

Evaluation of Quality Protein Maize Hybrids for Yield, Association of Yield with its Components and other Agronomic Traits at Bako, Ethiopia

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Abstract	Article Information
<p>Maize is an important food, feed, as well as raw material for producing high-quality protein and carbohydrates products in Africa including Ethiopia. The study was initiated with the objectives to evaluate quality protein maize pipeline varieties in terms of yield and yield related traits, and to investigate association of yield with its components and other desirable traits at Bako. Eighteen genotypes were planted in randomized complete block design with three replications. Highly significant difference were observed among the genotypes to 50% male flowering, days to 50% female flowering, maturity date, ears length and grain yield. Phenotypic coefficient of variation (PCV) was higher in magnitude than the genotypic coefficient of variation (GCV) in respect to all the characters: The character leaf area index, grain yield, 100 seed weight showed moderate PCV and GCV. Whereas male flowering date, female flowering date, days to maturity, plant height, ears height, ears diameter, number of kernel rows, and number of kernel ears showed low PCV and GCV. Heritability in broad sense was higher for male flowering date, female flowering date, days to maturity, plant height, grain yield, hundred seed weight and ears length. However, low heritability was recorded for leaf area index, number of kernel per ears and ears diameters. Based on variability study genotype BH540, BH542, BH543, Kuleni₂, and Obta, were identified as early in maturity; hence these can be used for developing early maturing genotypes. In present studies genotypic and phenotypic correlation of seed yield was positive and significantly related with, Leaf area index, Number of kernel per rows. This suggests that while selecting for improvement in seed yield is performed, this character can be kept in mind provided that the character should show high variability, which is the basis for selection to develop good quality protein maize. Improvement in seed yield could be achieved by direct or indirect selection for high grain yielding genotypes or for yield components positively associated to yield. It is expected that better performing varieties could be generated to increase productivity in Quality protein maize cultivars basically.</p>	<p>Article History: Received : 03-07-2015 Revised : 04-09-2015 Accepted : 06-09-2015</p> <p>Keywords: Quality protein maize Variability Correlation Genotypes Traits Heritability</p>
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INTRODUCTION

Maize is one of the worlds' three primary cereal crops. It occupies an important position in world economy and trade as a food, feed and industrial grain crop (Girma *et al.*, 2005). Maize demand is projected to increase by 50% worldwide and by 93% in sub-Saharan Africa between 1995 and 2020 (FAO, 2007). Though much of the global increase in use of maize is for animal feed, human consumption is increasing and accounts for about 70% of all maize consumption in sub Saharan Africa. It is also one of the major crops grown by small scale farmers in the semi-arid low rainfall areas of Ethiopia (Aquino, *et al.*, 2001). Some reports of diagnostic surveys indicated that 93% of the farmers in the lowlands of Ethiopia are maize growers. Maize grain is used for food, sale and marketing, local brewery and the Stover is used for construction, animal feed and domestic fuel (Tilahun and Teshome, 1987).

Maize is currently grown across 13 agro-ecological zones of Ethiopia which together cover about 90 percent of the country. Moreover, it is an increasingly popular crop in Ethiopia. The area covered by improved maize varieties grew from five percent of total area under maize cultivation in 1997 to 20 percent in 2006 (Byerlee *et al.*, 2007). The small-scale farmers that comprise some 80 percent of Ethiopia's population are both the primary producers and consumers of maize. The recent introduction of several new maize varieties in Ethiopia illustrates the potential importance of maize for food security and the contribution of improved maize varieties to country's agricultural sector (Alemu *et al.*, 2008).

Several hundred million people in developing countries rely on maize as their main staple food. However conventional maize (CM) has two significant flaws; it lacks

the full range of amino acids, namely lysine and tryptophan, needed to produce proteins, and has its niacin (vitamin B3) bound in an indigestible complex. In addition high diets in corn produce a condition known as wet-malnutrition that leads to 'Kwashiorkor' caused by a chronic lack of protein in the diet (Upadhyay *et al.*, 2009).

