Combing ability, Gene Action and Heterosis Estimation in Quality Protein Maize

Melkamu Elmyhum (MSc)*, Tadsse Dessalegn (PhD), Yigzaw Dessalegn (PhD)*****

*Amhara Regional Agricultural Research Institute at Adet Agricultural Research Center, Bahir dar, Ethiopia. Email: elmyhunmelkamu@yahoo.com or melke2005@yahoo.com
**Bahir dar University, Deprtment of plant sciences, Bahir dar, Ethiopia. Email: tadesseyfb@yahoo.com
*** Amhara Regional Agricultural Research Institute (ARARI), DGD of ARARI, Bahir dar, Ethiopia. Email: yigzawdessalegn@yahoo.com

Abstract- Maize is a major cereal for human nutrition in Ethiopia. For communities that rely heavily on maize as the main staple, development of maize cultivars with enhanced levels of two essential amino acids such as lysine and tryptophan are a must. The objectives of the study were to find out the combining ability, the nature and magnitude of gene action and heterosis of quality protein maize inbred lines. Six inbred lines and two testers were crossed 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 2011 at Adet. Although it was a one season trial, LN1, LN2 and LN5 were good general combiners for grain yield and yield component characters and can be used for development of hybrids. Hybrid HN7 (81.1%), HN8 (107.3%) and HN11 (88.3%) had higher magnitude of heterosis over the quality protein maize check but these hybrids were not superior over the normal maize check. From this result hybrid HN7, HN8 and HN11 can be exploited for future use and additional effort is required for the development of competent quality protein maize.

Index Terms- general combining ability, line by tester and specific combining ability

I. INTRODUCTION

Maize (Zea mays L.) is one of the important cereal crop grown in Ethiopia. In 2011/12 cropping season, maize is the first in total production over 6 million tonnes, and with yield per unit area 2.9 tonnes per hectare and second in area coverage among all the cereal crops (CSA, 2011/12). It is an essential food source in Ethiopia. All maize produced used for food. But almost all maize varieties cultivated in the country are normal maize varieties which are devoid of essential amino acids such as lysine and tryptophan. Million of smallholder farmers in the major maize producing regions of Ethiopia depend on maize for their daily food throughout the year and they have almost no access to protein sources like meat, eggs and milk for their daily consumption (Dereje *et al.*, 2001). One of the main nutritional limitations of normal maize is its poor nutritional profile because of a deficiency in essential amino acids such as lysine, tryptophan and methionine and an undesirable ratio of leucine and isoleucine (Bajaj *et al.*, 2007). Therefore, maize is a poor source of protein for both humans and monogastric animals. Thus, for communities that rely heavily on maize as the main staple, maize cultivars with an improved amino acid profile are a must.

Identification of opaque-2 gene (o2) can help the development of Quality protein maize (QPM) which solves the nutritional problem of normal maize. The mutant gene (o2) alters amino acid profile and composition of maize endosperm protein and result in two-fold increase in the levels of lysine and tryptophan compared to what is encountered in normal maize genotypes (Mertz, 1992; Villegas *et al.*, 1992). Because of the increase in concentration of these two essential amino acids, increased digestibility and increased nitrogen uptake relative to normal-endosperm maize (Mertz, 1992).

Heterosis is the phenomenon in which the cross of two inbreed lines produce hybrid that is superior in growth, size yield, or vigor of the F1 over the better parent (Lippman and Zamir, 2007). 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 objective of this study was to find out the combining ability, the nature and magnitude of gene action and heterosis of quality protein maize inbred lines.

