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Estimation of combining ability and heterosis of quality protein maize inbred lines

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Maize plays a great role for human food in Ethiopia. Even if it is cultivated for food, most improved varieties released were normal maize which are devoid of lysine and tryptophan. Combining ability analysis is one of the commanding means in identifying the best combiners that may be used in crosses either to exploit heterosis or to accrue productive genes. The objectives of this study were to examine combining ability of quality protein maize inbred lines, estimate the extent of heterosis and determine the nature of gene action. Six inbred lines were crossed with two testers (CML144 and CML159) to produce 12 F_1 hybrids. Twelve F_1 hybrids and two standard checks viz., BHQP542 and a normal maize hybrid, Jibat, were evaluated in a randomized complete block design with two replications in 2010/2011 at Ambo Agricultural Research Centre. Genetic differences were observed from mean squares of treatments for all traits except days to maturity, ear diameter, number of kernel rows per cob, protein content (%) and oil content (%). LN1 was good general combiner for grain yield. Hybrid HN7 (89.56%) and HN8 (85.63%) revealed significant positive standard heterosis and superior in mean performance for grain yield compared to check BHQP54. Therefore; even though it is a one year trial HN7 and HN8 could be exploited for commercial use.

Key words: Specific combining ability, general combining ability, gene action.

INTRODUCTION

Maize is physiologically more efficient cereal crop with high grain yield and wide adaptation (Shaw, 1988). In Ethiopia, maize grows from moisture stress areas to high rainfall areas and from lowlands to the highlands (Kebede et al., 1993). It is one of the important cereal crop grown for food in the country, and is the first in total production (6 million tonnes), and yield per unit area (2.9 tonnes per hectare) and second in area coverage among all the cereal crops in 2011/12 cropping season (CSA, 2011/12).

Maize is a major cereal for human nutrition in Ethiopia. About 40 improved maize varieties were released in the country since 1952 (EIAR, 2011). Of them only four varieties are quality protein maize (AMH760Q, BHQPY545 (Kello-1), Melkasa6Q and BHQP542). The remaining 36 varieties are normal maize varieties which are deficient in essential amino acid such as lysine and tryptophan. Lysine is the first limiting amino acid followed by tryptophan and threonine in the diets of non-ruminants and humans (Shimada and Cline, 1974). Lysine could also be limiting in poultry diet if protein sources (maize) other than soybean meal are used (Johnson et al., 2001). Substituting normal maize with high lysine maize on an equal weight basis can maintain proper amino acid balance (Wilson, 1991).

High proportion of zein (seed storage protein of maize) fraction which is completely devoid of lysine and tryptophan is the primary cause of poor protein quality in maize. A reduction in the zein fraction thus results in a proportional elevation of other fractions rich in lysine and an elevation of these two amino acids in protein,

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(Vassal, 2000). Therefore, for populations that depend heavily on maize as food source, maize cultivars with an improved amino acid profile must be developed. The discovery of mutant alleles, *opaque-2* (*o2*) (Mertz et al., 1964) by Purdue University researchers were found to alter the amino acid profile and composition of maize endosperm protein and result in twofold increase in the levels of lysine and tryptophan compared to what is encountered in normal maize genotypes. Yet, it expresses negative pleiotropic effects on the grain quality such as lower density, susceptibility to pests and diseases and a floury appearance (Vassal, 2001). The International Maize and Wheat Research Center (CIMMYT) has developed quality protein maize (QPM) that improves kernel quality characteristics over o2o2 soft genotypes, by introducing modifier genes and selecting for a hard, vitreous endosperm in o2o2 germplasm (Vassal, 2001).

Heterosis may be defined as the superiority of an F_1 hybrid over both of its parents in terms of yield and other characteristics (Bhat and Singh, 2005). Krivanek et al. (2007) declared that heterosis and combining ability is prerequisite for developing a good economically viable hybrid maize variety. Information on heterosis and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. Combining ability analysis is one of the powerful tools in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate productive genes. The objectives of this investigation were to estimate General combining ability (GCA) for parents and Specific combining ability (SCA) effects for single cross hybrids and to identify superior quality protein maize hybrids with good yield potential.