Quality protein maize (QPM) developed by the international maize and wheat improvement center (CIMMYT) in the late 1990's produces 70 to 100% more of lysine and tryptophan and yields 10% more grain than the most modern varieties of tropical maize (Vasal, 2000). These two amino acids allow the body to manufacture complete proteins, thereby eliminating wet-malnutrition. In addition tryptophan can be converted in the body to Niacin, which theoretically reduces the incidence of Pellagra. QPM offers 90% of the nutritional value of skim milk, the standard for adequate nutrition value (Upadhyay *et al.*, 2009). QPM varieties have yielded positive results in China, Mexico, and Central America for yield and reduction of wet malnutrition. In Africa, 17(South Africa, Burkina Faso, Cameroon, Ivory Coast, Ethiopia, Ghana, Guinea, Kenya, Malawi, Mali, Mozambique, Nigeria, Uganda, Senegal, Tanzania, Togo and Zimbabwe) countries have introduced and promoted QPM (Upadhyay *et al.*, 2009). QPM varieties adapted to Ethiopia and

competitive with grain yield with cultivated conventional maize are insufficient and only few hybrids had been released for planting since recent times. Hence this research proposal was designed with the objective of: To evaluate quality protein maize pipeline varieties in terms of yield and yield related traits at Bako, and to investigate association of yield with its components and other desirable traits.

MATERIALS AND METHODS

Description of Experimental Site

The trial was conducted at Bako Agricultural research center. It's located at 9°6' N latitude; 37°9' E longitude and 1650 m.a.s.l. The mean annual rainfall is 1200 mm, of which more than 80 percent is received between May and September. The mean minimum and maximum temperatures of the area are 13.7 and 27.9 °C, respectively. The soil is brown clay to sandy-clay loam Nitosols with a pH ranging from 5.3- 6.0.

Planting Materials

Thirteen quality protein maize pipelines and five checks (released hybrids) of maize were used for the trial. The seed source and pedigree of the pipelines are indicated in Table 1.

Table 1: Seed source and pedigree the experimental materials used for the study at Bako in 2013/14 cropping season

No.	Genotypes	Code	Seed source	Type
1	BK02-311-28(F2)B-1/CML144//CML142x144-7-B(F2)-9-2-1-1-2-1-1	BK02	BARC	Pipeline
2	BK02-311-28(F2)B-1/CML144//(GH-132-28)-22-1-6-1-1	BKOGH	BARC	Pipeline
3	BK02-Z-311-28(F2)B-1/CML144//(CML176xKULENii(F2)-4-3-1-1-1	BKOKU	BARC	Pipeline
4	CML144/CML159//CML142x144-7-B(F2)-9-2-1-1-2-1-1	CML1	BARC	Pipeline
5	CML144/CML159//CML176xKULENii(F2)-4-3-1-1-1	Kuleni2	BARC	Pipeline
6	CML144/CML159//BQOORC3#32-1-2-2-1-1-1	BQOORC	BARC	Pipeline
7	CML144/CML159//CML142x124-b(113)(F2)-1-1-1-2-2-1	CML2	BARC	Pipeline
8	CML144/CML159//CML142x144-7-B(F2)-9-2-1-1-1-1	CML3	BARC	Pipeline
9	CML144/CML159//CML142x144-7-b(F2)-9-2-1-2-1-1-1	CML5	BARC	Pipeline
10	CML144/CML159//CML142x144-7-b(F2)-9-2-1-2-2-1	CML6	BARC	Pipeline
11	CML144/CML159//CML142x144-7-b(F2)-9-2-2-1-1-1-1	CML4	BARC	Pipeline
12	CML144/CML159//CML176xKULENii(F2)-3-1-1-2-1-1	Kuleni1	BARC	Pipeline
13	Obatanpa-5-4-1-2/(GH-132-28)-22-1-6//CML144	Obat	BARC	Pipeline
14	BH543	BH543	BARC	Released
15	BH542	BH542	BARC	Released
16	BH661	BH661	BARC	Released
17	AMH760Q	AMH760	BARC	Released
18	BH540	BH540	BARC	Released

Experimental Design and Trial management

The trial consisted of 13 new quality protein maize pipelines and five standard checks as a total of eighteen treatments. The experimental design used was RCBD with three replications. Each variety was grown on 5.1 x 1.5 m (7.65m²) plot area with, 75 cm between rows and 30cm cm between plants. The distance between two blocks was 2 m and 1m between two successive plots. The total area of the experimental site was 576.45 m² (31.5 m length x 18.3 m width). Planting was done using two seeds per hill and 30 cm apart between hills. Thinning was performed at the three to five leaf stages to attain a final plant density of 44,444 plants ha⁻¹. All other management practices including planting, fertilization, weeding and harvesting were performed as per the recommendations for the location.

Data Collection

The following data were collected on plot bases:

Days to 50% Anthesis: the number of days from sowing to when 50% of the plants started to shedding pollen.

Days to 50% Silking: the number of days from sowing to when 50% of the plot produced 3 cm long silk.

Days to 90% Maturity: The number of days from sowing to when 90% of the plants in the plot reached physiological maturity which is indicated by the formation of black layer at the bases of ear kernels.

