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Testcross Performance and Heterosis of Selected Quality Protein Maize (QPM) (*Zea mays* L.) Inbred Lines

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ABSTRACT

One hundred thirty four genotypes were evaluated applying simple lattice design during 2007 cropping season. In this study BHQ542 maize variety and other checks were used at two locations. The study objective was to determine performance of the test crosses, heterosis and heterotic patterns of the inbred lines and testers and to identify promising crosses for future advanced trial. All agronomic and physiological data were recorded and analyzed. There was significant differences among genotypes for most of the traits with few exceptions. Based on the mean value of grain yield, sixteen crosses at Awassa and only four crosses at Melkassa were superior to QPM hybrid (BHQ542) but no crosses out yielded this check in the combined data. However, five lines crossed with T1 and seven lines crossed with T2 gave superior yield than the second best common check BH540 in the combined data. In this study crosses with T2 were superior to that of crosses with T1. Heterosis value varied highly for most of the traits studied at individual location and across locations. The highest heterosis over mid and better parent for grain yield was 189.47% (L36×T2) and 100.8% (L36×T2) at Awassa and 172.22% (L18×T2) and 62.65% (L35×T2) at Melkassa, respectively. Among the twenty maximum heterosis of grain yield only L5, L10, L15, L16, L18, L23, L28, L35, L36, L37 and L41 were common for both locations.

Key words: Quality protein maize, heterosis, heterotic pattern

INTRODUCTION

Maize is one of the most important cereals after wheat and rice and is widely distributed in the world. Maize originated in Central America and introduced to West Africa in the early 1500s by the Portuguese traders (Dowswell *et al.*, 1996) and it was introduced to Ethiopia (Huffnagel, 1961) during the 1600-1700s (Worku *et al.*, 2001b). Its production covers 1.3 million ha in the country.

In Ethiopia, maize grows from low lands to high lands (Mulatu *et al.*, 1993). Mulatu *et al.* (1993) noted that maize research in Ethiopia was started half a century ago. Since, the start of maize research more that 35 maize varieties have been released through research for different agro-ecologies of the country (Pixley, 2003). However from these, the share of quality protein maize was 7, 283 ha (Krivanek *et al.*, 2007). The quality aspect (specially the quality protein) of this crop has got attention just few years ago, even on the world level (CIMMYT, 2000).

Quality protein maize was discovered by Purdue University scientists in 1961 (Krivanek *et al.*, 2007). After repeated research on quality protein to improve the associated defects

Hussain *et al.* (2006), many breeding programs worldwide began converting normal maize endosperm populations and inbred lines to $\alpha 2$ versions through a direct backcross approach (Prasanna *et al.*, 2001). After conversion quality protein maize tasted like normal maize and yielded as much and more the normal maize while containing nearly twice the quantity of the essential amino acids (CIMMYT, 2000). Similarly, Tulu *et al.* (2001) reported that the quality protein maize hybrids have the potential to out yield their normal maize counterparts and disprove the common belief that quality protein maize is low yielding than normal maize.

Taking into account the importance of quality protein maize, Ethiopian Agricultural Research Institute started research on quality protein maize just few years ago and released the first QPM maize (BHQ542) in 2001 (Worku *et al.*, 2001a). This research project was initiated with the following objects (1) Determine performances of the top crosses, (2) Estimate heterosis and determine heterotic pattern of the 44 quality protein maize inbred lines and to identify promising crosses for further advanced trials.

MATERIALS AND METHODS

Site description: The research was conducted during the 2007 rainy season at two locations at Hawassa and Melkassa. The Hawassa site is located at 7°N and 38°31'E. latitude and longitude near Hawassa city; the capitals of South Nations Nationalities People Regional State, Ethiopia and lies at an altitude of 1700 m above sea level with the average annual rainfall of 1100 mm and with the average annual maximum and minimum temperatures of 27 and 12°C, respectively. The second site, Melkassa is located in the central Rift Valley of Ethiopia, 117 km from Addis Ababa southeast direction. It is situated at about 8°24'N latitude and 39°21'E longitude at an elevation of 1550 m above sea level. The area receives annual rain fall of 763 mm of which 70% comes during June to September and has an average maximum and minimum temperature of 28.4 and 14°C, respectively.

Experimental materials: Initially 45 inbred lines and their 90 crosses and checks were included in the experiment. The experiment whose results are reported in this paper consists of 44 quality protein maize inbred lines, two testers (the open pollinated variety Obatampa and the quality protein maize single cross hybrid CML144×CML159), their 88 top-crosses and checks in one experiment (Set I). The less vigorous lines were tested in a separate experiment (Set II) adjacent to the main trial (Set I) to avoid shading and resource competition effects of the crosses, testers and checks. Different checks including an already released quality protein maize variety from their respective location were included in the experiment. The checks were A-511, Melkassa 1, 2, 3, 4, 5, Katumani, Acv3, Acv6, BHQ542, Gibe and BH540 at Awassa and pool 15-c7 Melkassa 2, BHQ542, BH540 and Gibe at Melkassa. Table of Pedigree of parents and testers was not presented in this manuscript because of large volume.

The experiment was planted in two Sets as Set I and Set II. Set I experiment consisted of 100 genotypes (90 crosses and 10 checks). Set II experiment consisted of 49 genotypes (45 parents, 2 testers and 2 checks). At Awassa, the trial was planted on May 3, 2007 and at Melkassa it was planted on June 19, 2007. Each treatment was tested on a two- row plot. Each plot consists of two rows, each 4 m length and 1.5 m width. A spacing of 75 cm between rows and 25 cm between plants within a row was used. Plot area was, therefore, 6 m². During planting, two seeds per hill were sown and then thinned to recommended plants per plot at knee height.

Two types of fertilizers, DAP and urea, were used at the rate of 100 kg ha⁻¹ DAP at planting and 100 kg ha⁻¹ of urea in split application of 25% at planting and 75% at 37 days after emergence at Awassa and Melkassa. All cultural practices were used as recommended for each location. Border rows were planted at the two ends of each block to avoid border effects.

