mainly due to the use of inbred parents when crossed to recover their vigor and yield ability lost during inbreeding.

The difference in the magnitude of heterosis in different reports involving inbred parents is mainly attributed to the stage of inbreeding of the parents, the environmental conditions to which they were exposed, and the performance of the parental inbred lines [6]. According to Reif et al. [22], heterosis expression is in the range between 100% to 200% of grain yield over the parents, but in this study, there were crosses with high heterosis values in both MPH and BPH as compared with the range suggested by Reif et al., [22]. The crosses which had higher heterosis were: L6xT2 (222.07%), L7x T2 (243.58%), (L9XT2 (221.52), L10xT2 (208.31%), L11xT2 (249.27%), L14xT2 (240.52%), L17xT2 (329.89%), L19xT2 (282.57%) and L21xT2 (200.06%) over the mid-parent. L3xT2 (273.91%), L11xT2 (210.87%), L14xT2 (203.17%), L17xT2 (276.18%) and L19xT (2247.31%) over better-parent (Table 5). Other crosses had a value of heterosis between the minimum (100%) and maximum (200%). At Arsi-Negele, the following crosses had a value of heterosis between the range value of heterosis (100% to 200%) suggested by Reif et al. [22]. These crosses are: L7xT2 (104.15%), L8xT2 (102.56%) L10xT2 (128.38%), L11xT2 (115.53%), L18xT2 (102.20%) and L19xT2 (109.20%) over mid-parent and L10xT2 (11.27%) over the better-parent (Table 6).

At Ambo for DT, 10 crosses showed negative MPH and from these crosses, only one cross (L16xT2) showed a significant difference. Of the remaining crosses which had positive MPH, nine of them showed significant differences over the mid parent. The value of MPH for DT ranged from -3.12% (L16xT2) to 5.41% (L12xT1). For BPH, all crosses showed significant differences in the negative direction except three crosses which are showing nonsignificant variation. A similar result like DT was shown by crosses for both MPH and BPH by DS. The value for DS ranged from -12.19% (17 x T2) to 0.23% (L1xT1) for MPH and from -14.66% (L18xT1) to -2.75% (L13xT1) for BPH (Table 5). Most of the crosses showed negative MPH and BPH (Table 5 and 6) also showed negative SCA effects for DT and DS (data not shown). Similarly, Birhanu [6] reported negative MPH and BPH from most of crosses with negative SCA effects for DT and DS. This indicates parents were delayed in flowering compared to their offspring for DS and DT. At Arsi-Negele, a similar trend was observed for DT and DS for MPH and BPH with a slight difference in the magnitude of heterosis and level of variation (Table 6). The magnitude of MPH and BPH was smaller compared to the difference in Ambo. This indicates that parents were late in flowering at Ambo compared to crosses, whereas, at Arsi-Negele, crosses and parents were flowered relatively nearly on the same day compared with the result from Ambo. Similar to this study finding, Birhanu [6] and Beyene [7] observed significant negative heterosis in most of the crosses for MPH.

At Ambo, all crosses showed positive and significant MPH and BPH for both PH and EH. Similarly, most of the crosses showed positive and significant MPH and BPH with some exception of crosses showing negative MPH and BPH against their parents with nonsignificant variation in Arsi-Negele (Tables 5 and 6). The MPH for PH ranged from 21.29% (L1xT1) to 91.61% (L8xT2) whereas for BPH the value ranged between 10.76% (L1xT1) to 84.72% (L7xT1). MPH ranged from 47.85% (L3xT1) to 130.30 % (L10xT2) and for BPH, the value ranged from 30.0% (L4xT1) to 115.71% (L7xT1) for EH, respectively (Table 5). At Arsi-Negele, MPH and BPH values ranged from 8.86% (L15xT1) to 61.43% (L7xT1) and from -3.91% to 59.09% for the same crosses respectively for PH. These crosses also showed the lowest and highest MPH and BPH with the magnitude ranging from -2.68% to 93.49% and from -21.12% to 80.87% for EH, respectively (Table 6). The positive and significant heterosis observed for PH is evidence of the increase in plant vigor upon crossing. This result is in agreement with the previous report [6,7,23]. Beyene reported the range value from 36.0% to 115.0% for EH and from 25.7% to 95.2% for PH against mid-parents, he also reported the value of BPH ranged from

22.8% to 97.5% and 13.5 to 74.9% for EH and PH, respectively.

At Ambo, most of the crosses showed Signiant differences to the negative direction for MPH for ASI. Eight crosses showed positive and highly significant heterosis. This indicates that these crosses had substantially higher number of days than the average value of parents and their offspring. The values ranged from -700% to 400% obtained from L13xT1 and L13xT2, respectively. For BPH, most of the crosses had a negative value of heterosis and these crosses showed significant differences. The range value -116.67% to 200.0% BPH was recorded in L9xT1 and L13xT1 (Table 5). At Arsi-Negele, most of the crosses had positive MPH and five of them showed significant differences. Three crosses showed zero MPH heterosis, indicating that the average value of the parents was equal to the average value for crosses for ASI. Whereas some crosses showed negative heterosis but none of the crosses showed significant difference over the mid-parent value, this means the mid parent ASI values were higher than offspring values. Regarding BPH, 24 crosses showed negative BPH and from these crosses, only one cross (L14xT1) showed significant BPH, indicating that the crosses had shorter ASI relative to better parent ASI. There were three crosses (L8xT1, L10xT1, and L12xT1) that showed zero heterosis over better parent. The remaining crosses showed positive BPH, but the differences were not significant. The lowest (-55.56%) and highest (85.71%) were showed by L17xT1 and L2xT1, respectively (Table 6). In line with this study, Beyene [7] and Bitew [24] also reported significant positive and negative MPH and BPH in some of the crosses tested for mid-altitude materials.

For MD, MPH and BPH had negative magnitude for all crosses except L13xT1 for both MPH and BPH and L10xT2 for MPH which had positive magnitude heterosis but were not significantly different. Most of the crosses showed negative and significant heterosis for both MPH and BPH consistently. This indicates that most of the offspring/crosses were earlier in maturity than the mean value of the parents and the better parent of each cross. At Ambo, the lowest and highest value of heterosis was -2.58% and 0.92% for MPH and -4.31% and 0.79% for BPH, respectively (Table 5) which is in line with the report of Beyene [7] and Bitew [24] they reported negative heterosis whereas the result of this study in contrast to positive MPH and BPH reported by Birhanu, [6]. At Arsi-Negele, the heterosis for MD was the reverse result obtained at Ambo because of the environment in which maturity of parents was more forced at Arsi-Negele as compared with the crosses. In reality, parents are weaker than the hybrids/offspring of the parents to resist harsh conditions in maize. The results also confirmed that the parents were more forced to maturity than their offspring in Arsi-Negele, which is manifested by the positive magnitude of both MPH and BPH for all crosses. For MPH, from a total of 42 crosses, six of them showed positive and nonsignificant differences and 22 crosses had positive and significant BPH (Table 6). This positive magnitude of heterosis in crosses over the mid-parent and better parent indicates that parents were earlier than crosses for maturity. However, this value may not indicate the reality due to the existence of environmental pressure at Arsi-Negele. Based on this, it is better to rely on the results obtained at Ambo for this specific trait.

At Ambo, most of the crosses showed positive values for MPH and BPH for MOD except L2x xT1, and L17xT1 for both MPH and BPH and L11xT2 and L14xT1 for BPH. L11xT2, L14xT2, and L16xT1 showed zero heteroses for MPH and L3xT1, L19xT1, and L21xT1 for BPH. The crosses with negative heterosis values indicate that crosses showed good improvement for this trait than mid-parents or the better parent. Most of the crosses showed positive value and significant MPH, whereas, for BPH, few numbers of crosses showed significant heterosis. For crosses that had negative values, none of them showed a significant difference. The lowest (-25.0%) and highest (200.0%) values were recorded by L2xT1 for MPH and -30.0% and 150.0% by L17xT1 and L20xT2 for BPH, respectively (Table 5).

