

Standard heterosis in quality protein maize hybrids

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Maize as the main staple food, development of maize cultivars with enhanced levels of two essential amino acids such as lysine and tryptophan are a must. Most of the improved maize varieties released so far for commercial production are poor sources of quality protein since normal maize protein is deficient in two essential amino acids which are lysine and tryptophan. Developing quality protein maize (QPM) hybrids is therefore important to improve the human health. Determining the standard heterosis of QPM hybrids is an essential step to facilitate the development of QPM hybrids and their commercialization. This study was conducted to estimate standard heterosis of fifteen single-cross QPM hybrids. The crosses were made in a 6x6 half diallel mating design which produced fifteen F₁ single crosses. These single crosses along with three standard checks were evaluated for their grain yield and other traits, using alpha lattice design with three replications. L₃xL₄ gave the highest standard heterosis for grain yield over the best check BH546 (13.08%) and mean of the three checks, BH546, BH547 and BHQ548 (35.26%). L₃xL₆ and L₄xL₆ had also higher magnitude of standard heterosis over the checks. Thus, these hybrids can potentially be proposed for commercialization, and the breeding values of their parents can be exploited for QPM breeding.

Key words: grain yield, half-diallel, normal maize, quality protein maize, standard heterosis

INTRODUCTION

Maize (*Zea mays* L.) is the world's widely grown cereal and primary staple food crop in many developing countries. In Ethiopia, it is the most important strategic crop ranking first in annual total production and second in area coverage following teff. Millions 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). Normal maize varieties are deficient in two essential amino acid, lysine and tryptophan (Vasal, 2001), putting the people depending on

maize as their sole sources of protein at risk. Development of QPM hybrids is important to curb protein malnutrition among people in major maize producing and consuming areas of the country. The production and productivity of this crop in Ethiopia is 8.4 million tonnes harvest per annum and 3.94 t ha⁻¹, respectively (CSA, 2018). The average yield of maize in Ethiopia is by far lower than that of the world average, 5.4 t ha⁻¹ (FAO, 2016). This wide yield gap is attributed to an array of biotic and abiotic stresses (EARO, 2002) as well as socioeconomic constraints limiting adoption and dissemination of improved maize technologies. Production

and productivity of maize can be increased through use of improved hybrids along with appropriate agronomic practices. Breeding strategies for developing improved hybrids based on selection require acceptable level of heterosis. Heterosis is a phenomenon in which an F₁ hybrid of 2 genetically divergent parents demonstrate hybrid vigor over the mid parent value in measurable characters (Shull, 1908). It is an important crop genetics element that can help agriculture to meet the world's ever increasing food needs (Duvick, 1999). From commercial point of view, heterosis is measured as the degree of hybrid performance over the best available variety which is called standard heterosis (Virmani and Edwards, 1983). The type of parents chosen and measurement of trait determine the level of heterosis in maize (Ali et al., 2013). In this study we estimate the standard heterosis of 15 new single crosses QPM hybrids to assess their commercial values and the breeding values of their parental inbred lines.

MATERIALS AND METHODS

Experimental Sites

Bako national maize research center lies at 9°6' North latitude and 37°09' east longitude in the mid-altitude sub-humid maize agro-ecology of Ethiopia, at an altitude of 1650 meters above sea level (m.a.s.l.). During the main cropping season of 2017 the mean annual rainfall was 1598 mm and the maximum rainfall was received in the months of June to August. The mean minimum, mean maximum and average temperatures were 12.8, 29.0 and 20.09°C, respectively; and the relative humidity was 51.04% (BARC, 2017 unpublished weather data). The soil is reddish brown in color and clay loam in texture. Arsi-Negelle is a sub-station of Melkassa agricultural research center located at latitude of 7° 20'N, longitude of 38°9'E and at an altitude of 1960 m.a.s.l with long term average annual rainfall of 886 mm. The average annual temperature ranges from 9.1°C to 26°C. The soil at Arsi-Negelle is clay loam.