Data collection and analysis: The data collected were days to emergence, days to tasseling, days to silking, days to maturity, stand count at harvest, grain yield (kg plot⁻¹), total biomass (kg plot⁻¹), disease and lodging % (1-5), 1000 seed weight, plant height (cm), ear height (cm), No. of ears per plant, No. of seeds per plant, No. of tassel branching, weight of grain per plant, ear length, ear diameter, No. of kernel rows per ear, No. of kernels per ear and number of kernels per row. All data collected were subjected to analysis using SAS software at individual location and over locations but in this study those showed significant were reported. Those traits which manifested significant differences between the genotypes at either or both locations, subjected to L×T analysis of variance using SAS software; the elaborations given by Singh and Chaudhary (1977) were followed. The L×T analysis for data combined over location are presented in Table 2. One degree of freedom contrasts were used to compare the performance of crosses and lines, lines and testers and to compare the crosses of T1 with the crosses of T2. Locations were considered as fixed while genotypes were considered as random effect.

During analysis, the Better Parent Heterosis (BPH) and Mid Parent Heterosis (MPH) in percent were calculated for the characters that showed significant difference between genotypes as suggested by Falconer (1994).

RESULTS

Initially 45 quality protein maize lines with their 90 crosses and local checks were used in the experiment following simple lattice design. The data of line 15 was missing from both replications at Melkassa. Therefore, the line 15 and its crosses were discarded from all analysis and the remaining 88 top crosses that resulted from 44 lines crossed with two testers (Obatampa and CML144/CML159) were analyzed and presented in this study. The analysis was conducted for 20 traits of all genotypes used in the experiment (Table 1). Crosses were compared with checks, hybrids or open pollinated varieties, which are under production. Special emphasis was given to the comparison of the 88 L×T quality protein maize crosses with an already released three-way hybrid (BHQ542). Those quality protein maize new crosses with better or comparable yield as compared to the highest yielding hybrid or open pollinated varieties check were identified. For the traits whose f-test was significant at either or both locations, detailed L×T analysis of selected traits of pooled data was done and presented in Table 2.

According to analysis of variance in Table 1, there was significant differences among genotypes for days to emergence, days to tasseling, days to silking, days to maturity, tassel branching, plant height, ear length, ear diameter, No. of seed per plant, grain yield per plant, biomass, grain yield per hectare, No. of kernels per row, No. of kernel rows per ear, No. of kernel per ear and 1000 seed weight at Awassa. Similarly, there was significant difference among crosses for days to tasseling, days to silking, days to maturity, plant height, ear length, tassel branching, biomass yield, grain yield and No. of kernels per ear. At Melkassa, there was also significant difference among genotypes for days to emergence, days to tasseling, days to silking, days to maturity, tassel branching, plant height, ear height, ear length, ear diameter, disease severity, number of seeds per plant, grain yield per plant, biomass yield, grain yield, number of kernels per row, number of kernels row per ear, number of kernels per ear and 1000 seed weight.

Table 1: ANOVA of 20 traits at individual location and combined over locations

Mean squares										

Awassa			Melkassa			Combined				

Traits	Reps	Genotypes	Error	Reps	Genotypes	Error	Location	Genotypes	G×E	Error
df	1	145	145	1	139	139	1	133	133	265
DT	9.26	61.76**	2.45	11.44	12.66**	2.88	1430.81**	24.14**	12.77**	2.72
DS	2.684	57.88**	3.52	100.56	12.55**	3.71	2298.14**	20.54**	16.505**	3.205
DM	50.97	89.09**	2.58	58.59	51.85**	10.61	1212.00**	101.71**	17.32**	7.07
PH	85.49	2516.56**	180.01	13437.19	1715.89**	289.62	12395.56**	3850.5**	514.09**	258.53
EH	1242.11	2554.22 ^{NS}	2113.46	6883.67	555.65**	201.71	5682.96*	1833.51**	1403.35 ^{NS}	1253.44
YLD	2.265	23.088**	1.584	32.18	11.03**	2.29	128.58**	28.22**	6.53**	1.87
KPE	105523.36	21151.16**	2949.90	54905.00	22859.17**	2873.75	157177.53**	39223.18**	4870.22**	2793.72
TSW	163.138	5858.38**	1782.98	11662.48	6808.76**	2007.60	701144.86**	9212.48**	3017.38**	2023.42

*, **Significant at 5 and 1%, respectively, NS: Non significant, df: Degree of freedom, Reps: Replication, DT: Days to tasseling, DS: Days to silking, DM: Days to maturity, PH: Plant height, EH: Ear height, ED: Ear diameter, YLD: Grain yield, KPE: Kernel per ear, TSW: Thousand seed weight

Table 2: Line×tester analysis pooled over locations for yield and yield components

ANOVA				

Source of variation	df	GYLD	KPE	TSW
Environment	1	128.58**	157177.05**	701144.87**
Rep(env)	2	15.39**	51751.06**	6068.87*
Genotypes	133	28.23**	39250.91**	9209.92**
Crosses	87	5.14**	4121.03**	2217.21 ^{NS}
Parents	45	7.71**	18538.02**	7645.18**
Crosses vs. parents	1	2976.00**	3995862.08**	680241.89**
Genotypes×Env	133	6.52**	4853.34**	3015.06**
Crosses×Env	87	3.77**	3468.31**	2225.76 ^{NS}
Parents×Env	45	5.14**	7668.64**	3405.02**
Crosses×parents×Env	1	326.64**	5667.21**	56882.17**
Parents	45	7.71**	18538.02**	7645.18**
Lines	43	5.9**	9437.00**	7614.54**
Testers	1	6.86**	553.28 ^{NS}	1019.62 ^{NS}
Parents×Env	45	5.14**	7668.64**	3405.02**
Lines×Env	43	5.37**	7858.08**	3543.58**
Crosses	87	5.14**	4121.03**	2217.21 ^{NS}
Line	43	4.9**	5588.66**	2943.37*
Testers	1	115.37**	17385.19**	4184.63 ^{NS}
Crosses×Env	87	3.77**	3468.31**	2225.76 ^{NS}
Testers×Env	1	8.87*	67206.66**	12985.53*
Pooled error	264	1.78	2413.54	2009.84

*, **Significant at 5 and 1%, respectively, df: Degree of freedom, GYLD: Grain yield, KPE: Kernel per ear, TSW: Thousand seed weight, Env: Environment and NS: Non-significant

Similarly, there was significant variation among crosses for 14 traits out of 20 at Melkassa site (Table 1). The mean squares of genotypes at Awassa were non-significant for ear height, disease

severity, lodging and number of ears per plant. Similarly, at Melkassa non-significant difference was observed for lodging and number of ears per plant. For all genotypes, traits' mean performance was recorded at individual location and across location.