MATERIALS AND METHODS

The experiment was conducted at Ambo Agricultural Research Centers in 2011 cropping season. The experimental area at Ambo lies between 8°57' N latitude and 38°07' E longitude at an altitude of 2185 masl (EIAR, 2011). The soil of the centre is Vertisols consisting of 67% clay, 18% silt, 15% sand and 1.5% organic matter. The long term total annual rainfall is 1100 mm, with mean minimum and maximum temperatures of 11 and 26°C, respectively. A total of 12 experimental hybrids and two standard check varieties were used in this study. These experimental materials were obtained from Ambo high land maize breeding program, Ambo Plant Protection Research Center. The 12 experimental hybrids were generated by line x tester mating design between six QPM inbred lines and two testers. The parental inbred lines were developed by Ambo maize program through selfing from a QPM synthetic variety originally developed from highland inbred lines converted to QPM. QPM synthetic variety was developed by crossing highland inbred lines to QPM donor lines developed CIMMYT by diallel mating system. The lines (AMB06BSYN8Q6-2-4-1-2, AMB06BSYN8Q11-6-7-1-2, AMB06BSYN8 Q15-4-3-1-1, AMB06BSYN8Q 15-10-3-1-2, AMB06BSYN8Q18-7-3-1-2 and AMB06BSYN8Q19-12-1-2-2) were S4 generation stage and test crossed with QPM tester lines, CML144 and CML159. The resulting twelve crosses (AMB06BSYN8Q6-2-4-1-2/CML144, AMB06BSYN8Q11-6-7-1-2/CML144, AMB06BSYN8 Q15-4-3-1-1/CML144, AMB06BSYN8Q 15-10-3-1-2/CML144, AMB06BSYN8Q18-7-3-1-2/C ML144, AMB06BSYN8Q19-12-1-2-2/CML144, AMB06BSYN8Q6-2-4-1-2/CML159, AMB06BSYN8Q11-6-7-1-2/CML159, AMB06B SYN8Q15-4-3-11/CML159, AMB06BSY N8Q15 -10-3-1-2/CML159, AMB06BSYN8Q18-7-3-1-2/CML159, AMB06BSYN8Q19-12-1-2-2/CML159) and two standard checks viz., BHQP542 and a normal maize hybrid, Jibat (AMH851) were evaluated in a randomized complete block design with two replications in 2011 at Ambo. Each genotype was placed on one row plot of 5.1 m long with 30 cm intra row and 75 cm inter row spacing. The standard agronomic practices were adopted in order to ensure good crop stand. The recommended fertilizers rate 100 kg/ha DAP and 75 kg/ha UREA were applied. All of P_2O_5 and one -third of Nitrogen were applied at the time of planting. The remaining Nitrogen was divided in to two equal parts and applied 45 days after planting and at flag leaf stage.

Observations were recorded on days to 50% tasseling, days to 50% of silking, date of maturity, plant height, ear height, number of ears per plant, ear length, ear diameter, number of kernel rows per cob, number of kernels per row, 100-Grain weight, grain yield per plant, grain yield per hectare, protein (%), carbohydrate (%) and oil content (%). Observations for days to 50% tasselling and silking and grain yield were recorded on whole plot basis whereas for remaining characters data were taken on ten randomly selected competitive plants/ears from a plot and average values for each character were taken as the mean of the treatment. And the treatment mean was used for statistical analysis. Protein content (%), carbohydrate content (%) and oil content (%) were determined at Amhara Regional Agricultural Research institute (ARARI). The observations were recorded in the following manner.

Days to 50% tasseling

The number of days taking from emergence to the day on which 50% of plants in a treatment showing full tassel emergence were recorded as days to 50% tasseling.

Days to 50% silking

The number of days taking from the date of sowing to the day on which 50% of the plants in a treatment showing complete silk emergence were recorded as days to 50% of silking.

Date of maturity

The date when 50% of the plants whose husks are turned in to brown colour, was recorded as date of maturity.

Plant height (cm)

Plant height was expressed in centimeter by measuring the plant stalk from the ground level to the base of the last leaf sheath of the matured plant.

Ear height (cm)

Ear height was measured and recorded in centimeter as the length of plant from the ground level to the upper most ear bearing node.

Number of ears

The total number of ears per plant were counted and recorded.

Ear length (cm)

Length of the ear was measured and recorded in centimeter from the base to the tip of the ear at the time of harvest.

Ear diameter (cm)

Ear diameter was measured and recorded in centimeter as the thickness of the ear at the middle of the ear.

Number of kernel rows per cob

The number of kernel rows per cob were counted and recorded.

Number of kernels per row

Number of kernels in each kernel row was counted and average was recorded as number of kernels per row.

100-Grain weight (g)

Weight of 100 grains from a random sun dried sample from each plot was recorded in grams.