Plant Height (cm): heights of five randomly taken plants from each plot were measured from the ground level to

the base of tassel during dough stage and the average was recorded.

Physiological Maturity: Days to maturity were counted as the number of days from emergence to when 50% of the plants showed black layers on the tip of the kernel.

Ear Height (cm): ear heights of five randomly taken plants from each plot were measured from the ground level to the node bearing the upper useful ear during dough stage and the average was recorded.

Number of Ears Per Plant: Number of ears per plant from five randomly taken plants was counted and the average was recorded.

Ear Length (cm): Length of five randomly taken ears from each plot was measured and the average was recorded.

Ear Diameter (cm): Diameter of five randomly taken ears from each plot was measured using caliper and the average was recorded.

Number of Kernels Per Row: The number of kernels per row from five randomly taken ears per plot was counted and the mean recorded.

Number of Kernel Rows Per Ear: the number of kernel row per ears from five randomly taken ears from each plot was counted and the mean recorded.

100 Kernel Weight: Hundred kernels from each plot were counted by seed automatic seed counter and was weighed using sensitive balance and this was adjusted to 12.5%.

Bare Tips: number of uncovered ears on the tip of the ear were counted at harvest

Plant Aspect: plant aspects were rated on a scale bases of 1-5 (where 1= excellent and 5= poor) after physiological maturity.

Ear Aspect: rated on a scale bases of 1-5 (where 1= excellent and 5= poor) at harvest time.

Root Lodging: the number of plants whose stalk have been inclined below 45% from the ground were counted on a plot bases at harvest time.

Stalk Lodging: The number of plants whose stalk have been broken below the upper most ear were considered and counted as stalk lodging.

Grain Yield (kg/plot): The yield of grain each plot was weighed and adjusted to 12.5% moisture and converted to yield per hectare.

Leaf Area Index: The leaf area index was worked out using the formula given by Sestak (1971). The length and width of the fully opened and physiologically active leaves were measured with a meter road in centimeter on five plants per plot. Leaf area was then calculated by using the formula;

$$LA = L \times W \times K$$

Where, LA: Leaf area per plant (cm²); Length of leaf (cm); W: Width of leaf (cm) and Factor (0.75) or correction factor.

Statistical Data Analysis

Data was subjected to analysis of variance using SAS (SAS Institute, Inc., Cary, NC). Treatment means were separated by the Fisher's protected least significant difference test at $p = 0.05$ (SAS, 2004).

Estimation of Magnitude of Variation

The phenotypic and genotypic variances were estimated according to the method suggested by Burton and De Vane (1953).

$$\begin{aligned}\sigma_g^2 &= MS_g - MS_e / r \\ \sigma_p^2 &= \sigma_g^2 + \sigma_e^2 \\ \sigma_e^2 &= MS_e\end{aligned}$$

Where, σ_g^2 =genotypic variance; σ_p^2 =phenotypic variance; σ_e^2 =environmental variance; MS_g =Mean square due to genotypes; MS_e = Error mean square, and number of replications

The coefficient of variations at phenotypic, genotypic and environmental level variation was estimated using the formula adopted by Johnson *et al.* (1955).

$$PCV = [\sigma_p/x] * 100$$

$$GCV = [\sigma_g/x] * 100$$

Where, σ_p =phenotypic standard deviation ($\sigma_g + \sigma_e$); σ_g = genotypic standard deviation; x = Grand mean for the characteristic x ; PCV, GCV= Phenotypic and Genotypic coefficient of Variation respectively .

Heritability in broad sense for all characters was computed using the formula given by Falconer (1996) as:

$$H = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, H= heritability in broad sense; σ_p^2 = phenotypic variance and σ_g^2 = genotypic variance

The heritability percentage was categorized as low, moderate and high as follow by Robinson *et al.* (1955).

$$\begin{aligned}0 - 30\% &= \text{Low} \\ 30 - 60 &= \text{Moderate} \\ > 60 &= \text{High}\end{aligned}$$

Genetic advances (GA) under selection expected genetic advances where for each character at 5% selection intensity was computed by the formula described by Johnson *et al.*(1955a).

$$\text{Genetic Advances (GA)} = k \cdot \sigma_p \cdot H$$

Where: k = constant (selection differential where $k = 2.056$ at 5% selection intensity); σ_p =phenotypic standard deviation and H = Heritability in broad sense.

Genetic advances as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula

$$GAM = \frac{GA}{\bar{X}} \times 100 \text{ (Falconer, 1996).}$$

Where, GAM=genetic advances as percent of mean; GA=Genetic advances under selection; \bar{x} = Mean of population in which selection will be employed.