II. MATERIALS AND METHODS

The experiment was conducted at Adet Agricultural Research Center in 2011 cropping season. The experimental area at Adet is located within 11°17 'N latitude and 37 ° 43' longitude E at an altitude of 2240 masl. The soil type of the centre is Nitosol with pH 5.43. The long term total annual rainfall is 1091 mm, with an average minimum and maximum temperature of 18.2°C and 25.3°C, respectively. A total of 14 maize germplasms were used in this study. These germplasms were obtained from the Ambo National Maize Research centre. The lines were developed through selfing from a QPM synthetic variety originally developed from highland inbred lines converted to QPM by crossing to QPM donor lines developed CIMMYT by diallel mating system. The lines were S4 generation stage and test crossed with QPM tester lines, CML144 and CML159. The resultant twelve crosses (AMB06BSYN8Q6-2-4-1-2/CML144, AMB06BSYN8Q11-6-7-1-2/CML144, AMB06BSYN8Q15-4-3-1-1/CML144, AMB06BSYN8Q15-10-3-1-2/CML144, AMB06BSYN8Q18-7-3-1-2/CML144, AMB06BSYN8Q19-12-1-2-2/CML144, AMB06BSYN8Q6-2-4-1-2/CML159, AMB06BSYN8Q11-6-7-1-2/CML159, AMB06BSYN8Q15-4-3-1-1/CML159, AMB06BSYN8Q15-10-3-1-2/CML159, AMB06BSYN8Q18-7-3-1-2/CML159, AMB06BSYN8Q19-12-1-2-2/CML159) were evaluated with two standard checks viz., BHQP542 and a normal maize hybrid, Jibat (AMH851) in a randomized complete block design with two replications in 2011 at Adet. Each plot had one row each 5.1 m long. The standard of agronomic practices was adopted in order to ensure good crop stand. The recommended fertilizers rate 100kg/ha DAP and 75kg/ha UREA were applied. All of P_2O_5 and half of Nitrogen were applied at the time of planting. The remaining half of Nitrogen was applied 45 days after planting. Observations were recorded on days to 50 per cent tasseling, days to 50 percent 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, moisture content (%), 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 (%), carbohydrate (%) and oil content (%) were determined at Amara Regional Agricultural Research institute (ARARI).

III. RESULTS

The analysis of variance revealed that mean squares for entries were significant for all traits except ear length, ear diameter, number of kernels per row and yield per plant, signifying the presence of genetic variability among genotypes (Table 3.1). Analysis of variance for hybrids revealed that the mean sum of squares were highly significant for plant height, number of cobs per plot, 100-grain weight, protein content (%), starch content (%) and oil content (%), and significant for ear height, days to maturity, grain yield per ha and number of kernel rows per cob (Table 3.3) indicating that the tested hybrids varied from each other.

1.1. Mean performance

The mean value of plant height for hybrids varied from 150 cm for HN3 to 235 cm for HN11. Eleven hybrids showed significant plant height over check BHQP542 and all hybrids were shorter than check hybrid Jibat. Five hybrids were longer in ear height over the check BHQP542 and all hybrids produced shorter ear height than Jibat with range of 95cm to120cm. All hybrids were late in silking and tasseling as compared to check Jibat. But four and three hybrids were early in silking and tasseling with a range of 100 days to 107 days and 96.5 days to 105 days over check BHQP542, respectively.

The number of kernel rows per cob ranged from 12.7 (HN12) to 14.8 (HN1). All hybrids had higher number of kernel rows per cob than check BHQP542 whereas none of the hybrids exhibited higher number of kernel rows per cob than check Jibat. The number of cobs per plot varied from 8.5 (HN1 and HN9) to 19(HN8). Seven hybrids showed higher number of cobs per plot than check BHQP542 and one hybrid (HN8) disclosed more number of cobs per plot than both checks.

Hundred grain weight ranged from 18.8g (HN6) to 57.6g (HN10) and all hybrids were not superior to the two checks. Grain yield (Qha^{-1}) varied 15.8(HN3) to 63.9 (HN8) and six hybrids had better grain yield (Qha^{-1}) performance than BHQP542.

Six and four hybrids had higher protein content (%) over the check Jibat and BHQP542, respectively with range of 7.7% (HN9) to 10.3% (HN3). The range of starch content (%) was from 68.1(HN3) to 73.1(HN6). Two hybrids had higher starch content (%) over Jibat and one hybrid over the two checks. The oil content (%) of twelve hybrids varied from 3.35 to 5.25 and ten hybrids had higher oil content than only check Jibat.

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

Source variation	*Df*	PH	EH	DSS	DST	DSM	EL	ED	NKR	NK	GW	NCP	GYH
Replication	1	1032.1	0.32	0.89	0.89	36.6	12.1	0.092	0.87*	10.8	124.32	15.2	318.6
Entries	13	1959**	435.8*	20.9**	20.96**	60.7*	13.6	0.127	1.64**	65.7	2376009.6**	31.2**	387.3**
Error	13	249.4	149.6	3.35	3.4	16	6.45	0.065	0.18	26.2	962.9	7.1	92.1
R		0.89	0.74	0.86	0.86	0.79	0.69	0.67	0.90	0.71	0.99	0.81	0.81
CV		7.6	11.5	1.77	1.77	2.58	17.99	7.36	3.1	16.14	3.89	22	23.1
F		7.85	2.91	6.25	6.25	3.78	2.1	1.94	8.87	2.51	2467.64	4.38	4.2

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

Table 1. *Continued*

SOURCE VARIATION	*Df*	GYP	PC	SC	OC
Replication	1	664.9	0.09	1.75	0.006
Entries	13	1804.9	1.61**	4.19**	0.790**
Error	13	882.7	0.10	0.21	0.035
R		0.67	0.94	0.95	0.95
CV (%)		26.10	3.60	0.65	4.05
F		2.04	15.71	19.48	22.3

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

Where 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 (%) and OC=oil content (%), for all tables

Table 2. Mean performances of 14 entries (12 hybrids and 2 check hybrids) for twelve traits.