Grain yield per plant (g)

At the time of harvesting, fresh ear weight was recorded in kilo grams per plot. Grain yield per plot was calculated by using the formula given following. Grain yield per plant was calculated by dividing yield per plot to number of plants at the time of harvest.

$$\text{Yield per plot (kg/plot)} = \frac{\text{fresh ear weight x 100} - \text{AVM}}{\text{final stand harvest}} \text{ X K}$$

Where, $K = \frac{\text{average stand per plot of the trial x plot area x 0.9412}}{\text{100 x plot area}}$ and AVM = Average moisture.

Grain yield per hectare (ha)

At the time of harvesting, the cobs were recorded in each plot in kilograms. Grain yield per plot was converted in to yield per hectare and expressed in quintals per hectare by using the following formula.

$$\text{Yield (Q/ha)} = \frac{\text{fresh ear weight x 100} - \text{AVM}}{\text{final stand harvest}} \text{ X K}$$

Where, $K = \frac{\text{average stand of the trial x area (ha) x 0.9411}}{\text{100 x plot area}}$, and AVM = Average moisture

Determination of protein, carbohydrate and oil content

Three samples of maize kernels (25 g of each) were taken from each treatment. The protein, carbohydrate and oil content (%) of each sample was determined at ARARI quality laboratory using grain analyzer (near infrared spectrophotometer (NIRS)). The average of the three samples was used for statistical analysis.

The data were subjected to ANOVA using the SAS version 9. The magnitude of heterosis was estimated in relation to commercial check hybrid. It was calculated as percentage increase or decrease of the first filial generations (F1s) over the standard check (standard heterosis SC) using the methods of Turner (1953) and Hayes et al. (1955). The mean performance of the two checks in a given character was considered to work out the standard heterosis.

Heterosis over standard check (SC) = $\frac{F1 - SC}{SC} x100$

Where, F1 = mean performance of F1; SC = mean performance of the commercial checks. The combining ability variance analysis was based on the method developed by Kempthorne (1957).

RESULTS

Significant genetic differences ($p < 0.05$) were observed from mean squares of treatments for all traits except days to maturity, ear diameter, number of kernel rows per cob, protein content (%) and oil content (%) (Table 1) indicating the possibility carrying out genetic analysis. The analysis of variance for hybrids were highly significant for traits *viz*., plant height, ear height, days to 50% silking, days to 50% tasseling, ear length, number of kernels per row, 100-grain weight, grain yield per plant and grain yield per hectare, and significant for days to maturity, ear diameter, number of ears per plot and starch content (%) but exhibited non-significance for the remaining characters under study (Table 3).

Mean performances of hybrids

The mean performances of all 14 treatments (12 hybrids and the two checks) are shown in Table 2. The mean value of ear height for hybrids varied from 68 to 118.5cm. Five hybrids (HN1, HN2, HN6, HN7 and HN8) revealed higher ear height over the check BHQP542.For days to 50% silking and tasseling, all hybrids were late as compared to check Jibat and ten hybrids for days to 50% silking and eleven hybrid for days to 50% tasseling were early as compared to check BHQP542 with a range of 97.5 to 107.5 days for days to 50% silking and 96.5 to 109.5 days for days to 50% tasseling. One hybrid (HN8) exhibited higher ear length than check BHQP542 with a range of 9.39 to 16.4 cm. Four hybrids (HN1, HN9, HN11 and HN12) revealed higher 100-grain weight than the check BHQP542.Two hybrids (HN7 and HN8) disclosed significantly higher yield in quintal per hectare than BHQP542. The magnitude of grain yield per plant varied from 55.17 g (HN3) to 217.99 g (HN1) and only hybrid (HN1) had expressed significantly higher grain yield per plant over BHQP542.

Combining ability

The variation due to hybrids was further partitioned into lines, testers and line x tester interaction. The variance due to lines was statistically significant ($p < 0.05$) for all traits except for grain yield per plant, 100-grain weight,

Table 1. Analysis of variance of 14 treatments for 16 traits.

Source variation	Df	PH	EH	DSS	DST	DSM	EL	ED	NKR	NK	NCP	GW	GYH	GYP	PC	SC	OC
Replication	1	305.0	0.32	1.75	1.75	1.3	4.9	0.01	2.90	3.57	116.00	3.05	178.5	681.6	0.54	0.11	0.06
Genotypes	13	8219.7**	801.90**	43.86**	41.29**	20.7	8.7**	0.08	1.34	476.00**	64.90*	82.20**	1063.3**	4661.7**	1.54	1.05*	0.20
Error	13	1680.0	124.50	6.05	5.59	10.4	1.1	0.05	0. 79	1.96	16.88	16.80	189.8	720.9	0.60	0.28	0.11
R		0.83	0.86	0.87	0.88	0.67	0.89	0.61	0.61	0.96	0.81	0.83	0.85	0.86	0.72	0.78	0.65
CV (%)		14.10	11.40	2.45	2.38	1.80	7.40	5.30	7.60	4.43	21.90	14.10	24.45	17.44	7.70	0.77	6.50
F		4.89	6.44	7.24	7.38	1.99	6.93	1.61	1.39	22.88	3.84	4.89	5.60	6.47	2.56	3.65	1.85