The GA as percent of mean was categorized as low, moderate and high as following by Johnson *et al.* (1955) as follows.

0 - 10% = Low
10 – 20 = Moderate
> 20 = High

RESULTS AND DISCUSSION

Viability in Phonological Stages

There is a high significant difference among genotype for days to male and female flowering date, and female maturity date (Table 2). Genotypes took 80.6-84.3 days for male flowering and 80.6-85.7 days for female flowering. Genotypes CML₂, CML₁, BH540, AMH760Q, Kuleni₁, BH542, CML₃, BQOOR, CML₆, Obat, CML₄, BH661, BH543, BKOGH, CML₅, Kuleni₂, BKOKU and BKOKU, BKO2 were late in male flowering and CML₂, BH540, Kuleni₁, CML₁, BH542, BQOOR, CML₃, CML₆, Obat, Kuleni₂, AMH760Q, BKOKU, BKO2, CML₄, CML₅, BH543 and BH661 were late in female flowering. However, Genotypes CML₂ and CML₂ were early in male female flowering (Table 3). From the checks BH543 and BH661 varieties were late in male flowering or tasseling and took 83.7 and 83.3 days, respectively. However

BH542, AMH760Q and BH540 took relatively less number of days to reach days to flowering.

Table 2: Mean squares due to genotypes and error for grain yield and related traits of quality protein maize grown at Bako

Traits	Genotypes (DF=17)	Error (DF=34)
Male flowering	3.5	0.83***
Female flowering	4.9	0.74**
Female maturity	16.95	2.30***
Plant height	542.8	447.5 ^{ns}
Leaf Area Index	0.53	0.30*
Ear Height	288.7	414.9 ^{ns}
Plant aspect	0.12	0.03*
Ears aspect	0.12	0.081 ^{ns}
Stalk lodging	8.2	6.4 ^{ns}
Root lodging	34.4	15.9*
Bare tip	8.9	4.9 ^{ns}
Ears length	2.78	0.052***
Ears diameter	0.22	0.046***
No. of rows ⁻¹ ears	7.86	4.1*
No. of kernels ⁻¹ rows	2.78	0.48**
100 seed weight	68.2	10.98***
Grain yield	3.75	0.72***

Table 3: Agronomic trait of mean data parameter of thirteen quality protein maize pipelines and five standard checks

NO	Genotype	MFD	FFD	MD	PH	EH	LAI
1	BKKO2	84.3	84.7	159.	278.0	158.0	4.2
2	BKOKU	84.3	84.7	156.7	265.3	145.7	4.7
3	BQOORC	82.7	83.3	154.0	278.7	161.0	4.7
4	BKOGH	83.7	83.7	155.7	256.1	142.7	3.9
5	CML1	81.3	82.3	159.7	278.0	157.7	4.8
6	CML2	80.7	80.7	155.0	268.7	148.7	4.3
7	CML3	82.3	83.3	156.0	301.0	174.0	4.6
8	CML4	83.3	84.7	159.0	294.0	162.0	4.9
9	CML5	84.0	85.0	159.3	283.7	168.0	3.8
10	CML6	83.0	83.3	159.0	276.0	148.0	4.6
11	Kuleni1	82.0	82.3	154.0	291.3	165.3	4.5
12	Kuleni2	84.0	83.7	155.0	299.0	167.7	3.9
13	Obataba	83.3	83.3	154.3	276.7	153.7	4.2
14	AMH760Q	82.0	84.0	158.3	256.0	171.3	4.8
15	BH540	81.7	82.0	157.7	264.3	143.3	3.4
16	BH542	82.3	83.0	153.3	282.3	155.3	4.0
17	BH543	83.7	85.3	159.3	262.0	164.7	4.1
18	BH661	83.3	85.7	159.3	299.3	166.7	4.4
	Mean	82.9	83.6	156.8	280.0	158.5	4.3
	LSD (0.05)	1.5	1.4	2.5	35.1	33.1	0.9
	CV	1.1	1.0	0.96	7.6	12.9	12.7

MFD- male flowering date, FFD- female flowering date, MD- Maturity date, PH- plant height, EH- ear height, LAI- Leaf Area Index

The genotype took 153.3-159.6 days to maturity. Genotype CML₂, BH542, Kuleni₁, BQOORC, Obat, Kuleni₂, BKOGH, CML₃, BKOKU, BH540, AMH760Q2, BKO2, CML₄, CML₆, CML₅, BH543, BH661 and CML₂ were late in maturity date. However genotype CML₂ and BH542 were early in maturity (Table 3). In line with this result Lal and Dharendra (2014) reported that the existence of significant difference among quality protein

maize genotypes, this indicates the existence of sufficient variation in the material studied.