Hybrid No	PH	EH	DSS	DST	DSM	NKR	NCP	GW	GYH	PC	SC	OC
HN1	227.5	115.0	101.0	100.0	156.5	14.8	8.5	51.9	33.7	9.20	70.25	4.35
HN2	212.5	107.5	104.0	101.5	152.5	14.6	14.0	38.8	35.8	8.50	71.80	4.45
HN3	150.0	95.0	105.5	105.0	145.0	13.9	14.0	36.9	15.8	10.30	68.10	5.25
HN4	212.5	107.5	107.0	102.0	151.0	13.9	13.0	20.7	35.4	10.25	69.20	5.25
HN5	230.0	107.5	104.0	102.0	160.0	12.9	13.0	30.5	47.6	9.95	69.50	4.85
HN6	217.5	110.0	102.0	101.0	150.0	13.1	17.0	18.8	49.4	8.25	73.10	3.70
HN7	220.0	115.0	102.5	100.0	163.5	14.6	12.0	41.5	55.9	8.10	70.20	4.90
HN8	215.0	120.0	100.0	96.5	157.5	14.0	19.0	60.5	63.9	9.05	70.25	4.85
HN9	220.0	112.5	104.0	100.5	161.0	13.3	8.5	33.7	36.1	7.70	72.15	3.35
HN10	217.5	107.5	107.0	101.0	146.0	13.8	9.5	57.6	21.9	10.25	68.55	5.25
HN11	235.0	122.5	102.5	99.5	156.5	14.0	16.5	34.7	58.1	8.55	68.95	5.25
HN12	222.5	106.0	100.5	98.5	159.0	12.7	11.5	30.9	46.9	8.05	70.55	4.90
HN13	235.0	117.5	95.5	93.5	157.5	12.0	14.0	33.8	50.7	8.45	71.00	3.85
HN14	185.0	92.5	106.0	102.5	155.0	14.8	7.5	21.5	30.8	9.15	71.60	5.00
LSD (0.05)	24.65	18.93	2.86	2.86	6.16	0.92	4.18	46.2	14.96	0.48	0.70	0.28
LSD (0.01)	34.79	26.70	4.00	4.00	8.69	1.28	5.9	68	18.6	0.68	0.99	0.40

Where, 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= AMB06BSYN8Q6-2-4-1-2/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.

1.2. Analysis of Variance for combining ability

Lines significantly differed for all traits except for days to 50% tasseling, ear length, ear diameter, grain yield per plant and number of kernels per row. Testers significantly varied in days to 50% tasseling, plant height, days to maturity, yield per plant, grain yield per ha, protein content (%), starch content (%) and oil content (%).The line x tester interaction was significant for plant height, ear height, days to maturity, number of kernels per row, protein content (%), starch content (%) and oil content (%)(Table 3.3).

Specific Combining Ability (SCA) variance was higher than General Combining Ability (GCA) variance for all traits indicating predominance of dominance variance in controlling studied 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 the characters (Table 3.4). The ratio of additive to dominance variance was greater than unity for days to 50% silking, days to 50% tasselling, 100-grain weight and grain yield per plant indicative of equal importance of additive and non-additive gene action for these traits. It was less than unity for the remaining characters indicating the role of dominant genetic components than the additive component of variation.

1.2.1. General combining ability (GCA) effect

Estimates of GCA effects for sixteen characters are presented in Table 3.5. Line LN1 and LN2 were good general combiner for number of kernel rows per cob, number of cobs per plot and 100-grain weight. For grain yield (Qha^{-1}) trait significant and highest GCA effect was recorded in parental line LN5 and it showed significant GCA effects for plant height, protein content (%) and oil content (%). Line LN6 revealed significant positive GCA effect for starch content (%). Tester CML 159 had revealed significant positive GCA effects for 100-grain weight and oil content (%) but it had significant negative GCA effect for protein content (%).Tester CML144 had significant positive GCA effect for protein content.