Experimental Materials, Design and Management

Six QPM inbred lines, designated as L₁, L₂, L₃, L₄, L₅ and L₆ were used to form 15 single crosses using a half diallel mating design at Bako National Maize Research Center in 2016. The crosses were planted along with three similar maturity group standard checks (BH546, BH547 and BHQP548) at Bako and Arsi-Negelle during 2017 main cropping season. The experiment was planted using alpha lattice design (Patterson and Williams., 1976) with six plots per an incomplete block and 3 incomplete blocks with 3 replicates. Each entry was planted in a one row 5.1 m long plot with spacing of 0.75 m between rows and 0.30 m between plants within a row. The experimental materials were hand planted with 2 seeds per hill, which were later thinned to one plant to get the recommended planting density for the testing sites, 44,444 plants per hectare. Planting was conducted on the onset of the main rainy season after an adequate soil moisture level was reached to ensure good germination and seedling development. All cultural practices like weeding and

cultivation were done manually when necessary. Data on grain yield and other traits were collected on a plot and sampled plants/ears bases. Data collected on a plot basis include days to 50% silking, days to 50% anthesis, actual moisture content, field weight (kg/plot) while data recorded on sampled plants basis were plant height (cm) and ear height (cm). Grain yield per hectare was calculated based on field weight per plot, moisture content adjusted to 12.5%, 80% constant shelling percent and t/ha adjustment factor.

Data Analysis

Data were subjected to analyses of variance using PROC GLM procedure in SAS software version 9.0 (SAS, 2002). In the analysis, genotypes were used as fixed factor while replications, incomplete blocks within replication and locations were considered as random factors. This was specified using RANDOM statement in PROC GLM model of SAS. Before conducting the combined analysis, homogeneity of error variance of the two locations was determined. Combined ANOVA was performed only for traits where the error variances were homogenous. For traits that showed significant genotype by location interaction, correlation among the genotypes and the locations mean for each trait were checked to determine whether there is change of ranks among the genotypes across location. The magnitude of Standard heterosis (SH) was estimated as percentage increase or decrease in the mean of the F₁ diallel crosses in relation to the best check BH546 and the mean performance of the three check hybrids in a given character. Standard heterosis (SH) was calculated for characters that showed significant differences among genotypes following the method suggested by Falconer and Mackay (1996):

$$\%SH = \frac{F_1 - SV}{SV} \times 100$$

Where, F₁ = Mean value of a diallel cross

SV = Mean value of the standard checks (the three hybrids)

%SH = percent standard heterosis

Test of significance for Standard heterosis (SH) was made by using the t-test. The standard errors of the difference for heterosis and t-value were computed as follows:

$$t_{(\text{standard cross})} = \frac{SH}{SE(d)}$$

$$SE(d) = (\sqrt{2MSE/r})$$

Where SE(d) is standard error of the difference between two means

MSE = error mean square and
r = the number of replications
SH = standard heterosis

The computed t-value was tested against the t-value at degree of freedom of error.

RESULTS AND DISCUSSION

Analysis of variance

The combined analysis of variance showed significant differences among genotypes for grain yield and plant height

(Table 1). The interaction between genotypes and locations (GxL), was significant for days to anthesis and days to silking indicating non-consistent performance of the genotypes across locations for these traits. Traits that showed significant GxL interaction had different genotypic response to variable environmental conditions resulting in changes in the ranks of

Table 1. Results of the combined ANOVA for days to flowering, plant height and grain yield

| Source of variation | Degree of freedom | Days to Anthesis | Days to Silking | Plant Height (cm) | Grain Yield (t. ha ⁻¹) |
|---------------------|-------------------|---------------------|---------------------|----------------------|------------------------------------|
| Genotype | 17 | 24.50 ^{NS} | 27.33 ^{NS} | 1079.40*** | 7.24*** |
| Hybrid | 14 | 36.54 ^{NS} | 31.56 ^{NS} | 1448.03*** | 7.25** |
| Loc | 1 | 1112.34** | 1750.35** | 43906.72* | 43.41 ^{NS} |
| G x L | 17 | 14.28*** | 18.08*** | 108.22 ^{NS} | 0.87 ^{NS} |
| Error | 26 | 4.26 | 3.54 | 88.42 | 0.77 |
| Rep(Loc) | 2 | 5.24 ^{NS} | 2.07 ^{NS} | 1005.56* | 3.46* |
| Block (Rep*Loc) | 8 | 8.17 ^{NS} | 1.18 ^{NS} | 144.74 ^{NS} | 2.26* |
| CV | | 2.7 | 2.4 | 4.2 | 10.7 |

***, ** and * = significant at P<0.001, P<0.01 and P<0.05 level of probability respectively; GxL= genotype by environment interaction; Rep= Replication; Loc= location