In the analysis of variance pooled over location, all genotypes over location was analyzed and all of the traits studied showed highly significant variation ($p < 0.01$) except disease severity, lodging and number of ears per plant. Genotype \times Environment interaction was also significant for 15 of the 20 traits including grain yield (Table 2) and Genotype \times environment interaction was highly significant ($p < 0.01$) for 15 traits except for ear height, disease severity, lodging, No. of ears per plant and grain yield per plant. In the pooled analysis, location also showed significant ($p < 0.05$) and highly significant ($p < 0.01$) variation for some of the traits studied except for number of kernels row per ear indicating that mean values of those traits were highly influenced by the environment (Table 1). Hence, those genotypes, which showed significant variation in the analysis of variance over location, were subjected to L \times T analysis and results are presented in Table 2.

The extent of variation among genotypes was ranged from 13.96 t ha⁻¹ (L5 \times T2) to 2.6 t ha⁻¹ (L38) and the extent of variation among crosses was ranged from 13.96 t ha⁻¹ (L5 \times T2) to 6.96 t ha⁻¹ (L3 \times T1) at Awassa for grain yield. The best check at Awassa was Melkassa 4 which gave 13.72 t ha⁻¹. At Awassa those genotypes which gave comparable yield with the best check are L5 \times T2, L36 \times T2, L37 \times T2 and L41 \times T2 and gave yield of 13.96, 13.67, 13.62 and 13.58 t ha⁻¹, respectively. Only one cross (L5 \times T2) surpassed the best check and gave yield of 13.96 t ha⁻¹. The yield of best check is unusual. This might be due to the 2007 growing condition, which was more favorable than the previous seasons. The best check (BHQ542) gave yield of 12.7 t ha⁻¹ and 16 crosses were superior to this hybrid at Awassa. The local check BH540 gave only yields of 10 t ha⁻¹. Almost 72% of crosses were superior to this hybrid which is widely produced around Awassa with economic heterosis ranging from -29.92 (L3 \times T1) to 40.62 (L5 \times T2). At Awassa, L5 \times T2, L41 \times T2, L36 \times T2 and L37 \times T2 manifested highest economic heterosis of 40.62, 36.78, 37.71 and 37.19%, respectively.

The genotypes which manifested comparable grain yield at Awassa condition, still gave yield of 11.7, 9.05, 8.85 and 10.35 t ha⁻¹ at Melkassa condition. At Melkassa, the best check BHQ542 gave grain yield of 11.8 t ha⁻¹, but surpassed by only four crosses (L18 \times T2, L21 \times T2, L30 \times T2 and L35 \times T2). When the crosses compared with the local check Melkassa 2 (which gave 5.7 t ha⁻¹), all the crosses surpassed it with economic heterosis ranging from 2.44% (L17 \times T2) to 108.94% (L35 \times T2). Average location yield of crosses was 10.94 and 8.86 t ha⁻¹ at Awassa and Melkassa, respectively. The 2007 growing season was unique for Melkassa where the rain usually begins in the second week of June and ends in the first week of September with effective growing season of about 90 days.

During the 2007 growing season, the rain extended to the end of October and the distribution was unusual. As a result, even late maturing varieties such as Gibe composite and BH540 could reach maturity. This led to the unusually high yield at Melkassa, which was comparable to that of Awassa. Therefore, not all the top yielding crosses at Awassa repeated their performance at Melkassa. Among the 20 top yielding crosses, only ten were common for both locations. The common ones were L5 \times T2, L15 \times T2, L16 \times T2, L18 \times T2, L23 \times T2, L28 \times T2, L35 \times T2, L38 \times T2, L39 \times T2 and L41 \times T2. These crosses was superior not only to the already released QPM hybrids but also to the normal maize varieties under production at two locations and they seem to be promising future varieties and should be advanced further.

Table 3: Discriminating power of the two testers

Traits	Correlations			Traits	Correlations		
	Awassa	Melkassa	Combined		Awassa	Melkassa	Combined
DE	-0.280	0.151	-0.041	LOG	0.004	0.000	-0.067
DT	0.308*	0.479**	0.527**	NEPP	0.074	0.001	0.114
DS	0.286*	0.287*	0.469**	NSPP	0.077	0.104	0.164
DM	0.424**	0.238	0.453**	GYPP	-0.110	-0.074	-0.064
TB	0.148	-0.021	0.193	BYLD	0.183	0.172	0.193
PH	0.136	-0.008	0.131	GYLD	0.226	0.261	0.312*
EH	0.446**	-0.078	0.163	KPR	0.047	0.355**	0.251
ED	0.357**	0.438**	0.366**	RPE	0.362**	0.333*	0.415**
EL	-0.099	0.381	0.186	KPE	0.311*	0.382**	0.411**
DIS	0.017	0.086	-0.024	TSW	0.186	0.87**	0.342

*,**Significant at 5 and 1%, respectively, DE: Days to emergence, DT: Days to tasseling, DS: Days to silking, DM: Days to maturity, TB: Tassel branching, Ph: Plant height, EH: Era height, EL: Ear length, ED: Ear diameter, DIS: Disease, LOG: Lodging, NEPP: No. of ears per plant, NSPP: No. of seed per plant, GYPP: Grain yield per plant, BYLD: Biomass yield, GYLD: Grain yield, KPR: Kernel per row, RPE: Row per ear, KPE: Kernel per ear and TSW: 1000 seed weight

In the combined data, L×T analysis revealed highly significant difference (p<0.01) for all analyzed traits of genotypes (crosses and parents) (Table 2). Similarly crosses and parents also showed highly significant difference (p<0.01) for all traits except for days to emergence, ear height, ear diameter, No. of seed per plant and 1000 seed weight. Furthermore, crosses versus parents interaction was highly significant for entire traits studied in L×T analysis indicating the probability of potential crosses would come from parental genotype.