1.2.2. Specific combining ability (SCA) effects

A critical evaluation of the results with respect to SCA effects showed that none of the hybrid revealed desirable significant SCA effects for all the characters (Table 3.6). However; hybrid HN3, HN8 and HN10 were good specific combiners for protein content (%). Likewise, for starch content (%) hybrid HN2 and HN9 were good specific combiners. Hybrid HN3, HN7 and HN12 disclosed significant SCA effect for oil content (%).

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

Source of variation	*Df*	PH	EH	DSS	DST	DSM	EL	ED	GYH	NKR	NK	NCP
Hybrids(H)	11	1505.6**	457.5*	11	8.6	70.55*	15.4	0.14	2000.4	1.1*	73.5	32.3**
Lines(L)	5	1798.5**	482*	19.3*	7.28	65.6*	10.38	0.18	1866.4	1.7**	53.8	50.6**
Testers(T)	1	301**	12	8.2	40*	135.4*	24.6	0.001	7395.9*	0.23	30	7.7
L X T	5	1453.6**	522*	3.4	3.7	62.3*	18.6	0.12	1055.3	0.7	102*	18.9
Error	11	52.6	131	4.9	4.3	18.4	7.1	0.06	1453	0.3	28.6	6.14

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

Table 3. *continued.*

Source of variation	*Df*	GW	GYH	PC	SC	OC
Hybrids(H)	11	310.9**	421.5*	1.85**	4.56**	0.61**
Lines(L)	5	526.4**	527*	2.02**	4.83**	0.6**
Testers(T)	1	214.2	703.9*	3.8**	0.28*	0.07*
L X T	5	114.9	259.6	1.3**	5.15**	0.72**
Error	11	45.3	102	0.04	0.07	0.01

*, ** significant at 0.05, 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 parameters	PH	EH	DSS	DST	DSM	EL	ED	NKR	NK	NCP	GW	GYH
□□□GCA	48.4	12.6	0.54	0.39	2.4	0.39	0.005	0.04	1.56	1.36	14.82	17.4
□□□SCA	700.5	195.5	-0.75	-0.3	22.1	5.75	0.03	0.2	36.7	6.38	34.8	78.8
□□□GCA/□□□□SCA	0.07	0.06	0.72	-1.3	0.11	0.07	0.2	0.25	0.04	0.2	0.4	0.22
□□□□	193.6	50.4	2.16	1.56	9.6	1.56	0.02	0.16	6.24	5.44	59.28	69.6
□□□D	700.5	195.5	-0.75	-0.3	22.1	5.75	0.03	0.2	36.7	6.38	34.8	78.8
□□□□□□□□D	0.28	0.26	-2.88	-5.2	0.43	0.27	0.67	0.8	0.17	0.85	1.7	0.88

Table 4. *Continued*

Genetic parameters	GYP	PC	SC	OC
□□□GCA	87.7	0.07	0.13	0.02
□□□SCA	-198.8	0.63	2.54	0.35
□□□GCA/□□□□SCA	-0.44	0.11	0.05	0.06
□□□□	348.4	0.28	0.52	0.08
□□□D	-198.8	0.63	2.54	0.35
□□□□□□□□D	-1.7	0.44	0.2	0.22

Table 5. General combining ability (GCA) effects of parents in respect of thirteen characters at Adet

Line No	PH	EH	DSS	DST	DM	NKR	NCP	GW	GYH	GYP	PC	**SC**	**OC**
LN1	4.20	4.50	-1.58	0.62	5.12*	0.82*	2.79*	8.67*	3.04	32.21	-0.36**	0.01	-0.07
LN2	-5.80	3.25	-1.33	-1.62	0.12	1.17**	3.45*	11.62**	8.14	3.85	-0.23**	0.81**	-0.04
LN3	-7.08	-6.75	1.41	2.12	-1.87	-0.53	-1.79	-2.72	-15.74**	-24.73	-0.01	-0.09	0.39**
LN4	-4.58	-3.00	3.70**	0.87	-6.37*	0.72	-1.79	1.10	-13.07*	-24.20	1.23**	-1.34**	0.55**
LN5	12.90**	4.50	-0.08	0.12	3.37	-0.43	1.70	-5.47	11.11*	6.68	0.23*	-0.99**	0.35**
LN6	0.42	-2.50	-2.08	-0.87	-0.37	-1.76**	1.20	-13.20**	6.50	6.18	-0.86	1.61**	-0.39**
SEm±	3.60	5.70	1.10	1.03	2.14	0.39	1.23	3.36	5.04	19.18	0.10	0.13	0.05
LSD (0.05)	7.92	12.54	2.42	2.26	4.71	0.81	2.70	7.39	11.09	42.20	0.22	0.28	0.11
LSD (0.01)	11.18	17.70	3.41	3.19	6.64	1.09	3.82	10.43	15.65	59.57	0.31	0.40	0.15
Testers													
CML144	-2.08	-3.40	-0.58	1.29	-2.37	0.39	0.20	-5.10*	-5.40	-17.55	0.39**	0.10	-0.05*
CML159	2.08	3.40	0.58	-1.29	2.37	-0.39	-0.20	5.10*	5.40	17.55	-0.39**	-0.10	0.05*
SEm±	2.09	3.30	0.63	0.59	1.23	0.23	0.71	1.94	2.91	19.18	0.10	0.13	0.05
LSD (0.05)	4.60	7.26	1.26	1.29	2.70	0.47	1.56	4.26	6.40	42.20	0.22	0.28	0.11
LSD (0.01)	6.49	10.24	1.95	1.83	3.82	0.63	2.20	6.02	9.03	59.57	0.31	0.40	0.15