*, **; Significant at 0.05 and 0.01 levels of probability, respectively. PH, plant height (cm), EH, ear height(cm); DSS, days to 50% silking; DSM, days to maturity; DST, days to tasseling; EL, ear length (cm); ED, ear diameter (cm); NKR, number of kernel rows per cob; NK, number of kernels per row; NCP, number of cobs per plot; GYH,grain yield per hectare; GYP, grain yield per plant; GW, 100 grain weight (g); PC, protein content (%); SC, starch content (%); OC, oil content (%) for all tables..

Table 2. Mean performance of 14 treatments (12 hybrids and 2 check hybrids) for twelve traits at Ambo.

Hybrid no.	PH	EH	DSS	DST	NCP	GW	EL	NK	GYH	GYP	SC
HN1	222.5	114.5	98.0	98.0	21.0	33.4	14.10	31.5	70.90	217.99	68.35
HN2	234.5	113.5	100.0	98.0	26.5	25.7	15.20	32.0	54.31	131.98	69.25
HN3	143.0	68.0	110.5	109.5	11.0	25.9	9.39	32.0	15.15	55.17	69.10
HN4	212.5	97.0	97.5	97.5	10.0	29.4	14.20	35.5	36.48	154.87	68.10
HN5	220.5	102.0	102.5	102.0	20.5	28.2	13.85	31.5	59.45	188.14	68.15
HN6	217.5	113.0	98.5	97.5	24.5	21.7	14.65	32.0	69.42	156.19	69.90
HN7	234.0	118.5	97.5	97.0	22.5	30.5	15.35	31.5	80.91	182.10	68.70
HN8	238.0	118.5	98.5	97.0	21.0	31.7	16.40	35.5	79.23	178.28	70.05
HN9	209.5	91.0	98.0	96.5	13.5	40.9	15.20	35.0	48.99	155.24	69.90
HN10	126.0	49.0	107.5	106.5	10.0	30.8	9.90	31.0	14.66	56.01	69.00
HN11	203.5	103.5	100.5	99.5	18.0	33.9	15.20	31.5	59.79	176.55	68.45
HN12	214.5	104.5	100.0	99.0	19.5	34.6	14.90	30.5	60.31	156.76	70.05
HN13	181.0	98.5	90.5	90.5	27.5	34.4	16.30	37.5	92.26	207.58	69.05
HN14	203.0	84.0	101.0	100.5	15.0	23.5	13.30	34.5	42.68	136.13	69.95
LSD (0.05)	88.5	24.1	5.3	5.1	8.87	8.85	2.26	3.0	29.75	57.99	1.14
LSD (0.01)	123.6	33.6	7.4	7.1	12.37	12.3	3.15	4.2	41.49	80.87	1.59

HN1, AMB06BSYN8Q6-2-4-1-2/CML144; HN2, AMB06BSYN8Q11-6-7-1-2/CML144; HN3, AMB06BSYN8Q15-4-3-1-1/CML144; HN4, AMB06BSYN8Q15-10-3-1-2/CML144; HN5,AMB06BSYN8Q18-7-3-1-2/CML144; HN6,AMB06BSYN8Q19-12-1-2-2/CML144; HN7, AMB06 BSYN8Q6-2-4-1-2/CML159; HN8,AMB06BSYN8Q11-6-7-1-2/CML159; HN9,AMB06BSYN8Q15-4-3-1-1/CML159; HN10, AMB06BSYN8Q15-10-3-1-2/CML159; HN11, AMB06BSYN8Q18-7-3-1-2/ CML159 ; HN12, AMB06BSYN8Q19-12-1-2-2/CML159; HN13, Jibat check and HN14, BHQP542 check, for all tables.

number of kernel rows per ear and protein content (%). Variance due to testers was statistically significant ($p < 0.05$) for days to maturity, ear length, ear diameter, number of kernel rows per cob, 100-grain weight and protein content (%). Variance due to line x tester interaction was

Table 3. Line x tester analysis of 12 hybrids for sixteen traits.