Regarding CLR, all crosses had negative BPH, and most of the crosses except L4xT1 and L14xT1 for MPH. There were also some crosses which are explaining the difference significantly. The lowest (-55.56%) and the highest (10.0%) were obtained from (L7xT1) and L14xT1, respectively, for MPH. At Arsi-Negele, the lowest (-57.14%) and the highest (-7.69%) values of BPH were recorded by L7xT1 and L12xT1, respectively (Table 6). In contrast to the current study, Birhanu [6] reported both negative and positive MPH and BPH with a ranging value of -30.77 to 38.89 % and from -42.86 to 31.58%, respectively.

At Ambo, for EAS, most of the crosses showed negative values for both MPH and BPH. Twelve for MPH and 19 for BPH recorded negative values and showed significant heterosis over the mid-parent and better parent, respectively. This indicates that the crosses had better EAS scores (better looking ears) than their parents. Some crosses had zero heterosis, meaning that each cross was equal in magnitude to that of the value of mid-parent and better parent. There were also a few crosses that had positive and significant heterosis over the mid-parent and better parent. This indicates crosses were poor for EAS compared to the mid and better parents. The lowest and highest heterosis was -33.33% and 52.38% for MPH and -37.50% and 45.45% for BPH, and these records were obtained from L3xT2 and L13xT1, respectively (Table 5).

At Ambo, for PAS, only two crosses (L6xT1 and LL1xT2) had negative values for both MPH and BPH with a nonsignificant difference. L8xT2 and L3xT2 had zero heteroses for MPH. Cross: L3xT2, L8xT2 and L17xT1, and L20xT2 manifested by negative BPH. Generally, most of the crosses with a positive and significant difference for MPH and BPH implies hybrids fully fill the criteria of PAS poorly compared to parents with Ambo (Table 5). Beyene [7], in contrast, reported a higher number of crosses with positive and significant MPH and BPH.

At Ambo, all crosses had positive MPH except L1xT1 which showed negative MPH for EL. Out of the 41 crosses that had positive MPH, 25 of them showed significant differences. The value was ranged from -10.40% (L1xT1) to 61.80% (L8xT2). For BPH, most of the crosses had positive heterosis except for two crosses. Seventeen crosses had a positive magnitude and significant difference over the better parents. The magnitude of BPH ranged from -15.15% (L1xT1) to 54.55% (L6xT1) (Table 5). At Arsi-Negele, 28 crosses showed positive MPH and out of these, four of them showed significant differences with the mid-parent-parent value. Twenty-one crosses had positive heterosis and out of these, two crosses showed significant differences for BPH. The MPH and BPH ranged from -20.27 (L15xT1) to 32.85% (L7xT1) and from -26.25% to 31.89% in the same crosses, respectively (Table 6). For ED, the majority of crosses had positive and significant heterosis over mid-parent and better parent. However, there were two crosses for MPH and three crosses for BPH that had negative heterosis for Ambo. The value of MPH and BPH ranged from -2.55% (L13xT1) to 36.37% (L3xT1) and from -5.14% (L1xT1) to 31.94% (L8xT2) (Table 5). At Arsi-Negele, positive heterosis was obtained from 34 crosses and 29 crosses for MPH and BPH, respectively. Twelve crosses for MPH and five crosses for BPH positive heterosis showed a significant difference. Some crosses showed negative heterosis over the mid-parent and better parent. For ED, the magnitude of MPH and BPH ranged from -7.85% (L11xT1) to 22.47% (L5xT2), and from -11.36% (L9xT1) to 20.98% (L5 T2), respectively (Table 6). Even though there were some crosses with a negative magnitude over mid-parent and better parent, the result of this study is more similar to the previous report made by Birhanu [6] and Beyene [7]. These two authors observed positive and significant MPH and BPH in all crosses for EL and ED except for two crosses which are showing negative heterosis over better parent (2009) for ED.

For KPR, positive MPH was obtained from all crosses and most of the crosses showed significant differences. Similarly, most of the crosses had positive and significant BPH except for two crosses (L4xT1 and L13xT1). At Ambo, the magnitude of MPH and BPH ranged from 3.23% (L13xT1) to 99.07% (L17xT2) for MPH and from -5.96% (L4xT1) to 78.34% (L17xT2) for BPH (Table 5). In Arsi-Negele, out of 42 crosses, 38 crosses had positive heterosis over the mid-parent, again from these 38 crosses 20 of them showed a significant difference in mid-parent performance. For BPH, 31 crosses had positive heterosis and from these crosses, six of them had significantly different BPH. The magnitude of MPH and BPH ranged from -18.52% (L15xT1) to 53.51% (L14xT1) for MPH and from -25.13% (L15xT1) to 40.62% (L8xT2) for BPH (Table 6). The result obtained for MPH and BPH from Ambo, a place where high rainfall was recorded, is in line with the result reported by Birhanu [6], Beyene [7], and Patil et al*.* [23]. They reported positive and significant heterosis over the mid-parent and better parent. The magnitude of MPH and BPH in this study was lower compared with the findings reported by Birhanu [6]. He reported a higher value of MPH (ranging from 3.96 to 77.18 %) and MPH (ranging from 18.36 to 80.85%).

At Ambo, positive heterosis was obtained from 36 crosses for MPH and 26 crosses for BPH. Out of 36 crosses with a positive value of MPH, 18 of them showed significant differences and for BPH out of the 26 traits, nine of them showed significant differences. The value of the MPH

ranged from -40.56% (L2xT2) to 78.46% (L11xT2) and for BPH it ranged from -51.65% (L1xT1) to 75.37% (L11xT2) for TSW (Table 5). At Arsi-Negele, most of the crosses had positive values for both MPH and BPH for TSW. Twenty crosses showed a significant difference for MPH and 10 crosses for BPH. The lowest (-5.54%) and the highest (94.68%) MPH were obtained from L4xT1 and L7xT2, respectively. BPH is the lowest -13.93% and the highest (63.49%) obtained from the same crosses for BPH. However, there were also crosses with inferior performance than the mid-parent and better parent values. This is manifested by the negative MPH and BPH. The 2nd high yielder cross (L8xT2) had positive and showed significant MPH and BPH for this trait at Arsi-Negele (Table 6). Most of the crosses showed significant differences which are made from most of the lines crossed with T2, indicating that T2 had a good combining ability for TSW at Ambo and Arsi-Negele (Tables 5 and 6). Birhanu [6] and Beyene [7] reported positive magnitude and significant MPH and BPH which is similar to this study finding for TSW.

For BIOM, all crosses had positive MPH and BPH except one cross (L1xT1) which had negative heterosis, and the significant difference indicates that this cross manifested by lower BIOM performance than the mid-parent and better parent. Based on this, we can say the interaction between the male and female parents was weak to get the minimum possible heterosis. At Ambo, out of the crosses with positive values of heterosis, most of them showed significant MPH and BPH. The highest MPH (241.15%) and lowest BPH (183.05%) were obtained from L20xT2 and L11xT2, respectively (Table 5). Out of the crosses which had positive and significant MPH for BIOM, five of them were included in the top five crosses (L3xT2, L8xT2, L9xT1, L17xT2, and L18xT1) for GY at Ambo. At Arsi-Negele for BIOM, most of the crosses had positive MPH and 16 crosses had positive BPH. For MPH L7xT1 and L18xT1 showed significant differences with a positive magnitude, but for BPH none of the crosses showed significant differences. L1xT1, L9xT1, and L15xT1showed significant differences with negative values for both MPH and BPH. The crosses: L2xT1, L4xT1, L11xT1, L13xT1, L16xT1, and L17xT1 also had significant differences with negative magnitude for BPH. Crosses with negative MPH and BPH indicated that the hybrids are lower in BIOM than their mid-parent and better parent. The value of MPH ranged from -32.93% (L9xT1) to 50.77% (L18xT1) and BPH value ranged from -42.54% (L1xT1) to 19.67% (L2xT2) (Table 6). In line with the results obtained from Ambo, Birhanu [6] and Beyene [7] reported positive and highly significant MPH and BPH in all crosses tested. However, compare the results from Arsi-Negele, there was variation based on the direction of heterosis and magnitude as well due to the presence of random stress.