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

Where, LN1= AMB06BSYN8Q6-2-4-1-2, LN2= AMB06BSYN8Q11-6-7-1-2, LN3= AMB06BSYN8Q15-4-3-1-1, LN4= AMB06BSYN8Q15-10-3-1-2, LN5= AMB06BSYN8Q18-7-3-1-2 and LN6= AMB06BSYN8Q19-12-1-2-2.

2. Magnitude of Heterosis over the two Checks

The outcomes of standard heterosis for different characters that had significant mean squares are presented in Table 4.1. Eleven hybrids showed significant positive standard heterosis for plant height over BHQP542 and one hybrid (HN3) had expressed significant negative standard heterosis over Jibat. The highest significant positive standard heterosis was manifested by HN11 (27%) followed by HN5 (24.5%). For ear height, five hybrids (HN1, HN7, HN8, HN9 and HN11) revealed significant positive standard heterosis over BHQP542 and one hybrid (HN3) divulged significant negative standard heterosis over Jibat. The largest magnitude of significant positive standard heterosis was manifested by HN8 (29.7%) followed by HN1 and HN7 (24.5%).

All and nine hybrids disclosed significant positive and negative standard heterosis for number of kernel rows per cob over Jibat and BHQP542 respectively. HN1 (23.3%) recorded the highest standard heterosis followed by HN2 (21.7%) and HN7 (21.7%). No hybrid that had revealed significant positive standard heterosis for number of kernels per row.

The extent of standard heterosis was mostly in the negative direction for days to 50% silking and tasseling over BHQP542. The maximum negative heterosis for days to 50% siking and tasselling 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.

Eight hybrids showed high magnitude of significant positive standard heterosis over the check BHQP54 for cob numbers per plot. The largest magnitude of significant standard heterosis was manifested by hybrid HN8 (153.3%) followed by hybrid HN6 (126.7%). Only one hybrid HN8 (35.7%) revealed significant positive standard heterosis over the check Jibat.

For grain yield in quintal per hectare, six hybrids disclosed significant positive standard heterosis relative to check BHQP54 and hybrid HN7, HN8 and HN11 had expressed higher magnitude of significant positive standard heterosis (107.3% for HN8, 88.3 % for HN11 and 81.1% for HN7).

Hybrids HN3, HN4, HN5 and HN10 had higher positive standard heterosis for protein content (%) over check BHQP54 and Jibat.