Source of variation	*Df*	PH	EH	DSS	DST	DSM	EL	ED	GYP	NKR	NK	NCP	GW	GYH	PC	SC
Hybrids (H)	11	2497.4**	907.2**	34.8**	33.70**	22.98*	9.3**	0.09*	4908.80**	1.40	43.75**	65.1*	79.2**	977.30**	1.59	1.15*
Lines (L)	5	3024.9**	1407.7**	23.5*	22.28**	33.26*	9.1**	0.11*	612.90	1.00	17.96**	129.3**	16.7	1664.70**	0.74	2.14**
Testers (T)	1	104.2	88.2	4.2	7.04	66.70*	5.2**	0.32**	1.13	8.20*	1.50	13.5	242.5**	243.50	8.52**	1.50
L x T	5	2448.5	572.1**	52.2*	52.80**	3.96	10.4**	0.03	2119.20	0.91	78.00**	11.3	109.2**	436.60	1.05	0.10
Error	11	144.2	143.2	6.5	1.83	7.85	1.3	0.03	845.40	1.12	2.31	19.5	15.2	205.00	0.66	0.31

*, **; Significant at 0.05 and 0.01 levels of probability, respectively.

Table 4. Estimates of the variance due to GCA, SCA, dominance variance and additive variance for 16 traits.

Genetic parameter	PH	EH	DSS	DST	DSM	EL	ED	NKR	NK	NCP	GW	GYH	GYP	PC	SC	OC
σ^2_{GCA}	79.30	37.10	0.63	0.62	1.21	0.05	0.01	0.07	0.47	3.43	1.69	44.6	15.97	0.06	0.06	0.01
σ^2_{SCA}	1152.10	214.40	22.80	25.50	-1.93	4.50	-0.001	-0.11	37.84	-4.10	47.00	115.7	636.90	0.19	-0.11	-0.02
$\sigma^2_{GCA}/\sigma^2_{SCA}$	0.07	0.17	0.03	0.02	0.62	0.01	9.00	-0.66	0.01	-0.80	0.04	0.4	0.03	0.32	-0.60	-0.50
σ^2_A	317.20	148.50	2.50	2.48	4.84	0.18	0.02	0.28	1.88	13.70	6.76	178.5	63.90	0.25	0.25	0.04
σ^2_D	1152.10	214.40	22.80	25.50	-1.93	4.50	-0.001	-0.11	37.84	-4.10	47.00	115.7	636.90	0.19	-0.11	-0.02
σ^2_A/σ^2_D	0.28	0.69	0.11	0.09	-2.50	0.04	36.00	2.60	0.05	-3.35	0.14	1.5	0.10	1.30	-2.40	2.00

significant for ear height, days to 50% silking, days to 50% tasseling, ear length, number of kernels per row and 100-grain weight. Specific combining ability variance was important than general combining ability variance for all traits indicating preponderance of dominance variance in controlling these characters. The SCA variance to GCA variance ratio was lower than unity, which again confirms the predominance of non -additive gene action for the inheritance of these characters (Table 4).

General combining ability (GCA) effect

Estimation of GCA effect revealed that no parent was observed to be good general combiner for most traits (Table 5). However, the GCA effect for days to 50% tasseling and days to 50% silking recorded in the parental line LN1 and LN2 was significant and in the negative direction indicating the earliness of the parental lines. Similarly, LN1 was good general combiner for plant height, ear height and grain yield in quintal per hectare. LN2 had also expressed highest significant GCA effects for plant height, ear height, ear length and number of cobs per plot in positive direction. LN6 was good general combiner for starch content (%). Tester CML159 revealed significant GCA effects for 100-grain weight.

Specific combining ability (SCA) effect

A critical evaluation of the results with respect to SCA effects showed that none of the hybrid revealed desirable significant SCA effects for most characters (Table 6). But hybrid HN4 divulged significant SCA effect for plant height, ear height and ear length and HN9 also showed significant SCA effect for plant height and ear length. Hybrid HN4 and HN9 also exhibited negative significant SCA effects for days to 50% silking and tasseling. HN3 and HN10 had expressed negative significant SCA effects for plant height and ear height and positive significant SCA effects for days to 50% silking and tasseling.

Magnitude of heterosis over the two checks

The results of standard heterosis for different characters that had significant mean square are presented in Table 7. The percent of heterosis

Table 5. General combining ability (GCA) effects of parents in respect of eleven characters.