At Arsi-Negele, for HI, all crosses showed a positive value for MPH except L11xT1 which had a negative magnitude for both MPH and BPH, in addition, L10xT1, L21 xT1, and L21xT2 had a negative magnitude for BPH. For crosses with positive magnitude, 25 crosses showed significant MPH, whereas for BPH fifteen crosses explained the difference with significant variation. The MPH value ranged from - 0.79 % (L11xT1) to 106.44% (L5xT1). All of the five top crosses showed significant differences for MPH and three of the top five crosses (L5xT1, L8xT2, and L9xT1) had positive and significant heterosis for both MPH and BPH (Table 6). In line with this study's results for MPH and BPH, Birhanu [6] and Bitew [24] reported positive and significant MPH and BPH for most of the crosses tested for HI whereas Beyene [7] reported a highly significant difference in the positive side for both MPH and BPH in all crosses.

For LL, most of the crosses had positive and highly significant MPH except three crosses (L1xT1, L2xT2, and L6xT1) which had positive and nonsignificant MPH. Mostly the same trend was observed in crosses for BPH except for two crosses (L5xT2) which had a negative value and L6xT1 had zero heterosis. The highest MPH values (44.40%) and BPH (37.61%) were recorded by L18xT1 at Ambo (Table 5).

For MPH, most of the crosses had positive values of heterosis for LFPP, while eight crosses had a positive value of heterosis significant difference and there was one cross (L2xT1) with zero heterosis for MPH. Cross (L4xT1) also has shown zero heteroses over a better parent. Out of the crosses with positive values, only three crosses (L10xT2, L13xT2, and L17xT2) had significant BPH. There were also crosses with negative for both MPH and BPH. Some of the crosses showed significant differences in the negative direction at Ambo (Table 6). Similarly, Birhanu also reported a significant difference in the positive and negative direction for MPH and BPH [6]. The lowest (-14.10%) and highest (22.29%) heterosis values were recorded by

Table 5. Better-parent heterosis for trait heterosis determination of the 42 F1hybrids obtained by LxT and evaluated at Ambo in 2017

	GY		DT		DS		ASI		MD		PH	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1xT1	-34.13n	-41.26n	3.66b	-2.65n	0.23n	-3.50a	-100.0c	-100.0n	-2.22c	-2.85c	21.29c	10.76n
L1xT2	192.09c	138.34b	2.49n	-10.61c	-7.82b	-9.64c	33.33n	0.00n	-1.82b	-2.33b	79.91c	79.16n
L2xT1	70.25a	35.68n	3.00a	-10.31c	-6.39b	-9.69c	100.0c	25.00n	-0.92n	-1.31n	59.45c	42.01c
L2xT2	37.55n	26.11n	1.83n	-5.82c	-4.48b	-6.16c	-25.00a	-25.00n	-2.35c	-2.61c	41.50c	37.08c
L3xT1	79.61b	46.78n	1.41n	-5.09c	-4.40b	-6.36c	-60.00c	-75.00n	-1.57a	-1.83a	43.77c	39.54c
L3xT2	320.05c	273.91c	0.23n	-7.40c	-7.97b	-8.18c	-50.00c	-50.00n	-1.18n	-1.31n	65.93c	48.03c
L4xT1	-6.46n	-21.47n	3.22a	-5.80c	-2.05n	-5.70c	60.00c	0.00n	-1.44a	-1.82a	29.20c	15.97b
L4xT2	148.24c	114.59b	2.05n	-11.16c	-8.72b	-10.52c	25.00a	25.00n	-1.30a	-1.56a	79.95c	75.83c
L5xT1	71.62b	71.50b	4.32b	-8.73c	-5.54b	-11.25c	-33.33c	-63.63b	-1.96b	-2.59c	67.14c	62.50c
L5xT2	156.09c	91.35c	3.15a	-13.10c	-10.23b	-14.16c	-6.67n	-36.36n	-0.52n	-1.04n	67.96c	58.08c
L6xT1	112.15c	97.45c	1.18n	-6.04c	-5.77b	-8.10c	-50.00c	-71.42a	-1.18n	-1.31n	73.67c	71.04c
L6xT2	222.07c	153.58c	0.00n	-7.44c	-7.02b	-7.65c	9.09n	-14.29n	-0.26n	-0.26n	80.63c	63.29c
L7xT1	133.96c	106.54c	-0.72n	-2.86n	-3.52a	-4.20a	-75.00c	-85.71a	-1.44a	-1.57a	86.33c	84.72c
L7xT2	243.58c	182.87c	-1.90n	-9.76c	-8.54b	-9.58c	-27.27c	-42.86n	-1.57a	-1.83a	82.02c	68.19c
L8xT1	82.15c	61.48b	0.94n	-7.00c	-6.29b	-7.79c	-20.00n	-50.00n	-1.57a	-2.08b	79.19c	73.37c
L8xT2	190.70c	100.98b	-0.23n	-8.83c	-8.00b	-8.21c	25.00n	25.00n	-0.39n	-0.78n	91.61c	70.45c
L9xT1	161.59c	135.54c	1.41n	-6.48c	-7.15b	-9.45c	-128.57c	-116.67b	-1.18n	-1.81a	59.86c	57.96c
L9xT2	221.52c	160.14c	0.23n	-8.33c	-7.93b	-8.55c	0.00n	-16.67n	-0.78n	-1.30n	79.81c	63.05c
L10xT1	89.06c	70.94b	-0.48n	-3.80a	-4.24b	-4.69b	-66.66c	-80.00n	-0.66n	-1.05n	71.27c	63.54c
L10xT2	208.31c	148.57c	-1.65n	-8.37c	-7.87b	-9.13c	-55.55c	-60.00n	0.26n	-0.26n	90.03c	82.06c
L11xT1	99.36c	62.94a	-0.48n	-5.23b	-5.16b	-6.04c	-25.00n	-57.14n	-0.79n	-1.05n	60.99c	57.63c
L11xT2	249.27c	210.87c	-1.65n	-8.83c	-7.83b	-8.67c	-27.27c	-42.86n	-0.13n	-0.52n	78.29c	66.66c
L12xT1	81.52c	75.85b	5.41c	-7.69c	-3.78b	-9.24c	-100.00c	-100.00n	-2.58c	-4.31c	57.30c	49.22c
L12xT2	124.38c	71.43a	4.23b	-10.25c	-7.22b	-10.92c	-50.00c	-50.00n	-1.41a	-3.04c	65.77c	44.85c

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 5 (Continued)