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

Hybrid No	PH	EH	DSS	DST	DSM	NKR	NCP	GYP	GW	GYH	PC	SC	OC
HN1	5.83	3.41	-1.33	-1.29	-1.12	0.03	-1.95	-8.99	10.30	-5.67	0.15	-0.08	-0.22**
HN2	0.83	-2.83	1.41	1.20	-0.12	0.23	-2.71	-5.08	-5.70	-8.65	-0.67**	0.66**	-0.14
HN3	-5.41	-5.33	0.16	0.95	-5.62	0.23	2.54	-24.10	6.70	-4.70	0.90**	-2.13**	1.00**
HN4	-0.41	3.41	-0.58	-0.79	4.87	-0.01	1.54	-21.99	-13.30*	12.20	-0.39*	0.21	0.05
HN5	-0.41	-4.08	0.16	-0.04	4.12	-0.61	-1.95	10.93	3.00	0.17	0.30	0.16	-0.14
HN6	-0.41	5.41	0.16	-0.04	-2.12	0.11	2.54	5.24	-0.96	6.65	-0.29	1.16	-0.54**
HN7	-5.83	-3.41	1.33	1.29	1.12	-0.03	1.95	8.99	-10.30	5.67	-0.15	0.08	0.22**
HN8	-0.83	2.83	-1.41	-1.20	0.12	-0.23	2.71	5.08	5.70	8.65	0.67**	-0.66**	0.14
HN9	5.41	5.33	-0.16	-0.95	5.62	-0.23	-2.54	24.10	-6.70	4.70	-0.90**	2.13**	-1.00**
HN10	0.41	-3.41	0.58	0.79	-4.87	0.01	-1.54	-21.99	13.30*	-12.20	0.39*	-0.21	-0.05
HN11	0.41	4.08	-0.16	0.04	-4.12	0.61	1.95	-10.93	-3.00	-0.17	-0.30	-0.16	0.14
HN12	0.41	-5.41	-0.16	0.04	2.12	-0.11	-2.54	-5.24	0.96	-6.65	0.29	-1.16	0.54**
SEm±	5.10	8.09	1.56	1.46	3.03	0.38	1.75	26.95	4.75	7.14	0.14	0.18	0.07
LSD (0.05)	11.22	17.8	3.43	3.21	6.66	0.83	3.85	59.31	10.75	15.71	0.3	0.39	0.15
LSD (0.01)	15.84	25.12	4.84	4.53	9.41	1.18	5.60	85.11	14.75	22.17	0.43	0.55	0.21

and; Significant at 0.05 and 0.01levels of probability*

For starch content three hybrids (HN2, HN6 and HN9) and seven hybrids exhibited positive and negative standard heterosis over check Jibat respectively. And hybrid HN6 and nine hybrids exhibited significant positive and negative standard heterosis for the same trait over check BHQP54. Ten and one hybrids had disclosed significant positive and negative standard heterosis for oil content (%) over check Jibat respectively and four hybrids showed significant negative standard heterosis for this character over check BHQP54.

IV. DISCUSSION

Hybrids showed significant differences for most traits under study indicate the presence of high amount of differences for various traits that makes isolation possible for improvement of grain yield and yield component traits.

General combining ability (GCA) is the average performance of a strain in a serious of crosses which is associated with additive genetic effects while specific combining ability (SCA) is the deviation of individual crosses from the average performance of the parents involved that is associated with non- additive genetic effects (Falconer and Mackay, 1996; Kempthorne, 1957). High proportion of SCA variance than GCA variance for all traits under investigation indicated the greater role of non- additive genetic effects for controlling these characters. The ratio of GCA to SCA variance was lower than one, which again confirms the preponderance of non-additive gene action for the inheritance of the characters. These results are in the same trend with what obtained by Alamnie *et al* (2003), Wali *et al* (2010) and Sofi and Rather (2006).

The estimate of GCA effect of a parent is an important indicator of its potential for generating superior breeding genotypes. SCA effect used to determine the deviation of the performance individual crosses from the average performance of the parents involved (Falconer and Mackay, 1996). Parents (lines and testers) showed GCA effects with different magnitudes and directions indicating the presence of adequate diversity in the genetic constitution of parents. Inbred line LN5 was good general combiner for grain yield (Qha^{-1}). Line LN1 and LN2 were good general combiner for number of kernel rows per cob, number of cobs per plot and 100-grain weight.

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

Hybrid No	PH		EH		DSM		NKR		GW		DST	
	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542
HN1	-3.20	22.90	-2.10	24.50	-0.60	0.90	23.30**	0.00	53.60**	141.40**	6.90**	-2.40
HN2	-9.60	14.90	-8.50	16.20	-3.20	-1.60	21.70**	-1.40**	14.80**	80.50**	8.60**	-0.90
HN3	-36.20**	-18.90	-19.10	2.70	-7.90	-6.50	15.80**	-6.10**	9.20**	71.60**	12.30**	2.40
HN4	-9.60	14.90	-8.50	16.20	-4.10	-2.60	15.80**	-6.10**	-38.80**	-3.70	9.10**	-0.50
HN5	-2.10	24.30	-8.50	16.20	1.60	3.20	7.50**	-12.80**	-9.90**	41.60**	9.10**	-0.50
HN6	-7.40	17.60	-6.40	18.90	-4.80	-3.20	8.80**	-11.80**	-44.50**	-12.80**	8.00**	-1.50
HN7	-6.40	18.90	-2.10	24.50	3.80	5.50	21.70**	-1.40**	22.90**	93.00**	6.90**	-2.40
HN8	-8.50	16.20	2.10	29.70*	0.00	1.60	16.70**	-5.40**	78.90**	181.40**	3.20	-5.80**
HN9	-6.40	18.90	-4.30	21.60	2.20	3.90	10.80**	-10.10**	-0.30	56.70**	7.50**	-1.90
HN10	-7.40	17.60	-8.50	16.20	-7.30	-5.80	15.00**	-6.80**	70.30**	167.70**	8.00**	-1.50
HN11	0.00	270	4.30	32.40*	-0.60	0.90	16.70**	-5.40**	2.50	61.20**	6.40**	-2.90
HN12	-5.30	20.30	-9.80	14.60	0.90	2.60	5.80**	-14.20**	-8.60**	43.70**	5.30**	-3.90
SEm±	15.79		12.22		3.98		0.42		1.44		1.81	
CD at 5%	34.10		26.40		8.60		0.90		3.70		3.90	
CD at 1%	45.30		36.40		12.00		1.30		5.70		5.50	