In the correlation analysis, the rank correlations (Table 3) between the crosses of lines with the two testers were also low for most of the traits and were statistically non-significant, indicating that the two testers ranked the lines in a different manner. Although, the two testers differed in only few traits, they ranked the lines in a completely different order. Hence, in combined data over the two locations, the f-test of nine traits were statistically significant for the crosses of both testers while only three traits were significant for only one tester. It is surprising to note that Tester Obatampa per se performance was superior to CML 144/ CML 159 in most of yield components such as number of seeds per plant, grain yield per plant, No. of kernel per row, No. of kernel rows per ear, No. of kernels per ear and 1000 seed weight; but the crosses gave low yield per hectare. The high biomass production coupled with higher harvest index of 0.37 and 0.35 for lines crossed with CML144/CML enabled them to produce higher grain yields than Obatampa crosses. Consequently, all elite crosses at each location are those of lines crossed with T2. Maximum yield 13.67 and 12.85 t ha⁻¹ was from lines crossed with T2 while 12.8 and 9.65 t ha⁻¹ was from lines crossed with T1 at Awassa and Melkassa, respectively. It is only by their average grain yields over the two testers that the best yielding crosses of lines were determined.

At a specific location (Awassa or Melkassa), the two testers were ranked the 44 lines differently. Hence, there were big rank changes in yield between the two crosses of a single line. The crosses of the same line with T2 was the second highest yielding in the combined data but was 41 1st when crossed with T1. The rank correlation between the crosses of the two testers by the 20 traits was therefore low and statistically non-significant for the majority of the traits at Awassa, Melkassa and in the combined data (Table 3).

Mean comparisons: The interaction of genotypes with the environments and similarly the interaction of its components (crosses, parents and crosses versus parents) was significant for all traits but for ear height (Table 2). The crosses×environment interaction was significant for most of the traits but for days to emergence, ear height, ear diameter, No. of seeds per plant, No. of kernel row per ear and 100 seed weight. The crosses×parents×environment component was non-significant for days to emergence, days to tasseling, ear height, No. of kernel per row and No. of kernels per ear. The lines×environment component were significant for all the 20 traits studied indicating the inconsistency of performance of the lines over the environments. The lines×testers×component was non-significant for almost all traits except for days to tasseling, days to silking, days to maturity, tassel branching, biomass and grain yield. The difference between lines and testers was little affected by the change of the environment.

The trend of genotypic variability of days to tasseling and days to silking followed that of days to maturity, while the trend of other quantitative traits followed that of the grain yield and 1000 seed weight (Fig. 1). Wide variability among genotypes (lines, testers and crosses) was observed in the mean comparisons. When the mean performance of genotypes (Crosses, lines and testers) compared, at Awassa (Fig. 1), the mean values of testers exceeded mean values of lines for different traits, which revealed significant difference in the preliminary analysis at individual location and across locations. The variation between mean values of yield of lines and testers was detected and such variation is supporting crossing of lines with testers, which were used as genotypes in this experiment. Moreover, the analysis of variance of L×T analysis showed similar trend of variation (Fig. 1). On the other hand at Melkassa, the mean comparison revealed that testers out yielded lines and showed superior performance in some traits studied (Fig. 2). In this location great variation was observed for the traits such as plant height, ear height, No. of seeds per plant, biomass yield, grain yield, No. of kernels per ear and 1000 seed weight (Fig. 2). The outstanding performance of testers was similar across locations for the trait, which showed significant variation. In similar way, L×T analysis confirmed the above mean comparisons of lines and testers so that the top crossing was made and it was promising for the presence of heterosis of grain yield.

In the mean comparison of traits pooled over location, similar results were observed for lines versus testers and crosses versus lines except No. of kernel per row and No. of kernel per ear (Fig. 3). In this case, the two traits of tester gave mean value of 37.75 and 694.25 while the same traits in crosses observed to give the mean value of 36.43 and 606.08. Though the testers mean value was greater for the above traits, it does not mean that it yields too. In the case of yield and other yield related traits, crosses surpassed the testers (Fig. 3). Thus, crosses were earlier for days