	GY		DT		DS		ASI		MD		PH	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L13xT1	-24.34n	-37.15n	2.33n	-5.00b	-1.17n	-2.75	-700.00c	200.00n	-1.83b	-2.09b	39.79c	20.13b
L13xT2	136.95c	107.16b	1.15n	-9.54c	-6.63b	-6.84c	400.00c	25.00n	0.92n	0.79n	78.52c	66.25c
L14xT1	81.57b	48.36n	2.77a	-5.85c	-4.71b	-9.40c	-53.84c	-75.00c	-1.56a	-2.33b	56.82c	52.45c
L14xT2	240.52c	203.17c	1.60n	-9.90c	-8.60b	-11.53c	-12.50n	-41.66a	-0.65n	-1.30n	76.51c	57.70c
L15xT1	144.02c	101.33c	2.33n	-7.72c	-5.28b	-8.03c	20.00n	-25.00n	-1.44a	-1.82a	50.82c	43.71c
L15xT2	174.36c	141.64c	1.15n	-10.45c	-8.35b	-9.37c	50.00c	50.00n	-1.57a	-1.82a	72.04c	50.94c
L16xT1	65.47b	59.07a	-1.94n	-5.71b	-3.54a	-3.77a	9.09n	-40.00n	-1.71b	-1.84a	60.28c	54.16c
L16xT2	135.83c	81.18b	-3.12a	-14.41c	-8.12b	-9.58c	100.00c	40.00n	-0.26n	-0.52n	66.79c	58.64c
L17xT1	138.08c	97.60c	3.22a	-8.48c	-6.09b	-10.34c	-33.33c	-62.50a	-0.65n	-1.30n	75.08c	70.83c
L17xT2	329.89c	276.18c	2.05n	-14.28c	-12.19b	-14.66c	0.00n	-25.00n	-1.82b	-2.33b	80.15c	68.97c
L18xT1	165.19c	131.10c	1.87n	-10.09c	-8.54b	-10.81c	-20.00n	-50.00n	-1.44a	-1.82a	74.07c	68.95c
L18xT2	126.09c	88.37a	0.69n	-8.71c	-6.57b	-7.20c	75.00c	75.00n	-2.35c	-2.61c	71.79c	53.26c
L19xT1	117.13c	52.40a	0.47n	-4.71b	-4.67b	-5.99c	-33.33n	-60.00n	-0.92n	-1.05n	63.26c	60.00c
L19xT2	282.57c	247.31c	-0.70n	-10.23c	-9.174b	-9.58c	11.11n	0.00n	-1.05n	-1.05n	74.44c	57.00c
L20xT1	110.29c	71.74b	2.55n	-7.23c	-2.48n	-6.89c	83.33c	0.00n	-1.30a	-1.82a	75.21c	74.30c
L20xT2	194.94c	162.72c	1.38n	-10.40c	-7.31b	-9.91c	46.66c	0.00n	-1.18n	-1.56a	74.85c	61.05c
L21xT1	101.30c	78.38b	1.64n	-1.84n	-2.07n	-4.91b	-100.00c	-100.00b	-1.70b	-1.83a	74.26c	64.58c
L21xT2	200.06c	146.20c	0.46n	-8.29c	-6.09b	-7.14a	63.63c	28.57n	-0.79n	-0.79n	89.51c	83.59c
Minimum	-34.13	-41.26	-3.12	-14.42	-12.19	-14.66	-700.00	-116.67	-2.58	-4.31	21.29	10.76
Maximum	329.89	276.18	5.41	-1.84	0.23	-2.75	400.00	200.00	0.92	0.79	91.61	84.72
CD,0.05	1.48	1.70	2.99	3.45	3.11	3.59	2.10	2.42	2.37	2.73	14.88	17.18
CD,0.01	1.97	2.28	3.99	4.61	4.16	4.81	2.81	3.24	3.17	3.66	19.90	22.98
CD,0.001	2.59	2.99	5.24	6.05	5.46	6.31	3.68	4.25	4.16	4.80	26.12	30.16

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 5 (Continued)

	EH		MOD		EAS		PAS		EL		KPR	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1xT1	48.63c	36.42c	83.33b	37.50n	45.45c	33.33b	100.0c	100.00c	-10.40n	-15.15n	27.80n	9.60n
L1xT2	109.13c	95.72c	80.00a	50.00n	-30.76b	-35.71c	15.79n	0.00n	30.55n	28.93n	46.48b	39.16a
L2xT1	80.95c	49.28c	-25.00n	-25.00n	-4.76n	-9.09n	36.84c	18.18n	31.62n	16.66n	60.98n	31.12a
L2xT2	75.12c	65.68c	28.57n	12.50n	20.00n	7.14n	54.54c	54.54c	29.15n	19.01n	36.74a	22.50n
L3xT1	47.85c	37.42c	33.33n	0.00n	0.00n	-18.75a	33.33c	7.69n	15.38n	13.64n	34.08n	19.87n
L3xT2	84.90c	50.30c	60.00n	33.33n	-33.33c	-37.50c	0.00n	-7.69n	51.00b	46.87b	75.73c	75.00c
L4xT1	49.79c	30.00b	57.14a	37.50n	30.43b	15.38n	66.66c	50.00c	1.61n	-4.55n	4.03n	-5.96n
L4xT2	103.90c	102.91c	50.00n	50.00n	-18.51a	-21.42a	23.80a	18.18n	28.27n	25.63n	37.19a	36.07n
L5xT1	91.57c	78.57c	57.14a	37.50n	33.33b	27.27a	33.33b	20.00n	21.48n	18.84n	52.25n	45.69b
L5xT2	100.00c	84.29c	116.66c	116.66c	-12.00n	-21.42a	23.80a	18.18n	37.45a	28.98n	44.96b	35.50a
L6xT1	98.67c	85.71c	66.66a	25.00n	-4.35n	-15.38n	44.44c	30.00b	54.54c	54.55b	63.23n	47.01b
L6xT2	112.92c	73.91c	120.00c	83.33a	-11.11n	-14.29n	-4.76n	-9.09n	42.29b	36.36a	69.29c	68.59c
L7xT1	118.84c	115.71c	66.67n	25.00n	4.00n	-13.33n	41.17c	33.33b	49.62b	46.37b	61.67n	53.64c
L7xT2	115.12c	88.23c	80.00a	50.00n	-24.13b	-26.66b	20.00a	9.09n	43.63b	34.78a	71.09c	61.02c
L8xT1	92.47c	71.50c	116.66c	62.50a	26.31a	20.00n	41.17c	33.33b	23.74n	17.80n	23.62n	20.89n
L8xT2	114.94c	68.71c	140.00c	100.0b	-4.35n	-21.42a	0.00n	-9.09n	61.80c	47.94b	79.85c	58.23c
L9xT1	72.97c	64.10c	83.33b	37.50n	-25.00a	-35.71c	11.11n	0.00n	42.46b	30.00a	51.46n	48.10b
L9xT2	100.77c	66.02c	40.00n	16.67n	-21.42a	-21.42a	14.29n	9.09n	59.43b	40.00b	71.94c	51.26c
L10xT1	92.56c	85.00c	22.22n	10.00n	12.00n	-6.67n	52.94c	44.44c	28.37a	15.85n	26.52n	22.22n
L10xT2	130.30c	106.20c	37.50n	10.00n	-10.34n	-13.33n	10.00n	0.00n	41.05b	22.56n	49.64c	30.24a
L11xT1	89.47c	80.00c	22.22n	10.00n	16.67n	0.00n	44.44c	30.00b	30.30a	30.30n	35.23n	25.83n
L11xT2	114.03c	93.65c	0.00n	-20.00n	-21.42a	-21.42a	-4.76	-9.09n	58.10b	51.51b	67.19c	60.76c
L12xT1	89.86c	80.12c	12.50n	12.50n	0.00n	0.00n	41.17c	33.33b	14.87n	5.30n	31.43n	21.85n
L12xT2	75.96c	45.51c	28.57n	12.50n	-25.00a	-35.71c	40.00c	27.27b	39.39a	33.07n	53.41b	48.06b

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 5 (Continued)