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

Table 7. *Continued*

Hybrid No	DSS	NCP	GYH	PC	SC	OC

	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542	Jibat	BHQP542
HN1	5.80**	-4.70*	-39.30*	13.30**	-33.70**	9.10	8.87**	0.55*	-1.06*	-1.89**	12.99**	-13.00**
HN2	8.90**	-1.90	0.00	86.70**	-29.50**	16.00	0.59*	-7.10**	1.13**	0.28	15.58**	-11.00**
HN3	10.50**	-0.50	0.00	86.70**	-68.80**	-48.70**	21.89**	12.57**	-4.08**	-4.89**	36.36**	5.00**
HN4	12.00**	0.90	-7.10*	73.30**	-30.20**	14.80	21.30**	12.02**	-2.54**	-3.35**	36.36**	5.00**
HN5	8.90**	-1.90	-7.10*	73.30**	-6.30	54.20**	17.75**	8.74**	-2.11**	-2.93**	25.97**	-3.00**
HN6	6.80**	-3.80	21.40**	126.70**	-2.60	60.30**	-2.40**	-9.84**	2.96**	2.09**	-3.89**	-26.00**
HN7	7.30**	-3.30	-14.30**	60.00**	10.10	81.10**	-4.10**	-11.48**	-1.13**	-1.96**	27.27**	-2.00**
HN8	4.70*	-5.70*	35.70**	153.30**	26.00*	107.30**	7.10**	-1.09**	-1.06**	-1.89**	25.97**	-3.00**
HN9	8.90**	-1.90	-39.30**	13.30**	-28.80*	17.10	-8.87**	-15.85**	1.62**	0.77*	-12.99**	-33.00**
HN10	12.00**	0.90	-32.10**	26.70**	-56.90**	-29.10**	21.30**	12.02**	-3.45**	-4.26**	36.36**	5.00**
HN11	7.30**	-3.30	17.90**	120.00**	14.50	88.30**	1.20**	-6.56**	-2.89**	-3.70**	36.36**	5.00**
HN12	5.20*	-5.20*	-17.90**	53.30**	-7.40	52.30**	-4.73**	-12.02**	-0.63	-1.47**	27.27**	-2.00**
SEm±	1.81		2.68		9.58		0.22		0.32		0.13	
CD at 5%	3.90		5.80		20.70		0.48		0.70		0.28	
CD at 1%	5.50		8.00		28.90		0.68		0.99		0.40	

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

Tester CML 159 had revealed significant positive GCA effects for 100-grain weight and oil content (%) and tester CML144 had significant positive GCA effect for protein content (%).These result indicated that LN5, LN1 and LN2 contributed to increased grain yield in their crosses. And tester CML144 and CML 159 can be used for quality improvement. Alamnie *et al* (2003) reported that four lines, namely, HYD.SEL 13, HYD.SEL 10, HYD.SEL 14, and HYD.SEL 6 among females and CI-5 among males were good general combiners for increase in grain yield.

SCA effects for yield and yield contributing traits show that the hybrids had better or poorer performance than the expected GCA effects of their respective parents. No hybrid that was best specific combiner for grain yield. However; hybrid HN3, HN8 and HN10 were good specific combiners for protein content (%).

Hybrids showed superiority over standard checks for various traits indicating the presence of substantial heterosis in the hybrids and the potential of inbred lines for hybrid development. Five hybrids (HN5, HN6, HN7, HN8 and HN11) showed superiority for grain yield (Qha^{-1}) over the standard check BHQP54 but all hybrids were not superior compared to the normal maize hybrid check for the same trait proposes the need for additional effort for the development of competent quality protein maize germplasm. These results are in line with Dagne Wegary (2008). Almost all hybrids had expressed negative standard heterosis over BHQP54 and positive standard heterosis over Jibat indicating earliness and lateness compared to BHQP54 and Jibat respectively. Hybrid HN3, HN4, HN5 and HN10 revealed high amount of protein over checks. Heterosis responses of hybrids largely depend on genetic diversity of parents and environmental conditions (Hallauer and Miranda, 1988). Heterosis response increases with increased genetic diversity.