Line no.	PH	EH	DSS	DST	EL	NKR	NCP	GW	GYH	GYP	SC
LN1	21.90**	17.08*	-3.00*	-2.40**	0.70	-0.96	3.60	1.40	21.80*	49.10*	-0.56
LN2	29.90**	16.60*	-1.50	-2.10**	1.80**	1.29	5.60*	-1.90	12.60	4.20	0.57
LN3	-30.10**	-19.90**	3.50*	3.10**	-1.70	1.04	-5.90*	2.80	-22.10*	-45.70	0.42
LN4	-37.10**	-26.40**	1.75	2.10**	-1.90**	0.79	-8.20**	-0.50	-28.60*	-45.50	-0.53
LN5	5.70	3.30	0.75	0.90	0.50	-0.96	1.10	0.50	5.50	32.40	-0.78*
LN6	9.70	9.30	-1.50	-1.60	0.70	-1.21	3.80	-2.40	10.70	5.50	0.89*
SEm±	6.00	5.90	1.27	0.67	0.57	0.75	2.20	1.90	7.16	14.50	0.27
LSD (0.05)	13.20	12.98	2.79	1.47	1.25	1.65	4.80	4.18	15.60	31.90	0.59
LSD (0.01)	18.60	18.30	3.90	2.08	1.77	2.33	6.80	5.90	22.20	45.04	0.83
Testers											
CML144	-2.08	1.90	0.42	0.54	-0.50	-0.04	0.80	-3.20*	-3.20	-0.22	-0.28
CML159	2.08	-1.90	-0.42	-0.54	0.50	0.04	-0.80	3.20*	3.20	0.22	0.28
SEm±	3.50	3.50	0.70	0.39	0.32	0.40	1.27	1.10	4.13	8.39	0.16
LSD (0.05)	7.70	7.70	1.54	0.85	0.70	0.88	2.79	2.42	9.09	18.47	0.35

*, **; Significant at 0.05 and 0.01 levels of probability, respectively; LN1, AMB06BSYN8Q6-2-4-1-2, LN2, AMB06BSYN8Q11-6-7-1-2, LN3, AMB06BSY N8Q15-4-3-1-1, LN4, AMB06BSYN8Q15-10-3-1-2, LN5, AMB06BSYN8Q18-7-3-1-2; LN6, AMB06BSYN8Q19-12-1-2-2, for all tables.

Table 6. Specific combining ability (SCA) effects of test cross hybrids of maize in respect of eleven characters

Hybrid no.	PH	EH	DSS	DSM	EL	NKR	NK	NCP	GYH	GW	SC
HN1	-7.80	-3.90	-0.20	-0.04	-0.20	0.40	0.04	-1.50	-1.80	4.70	0.10
HN2	-3.80	-4.40	0.30	-0.29	-0.10	0.30	-1.71	2.00	-9.30	0.20	-0.13
HN3	-35.30**	-13.40	5.80**	5.96**	-2.40*	0.20	-1.46	-2.00	-13.70	-4.30	-0.13
HN4	41.20**	22.10*	-5.40*	-5.04**	2.60**	0.20	2.29	-0.75	14.10	2.50	-0.18
HN5	6.10	-2.70	0.60	0.71	-0.20	-0.10	0.04	0.50	3.00	0.30	0.13
HN6	-0.60	2.30	-1.20	-1.29	0.30	-0.30	0.79	1.75	7.70	-3.30	0.20
HN7	7.80	3.90	0.20	0.04	0.20	0.40	-0.04	1.50	1.80	-4.70	-0.10
HN8	3.80	4.40	-0.30	0.29	0.10	0.30	1.71	-2.00	9.30	-0.20	0.13
HN9	35.30**	13.40	-5.80**	-5.96**	2.40*	-0.20	1.46	2.00	13.70	4.30	0.13
HN10	-41.20**	-22.10*	5.40*	5.04**	-2.60**	-0.20	-2.29	0.75	-14.10	-2.50	0.18
HN11	-6.40	2.70	-0.60	-0.71	0.20	0.10	-0.04	-0.50	-3.00	-0.30	-0.13
HN12	0.60	-2.30	1.20	1.29	-0.30	0.30	-0.79	-1.75	-7.70	3.30	-0.20
SEm±	8.50	8.50	1.80	0.95	0.80	0.70	1.07	3.10	10.12	2.75	0.39
LSD (0.05)	18.70	18.70	3.96	2.09	1.76	1.54	2.35	6.82	22.27	6.05	0.85
LSD (0.01)	26.40	26.40	5.59	2.95	2.48	2.17	3.32	9.62	31.43	8.54	1.21

*and**; Significant at 0.05 and 0.01 levels of probability.

Table 7. The nature and magnitude of heterosis for candidate hybrids relative to two checks.