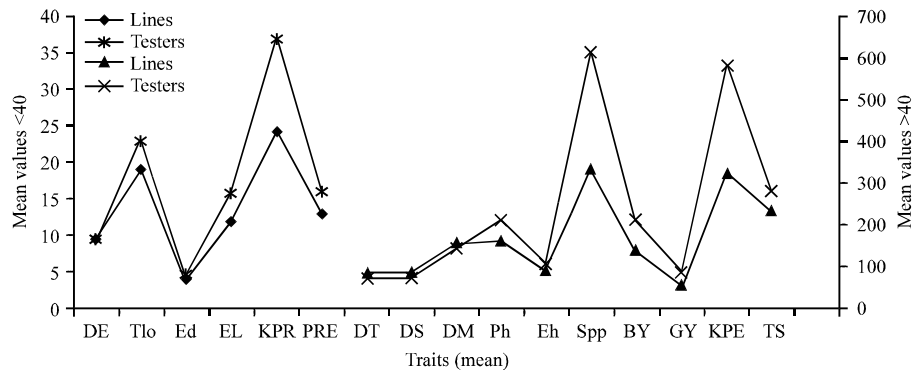


Fig. 1: Comparisons at Awassa

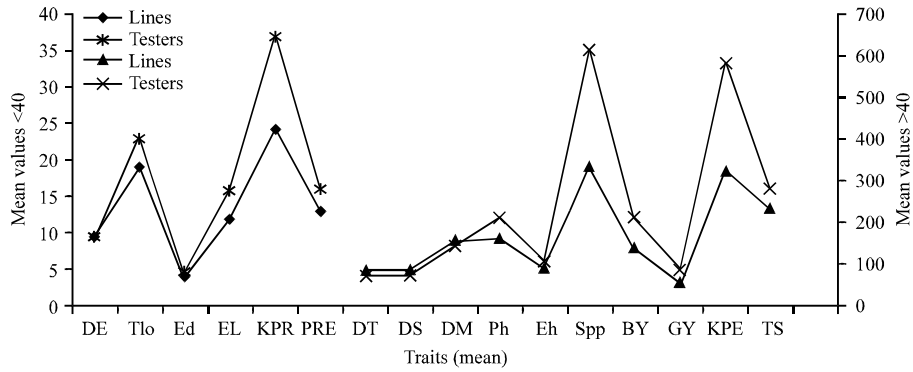


Fig. 2: Comparisons at Melkassa

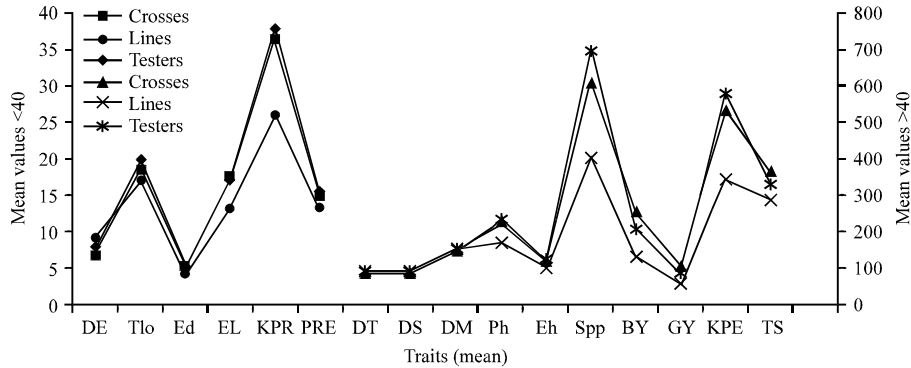


Fig. 3: Comparisons of pooled data

to tasseling, days to silking and days to maturity. On the other hand, lines gave lower mean values of plant height, ear height, kernel per plant, biomass yield, grain yield, kernel per row, kernel per ear and 1000 seed weight than testers and crosses. This shows that the diverse variability of genotypes during crossing brought the out-standing crosses with higher mean values of grain yield and yield related traits. The mean square due to lines was statistically significant for all the studied characters (Table 2). For example in the combined data, days to maturity ranged from 143-156 days, tassel branching from 11-24 branches, ear length from 10.4-16.1 cm, No. of seeds per plant from 214-566, grain yield $t\ ha^{-1}$ from 2.3-7.11 $t\ ha^{-1}$, 1000 seed weight from 205-366 g. Some lines had 1000 seed weight comparable to that of the crosses. The crosses also compared with testers in the combined data. The crosses were taller than testers and produced more biomass and grain yield than testers. It can be generalized that the maturity trait manifested negative over-dominance for some crosses. As result, there could be a possibility to identify the promising crosses based on yield performance, heterosis and combing ability (not presented).

Heterosis: The heterosis of the F1 (the crosses) over the mid parents and the better parents was computed and the results were presented in the Table 5 and discussed here to some extent for some characters in combined analysis. For maturity traits such as days to tasseling, silking and days to maturity, the better parent was the one, which was earlier from the parents. For other traits, the better parent was the one with the higher value of the trait. The deviations of the F1 mean from

mid parents either in the positive or in the negative direction was an indication of the presence of dominant gene action. All crosses tasseled and matured earlier than the earliest parent, which was the tester. The lines were flowered later than crosses and testers. At Awassa, traits like days to tasseling, days to maturity, plant height, ear length, biomass yield, grain yield, number of kernel per ear and number of kernel row per ear showed significant heterosis over mid and better parents (table not presented in this manuscript). In the analysis of heterosis, 98.8 and 81.8% of crosses manifested positive and significant heterosis over mid and better parents, respectively for grain yield indicated that those crosses have great potential for future use.

Regarding heterosis of lines crossed with testers, maximum negative heterosis obtained on average from inbred line crossed with T1 (Obatampa). The range of maturity of the lines was from 140-160 days. T1 matured in 150 days while T2 matured in 143 days. The range of maturity for the crosses (130-141 days) was narrower than that of lines. Although, lines crossed with T1 were in general earlier than that of lines crossed with T2, crosses with the highest better parent heterosis were obtained from Top crosses of lines crossed with T2 for grain yield and other agronomic traits except maturity traits. Better Parent Heterosis (BPH) was computed by comparing earliness of the crosses with earliness of the testers except in the 14 lines, which were earlier than the earliest tester. In most cases, therefore, BPH for lines crossed with T2 was higher than that of lines crossed with T1. The grain-filling period was longer for lines crossed T2 than T1 and it matured about seven days later than T1 (143 vs. 150 days).

From the inbred lines those crossed with T2 (tester two) (CML144/159) showed higher performance and heterosis over mid parent and better parent for most of the traits studied. Hence, regarding the most important economic trait (grain yield), L36×T2, L38×T2, L5×T2, L26×T2 and L41×T2 manifested maximum heterosis over mid parent and better parent at Awassa.

For grain yield, L36×T2 and L9×T2 expressed maximum and minimum heterosis of 189.47 and 45.21%, respectively over mid parents at Awassa. Referring inbred line crossed with T1, L38×T1 gave positive and significant heterosis of 131.9 and 51.47% over mid and better parents. From the crosses with T1, 98.86% manifested positive and significant heterosis over mid parent. Lines crossed with T1, showed low heterosis compared with crosses of T2. Thus, lines crossed with T1 and T2 expressed significant heterosis ranging from 131.9% (L38×T1)-32.63% (L14×T1) and from 189.47% (L36×T2)-54.4% (L4×T2), respectively over mid parents for grain yield. On the other hand, lines crossed with T1 manifested positive and significant better parent heterosis ranging from 51.47% (L38×T1)-25.26% (L31×T1), while lines crossed with T2 had heterosis that ranged from 114.15% (L5×T2)-17.09% (L9×T2). The cross L5×T2 gave the highest BPH of 7.4 t ha⁻¹ for grain yield. Moreover, the top yielder at Awassa L36×T2 expressed maximum heterosis of 189.47 and 109.71% over mid and better parent, respectively.

Referring heterosis of grain yield at Melkassa, most of the lines crossed with T1 showed no heterosis (over mid and better parent) but lines crossed with T2 revealed maximum and positive heterosis over mid and better parent. At this site in general, the better parent performance was low for yield and yield related traits. Here, L35×T2 gave the maximum better parent heterosis of 62.65% and it was one of the best lines crossed with T2, which gave high yield. At Melkassa, of all crosses studied, L18×T2 and L17×T2 gave maximum and minimum mid-parent heterosis of 172.22 and -25.88%, respectively indicated that maximum and minimum heterosis for grain yield was obtained from inbred lines crossed with T2.