	EH		MOD		EAS		PAS		EL		KPR	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L13xT1	66.81c	32.85c	57.14a	37.50n	52.38c	45.45c	68.42c	45.45c	4.13n	-4.55n	3.23n	-4.64n
L13xT2	108.64c	89.21c	66.66a	66.66a	-20.00a	-28.57b	9.09n	9.09n	54.10b	47.10a	31.85a	27.74n
L14xT1	73.28c	66.44c	0.00n	-10.00n	-9.09n	-16.67n	41.17c	33.33b	18.70n	10.61n	7.04n	0.66n
L14xT2	98.42c	65.78c	62.50b	30.00n	-15.38n	-21.42a	20.00a	9.09n	32.76a	28.93n	41.10b	34.20a
L15xT1	67.33c	56.87c	100.00c	50.0a	18.18n	8.33n	73.33c	62.50c	12.78n	11.94n	30.81a	26.49n
L15xT2	87.78c	53.75c	140.00c	100.00b	-15.38n	-21.42a	33.33c	9.09n	23.92n	17.91n	46.35b	35.45a
L16xT1	85.24c	61.42c	0.00n	0.00n	4.76n	0.00n	50.00c	50.00c	30.43a	25.00n	34.48a	29.14n
L16xT2	87.37c	85.57c	28.57n	12.50n	-12.00n	-21.42a	15.79n	0.00n	34.33a	23.61n	59.07c	48.19b
L17xT1	123.80c	101.42c	-22.22n	-30.00n	4.35n	-7.69n	75.00c	75.00c	43.93b	43.93b	56.09c	27.15n
L17xT2	123.36c	113.39c	50.00a	20.00n	-25.92b	-28.57b	5.26n	-9.09n	48.62b	42.42a	99.07c	78.34c
L18xT1	98.64c	89.03c	83.33b	37.50n	4.76n	0.00n	52.94c	44.44c	20.28n	11.69n	66.78c	49.66b
L18xT2	86.77c	54.83c	140.00c	100.00b	-12.00n	-21.42a	40.00b	27.27b	13.46n	1.30n	63.33c	63.33b
L19xT1	92.06c	72.85c	33.33n	0.00n	4.00n	-13.33n	75.00c	75.00c	40.27b	29.48a	48.65c	37.08a
L19xT2	108.41c	99.10c	140.00c	100.00b	-24.13b	-26.66b	26.31a	9.09n	53.07c	35.90a	67.27c	62.35c
L20xT1	100.72c	98.57c	116.66c	62.50a	0.00n	-8.33n	50.00c	50.00c	39.30b	35.60a	63.56c	39.73b
L20xT2	102.51c	76.64c	200.00c	150.00c	0.00n	-7.14n	5.26n	-9.09n	56.09c	53.59b	69.16c	60.00b
L21xT1	107.40c	100.00c	33.33n	0.00n	4.35n	-7.69n	55.55c	40.00c	10.45n	8.82n	31.00a	24.50n
L21xT2	104.31c	82.30c	100.00b	66.66a	-18.51a	-21.42a	23.80a	18.18n	52.53c	44.11b	53.90c	44.84b
Minimum	47.85	30.00	-25.00	-30.00	-33.33	-37.50	-4.76	-9.09	-10.40	-15.15	3.23	-5.96
Maximum	130.30	115.71	200.00	150.00	52.38	45.45	100.00	100.00	61.80	54.55	99.07	78.34
CD,0.05	11.18	12.91	0.85	0.99	0.58	0.67	0.47	0.55	3.13	3.61	6.39	7.37
CD,0.01	14.95	17.26	1.14	1.32	0.78	0.90	0.63	0.73	4.18	4.83	8.54	9.86
CD,0.001	19.62	22.65	1.50	1.73	1.02	1.18	0.83	0.96	5.49	6.34	11.21	12.94

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 5 (Continued)

	ED		TSW		BIOM		LL		LFPP		LFBE	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1xT1	-0.02n	-5.14n	-39.86b	-51.65c	-20.21n	-23.15n	10.78n	3.63n	2.30n	-6.32n	-11.95n	-20.58a
L1xT2	22.03c	12.07a	34.91a	10.49n	83.28n	39.78n	32.57c	29.64b	13.92a	13.92n	-7.41n	-8.54n
L2xT1	24.44c	23.07c	20.83n	0.37n	58.60n	34.41n	25.64c	21.97b	9.20n	0.00n	-19.35a	-26.47b
L2xT2	7.10n	4.60n	-40.56b	-49.65c	66.92n	51.56n	34.49c	32.33c	2.53n	2.53n	-19.51n	-21.43n
L3xT1	13.36a	1.79n	6.40n	1.46n	30.24n	19.82n	20.19b	15.91a	-13.81a	-17.89b	-27.47b	-35.29c
L3xT2	36.37c	26.39c	60.86c	56.98b	144.78a	80.69a	23.12b	13.67n	7.88n	3.49n	-2.50n	-2.50n
L4xT1	4.76n	1.02n	-19.21n	-28.06n	15.23n	6.71n	30.05c	23.89b	0.00n	-9.47n	-28.26b	-35.29c
L4xT2	27.43c	18.87c	25.35n	14.04n	168.54a	123.63a	23.64b	23.23c	-14.10a	-15.19n	-37.03c	-37.80b
L5xT1	21.72c	18.67c	-8.50n	-29.46a	128.03b	126.68a	17.46b	7.94n	-13.36a	-14.73a	-41.17c	-41.17c
L5xT2	35.63c	27.86c	22.10n	-4.25n	137.30a	85.13a	7.18n	-5.49n	-13.45a	-19.57b	-43.95c	-50.00c
L6xT1	19.41c	13.45a	37.98a	24.98n	79.94n	59.80n	1.00n	0.00n	-6.29n	-13.68a	-40.62c	-44.11c
L6xT2	21.80c	19.71b	57.92c	46.19b	72.25n	24.04n	30.48c	23.51b	9.43n	8.75n	-11.76n	-16.67n
L7xT1	13.69b	10.27n	18.59n	9.45n	133.58b	130.11a	18.26b	15.85a	-2.89n	-11.58n	-24.21b	-29.41b
L7xT2	16.38b	15.91b	59.77b	44.27a	139.98a	86.01a	23.01b	15.27a	15.92a	15.19n	-10.71n	-14.77n
L8xT1	10.56a	8.46n	30.73n	26.59n	50.03n	18.31n	22.14b	19.55a	-8.70n	-11.58n	-33.65c	-34.90c
L8xT2	34.00c	31.94c	55.36b	54.03b	89.66a	25.86a	25.99c	22.94b	11.91n	5.62n	-9.68n	-20.75a
L9xT1	14.47b	11.87a	36.16a	24.24n	152.24b	148.15b	23.56b	21.57b	5.95n	3.16n	-11.76n	-11.76n
L9xT2	32.09c	30.55c	58.60c	47.94b	239.97c	163.25b	20.60b	17.08a	-2.96n	-8.89n	-27.47b	-35.29c
L10xT1	5.57n	4.98n	35.71n	33.88n	157.94b	156.92b	35.78c	30.03c	5.20n	-4.21n	-16.13n	-23.52a
L10xT2	24.94c	20.06c	66.98c	60.91b	184.00b	121.89a	24.50b	24.22b	22.29b	21.52b	6.10n	3.57n
L11xT1	7.35n	4.79n	25.75n	24.94n	23.03n	2.15n	20.90b	18.95a	2.22n	-3.16n	-15.63n	-20.58a
L11xT2	20.77c	14.00b	78.46c	75.37c	204.61a	183.05a	17.07a	12.94n	5.88n	0.00n	5.88n	0.00n
L12xT1	7.39n	-0.73n	1.66n	-20.87n	27.14n	1.02n	2.13n	1.05n	-8.16n	-11.76n	-8.16n	-11.76n
L12xT2	27.80c	14.46b	21.86n	-3.48n	53.44n	2.34n	11.63n	3.23n	3.45n	-4.25n	3.45n	-4.25n

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 5. (Continued)