Hybrid no.	PH		EH		EL		NKR		GW		DSS	
	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542
HN1	22.93	9.61	16.24	36.31**	-13.50**	6.01**	Jibat	BHQP542	-2.79**	42.28**	8.29**	-2.49
HN2	29.56	15.52	15.23	35.12**	-6.75**	14.29**	-16.00**	-8.69**	-25.39**	9.19*	8.29**	-2.49
HN3	-20.99	-29.56	-30.96*	-19.05	-42.39**	-29.39**	-14.67**	-7.23**	-24.83**	10.02*	20.99**	8.95**
HN4	17.40	4.68	-1.52	15.48	-12.88**	6.77**	-14.67**	-7.23**	-14.65**	24.91**	7.73**	-2.98
HN5	21.82	8.62	3.55	21.43	-15.03**	4.14**	-5.33**	2.89	-17.98**	20.04**	12.71**	1.49
HN6	20.17	7.14	14.72	34.52**	-10.12**	10.15**	-16.00**	-8.69**	-37.05**	-7.87	7.73**	-2.98
HN7	29.28	15.27	20.30	41.07**	-5.83**	15.41**	-14.67**	-7.23**	-11.44*	29.62**	7.18*	-3.48
HN8	31.49	17.24	20.30	41.07**	0.61	23.31**	-16.00**	-8.69**	-7.79	34.96**	7.73**	-2.98
HN9	15.75	3.20	-7.61	8.33	-6.75**	14.29**	-5.33**	2.89	18.82**	73.91**	6.63*	-3.98
HN10	-30.39	-37.92	-50.25**	-41.67**	-39.26**	-25.56**	-6.67**	1.45	-10.59*	30.85**	17.68**	5.97*
HN11	12.43	0.25	5.08	23.21	-6.75**	14.89**	-17.33**	-10.14**	-1.42	44.27**	9.94**	-0.99
HN12	18.51	5.67	6.09	24.21*	-8.59**	12.03**	-16.00**	-8.69**	0.73	47.42**	9.39**	-1.49
SEm±	40.99		11.16		1.05		1.4		1.05		2.36	
CD at 5%	88.50		24.10		2.26		3.00		2.26		5.30	
CD at 1%	123.50		33.60		3.15		4.20		3.15		7.40	

Hybrid no.	GW		DSS		GYP		GYH		SC		NCP	
	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542
HN1	-2.79**	42.28**	8.29**	-2.49	5.01	60.13*	-23.18	66.03**	-1.01	-2.29**	-23.63**	40.00**
HN2	-25.39**	9.19*	8.29**	-2.49	-36.42	-3.04	-41.13*	27.23	0.29	-1.00	-3.63	76.67**
HN3	-24.83**	10.02*	20.99**	8.95**	-73.42**	-59.47*	-83.58**	-64.50**	0.07	-1.21*	-60.00**	-26.67**
HN4	-14.65**	24.91**	7.73**	-2.98	-25.39	13.77	-60.45**	-14.53	-1.38*	-2.64**	-63.63**	-33.33**
HN5	-17.98**	20.04**	12.71**	1.49	-9.36	38.20	-35.55*	39.29*	-1.30*	-2.57**	-25.45**	36.67**
HN6	-37.05**	-7.87	7.73**	-2.98	-24.76	14.74	-24.77	62.63**	1.23*	-0.07	-10.91**	63.33**
HN7	-11.44*	29.62**	7.18*	-3.48	-12.28	33.77	-12.29	89.56*	-0.51	-1.79**	-18.18**	50.00**
HN8	-7.79	34.96**	7.73**	-2.98	-14.11	30.97	-14.12	85.63*	1.45*	0.14	-23.63**	40.00**
HN9	18.82**	73.91**	6.63*	-3.98	-25.21	14.04	-46.90**	14.77	1.23*	-0.07	-50.91**	-10.00*
HN10	-10.59*	30.85**	17.68**	5.97*	-73.02**	-58.85*	-84.10**	-65.64**	-0.07	-1.36*	-63.63**	-33.33**
HN11	-1.42	44.27**	9.94**	-0.99	-13.98	31.17	-35.19*	40.08*	-0.87	-2.14**	-34.54**	20.00**
HN12	0.73	47.42**	9.39**	-1.49	-24.48	15.15	-34.63*	41.29*	1.45*	0.14	-29.09**	30.00**
SEm±	1.05		2.36		26.85		13.78		0.53		4.11	
CD at 5%	2.26		5.30		57.99		29.75		1.14		8.87	
CD at 1%	3.15		7.40		80.87		41.49		1.59		12.37	

*and **; Significant at 0.05 and 0.01 levels of probability, respectively.

over the two standard checks (Jibat and BHQP542) for plant height ranged from -30.39 to 29.56 cm and -37.92 to 17.24 cm, respectively. Five hybrids (HN1, HN2, HN7, HN8 and HN9) had significant positive standard heterosis over BHQP542 and two hybrids (HN3, HN10) revealed significant negative standard heterosis over Jibat for ear height. HN7 and HN8 had expressed the highest significant positive standard heterosis (41.07%) followed by HN1 (36.31%) for this trait. For ear length, two hybrids HN3 and HN10 exhibited significant negative standard heterosis over Jibat and BHQP542 and one hybrid HN8 (23.1%) exhibited significant positive standard heterosis over BHQP542.