Growth Parameters

Non- significant differences were observed among genotype for plant and ears height (Table 2). However, the genotypes showed a significant difference for leaf area index (Table 2). On average the genotypes gave a

leaf area index of 4.3, with the maximum recorded from CML4 but not statistically different from almost all the genotypes except CML5 and BH540 (Table 3). Significant differences were observed among genotypes tested for plant aspect and root lodging (Table 2). However, non-significant differences were observed among genotypes for ear aspect, stalk lodging and bare tip. Plant aspect rating ranged from 2.0 to 2.5. Generally most of the genotype fell within the range of preference by the breeders for their plant aspect (Table 5). Mbuya *et al.* (2010) reported similar results for plant aspect in quality protein maize selected for Savanna agro-ecologies.

Yield and Yield Components

High significant differences were observed among genotypes tested for number of kernel per ears, ear length, number of rows per ears; hundred seed weight and grain yield (Table 2). Number of kernel per row ranges from 10.21 to 13.79 for BKO₂ and BKOKU genotypes. Thus, genotypes BKO₂, AMH760Q, CML₆, CML₁, CML₃, CML₄, CML₃, kuleni₁, CML₅, BH661, BH543, BKOGH, BH540, Obat, BQOORC, BH542, CML₂, Kuleni₂ and BKOKU gave the highest number of kernels per row as compared to the rest genotypes (Table 4). Ear length ranges from 20.2 to 21.1 with an average of 21.2cm. The maximum ear length was obtained from genotypes CML₂, CML₁, BH540, AMH760Q, Kuleni₁, BH542, CML₃, BQOORC, CML₆, Obatmba, CML₄, BH661, BKOKU, BH543, BKOGH, CML₅, Kuleni₂ and BKO₂ (Table 4).

On average the genotypes gave 35.0 with the range from 27.3 to 42.7 gram hundred seed weight (Table 4).

Genotypes BH542, CML₂, Kuleni₂, Obatmba, CML₃, CML₅, BKOKU, BQOORC, BKOGH, Kuleni₁, CML₆, CML₁, CML₄, AMH760Q, BKO₂, BH543, BH661 and BH540 were identified for their highest hundred seed weight (Table 4). On average the genotypes tested gave 8.4t/ha grain yield, with the range of 5.8 to 10.1 for BH542 and CML₄ genotypes (Table 4) and genotypes BH542, BH543, BH540, BKOGH, BQOORC, BKO₂, Obat, CML₅, CML₂, AMH760Q, CML₆, BKOKU, Kuleni₁, BH661, Kuleni₂, CML₁, CML₃ and CML₄ were gave better grain yields (Table 4) as compared to the rest genotypes. High grain yield potential was shown in the experiment of QPM Pipelines in CML₄ had higher grain yields than the best hybrid check, BH661, which yielded 9.4 t ha⁻¹. In line with this result Mbuya *et al.* (2010) reported that the agronomic performance of other QPM and normal varieties were equal or slightly better than the genetically improved normal varieties currently released or the local farmer variety.

Estimates of Means, Ranges, Phenotypic and Genotypic Coefficients of Variations

In general, quality characters had moderate genotypic and phenotypic coefficients of variability. Hundred seed weight had moderate GCV and PCV followed by grain yield. However, these coefficients variability were very low for ears length. Among the yield and yield related characters number of kernel per row and plant height, leaf area index number of kernel per ears, days to maturity, days to female flowering, days to male flowering, ears length and ears diameter respectively (Table 6).

Table 4: Mean grain yield, ear length, ears diameter, number of kernel per ears, number of kernel per row, 100 seed weight of thirteen quality protein maize pipelines and five checks (released hybrids of maize)