	ED		TSW		BIOM		LL		LFPP		LFBE	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L13xT1	-2.55n	-3.21n	-31.56a	-39.75a	24.04n	10.83n	30.65c	28.02c	5.14n	-3.16n	-6.67n	-17.65n
L13xT2	22.41c	17.48b	38.46a	24.49n	184.31a	144.58a	30.38c	27.10b	20.75b	20.00a	13.92n	12.50n
L14xT1	8.02n	-2.45n	8.06n	-10.24n	44.08n	34.29n	23.40b	22.78b	-3.78n	-6.32n	-19.80a	-20.58a
L14xT2	21.40c	6.32n	54.33c	30.72a	190.09b	140.23a	41.03c	35.43c	2.96n	-3.33n	-16.67n	-24.99b
L15xT1	16.53c	10.70a	3.28n	-21.30n	143.80b	136.90a	30.34c	24.69b	0.55n	-3.16n	-13.86n	-14.71n
L15xT2	20.86c	11.13a	36.20b	5.55n	116.38n	73.22n	31.27c	31.12c	-0.60n	-5.68n	-16.67n	-24.99b
L16xT1	16.41c	8.79n	27.30n	11.08n	82.83n	71.91n	39.80c	31.34c	1.18n	-9.47n	-14.77n	-26.47b
L16xT2	22.86c	11.19a	57.72c	40.53a	187.39b	136.24a	24.55b	22.34a	14.29n	11.39n	1.30n	-2.50n
L17xT1	7.62n	-0.52n	5.66n	-19.87n	168.61b	141.10a	40.10c	30.64c	-3.30n	-7.37n	-17.34a	-20.58a
L17xT2	25.67c	12.54b	54.25c	18.95n	172.27a	133.23n	36.43c	32.96c	21.68b	16.09a	3.45n	-4.25n
L18xT1	21.14c	16.36b	17.15n	-7.81n	84.50a	63.75n	19.71a	9.27n	-5.82n	-6.32n	-22.11b	-23.58b
L18xT2	16.08b	7.88n	16.77n	-6.46n	75.75n	26.50n	44.40c	37.61c	17.91b	8.51n	0.00n	-12.26n
L19xT1	20.88c	17.21b	14.45n	-10.94n	42.52n	36.91n	26.78c	25.50b	-4.40n	-8.42n	-11.96n	-20.58a
L19xT2	24.50c	24.03c	33.71a	5.89n	105.01n	56.06n	33.04c	28.39c	13.25a	8.05n	14.81n	13.42n
L20xT1	25.27c	18.31c	32.86a	4.03n	125.94a	116.68a	24.50c	23.03b	9.19n	6.32n	2.00n	0.00n
L20xT2	28.85c	17.81c	17.45n	-6.40n	241.14c	175.94b	15.83a	9.45n	12.43n	5.56n	-8.99n	-17.35n
L21xT1	14.03b	13.61a	-4.78n	-20.20n	40.66	31.12n	26.84c	20.96a	5.03n	-1.05n	-7.22n	-11.76n
L21xT2	33.04c	28.99c	48.17b	26.64n	199.98c	123.50a	35.47c	35.17c	15.33a	11.91n	4.65n	-2.17n
Minimum	-2.55	-5.14	-40.56	-51.65	-20.21	-23.15	1.00	-5.49	-14.10	-19.57	-43.96	-50.00
Maximum	36.37	31.94	78.46	75.37	241.15	183.05	44.40	37.61	22.29	21.52	14.81	13.42
CD,0.05	0.35	0.40	59.78	69.03	6.58	7.60	11.27	13.02	1.76	2.03	1.34	1.55
CD,0.01	0.46	0.54	79.96	92.33	8.81	10.17	15.08	17.41	2.35	2.71	1.79	2.07
CD,0.001	0.61	0.70	104.91	121.14	11.55	13.34	19.78	22.84	3.08	3.56	2.35	2.72

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 6. Better-parent heterosis for trait heterosis determination of the 42 F1hybrids obtained by LxT and evaluated by Arsi-Negele in 2017

	GY		DT		DS		ASI		MD		PH		EH	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1xT1	-4.74n	-20.17n	0.00n	-0.52n	0.76n	0.51n	27.27n	16.67n	0.91n	0.30n	10.36n	4.26n	9.28n	6.00n
L1xT2	74.13n	70.05n	-3.19n	-5.70n	-2.55n	-3.54n	12.50n	-18.18n	3.56c	0.91n	31.09c	23.10b	33.33b	32.63a
L2xT1	24.78n	3.57n	-5.51a	-5.76a	-2.03n	-2.03n	100.0a	85.71n	0.76n	0.30n	23.00b	11.49n	19.32n	5.00n
L2xT2	5.06n	1.40n	2.41n	0.53n	2.81n	2.03n	11.11n	-9.09n	2.48c	0.00n	12.82n	1.68n	25.15n	12.63n
L3xT1	43.00n	18.39n	-0.79n	-1.05n	0.51n	0.51n	38.46n	28.57n	1.39a	0.31n	17.94b	9.93n	15.65n	2.31n
L3xT2	65.88a	59.61n	-5.63a	-7.36a	-5.37n	-6.09n	0.00n	-18.18n	5.36c	4.37c	23.92c	16.17a	28.00b	10.77n
L4xT1	7.66n	-8.87n	0.53n	0.00n	0.00n	0.00n	-14.29n	-25.00n	1.52a	1.22n	21.57b	11.49n	24.73a	16.00n
L4xT2	73.41b	71.37a	-5.37a	-6.87a	-4.86n	-5.58n	5.26n	-9.09n	3.57c	1.22n	23.04b	12.18n	14.92n	9.47n
L5xT1	84.99c	68.24b	-2.83n	-4.55n	0.76n	0.51n	233.33a	66.67n	2.90c	2.75c	31.83c	26.66c	35.48b	25.64a
L5xT2	84.93b	72.57b	-4.46n	-8.08b	-3.57n	-4.55n	27.27n	-36.36n	4.06c	2.14b	26.57c	22.35b	27.35a	15.38n
L6xT1	12.08n	8.86n	1.33n	-0.52n	0.26n	-0.51n	-25.00n	-40.00n	0.91n	0.61n	43.03c	37.94c	42.97c	24.44a
L6xT2	64.60b	44.27n	-3.54n	-3.80n	-2.06n	-2.06n	23.81n	18.18n	3.57c	1.22n	29.12c	25.29c	39.13c	18.52n
L7xT1	104.15c	78.92c	-1.86n	-3.14n	-1.02n	-1.02n	17.65n	-9.09n	2.61c	1.83a	61.42c	59.09c	93.49c	80.87c
L7xT2	85.53b	80.19b	-6.23a	-6.98a	-7.41b	-8.12a	-27.27n	-27.27n	3.77c	2.48c	33.33c	32.23c	41.90c	29.56a
L8xT1	81.32c	64.71c	-0.26n	-0.52n	-0.25n	-0.51n	0.00n	0.00n	1.67b	1.52a	40.44c	25.41c	34.05c	4.47n
L8xT2	102.56c	59.97b	-5.63a	-7.36a	-4.62n	-5.10n	17.65n	-9.09n	4.36c	2.13b	29.60c	16.38b	29.19c	-1.12n
L9xT1	34.74n	11.80n	0.52n	0.52n	-0.25n	-0.51n	-23.08n	-28.57n	1.99b	1.83a	28.93c	18.57b	33.87c	13.10n
L9xT2	79.92b	73.58a	-6.95c	-8.90b	-3.06n	-4.04n	77.77a	45.45n	3.75c	1.84a	25.86c	16.42b	26.66b	4.83n
L10xT1	40.89n	12.94n	-0.53	-1.05n	0.25n	0.00n	20.00n	0.00n	1.38a	0.61n	28.51c	21.67b	22.27a	8.53n
L10xT2	128.38c	111.27c	-6.98b	-8.46b	-5.10n	-6.06n	30.00n	18.18n	5.97c	4.65c	29.34c	23.19c	33.93	16.28n
L11xT1	-7.07n	-25.87n	0.27n	-2.09n	0.00n	-1.02n	-5.88n	-27.27n	1.52a	1.52a	28.33c	25.71c	34.59b	27.92a
L11xT2	115.33c	98.00b	-9.04b	-9.28b	-7.49b	-7.73a	18.18n	18.18n	4.21c	2.14b	29.60c	27.75c	40.77c	30.63a
L12xT1	51.88a	28.73n	0.52n	0.52n	0.76n	0.51n	7.69n	0.00n	1.984b	1.82a	25.28c	13.93a	51.56c	37.39c
L12xT2	63.96a	62.29a	-2.14n	-4.19n	-2.04n	-3.03n	0.00n	-18.18n	4.04c	1.82a	22.66c	12.19a	22.01a	8.13n