According to the analysis of better parent heterosis, twenty lines crossed with T2 were identified and marked in the table that can give the highest yield in the combination. These combinations

Table 4: Heterotic combinations of QPM inbred lines crossed with T1 and T2

Testers	QPM inbred Lines												
Category A	L18	L38	L23	L15	L37	L35	L28	L41	L39	L16	L44	L19	L11
Category B	L38	L15	L5	L18	L35	L23	L39	L41	L37	L28	L16	L44	L11
	L24	L19	L36	L37	L42	L44							
Category C	L38	L15	L16	L18	L35	L23	L28	L39	L41	L44	L19	L11	

Category A: T1 (Obatampa), Category B: T2 (CML144×CML159), Category C: Common well combiner to both testers

consists of some groups which can be suggested for immediate use after a verification trail and others which requires further recurrent selection for identifying of high yielding varieties.

Yield related traits, such as No. of kernels per ear, No. of kernels per row and 1000 seed weight exhibited significant heterosis of 42.04, 36.33 and 6.82% over mid and better parents, respectively. This variation found to be small but can be an indication of importance for selection of grain yield in addition to other important criterion for selection. This is referred as indirect selection.

For the physiological traits such as plant height and ear length 53.41 and 50.0% of crosses expressed positive and significant heterosis over mid parent, respectively while none of crosses showed heterosis over better parent at Awassa and for ear diameter, 69.32% of crosses over mid parent and 10.23% of crosses over better parent exhibited positive and significant heterosis. At Melkassa for plant height, ear length and ear diameter, 82.95, 39.77 and 12.55% of crosses exhibited heterosis over mid parents revealing the dominance effects in their inheritance, while no better parent heterosis was observed.

Heterotic patterns: Based on gca and sca effects (data not presented here) and heterosis of mid and better parents across locations the best combination patterns between testers and selected quality protein inbred lines was identified and the results of some traits are presented in the Table 4. In the analysis, almost all inbred lines crossed with T2 gave more or less higher mean yield (Table 2), showed maximum heterosis over mid parent and better parent and similar results were observed in the combined heterosis analysis (Table 5). Thus, based on combined heterosis over locations, 95.45 and 84.09% of inbred lines with T2 showed the presence of exploitable heterosis over mid and better parents for grain yield, respectively. Those traits, which showed significant heterosis across location, are presented in Table 4. Hence, those combinations, which showed exploitable positive heterosis at individual location and across locations, performed consistently for yield and other yield related traits in 2007 growing season. In Table 4 the best heterotic combinations are presented and could be used for further breeding activities.

DISCUSSION

The aim of this study was to see the performance of test crosses of QPM lines with testers and to determine the heterosis and heterotic groups. In both locations most of the crosses out yielded the testers and lines. Sixteen crosses were superior to BHQ542 and 72% of the crosses was superior to BH540 at Hawassa where as at Melkassa only four crosses surpassed the best check BHQ542 and all crosses surpassed the local check Melkassa 2. Worku *et al.* (1996) and Tulu *et al.* (2001) reported that QPM hybrids produced higher or comparable grain yield as the normal maize check BH540 cited by Worku *et al.* (2001a). In the comparisons of QPM maize with the commercialized normal maize at Pakistan, four QPM hybrids out yielded the top commercial maize varieties

Table 5: Mid and better parent heterosis of yield related traits combined over location

Crosses	BYLD		GYLD		KPE		KPR		TSW	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L1×T1	23.44	10.50	17.46	-0.71	-2.82	-17.56	-0.43	-8.15	14.86	10.39
L2×T1	36.21*	14.72	30.08	5.78	12.09	-14.35	13.57	-5.19	21.95	9.23
L3×T1	29.47	6.80	2.16	-20.22	3.26	-13.51	-1.32	-12.33	1.55	1.47
L4×T1	47.9*	3.10	47.14*	1.60	36.2**	-1.03	31.9**	3.50	11.17	-1.73
L5×T1	30.35	-6.75	26.28	-9.84	22.35*	-7.83	17.64*	-3.10	19.97	5.38
L6×T1	0.96	-6.02	17.24	4.61	1.21	-13.52	3.89	-10.04	13.03	6.55
L7×T1	32.43	-2.60	26.32	-6.53	9.30	-17.90	9.37	-9.91	15.89	11.35
L8×T1	35.15*	19.93	31.95*	9.58	22.57*	-12.64	15.84	-10.99	11.18	10.47
L9×T1	24.11	9.74	25.22	4.38	3.92	-9.89	2.34	-5.86	9.85	7.46
L10×T1	28.91	-2.93	35.24*	-4.05	34.9**	-6.96	29.1**	-4.85	5.57	-1.60
L11×T1	18.60	-2.77	34.85*	8.80	7.84	-11.76	9.91	-5.46	22.17	9.47
L12×T1	11.67	-7.79	16.34	-2.56	17.90	-7.36	16.09*	-1.01	-2.13	-15.07
L13×T1	39.38*	9.94	28.62	0.74	24.84*	-2.14	16.06*	-2.83	25.42	7.10
L14×T1	27.63	3.58	25.50	0.31	18.99*	-3.75	13.62	-5.79	15.59	3.87
L15×T1	61.95**	5.15	54.38**	2.65	23.11*	-3.86	12.94	-5.19	13.07	6.36
L16×T1	40.43*	17.90	41.52*	11.83	16.48	-2.75	7.92	-5.86	26.91*	13.05
L17×T1	20.29	14.11	14.62	-0.35	14.91	-6.49	9.54	-6.00	17.84	10.71
L18×T1	64.06**	10.89	72.46**	8.08	17.40	-8.06	19.71*	-2.76	9.43	7.68
L19×T1	47.44**	34.96	38.51*	17.79	13.78	-10.18	16.20*	-2.09	22.77*	18.55
L20×T1	19.70	-9.09	35.61*	2.93	22.08*	-5.51	12.70	-7.28	10.31	3.90
L21×T1	92.94**	29.19	57.12**	9.33	18.68*	-4.98	17.63*	-0.13	35.55*	12.61
L22×T1	32.00	-5.69	32.31	-3.30	20.52*	-8.80	14.98	-6.33	27.04*	10.52
L23×T1	61.36**	11.32	61.66**	8.94	16.91	-8.65	11.79	-6.67	19.53	5.58
L24×T1	31.10	7.27	19.26	1.42	21.89*	-3.47	17.61*	-2.96	17.06	-0.02
L25×T1	16.20	-6.06	10.59	-4.32	8.35	-6.95	5.41	-3.43	29.24*	5.76
L26×T1	55.19**	20.25	37.71*	4.15	9.94	-9.70	12.30	-5.19	28.09*	7.31
L27×T1	36.60*	8.20	43.81*	9.23	31.43**	0.10	29.52**	5.46	31.87*	14.25
L28×T1	27.67	-4.20	48.59**	10.65	23.62*	1.53	14.17	-0.33	20.66	-0.92
L29×T1	51.19*	-3.14	34.02	-13.38	12.85	-8.79	11.94	-3.30	7.80	-1.19
L30×T1	27.16	-0.37	31.10	-0.26	15.06	-12.30	5.69	-8.02	7.11	6.94
L31×T1	57.04**	5.17	53.08**	2.91	32.38**	-3.05	25.13**	-1.82	27.13*	9.35
L32×T1	11.11	-20.30	19.38	-12.75	14.54	-11.02	8.29	-8.42	2.69	0.39
L33×T1	32.26*	12.27	55.23**	15.45	16.05	-10.75	13.84	-7.95	29.07**	13.70
L34×T1	43.09*	15.38	28.67	3.36	15.70	-6.65	18.01*	1.82	42.01**	13.76
L35×T1	54.50**	9.26	50.10**	10.03	7.62	-12.43	17.79*	-2.22	19.15	10.63
L36×T1	39.26*	11.86	30.22*	12.26	18.10*	-4.25	13.11	-3.77	16.51	1.63
L37×T1	53.83*	6.89	53.53**	10.00	10.02	-2.84	10.70	0.33	2.38	0.86
L38×T1	77.19**	13.14	68.31**	6.53	20.86*	1.95	17.39*	-1.01	35.06*	9.79
L39×T1	44.33*	7.49	43.10*	4.30	23.44*	2.09	13.22	-3.30	1.10	-2.32
L40×T1	19.19	2.49	28.42	3.46	4.86	-9.98	3.32	-10.85	-0.98	-2.31
L41×T1	45.28*	16.92	46.04**	10.43	33.34**	4.09	22.58**	1.55	19.24	13.74
L42×T1	17.90	-10.41	34.48*	-2.37	12.00	-11.26	23.15**	1.14	15.71	13.41
L43×T1	21.79	-11.62	29.96	-1.31	8.46	-6.60	6.38	-2.29	9.37	6.45
L44×T1	62.57**	26.03	39.86*	8.55	0.70	-12.53	2.27	-7.41	31.84*	21.05
L1×T2	37.02*	36.23*	40.93*	31.62*	3.80	-12.97	3.51	-6.05	11.08	10.39
L2×T2	49.83*	39.04*	43.89*	28.60	5.12	-20.47	10.75	-8.84	20.43	11.25