No	Genotype	EL	ED	NKE	NKR	Gytha	HSW
1	BKO ₂	21.1	21.2	34.51	10.2	7.8	40
2	BKOKU	21.1	21.2	33.12	13.8	9.3	33.3
3	BQOORC	20.7	20.8	32.2	12.7	7.6	33.3
4	BKOGH	20.9	20.9	34.12	11.9	7.5	34.0
5	CML ₁	20.3	20.6	33.98	11.3	9.4	36.0
6	CML ₂	20.2	20.2	35.00	13.3	8.4	28.0
7	CML ₃	20.6	20.8	35.57	11.4	9.9	32.0
8	CML ₄	20.8	20.2	38.10	11.4	10.1	38.0
9	CML ₅	21.0	21.3	34.17	11.4	8.1	32.0
10	CML ₆	20.8	20.8	34.72	11.1	8.9	35.3
11	Kuleni ₁	20.5	20.6	33.13	11.4	9.3	34.7
12	Kuleni ₂	21.0	20.9	34.59	13.4	9.4	28.7
13	Obataba	20.8	20.8	31.45	12.5	8.1	29.3
14	AMH760Q	20.5	20.0	32.71	10.9	8.6	38.0
15	BH540	20.4	21.5	32.98	12.2	7.0	42.7
16	BH542	20.6	20.8	31.92	12.9	5.8	27.3
17	BH543	20.9	21.34	33.59	11.8	7.2	41.3
18	BH661	20.8	20.4	36.20	11.5	9.3	41.3
	Mean	20.7	20.9	34.0	11.9	8.4	34.7
	LSD (0.05)	0.37	0.36	5.9	1.2	1.4	5.5
	CV	1.1	1.0	5.9	5.8	10.0	9.5

EL=Ears Length, ED= Ears diameter, NKR=Number of kernel per rows, NKE=Number of kernel per ears, Gytha =Grain yield tone per hectare

Table 5: Mean value of plant aspect, ears aspect, bare tip, stalk and root logging for 13 QPM and 5 standard checks maize varieties at Bako Agricultural research station 2013

No	Genotype	Plant aspect	Ears aspect	Bare Tip	Stalk Logging	Root Logging
1	BKO2	2.2	2.3	5.0	3.0	3.7
2	BKOKU	2.3	2.5	2.7	3.0	2.7
3	BQOORC	2.5	2.3	5.3	4.3	10.7
4	BKOGH	2.5	2.5	3.3	5.0	7.3
5	CML1	2.0	2.5	7.3	4.3	7.0
6	CML2	2.5	2.5	6.3	6.0	9.0
7	CML3	2.0	2.5	2.3	3.3	2.6
8	CML4	2.0	2.5	4.3	3.7	4.0
9	CML5	2.2	2.5	3.3	5.3	6.3
10	CML6	2.2	2.5	2.0	2.0	2.7
11	Kuleni1	2.5	2.5	7.0	4.3	1.4
12	Kuleni2	2.2	2.5	2.0	5.0	5.3
13	Obta	2.5	2.5	4.0	4.7	9.7
14	AMH760Q	2.2	2.0	2.3	4.0	5.3
15	BH540	2.5	2.0	3.3	8.3	6.7
16	BH542	2.3	2.2	4.0	7.7	13.7
17	BH543	2.2	2.2	3.7	3.0	5.3
18	BH661	2.0	2.0	6.3	6.0	8.7
	Mean	2.3	2.4	4.2	4.7	2.2
	LSD(0.5)	0.3	8.4	3.6	4.2	6.6
	CV(%)	8.8	12.1	NS	NS	Ns

LSD=Least significant difference, CV=Coefficients variation

Table 6: Estimates of range, mean, genetic components of variance, heritability and genetic advance of QPM genotype

Trait	Range	Mean	SE+	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	H ²	GA	GAM
MFD	80.6-84.3	82.9	1.3	1.41	1.15	0.83	1.6	1.40	0.88	2.5	3.05
FFD	80.6-84.3	83.6	1.4	1.68	1.44	0.74	2.00	1.70	0.86	2.97	3.55
DM	153-159	156.8	2.7	3.1	2.7	2.29	1.97	1.72	0.87	5.55	3.54
PH	256-301	280	21.6	22.23	6.8	447.7	7.9	2.5	0.90	41.17	14.7
LAI	3.4-4.9	4.31	0.6	0.64	0.33	0.30	14.8	7.6	0.05	0.007	0.16
EL	71.7-86.2	20.74	0.3	0.36	0.28	0.05	1.7	1.35	0.77	0.57	2.75
NKE	157-190.4	34	2.3	2.55	1.38	4.6	7.5	4.1	0.54	2.83	8.32
NKR	51.1-68.9	11.94	1.1	1.27	1.07	0.48	10.6	8.96	0.84	2.19	18.36
Gytha	5.8-10.1	8.4	1.2	1.49	1.23	0.72	17.7	14.6	0.83	2.5	3.02
HSW	27.3-42.7	34.7	5.3	6.29	5.34	10.92	18.1	15.4	0.85	10.99	31.7
ED	20.1-21.4	20.9	0.35	0.56	0.14	0.04	2.7	0.64	0.24	0.27	1.32

Ears Length, Ears diameter, NKR=Number of kernel per rows, NKE=Number of kernel per ears, Gytha =Grain yield tone per hectare, σ^2_p = Phenotypic variance, σ^2_g =genotypic variance, σ^2_e = error variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H²=Heritability (broad sense), GA= Genetic advance, GAM= genetic advance as percent of mean, MFD=Male flowering date, FFD=female flowering date, MD=Days to maturity, PH=Plant height, EH=Ears height, LAI=Leaf area index and HSW=100 Seed weight

Estimates of Variance Components

Estimates of variance components for the traits recorded are indicated in Table 6. Male flowering date, female flowering date, days to maturity, plant height, ears height, leaf area index, ears length, ears diameters, number of kernel per ears, number of kernel per row, grain yield tone per hectare, 100 seed weight had exhibited moderate genotypic and phenotypic coefficient of variances (Table 6).