Table 2. Mean values for days to flowering, plant height and grain yield of 18 F₁ hybrids of maize evaluated at Arsi-Negelle, Bako and combined across locations in 2017

| Cross | Bako | | Arsi-Negelle | | Combined Across location | |
|--------------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|-----------------------------------|
| | Day to Anthesis | Days to Silking | Day to Anthesis | Days to Silking | Plant Height (cm) | Grain Yield (t.ha ⁻¹) |
| L ₁ XL ₂ | 72.50 | 74.50 | 73.00 | 78.00 | 216.25 | 6.68 |
| L ₁ XL ₃ | 73.50 | 74.00 | 79.00 | 81.00 | 212.25 | 7.87 |
| L ₁ XL ₄ | 74.00 | 75.00 | 81.00 | 83.50 | 234.25 | 8.79 |
| L ₁ XL ₅ | 71.00 | 71.00 | 85.00 | 88.00 | 185.25 | 5.33 |
| L ₁ XL ₆ | 75.00 | 78.00 | 81.00 | 84.00 | 251.75 | 8.04 |
| L ₂ XL ₃ | 71.00 | 72.00 | 71.50 | 76.00 | 220.75 | 8.87 |
| L ₂ XL ₄ | 72.00 | 74.00 | 79.50 | 83.00 | 232.50 | 8.92 |
| L ₂ XL ₅ | 70.00 | 68.00 | 80.00 | 82.00 | 207.00 | 6.72 |
| L ₂ XL ₆ | 72.00 | 74.50 | 90.00 | 93.00 | 240.00 | 7.88 |
| L ₃ XL ₄ | 73.00 | 73.00 | 81.50 | 85.00 | 229.75 | 10.55 |
| L ₃ XL ₅ | 68.00 | 72.00 | 77.50 | 82.50 | 217.00 | 8.61 |
| L ₃ XL ₆ | 75.50 | 76.00 | 89.50 | 91.50 | 250.25 | 9.94 |
| L ₄ XL ₅ | 71.00 | 71.00 | 79.00 | 81.00 | 203.50 | 7.32 |
| L ₄ XL ₆ | 75.50 | 75.50 | 81.50 | 83.50 | 247.75 | 9.45 |
| L ₅ XL ₆ | 74.50 | 74.00 | 80.00 | 83.00 | 236.25 | 8.29 |
| BH546 | 71.00 | 75.00 | 79.50 | 82.50 | 235.75 | 9.33 |
| BH547 | 71.50 | 72.50 | 81.00 | 84.00 | 222.00 | 8.27 |
| BHQ548 | 77.00 | 78.00 | 80.00 | 84.00 | 195.75 | 5.97 |
| Maximum | 77 | 78.00 | 90.00 | 93.00 | 250.25 | 10.55 |
| Minimum | 68 | 68.00 | 71.50 | 76.00 | 185.25 | 5.97 |
| Mean | 72.67 | 73.78 | 80.53 | 83.64 | 224.33 | 8.22 |
| LSD | 3.97 | 2.55 | 4.89 | 5.16 | 15.52 | 1.81 |

Table 3. Standard heterosis of crosses over the best check and mean of the three checks for flowering, plant height and grain yield in 2017