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 6 (Continued)

	GY		DT		DS		ASI		MD		PH		EH	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L13xT1	18.74n	-9.34n	1.31n	1.04n	1.01n	0.50n	-7.69n	-14.29n	0.46n	0.00n	18.24a	3.40n	22.22n	-1.00n
L13xT2	79.22a	56.17n	-4.53n	-6.77a	-5.34n	-6.53a	-22.22n	-36.36n	2.48c	0.00n	34.29c	16.80a	35.03a	11.58n
L14xT1	70.10b	36.37n	-1.31n	-1.57n	-2.99n	-4.88n	-33.33n	-53.33a	2.00b	1.22n	39.04c	30.71c	51.35c	37.70c
L14xT2	56.00n	44.33n	-4.02n	-5.79n	-3.26n	-5.85n	7.69n	-6.67n	5.03c	3.72c	18.81b	12.36n	28.11b	13.93n
L15xT1	-10.36n	-17.88n	0.27n	-1.57n	1.55n	0.00n	38.46n	28.57n	0.46n	0.31n	8.86n	-3.91n	-2.68n	-21.12a
L15xT2	38.31n	9.99n	-4.09n	-4.35n	-4.42n	-5.15n	-11.11n	-27.27n	2.81c	0.92n	14.49a	1.63n	8.59n	-13.66n
L16xT1	49.19a	36.35n	-4.95n	-9.42b	-3.17n	-7.10a	42.86n	25.00n	1.84b	1.52a	45.77c	39.57c	59.59c	58.00c
L16xT2	38.42n	28.53n	-3.37n	-6.01n	-2.93n	-6.19n	5.26n	-9.09n	2.03b	0.31n	16.55a	10.92	6.74n	5.10n
L17xT1	47.80a	19.46n	-0.53n	-2.09n	-2.30n	-3.05n	-46.67n	-55.56n	1.67b	1.52a	40.96c	36.17c	61.38c	59.80c
L17xT2	72.59a	61.27a	-3.80n	-4.32n	-4.12n	-4.12n	-10.00n	-18.18n	1.55a	-0.61n	23.85c	18.90a	30.96b	26.47a
L18xT1	92.38c	53.05a	-6.13a	-7.85b	-4.37n	-5.58n	42.86n	25.00n	0.92n	0.31n	41.40c	41.10c	48.38c	37.60b
L18xT2	102.06c	85.21b	-7.35b	-7.60a	-3.63n	-4.12n	68.42a	45.45n	4.86c	3.40c	29.11c	28.57c	20.75n	9.40n
L19xT1	109.20c	69.00b	-6.35a	-7.32a	-5.82a	-6.06n	5.88n	-18.18n	2.74c	2.43c	38.77c	33.33c	76.71c	67.00c
L19xT2	93.41b	80.62b	-6.48a	-7.48a	-4.59n	-5.56n	27.27n	27.27n	3.57c	1.22n	36.30c	31.76c	58.69c	53.68c
L20xT1	87.22n	40.98n	-3.96n	-4.71n	-1.77n	-2.02n	50.00n	20.00n	2.29c	2.14b	44.88c	42.21c	60.93c	50.43c
L20xT2	68.11a	44.01n	-4.58n	-5.85n	-1.02n	-2.02n	61.90a	54.55n	4.37c	2.45c	28.38c	26.80c	27.61a	16.52n
L21xT1	27.91n	8.63n	-1.06n	-2.09n	-2.54n	-2.54n	-37.50n	-50.00n	1.68b	1.22n	39.51c	34.46c	44.49c	38.53b
L21xT2	61.53a	60.28a	-2.16n	-3.21n	-3.32n	-4.06n	-23.81n	-27.27n	5.01c	3.39c	36.40c	30.67c	34.31b	25.68a
Minimum	-10.36	-25.87	-9.04	-9.42	-7.49	-8.12	-46.67	-55.56	0.46	-0.61	8.86	-3.91	-2.68	-21.12
Maximum	128.38	111.27	2.41	1.04	2.81	2.03	233.33	85.71	5.97	4.66	61.43	59.09	93.49	80.87
CD,0.05	1.70	1.96	4.80	5.54	5.39	6.22	2.99	3.45	1.96	2.26	14.83	17.13	11.33	13.09
CD,0.01	2.27	2.63	6.42	7.41	7.21	8.32	4.00	4.62	2.62	3.03	19.84	22.91	15.16	17.50
CD,0.001	2.98	3.45	8.42	9.72	9.46	10.92	5.25	6.06	3.44	3.97	26.03	30.06	19.89	22.97

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 6 (Continued)

	CLR		EL		KPR		ED		TSW		BIOM		HI	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1xT1	-4.35n	-15.38n	-11.59n	-12.86n	19.10n	-0.63n	-1.66n	-1.83n	-4.35n	-11.13n	-32.41a	-42.53b	34.94n	31.67n
L1xT2	-14.29n	-18.18n	-1.37n	-5.27n	37.96a	22.47n	14.32a	12.38n	23.74n	16.89n	19.99n	19.67n	38.12n	31.22n
L2xT1	-30.43n	-38.46a	2.22n	1.47n	7.37n	-4.38n	5.04n	4.05n	35.73a	34.91a	-21.17n	-36.29b	54.75a	49.96a
L2xT2	-4.76n	-9.09n	-16.78n	-21.71a	12.55n	7.25n	-4.39n	-5.29n	-5.16n	-6.26n	-22.94n	-27.74n	28.38n	27.85n
L3xT1	-9.09n	-23.08n	12.41n	11.59n	40.92b	23.75n	9.72n	-5.06n	-2.20n	-13.39n	-8.08n	-19.28n	59.12a	51.30a
L3xT2	-20.00n	-27.27n	8.27n	3.28n	49.80c	40.57b	16.25a	2.23n	30.23n	13.57n	19.13n	15.02n	29.11n	19.61n
L4xT1	4.76n	-15.38n	-6.15n	-10.29n	10.00n	-10.63n	0.60n	-0.68n	-5.54n	-13.93n	-19.28n	-35.93a	27.81n	19.02n
L4xT2	-5.26n	-18.18n	-4.35n	-13.16n	20.17n	3.62n	10.99n	10.31n	22.92n	13.84n	15.21n	5.65n	45.16a	38.77n
L5xT1	-33.33n	-46.15b	6.96n	6.57n	24.32a	19.65n	13.87a	13.11a	9.62n	-2.33n	-15.68n	-22.99n	106.44c	104.26c
L5xT2	-15.79n	-27.27n	2.42n	-2.64n	26.04a	13.30n	22.47c	20.98b	51.26b	32.70a	-10.53n	-17.15n	77.27b	70.71b
L6xT1	-28.00n	-30.77n	14.48n	7.79n	13.70n	3.75n	-4.96	-7.82n	24.09n	22.74n	-22.09n	-22.63n	43.73n	39.39n
L6xT2	-30.43n	-33.33n	17.65n	16.89n	42.96b	39.85a	1.37n	0.16n	33.59a	29.84n	-4.30n	-17.99n	67.12b	57.84a
L7xT1	-55.55c	-57.14c	32.85b	31.89b	22.68n	20.00n	4.88n	0.66n	56.14b	33.05n	34.43a	3.20n	44.89a	25.19n
L7xT2	-36.00a	-42.85b	13.10n	7.89n	32.65n	26.15n	5.29n	2.93n	94.67c	63.48c	8.72n	-4.30n	62.86c	44.11a
L8xT1	-23.08n	-23.08n	4.11n	-2.56n	15.00n	15.00n	3.99n	0.80n	21.84	15.24n	19.63n	16.20n	49.92a	33.72n
L8xT2	-41.66a	-46.15b	11.68n	10.25n	51.00c	40.62b	15.03a	13.60a	40.74b	35.40a	21.49n	6.13n	64.96c	50.82a
L9xT1	-16.13n	-27.77a	15.87n	9.09n	27.97a	24.37n	-4.10n	-11.36n	8.47n	1.52n	-32.92a	-41.33b	100.04c	86.76b
L9xT2	-17.24n	-33.33b	22.87a	22.08a	28.71a	23.18n	2.18n	-3.88n	41.78b	30.53n	16.42n	12.91n	49.58a	36.14n
L10xT1	-18.52n	-21.43n	18.75a	3.26n	32.88b	22.50n	-0.61n	-5.15n	21.15n	18.75n	29.34n	-2.36n	3.14n	-5.96n
L10xT2	-36.00a	-42.85b	10.71n	1.09n	29.67a	28.26n	9.54n	6.45n	32.40a	27.56n	17.62n	1.39n	82.04c	70.27b
L11xT1	-46.15b	-46.15b	-0.74n	-1.46n	18.49	8.12n	-7.85n	-8.81n	19.01n	13.72n	-13.20n	-33.84a	-0.79n	-10.59n
L11xT2	-8.33n	-15.38n	13.28n	6.58n	29.63a	26.81n	6.51n	5.62n	48.79b	39.80a	15.54n	0.78n	69.61c	56.74b
L12xT1	-4.00n	-7.69n	3.71n	2.95n	5.16n	1.87n	1.62n	-4.11n	12.41n	10.58n	3.86n	-18.92n	41.97a	28.84n
L12xT2	-21.74n	-25.00n	0.70n	-5.27n	33.33b	28.00a	10.72a	2.65n	26.63n	26.47n	32.67n	19.22n	18.02n	9.84n