Out of twelve hybrids, none of them revealed significant positive standard heterosis over Jibat and BHQP542 for number of kernels per row. Nine hybrids divulged significant negative standard heterosis over Jibat. These hybrids had revealed negative standard heterosis over the check BHQP542 but they are non-significant. Significant positive standard heterosis was observed in four hybrids (HN1, HN9, HN11 and HN12) for 100 grain weight over BHQP542 and one hybrid HN6 had significant negative standard heterosis over Jibat.

Significant standard heterosis was mostly in negative direction for days to 50% tasselling and silking over BHQP542 except (HN3, HN5 and HN10). The maximum negative heterosis for days to 50% tasselling and silking was recorded for hybrid HN8 followed by hybrid HN12. But significant standard heterosis for all hybrids was in positive direction for days to 50% tasselling and silking over Jibat.

Only hybrid HN1 (60.13%) had showed large magnitude of significant standard heterosis for grain yield per plant over the check BHQP542. For grain yield in quintal per hectare, two hybrids HN7 (89.56%) and HN8 (85.63%) revealed significant positive standard heterosis compared to check BHQP542 and six hybrids had expressed significant negative standard heterosis compared to check Jibat.

DISCUSSION

The study revealed considerable variability in treatments as well as hybrids which is encouraging for selection of desirable genotypes. Differences among lines and testers were statistically significant for most traits. This indicates that the inbred lines behaved differently in their respective hybrids, and that greater diversity exists between the two testers. Similarly, significant line x tester interaction indicated that the inbred lines performed differently in their respective hybrids depending on the type of testers used for these traits. These results are in line with Mosa (2010) conclusions.

There was preponderance of SCA variances showing the greater importance of non-additive genetic component in the inheritance of studied traits. Alamnie et al. (2003), Wali et al. (2010) and Sofi and Rather (2006) reported that SCA variance was dominance for the inheritance of yield and yield component traits.

The present results indicated that LN1 was obtained superior for GCA effects for grain yield, plant height and ear height. LN2 provided important GCA effects for plant height, ear height, ear length and number of cobs per plot. Ahmad and Saleem (2003) reported that the inbred parent TZI-7103 had eminent GCA effects for half of the traits including grain yield. The GCA effects for days to 50% tasseling and days to 50% silking recorded in the parental line LN1 and LN2 were significant and in the negative direction indicating the earliness of the parental lines. Uddin et al. (2006) and Sundararajan and Kumar (2011) revealed the importance of negative GCA effect for days to 50% tasseling and days to 50% silking to develop early maturing varieties.

The specific combining ability effect is an essential criterion to determine the usefulness of hybrids. HN4 and HN9 had significant negative SCA effects for days to 50% tasseling and days to 50% silking showing their earliness. Uddin et al. (2006) described eleven and fourteen hybrids exhibited significant negative SCA effects for days to 50% tasseling and days to 50% silking, respectively indicating early maturing.

Hybrid HN7 and HN8 showed significant negative standard heterosis for days to 50% tasseling and days to 50% silking and at the same times they had significant standard heterosis for grain yield in quintal per hectare over BHQP542. Uddin et al. (2006) observed similar results.

CONCLUSION AND RECOMMENDATION

Considerable variability was observed in treatments and hybrids that show selection process is desirable. Statistical significance differences were examined in lines, testers and line x tester interaction for most traits showing lines behaved differently in their hybrids depending on the type of tester involved. SCA variance played greater role in controlling most of the studied characters.

LN1 was higher for GCA effects for grain yield in quintal per hectare and it had negative significant GCA effects for days to 50% tasseling and days to 50% silking and it can be used to develop high yielding early maturing variety.

SCA effects for days to 50% tasseling and days to 50% silking were in the negative direction for hybrid HN4 and HN9 indicating they are early maturing hybrids. HN7 and HN8 revealed higher standard heterosis for grain yield per hectare as compared to quality protein maize standard check and they had negative standard heterosis for days to 50% tasseling and days to 50% silking. So HN7 and HN8 could be recommended for commercial utilization.

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