| | Combined across location | | | | Bako | | | | Arsi-Negelle | | | |
|--------------------------------|--------------------------|----------------|--------------|----------------|------------------|----------------|-----------------|----------------|-----------------|----------------|------------------|----------------|
| | Grain yield | | Plant height | | Days to anthesis | | Days to silking | | Days to silking | | Days to anthesis | |
| | BH546 | Mean of Checks | BH546 | Mean of Checks | BH546 | Mean of Checks | BH546 | Mean of Checks | BH546 | Mean of Checks | BH546 | Mean of Checks |
| L ₁ XL ₂ | -28.40*** | -14.36*** | -8.27 | -0.71 | 2.11 | -0.96 | -0.67 | -0.93 | 0.00 | -8.94** | -5.45* | -6.59* |
| L ₁ XL ₃ | -15.65*** | 0.90 | -9.97 | -2.55 | 3.52 | 0.41 | -1.33 | -1.60 | 7.59** | -1.46 | -1.82 | -2.99 |
| L ₁ XL ₄ | -5.79*** | 12.69*** | -0.64 | 7.55 | 4.22* | 1.09 | 0.00 | -0.27 | 9.88*** | 1.04 | 1.21 | 0.00 |
| L ₁ XL ₅ | -42.87*** | -31.67*** | -21.42* | -14.94 | 0.00 | -3.01 | -5.33*** | -5.59*** | 14.12*** | 6.02* | 6.67* | 5.39* |
| L ₁ XL ₆ | -13.83*** | 3.08** | 6.79 | 15.59 | 5.63* | 2.46 | 4.00*** | 3.72** | 9.88*** | 1.04 | 1.82 | 0.60 |
| L ₂ XL ₃ | -4.93*** | 13.72*** | -6.36 | 1.35 | 0.00 | -3.01 | -4.00*** | -4.26*** | -2.10 | -10.81*** | -7.88** | -8.98** |
| L ₂ XL ₄ | -4.39*** | 14.36*** | -1.38 | 6.75 | 1.41 | -1.64 | -1.33 | -1.60 | 8.18** | -0.84 | 0.61 | -0.60 |
| L ₂ XL ₅ | -27.97*** | -13.85*** | -12.20 | -4.96 | -1.41 | -4.37* | -9.33*** | -9.57*** | 8.75** | -0.21 | -0.61 | -1.80 |
| L ₂ XL ₆ | -15.54*** | 1.03 | 1.80 | 10.19 | 1.41 | -1.63 | -0.67 | -0.93 | 18.89*** | 12.26*** | 12.73*** | 11.38*** |
| L ₃ XL ₄ | 13.08*** | 35.26*** | -2.55 | 5.49 | 2.18 | -0.27 | -2.67* | -2.93** | 10.43*** | 1.66 | 3.03 | 1.80 |
| L ₃ XL ₅ | -7.72*** | 10.38*** | -7.95 | -0.37 | -4.23* | -7.10** | -4.00*** | -4.26*** | 5.81* | -3.33 | 0.00 | -1.20 |
| L ₃ XL ₆ | 6.54*** | 27.44*** | 6.15 | 14.90 | 6.34** | 3.14 | 1.33 | 1.06 | 18.44*** | 11.64*** | 10.91*** | 9.58** |
| L ₄ XL ₅ | -21.54*** | -6.15*** | -13.68 | -6.57 | 0.00 | -3.01 | -5.33*** | -5.59*** | 7.59** | -1.46 | -1.82 | -2.99 |
| L ₄ XL ₆ | 1.29 | 21.15*** | 5.09 | 13.75 | 6.34** | 3.14 | 0.67 | 0.40 | 10.43*** | 1.66 | 1.21 | 0.00 |
| L ₅ XL ₆ | -11.15*** | 6.28*** | 0.21 | 8.47 | 4.93* | 1.78 | -1.33 | -1.60 | 8.75** | -0.21 | 0.61 | -0.60 |

***= Significant at P<0.001 level of probability, ** significant at P<0.01, * = Significant at P<0.05.

genotypes and making interpretation of data for the traits location specific (Asefa et al., 2008).

Mean performance

Mean grain yield pooled across location ranged from 5.33 for L₁xL₅ to 10.55 t ha⁻¹ for L₃xL₄ (Table 2). The top yielding crosses that performed higher than or as high as the check BH546 (9.33 t ha⁻¹) were L₃xL₄, L₃xL₆ (9.94 t ha⁻¹), and L₄xL₆ (9.45 t ha⁻¹). L₃ and L₄ can be considered heterotic inbred lines with high breeding value. Whereas L₁ and L₅ which gave the lowest yielding hybrid were also involved in many of the crosses with low grain yield suggesting their poor breeding values. Maximum plant height was 251.75 cm for L₁xL₆ and the minimum was 185.25 cm for L₁xL₅. At Bako the maximum number of days to anthesis (77) was recorded for BHQ548 while lowest number of days to anthesis (68) was recorded for L₂xL₅ (Table 2). Number of days to silking ranged from 68 days for L₂xL₅ to 78 days for L₁xL₆ and BHQ548. At Arsi-Negelle Number of days to anthesis ranged from 71.5 for the cross L₂xL₃ to 90.0 for the cross L₂xL₆, while number of days to silking varied from 76.0 for the cross L₂xL₃ to 93.0 the cross L₂xL₆.