Table 5: Continue

Crosses	BYLD		GYLD		KPE		KPR		TSW	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
L3×T2	34.84	22.20	46.59*	25.03	12.86	-6.56	5.76	-7.48	9.37	5.83
L4×T2	53.30*	14.46	52.97*	13.11	19.37	-14.02	15.36	-10.60	31.31*	19.64
L5×T2	139.93**	84.58**	131.46**	77.96**	28.40**	-4.19	24.94**	1.49	23.06	11.40
L6×T2	25.90	21.39	41.59*	40.60*	-0.40	-15.91	5.41	-10.08	14.07	11.12
L7×T2	47.83*	17.44	48.07*	18.67	19.86*	-10.83	17.66*	-4.42	12.19	11.47
L8×T2	30.23	28.20	50.49**	37.76*	24.58*	-11.96	25.24**	-4.94	5.45	1.32
L9×T2	27.32	24.83	32.26	21.59	3.56	-11.28	-0.14	-9.62	18.16	16.75
L10×T2	95.01**	59.18**	74.45**	33.13*	30.14**	-10.99	36.42**	-0.58	10.51	6.39
L11×T2	84.41**	65.95**	73.57**	53.72**	10.44	-10.63	12.85	-4.35	19.84	10.76
L12×T2	52.08*	37.97*	48.93**	37.64*	11.94	-12.96	11.42	-6.37	17.95	5.44
L13×T2	56.73**	34.97	60.84**	37.68*	7.01	-16.98	10.36	-8.91	34.60*	18.33
L14×T2	93.20**	71.88**	65.41**	44.93**	10.53	-11.56	14.60	-6.31	22.61	13.65
L15×T2	135.92**	62.00**	132.24**	64.26**	26.26**	-2.41	17.15*	-3.05	16.25	12.98
L16×T2	87.12**	73.02**	93.88**	67.66**	10.40	-8.89	12.07	-3.70	19.65	9.89
L17×T2	-0.49	-5.90	12.51	8.48	6.58	-14.23	7.50	-9.10	12.31	9.02
L18×T2	112.17**	52.76**	130.08**	51.68**	13.46	-12.06	13.03	-9.43	10.11	8.17
L19×T2	61.76**	58.74**	67.38**	57.41**	18.41*	-7.50	19.07*	-1.10	7.98	0.93
L20×T2	33.14	9.76	51.68*	25.22	25.06*	-4.19	15.87*	-5.98	20.88	17.64
L21×T2	106.07**	46.74*	91.46**	42.86*	16.28	-7.90	20.99*	1.23	51.60**	29.51
L22×T2	48.74*	14.25	66.70**	31.72*	10.04	-17.54	9.71	-11.84	20.58	8.07
L23×T2	100.34**	47.74**	123.69**	60.73**	27.36**	-1.51	23.32**	1.49	25.41	14.18
L24×T2	56.17**	40.23*	71.17**	60.96**	26.35**	-0.99	22.83**	-0.06	23.30	8.41
L25×T2	49.71*	32.58	53.02**	46.72**	7.46	-8.82	5.81	-4.61	41.76**	19.21
L26×T2	65.05**	39.25*	68.41**	38.47*	7.39	-12.78	9.85	-8.58	30.40*	12.38
L27×T2	55.70**	34.72*	66.75**	37.77*	32.25**	-0.26	30.74**	5.00	21.53	8.45
L28×T2	90.84**	55.16**	95.70**	58.03**	18.58*	-3.69	12.75	-3.05	22.13	3.06
L29×T2	95.80**	32.32	91.55**	31.00*	14.14	-8.74	14.29	-2.73	9.62	3.71
L30×T2	92.27**	64.27**	83.72**	52.07**	32.46**	-0.03	16.58*	-0.06	2.78	-0.77
L31×T2	63.98*	16.79	92.01**	37.58*	35.52**	-1.65	27.76**	-1.04	9.39	-3.10
L32×T2	95.23**	50.65**	100.11**	58.11**	26.98**	-2.35	24.27**	3.57	6.36	0.61
L33×T2	48.26*	38.81*	71.03**	37.91*	20.86*	-7.98	26.59**	0.97	30.88*	18.84
L34×T2	68.02**	48.37**	56.72**	38.10*	15.80	-7.58	12.97	-3.96	45.74**	19.86
L35×T2	112.04**	60.95**	127.28**	80.21**	17.73	-5.26	23.05**	0.71	26.79*	21.58
L36×T2	89.86**	66.93**	64.98**	57.58**	15.01	-7.78	21.30*	1.69	34.35*	20.75
L37×T2	126.70**	68.60**	101.83**	55.84**	17.35*	2.34	14.93*	2.53	2.19	0.26
L38×T2	130.60**	55.25**	140.30**	60.30**	24.13**	3.49	21.95**	1.36	27.64	6.60
L39×T2	89.03**	52.37**	106.77**	62.85**	13.37	-7.29	16.27*	-2.14	-3.70	-3.78
L40×T2	65.60**	57.32**	70.51**	50.77**	10.41	-6.35	16.34*	-1.10	8.97	3.99
L41×T2	102.98**	78.86**	101.91**	65.96**	34.58**	3.98	22.89**	0.39	24.09*	22.37
L42×T2	70.82**	40.90*	104.81**	60.57**	21.97*	-4.38	25.54**	1.69	23.57*	21.85
L43×T2	58.96*	24.32	64.92**	36.21*	13.25	-3.63	12.45	1.62	18.81	11.91
L44×T2	85.48**	56.58**	78.24**	50.99**	10.45	-5.23	17.70*	4.87	14.83	8.85
LSD	6.03		2.21		81.09		4.88		74.00	