Phenotypic coefficient of variability (PCV) values ranged from 1.7 % for ears length to 18.13% for 100 seed weight, whereas the genotypic coefficient of variability

(GCV) ranged from 1.35 % for ears length to 15.4 for 100 seed weight. In addition, PCV value was generally higher than their corresponding GCV values for all the characters considered (Table 6). According to Deshmukh *et al.* (1986) PCV and GCV values roughly more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Based on this delineation, PCV value was low for number of kernel per row, plant height, leaf area index, number of kernel per ears, days to maturity, days to female flowering, days to male flowering, ears length; medium for Hundred seed weight had the moderate and grain yield.

Genotypic coefficient of variability (GCV) values were low for number of kernel per row, plant height, leaf area index, number of kernel per ears, days to maturity, days to female flowering, days to male flowering, ears length; medium for Hundred seed weight had the moderate and grain yield (Table 6). The low GCV values of these characters suggest that the possibility of improving these trait through selection expression. The difference between PCV and GCV values was medium for hundred seed weight; grain yield leaf area index and medium hundred seed weight and grain yield the influence of environment on these characters. However, this difference was low for number of kernel per row, plant height, leaf area index, number of kernel per ears, days to maturity, days to female flowering, days to male flowering, ears length suggesting minimal influence of environment on the of the characters, thereby having the highest estimates of heritability. Similar result was reported by Yucel *et al.* (2006) for days to flowering, plant height and harvest index.

Estimation of Heritability in Broad Sense and Genetic Advance

Estimates of heritability in broad sense ranged from 0.5% for leaf area index to 90 % for plant height (Table 6). The heritability percentage was categorized as low, moderate and high as follow by Robinson *et al.* (1955). If heritability of a character is very high, say 60% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 60% or less, selection may be considerably difficult or virtually impractical due to the masking effect of environment. Considering this benchmark, heritability estimate was high (>60%) for hundred seed weight, days to female flowering, Ears length, grain yield, number, hundred seed weight, days to maturity,

days to male flowering and plant height. It was moderate (10-20%) for the remaining quantitative characters.

Genetic advances(GA) under selection expected genetic advances where for each character at 5% selection intensity was computed by the formula described by Johnson *et al.*(1955a). Estimates of GA for grain yield was 2.5 tons ha⁻¹ per hectare indicating that whenever we select the best 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 2.5 tons per hectare (Table 6). Maximum genetic advance (>20) as percent of mean (GAM) at 5% selection intensity was recorded for plant height and hundred seed weight (Table 6). Between 0-10genetic advance as percent of mean (GAM) at 5% selection intensity was recorded for leaf area index, number of kernels per rows, ears length, plant height, grain yield, days to female flowering, days to maturity, days to male flowering, number of kernels per ears and 100 seed weight (Table 6).

Estimates of Correlation Coefficients at Phenotypic and Genotypic Levels

Grain yield is the result of many characters which are interdependent. Breeders always look for genetic variation among traits to select desirable types. Some of these characters are highly associated among themselves and with grain yield. The analysis of the relationship among these characters and their association with grain yield is essential to establish selection criteria (Sing *et al.*, 1990). Estimates of phenotypic and genotypic correlation coefficient between each pair of characters are presented in (Table 7). The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the presence of inherent association among various characters.