Standard Heterosis

The standard heterosis in positive direction was considered to be desirable for Grain yield. L₃xL₄ showed the highest standard heterosis for grain yield over the best check BH546 (13.08%) and over mean of the three checks (35.26%), while L₁xL₅ showed the lowest standard heterosis over the best check BH546 (-42.87%) and over mean of the three checks (-31.67%). Two crosses L₃xL₄ and L₃xL₆ expressed positive and significant heterosis over BH546 and mean of the three checks (table 3). In line with the current study (Gebre, 2017) reported both significant positive and negative standard heterosis for grain yield. Standard heterosis over BH546 for plant height ranged from -21.42% for L₁xL₅ to 6.79% for L₁xL₆. Whereas, standard heterosis over mean of the three checks ranged from -14.94% for L₁xL₅ to 15.59% for L₁xL₆. None of the crosses expressed significant heterosis for plant height either in the positive or negative direction over mean of the checks. Cross L₁xL₅ showed negative and significant heterosis over BH546. Similarly, (Gudeta *et al*, 2015) reported standard heterosis ranging from negative to positive for plant height. At Bako, standard heterosis over BH 546 ranged from -4.23 % for L₃xL₅ to 6.34% for L₃xL₆ and L₄xL₆ and over mean of the checks ranged from -7.10 % for L₃xL₅ to 3.14% for L₃xL₆ and L₄xL₆. L₃xL₅ showed negative and significant heterosis over both BH546 and mean of the checks. For number of days to silking, heterosis over BH 546, ranged from -9.33 % to 4.00% and over mean of the three checks ranged from -9.57 % to 3.72%. The minimum standard heterosis was found for L₂xL₅ while the maximum was for L₁xL₆. Eleven crosses showed negative heterosis over BH546 and mean of the 3 checks, out of them L₁xL₅, L₂xL₃, L₂xL₅, L₃xL₄, L₃xL₅ and L₄xL₅ showed negative and significant heterosis over BH546 and mean of the three checks. At Arsi-Negelle, standard heterosis over BH546 for the number of days to anthesis ranged from -2.10% for L₂xL₃ to 18.89% for L₂xL₆. Heterosis over mean of the checks ranged from -10.81% for L₂xL₃ to 12.26% for L₂xL₆.

Two crosses L₁xL₂ and L₂xL₃ expressed negative and significant heterosis over mean of checks but none of the crosses showed negative and significant standard heterosis over the best check BH546. Eleven crosses showed positive days to anthesis heterosis over BH546 while only three crosses showed positive and significant standard heterosis over mean of the three checks. In line with this study, significant level of negative heterosis for days to anthesis was reported by previous works (Shushay, 2011; Singh et al., 2012; Talukder et al., 2016 and Gebre, 2017). The current result agreed with (Bitew, 2016) who reported both significant positive and negative standard heterosis for this trait and contrasts with the findings of (Matin et al., 2016) who reported only significantly positive heterosis for number of days to anthesis on different set of genotypes. At Arsi-Negelle standard heterosis over BH 546 for number of days to silking ranged from -7.88% in L₂xL₃ to 12.73% for L₂xL₆ and over mean of the checks ranged from -8.98% for L₂xL₃ to 11.38% for L₂xL₆. Two crosses L₁xL₂ and L₂xL₃ expressed negative and significant heterosis in the desired direction while L₁xL₅, L₂xL₆ and L₃xL₆ expressed positive and significant heterosis over BH546 and mean of the check hybrids. The current result agreed with (Melkamu, 2013; Bitew, 2016; Matin et al., 2016 and Talukder et al., 2016), who reported both positive and negative significant level of standard heterosis for number of days to silking. Significant negative standard heterosis for days to flowering is desirable as it indicates early maturity of the crosses than the standard checks.

CONCLUSION

L₃x L₄, L₃ x L₆ and L₄ x L₆ are promising crosses. In addition, their parental inbred lines can be exploited in future QPM breeding works for their favorable breeding values. Further evaluation of the promising QPM hybrids is recommended to see their consistency across seasons.

AUTHOR CONTRIBUTIONS

Haimanot Beruk initiated the concept, designed and conducted the experiment, structured and wrote the original draft, and performed reviewing and editing the manuscript, and prepared the final paper. Hussien Mohammed and Girum Azmach enriched the research concept, supervised the work, contributed to structuring and reviewing the manuscript.

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COMPETING INTERESTS

The authors declare that they have no competing interest

ETHICS APPROVAL

Not applicable

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