**, *Significant at 5 and 1%, respectively, BYLD: Biomass yield, GYLD: Grain yield, KPE: Kernel per ear, KPR: Kernel per row and TSW: 1000 seed weight

(Hussain *et al.*, 2006). In our case, the normal maize lines crossed with the tester (which is called the lysine and tryptophan donors) showed exiting performance in the two location as compared to that in the Pakistan. This indicates the potential of gaining many QPM maize commercial varieties to Ethiopian Farmers through crossing the parent lines of top performing commercial maize varieties with the two testers that has been used in this experiment. Taking into account the importance of QPM maize for food security and the number of malnourished people in the developing country, maize scientists has been convinced to go for quality maize research since ninth (Hussain *et al.*, 2006). In this study most of the crosses in both locations showed significant performance and heterosis as well. Strongly in line with this result Rodrigues and Chaves (2002) reported that the significance of varietal performance of crosses or QPM maize coupled with its significant average heterosis can be used as the best indicator of heterotic pattern. The dominant gene action was reported by different studies for the presence of heterosis but the genetic base of heterosis was not clear so far. However, the report of Yao *et al.* (2013) suggest that a major component of heterosis is a mechanism that is modulated by dosage-sensitive factors that involves allelic diversity.

The interaction of genotypes with the environments and similarly the interaction of its components (crosses, parents and crosses vs. parents) was significant for all traits but for ear height (Table 3). Similar result was reported by Rodrigues *et al.* (2006) for crosses versus parent's interaction across location. The crosses \times location interaction was significant for most of the traits but for days to emergence, ear height, ear diameter, number of seeds per plant, number of kernel row per ear and 100 seed weight. This is in agreement with the findings of Hussain *et al.* (2006) who reported the interaction of crosses \times location which was statistically highly significant reflecting the importance of G \times E.

Heterosis: According to the analysis of heterosis , 68.2 and 43.18% of crosses over mid parents and better parents, respectively showed significant heterosis for days to tasseling at Awassa in the opposite direction. Similarly, for days to maturity all crosses manifested highly significant heterosis over mid and better parents in the negative direction. In general, the crosses were earlier than the earliest parent, which was in most case the tester and more vigorous than both parents possessing high values for the quantitative traits measured. Almost all of the crosses had negative mid parent and better parent heterosis for the three maturity traits such as days to tasseling, days to silking and days to maturity. For maturity trait, L17 \times T2 and L7 \times T1 exhibited the highest and lowest heterosis of 3.7 and -14.4% over mid and better parents, respectively.

At Awassa, maximum heterosis of 189.47% (L36 \times T2) was obtained and followed by 189.09% (L15 \times T2) and 180.25% (L38 \times T2) over mid parent. These crosses also showed better parent heterosis of 109.71, 100.72 and 94.26%, respectively. Similar to the present findings, Hussain *et al.* (2006) obtained four quality protein maize hybrids which are with better and comparable performance to best commercial check. In addition Saleh *et al.* (2002) reported superior and comparable performance of quality protein maize varieties for grain yield and for some yield related characters. For maturity, yield and quality characters Netravati *et al.* (2013) reported the presence of heterosis over better parent and standard check which is in line with the findings in this research.

Different studies reports the role of gene frequency for the expression of heterosis of grain yield. Gardner and Eberhart (1966) suggested that mid parent heterosis depends on the existence of dominance effects and of gene frequency differences among population considered. Similarly, better

parent heterosis depends on the existence of differences among gene frequencies of a variety in relation to the mean gene frequency of the parents in the same group. Thus, a significant mid-parent heterosis effect indicates divergence among the gene frequencies of the population for the loci displaying dominance. Thus, a recurrent selection program lead to an increase in the heterosis among these populations if there would be an increase in gene frequency divergence. However, if such an increase is the same, both in direction and magnitude, in the two populations, the heterosis will remain unchanged, as stated by Hallauer and Filho (1981).

Based on the heterosis and other parameter identifying the heterotic pattern, heterotic combinations were reported for maximum exploitation of yielding potential of a given crop. Similar to the heterotic pattern report in this study, several authors have reported heterotic patterns used in the major maize production regions of the world (Wellhausen, 1978; Parra and Hallauer, 1997). In this research, line per se performance was compared with its respective testcross and similar result was obtained to that of Kebede *et al.* (2012). Acceptable level of protein quality in the QPM is very important since the protein content in QPM is affected by heterotic pattern (Ikramullah *et al.*, 2011); indicating identification of heterotic pattern as one step forward in the improvement of QPM varieties.

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