V. CONCLUSION

Combining ability analysis and estimation of heterosis are important breeding methods to develop high yielding hybrid in maize. High amount of differences were observed among hybrids for most traits which indicate the possibility of selection for improvement of yield and yield related traits. Non- additive gene action is more important for controlling most traits under study.

Since this exploration is a one year and location trial, it is suggested to evaluate in multilocation trial on large scale basis before their commercial cultivation of identified promising hybrids for grain yield and their stability over locations and seasons.

Even if it is a one year trial, LN1, LN2 and LN5 showed desirable GCA effects for grain yield and yield contributing traits and can be used for development of hybrids. Moreover; there were hybrids (HN5 (54.2%), HN6 (60.3%), HN7 (81.1%), HN8 (107.3%) and HN11 (88.3%)) that had higher magnitude of heterosis over the quality protein maize check but these hybrids were not superior over the normal maize check. From this result hybrid HN8 and HN11can be exploited for future use and additional effort is required for the development of competent quality protein maize.

ACKNOWLEDGMENTS

First of all, I would like to convey my exceptional thanks and appreciation to my advisor Dr. Tadesse Dessalegn for his close supervision, assistance, constructive criticism, support and generosity during the whole period of my study. I would also like to thank my co-advisor Dr. Yigzaw Dessalegn for his guidance, encouragement, all-rounded support and valuable comments. I would like to thank Mr. Kassa Yihun (Ambo Agricultural Research Center) who provided me the planting materials and valuable information used for the study. I am indebted to Adet Agricultural Research Center for providing technical and financial assistance during my study. I also thank the Amhara Regional Agricultural Research Institute (ARARI) for the training opportunity given to me.

REFERENCES

[1] Alamnie, A., Naykar N.Y. and Wali M.C. 2003. Combining Ability, Heterosis and per se Performance of Height Characters in Maize. Karnataka J. Agril. Sci.16 (1):131-133.

[2] CSA. 2011/12. Report on Area and Production of Major crops, Addis Ababa, Ethiopia.

[3] Dagne Wegary. 2008. Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. Phd thesis,University of the Free State, South Africa, p225.

[4] Dereje Bacha, mosisa Worku, Hadji Tuna, Wonde Abera, Twumasi Afiriyie S., Mandefro Nigusie, Leta Tulu, Legesse Wolde and Abdissa Gemeda. 2001. On-farm evaluation of cimmyt's quality protein maize varieties in Ethiopia. Seventh eastern and southern African Regional maize conference, feburary 11th - 15th, 2001. Jimma Agricultural Research center, Jimma, Ethiopia, p77-79.

[5] Falconer D.S and Mackay T.F.C. 1996. Introduction to quantitative genetics. 4th ed. Lndon, Longman, p464.

[6] Hallauer A.R. and Miranda J.B. 1988. Quantitative genetics in maize breeding. Iowa State University Press. Iowa, 123p.

[7] Kempthorne O.1957. An Introduction to Genetics Statistics. John wiley and sons, New York. p457.

[8] Krivanek A. F., De Groote H., Gunaratna N. S., Diallo A. O. and Dennis. 2007. Breeding and disseminating quality protein maize (QPM) for Africa. Afr. J. Biotechnol. 6 (4): 312-324.

[9] Lippman Z. B. and Zamir D. 2007. Heterosis: revisiting the magic. Trends Genet. 23: 60–66.

[10] Mertz E.T. 1992. Discovery of high-lysine, high tryptophan cereals. In: Mertz E. T. (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minesota, USA. p. 1-8.

[11] Sofi P.and Rather A.G., 2006. Genetic analysis of yield traits in local and cimmyt inbred line crosses using line x tester analysis in maize (Zea mays L.). Asian J. plant sci. 5:1039-1042.

[12] Villegas E., Vassal S.K. and Bjarnason M. 1992. Quality protein maize – What is it and how was it developed. In: Mertz E. T (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minnesota, USA. pp. 27-48.

[13] Wali M.C., Kachapur R.M., Chandrashekhar C.P., Kulkarni V.R., and Devara N. S.B., 2010. Gene action and combining ability studies in single cross hybrids of maize (Zea mays L.). Karnataka J. Agric. Sci., 23: 557-562.