Table 7: Correlation of grain yield with others characters among 13 QPM pipe lines and 5 checks maize

Traits	PH	EH	MFD	FFD	MD	LAI	NKE	NKR	EL	ED	HSW	GY
PH	1	0.68***	0.08 ^{ns}	0.11 ^{ns}	0.5 ^{ns}	0.03 ^{ns}	0.27*	-0.16 ^{ns}	0.08 ^{ns}	0.11 ^{ns}	0.05 ^{ns}	0.22 ^{ns}
EH		1	0.10 ^{ns}	0.23 ^{ns}	0.04 ^{ns}	0.02 ^{ns}	0.09 ^{ns}	-0.09 ^{ns}	0.10 ^{ns}	0.23 ^{ns}	0.05 ^{ns}	0.11 ^{ns}
MFD			1	0.79***	0.22 ^{ns}	-0.005 ^{ns}	0.02 ^{ns}	0.02 ^{ns}	1.00***	0.79**	0.08 ^{ns}	-0.03 ^{ns}
FFD				1	0.04 ^{ns}	0.09 ^{ns}	0.11 ^{ns}	-0.22 ^{ns}	0.79 ^{ns}	1.00***	0.32**	0.11*
MD					1	0.06	0.31	-0.52**	0.22 ^{ns}	0.42**	0.62**	0.16 ^{ns}
LAI						1	0.03 ^{ns}	-0.14 ^{ns}	-0.006 ^{ns}	0.9 ^{ns}	0.01 ^{ns}	0.25 ^{ns}
NKE							1	-0.19 ^{ns}	0.02 ^{ns}	0.11 ^{ns}	0.15 ^{ns}	0.50***
NKR								1	0.02 ^{ns}	-0.22 ^{ns}	-0.51***	-0.10 ^{ns}
EL									1	0.79***	0.08 ^{ns}	-0.03 ^{ns}
ED										1	0.32*	0.11
HSW											1	0.07
GY												1

MFD=Male flowering date, FFD=female flowering date, MD=Days to maturity, PH=Plant height, EH=Ears height, LAI=Leaf area index, Ears length, ED=Ears diameters, NKE=Number of kernel per ears, NKR= Number of kernel per row, Gytha=Grain yield tone per hectare, HSW=100 Seed weight

Correlation of Grain Yield with other Characters

Grain yield showed positive and significant association with days to male flowering, days to female flowering, plant height, ears height, and leaf area index, ears length, number of kernel per rows, and 100 seed weight (Table 7). At genotypic level, grain also had positive and high correlation with male flowering date, female flowering date, plant height, ears height, leaf area index, number of kernel per ears, days to maturity, ears diameter except

for 100 seed weight and number of kernel per rows. Grain yield had negative genotypic correlation with for 100 seed weight and number of kernel per rows with plant height (Table 7).

Correlations among other Characters

Male flowering date had positive and significant phenotypic and genotypic correlation (Tables 7) with days to maturity, plant height, ears height, ears length, ears

diameter, number of kernel per ears and 100 seed weight. Female flowering date had positive and significant phenotypic and genotypic correlation with male flowering, days to maturity, plant height, leaf area index, rust, ears length, number of kernel per ears and 100 seed weight. Days to maturity had positive and significant phenotypic and genotypic correlation with plant height, ears height, leaf area index, ears length, ears diameter, number of kernel per ears and 100 seed weight. Pant height had positive and significant phenotypic and genotypic correlation with leaf area index, ears length and 100 seed weight. Ears height had positive significant phenotypic correlation with leaf number of cobs/ears harvest, ear length, number of kernel per ears and 100 seed weight. Leaf area index had positive and significant phenotypic correlation with ears length, and number of kernel per ears. Ears length had positive and significant phenotypic and genotypic correlation with 100 seed weights. Ears diameter had positive and significant phenotypic and genotypic correlation with number of kernel per rows and 100 seed weights.

CONCLUSION

Thirteen QPM genotypes and five checks (QPM and non-QPM hybrid varieties) were planted in randomized complete block design at Bako to evaluate quality protein maize pipeline varieties in terms of yield and yield related traits, and to investigate association of yield with its components and other desirable traits. In the present investigation, analysis of variance revealed significant difference among the genotypes for all the traits measured indicating the existence of sufficient variation in the material studied. The character LAI, grain yield, 100 seed weight showed moderate PCV and GCV. Days to maturity, plant height, ears height, leaf area index, ears length, ears diameter, number of kernel per rows, days to male flowering, grain yield tone per hectare. This indicates that there is a lesser influence of environment in the expression of characters which are suitable for selection. The character days male flowering date, female flowering date, days to maturity, plant height, grain yield, hundred seed weight, ears length were showed high heritability but low level of variability; hence these characters are not amenable for selection in the present studies.

Based on variability study genotype BH540, BH542, BH543, Kuleni2, and Obta, was identified as early in maturity, hence these can be used for developing early maturing genotypes. In present studies genotypic and phenotypic correlation of seed yield was positive and significantly related with, grain yield tone per hectare, leaf area index, number of kernel per rows. This suggests that while selecting for improvement in seed yield is performed, this character can be kept in mind provided that the character should show high variability, which is the basis for selection to develop good quality protein maize.

Conflict of Interest

Authors declared no conflict of interest.

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