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

Table 6 (Continued)

	CLR		EL		KPR		ED		TSW		BIOM		HI	
Code	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L13xT1	-4.35n	-15.38n	8.95n	-1.46n	15.67n	-3.13n	4.93n	1.56n	2.65n	-0.96n	-16.38n	-38.54a	35.38n	29.50n
L13xT2	-4.76n	-9.09n	0.76n	-13.16n	16.26n	3.62n	7.84n	6.33n	28.04a	25.70n	16.95n	-2.52n	47.64a	45.08n
L14xT1	10.00n	-15.38n	26.82a	14.71n	53.51c	29.99a	14.66b	10.58n	35.59a	25.20n	6.04n	-12.16n	53.76a	53.73a
L14xT2	-11.11n	-27.27n	-3.82n	-17.11n	-0.40n	-10.14n	12.45a	6.50n	50.40b	36.64a	6.40n	2.83n	35.63n	31.98n
L15xT1	-25.00n	-30.77n	-20.27a	-26.25a	-18.52n	-25.13a	1.26n	-2.70n	25.77n	20.00n	-29.79a	-32.11a	25.21n	11.42n
L15xT2	-45.45a	-45.45a	-6.41n	-8.75n	0.91n	-13.09n	9.36n	3.20n	46.83b	42.52b	-0.38n	-12.63n	41.13a	28.73n
L16xT1	-23.81n	-38.46a	14.29n	11.77n	11.92n	5.62n	8.70n	5.71n	27.86a	17.82n	-18.74n	-33.59a	76.96c	57.53b
L16xT2	-26.32n	-36.36n	-7.80n	-14.48n	-1.43n	-2.82n	5.29n	0.54n	36.73b	28.07a	-8.65n	-13.18n	49.18b	36.13n
L17xT1	-20.00n	-23.08n	6.98n	1.47n	40.14b	24.37n	-2.78n	-5.23n	17.57n	5.61n	-3.38n	-27.35a	43.64n	28.35n
L17xT2	-21.74n	-25.00n	11.68n	0.66n	33.58a	26.81n	15.54b	10.58n	63.86c	49.56c	24.24n	6.57n	28.89n	18.07n
L18xT1	-14.29n	-30.77n	7.36n	7.36n	26.75a	12.50n	12.60a	6.65n	3.35n	-9.32n	50.76b	6.14n	17.62n	0.50n
L18xT2	-26.32n	-36.36n	-2.78n	-7.89n	43.50b	36.23a	18.67b	14.46a	4.87n	-6.55n	27.80n	0.93n	51.31b	32.36n
L19xT1	-23.81n	-38.46a	5.41n	-2.50n	21.68	17.50n	8.49n	3.11n	17.97n	8.32n	21.30n	-4.11n	70.41b	64.46b
L19xT2	-15.79n	-27.27n	6.41n	3.75n	31.70a	26.85n	22.43c	18.50b	31.11a	22.38n	10.32n	0.67n	68.83b	67.42b
L20xT1	-30.76a	-30.77n	21.26n	13.24n	29.07a	13.75n	9.31n	7.74n	28.89a	20.02n	18.83n	-14.00n	52.30a	44.52n
L20xT2	-41.66a	-46.15b	-4.44n	-15.13n	13.85n	7.25n	8.73n	5.19n	46.13c	38.36b	2.69n	-16.03n	57.80b	53.79a
L21xT1	-21.74n	-30.77n	-10.61n	-13.24n	-0.99n	-6.25n	-1.57n	-2.10n	17.85	5.58n	9.06n	-20.28n	9.32n	-8.78n
L21xT2	-42.85a	-45.45a	-4.29n	-11.84n	10.32n	8.39n	6.91n	4.36n	37.48b	25.14n	36.33n	12.89n	9.98n	-6.12n
Minimum	-55.56	-57.14	-20.27	-26.25	-18.52	-25.13	-7.85	-11.36	-5.54	-13.93	-32.93	-42.54	-0.79	-10.59
Maximum	10.00	-7.69	32.85	31.89	53.51	40.62	22.47	20.98	94.68	63.49	50.77	19.67	106.44	104.27
CD,0.05	0.94	1.08	2.28	2.64	5.97	6.90	0.44	0.51	76.49	88.32	2.28	2.63	17.93	20.70
CD,0.01	1.26	1.45	3.05	3.52	7.99	9.23	0.59	0.68	102.31	118.14	3.05	3.52	23.98	27.69
CD,0.001	1.65	1.90	4.00	4.62	10.48	12.11	0.77	0.89	134.24	155.00	4.00	4.62	31.46	36.33

n=non-significant difference, a, b, c = significant at alpha 0.05,0.01,0.001 level, respectively

L4xT2 and L10xT2, respectively, for MPH, whereas for BPH was -the lowest (19.57%) and highest (21.52%) for L5xT2 and L10xT2, respectively (Table 5).

At Ambo for LFBE, most of the crosses had negative and significant heterosis over both mid-parent and better parent. Some crosses had negative and positive values of heterosis for MPH and BPH with a nonsignificant difference. The negative heterosis value indicates that the parents had a greater number of leaves below the uppermost ear compared to their offspring. The MPH values ranged from -43.96 % (L5xT2) to 14.81% (L19xT2), whereas for BPH the values ranged from -50.0% to 13.42% in the same crosses (Table 5). In general, the higher value for better parent heterosis for different traits indicates that the parents which form the specific cross came from genetically distant group. Whereas the crosses which showed relatively lower of MPH value for quantitative traits highlight that the crosses were formed from parents inter related each other or closely related genetically.

4. CONCLUSION

The crosses that showed negative heterosis was the cross-product of lines with negative SCA effects for DS and DT, highlighting the parents are late for flowering compared to their crosses. For quantitative traits (GY, PH, EH, EL, KPR, ED, TSW, and BIOM), the value of the mid-parent and better parent heterosis indicates the positive value by most of the crosses whereas for phenology traits (DS, DT, and DM) both mid-parent and better parent heterosis showed to the negative side under ideal location that is Ambo but under location, with some natural stress (Arsi-Negele) this conclusion is somehow contrasted. To be clearer, for such kinds of information about our germplasm, it is advisable to evaluate the new germplasms in different testing environments. In general, for-grain yield and yield related traits, both the MPH and BPH values were found in the positive direction for almost all crosses. This highlights that the crosses evaluated in the study were created from genetically diverse inbred parents.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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