

Evaluation of Quality Protein Maize (*Zea mays* L) Hybrids at Jimma, Western-Ethiopia

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Abstract

Maize is an important food crop in Ethiopia. But its nutritional quality is poor as its seed protein is devoid of two essential amino acids (lysine and tryptophan). The objective of the present study was to evaluate the performance of Quality Protein Maize (QPM) hybrids developed by CIMMYT. Forty three QPM hybrids and 2 checks were tested using 5X9 alpha lattice design with two replications. Data were subjected to ANOVA using SAS version 9.2. The ANOVA revealed very highly significant differences among the genotypes ($p < 0.001$), for 50% tasseling, ear height, plant count and grain yield. High phenotypic variances were observed for ear height, number of rows/ear, number of grains/row and grain yield. The phenotypic coefficient of variation and genotypic coefficient of variation were high for ear height, plant count, number of rows/ear, number of grains/row and grain yield. The maximum (0.91) and minimum (0.23) broad sense heritability's were recorded for number of rows/ear and days to 50% tasseling respectively.

Keywords: Quality protein Maize (QPM); Phenotypic variability; Genotypic variability; Heritability

Introduction

Zea mays L. (Family Poaceae; Subfamily Panicoideae; Genus *Zea*) is an important annual food crop of the world. *Z. mays* L. (maize) is one of the five species in Genus *Zea*, the others being *Z. diploperennis* HH, *Z. luxurians*, *Z. nicaraguensis* HH, and *Z. perennis* (United States Department of Agriculture [1]). The species of *Zea* have chromosome number of $2n=20$; except *Z. perennis* with $2n=40$ [2]. Maize occupies an important position in the world economy and trade as a food, feed and an industrial grain crop. Several million people in the developing world including Ethiopia consume maize as a principal staple food and derive their protein and calorie requirements from it. The grain accounts for about 15 to 56% of the total daily calories in diets of people in several developing countries in Africa and Latin America, where animal protein is scarce and expensive [3]. In Ethiopia, it is produced for food among low-income families served in different forms of dishes. It is also used in the production of traditional alcoholic beverages for household consumption and family-based businesses. The leaf and stalk are used for animal feed while dried stalk and ear are used for fuel.

Although several hundred million people rely on maize for their principal daily food and for feeding their livestock, it lacks the full range of essential amino acids, namely lysine and tryptophan needed to produce proteins [4]. Until the early 1970s, protein deficiency was believed to be the most serious cause of malnutrition for people who use maize as their principal staple food. In 1963, scientists at Purdue University discovered a mutant maize variety, named as Opaque-2, with twice the normal levels of lysine together and elevated levels of tryptophan [5]. The discovery of Opaque-2 was heralded as a significant breakthrough in the global alleviation of protein deficiency. The genetic system that confers high levels of lysine and tryptophan in maize endosperm protein is the recessive allele of the Opaque-2 gene mapped to short arm of chromosome 7 of maize [6]. The improved protein quality of maize mutants is due to repression of zein synthesis thus increase in non-zein fraction yielding increased lysine and tryptophan [7]. Hence, though this mutant aroused tremendous interest and enthusiasm for its possible use in developing maize with

superior protein quality, the pleiotropic effects of such mutations began to be recognized. The trait was found to be closely associated with several undesirable ones. The Opaque-2 maize kernels were dull and chalky, had 15-20% less grain weight and were more susceptible to several diseases and insects [8] leading to the loss of interest towards it among scientists. Fortunate enough, few international researchers had continued their systematic research activities on refining the original Opaque-2 variety with the aim of maintaining its nutritional quality while making it competitive with conventional varieties of improved maize. And over time, breeders in the International Maize and Wheat Improvement Center (CIMMYT) found modifier genes that restored the desirable hard endosperm phenotype in materials containing the recessive Opaque-2 mutation. These agronomically acceptable and nutritionally enhanced materials later came to be known as Quality Protein Maize (QPM) [9-11]. QPM contains nearly twice as much usable protein as other maize grown in the tropics and yields 10% more grain than traditional varieties of maize [12].

Despite its importance, the cultivation and use of QPM is not expanding throughout the world including in Ethiopia. This is mainly due to poor adaptation of QPM lines in different agro-ecological conditions of the world. The best option of utilizing the QPM germplasm is carrying out different adaptation trials of the QPM hybrids developed by CIMMYT and other research groups to select high performing and stable materials for a given agro-ecology. In Ethiopia, there are few QPM hybrids that perform well, namely:

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BHQP-542 [13], Gibessa, BHQ-542 [14], BHQPY-545 and Melkassa-6Q [15]. All are released to farmers and are benefitting them. However, these activities alone do not suffice in answering the nutritional needs of a large sector of the Ethiopian people who principally depend on maize for staple food. Hence, it is necessary and helpful to evaluate the different QPM hybrids. And yet, very little has been done in evaluating QPM hybrids in Ethiopia. This paper reports the findings of a study aiming at evaluating the performance of CIMMYT's QPM experimental hybrids in Jimma, Western Ethiopia.

Materials and Methods

Description of study area

The experiment was conducted between July and October 2009 at the research field of Jimma University College of Agriculture and Veterinary Medicine called Eladalle (altitude: 1722 m; latitude: 7° 33' 0" N; longitude: 36° 57' 0" E). Eladalle has: (a) mean maximum and minimum annual temperatures are 26.8°C and 11.4°C, respectively; (b) mean maximum and minimum relative humidity in the area are 91.4% and 39.92%, respectively; (c) mean annual rainfall of 951.5 mm; and (d) reddish-brown clay soil with pH ranging from 5.07 to 6.0 [16].

Experimental materials

QPM hybrids obtained from CIMMYT were used in the study. The materials consisted of 43 three way hybrids and two checks (one commercial and another local). Details of materials are shown in Table 1.

Experimental designs and procedure

The materials were sown in alpha lattice (5×9) with 5 plots per block with two replications in a 5 meters single row plot with spacing of 0.75 meters between rows, and 0.3 meters between plants. Though it may be argued that the number of replications is small, the efficiency of alpha-lattice design increases precision of the experiment. All agronomic

practices including land preparation, weeding, and fertilization were applied to all plots as per standard practices for maize.

Data sources

Data were collected on the whole plot basis for days for 50 percent tasseling, plant count and grain yield, whereas plant height, ear height, number of kernels row/ear and numbers of kernels per row were taken on the basis of five randomly selected plants and 100-kernel weight was also taken from composite seeds of all the plants from the plot after removing the plants at the ends of the rows.

Data analysis

Data collected for each trait were analyzed using ANOVA using SAS Software, Version 9.2 [17]. Least significant difference (LSD) was employed in comparing the means. Phenotypic and genotypic variances; and phenotypic and genotypic coefficients of variations were computed using GENRES Version 7.01 [18].

Grain yield

The grain yield was adjusted to a uniform moisture level i.e., 15%. The following formula were used to convert this yield in kg/ha.

$$Yield = Fresh\ Weight \times \left[\frac{100 - Moisture}{100} \right] \times \left[\frac{1.176 \times 0.8 \times 100}{Plot\ Size\ in\ m^2} \right]$$

Plot size being 3.75 m²; 1.176 is constant, 0.8 is shelling ratio,

Heritability in the broad sense

Since the experiment was conducted in single location, Heritability in the Broad Sense was calculated using GENRES based on components of variance as:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Entry	Name	Origin	Entry	Name	Origin
1	CKH-08001:	KB08B-0B20-1/2	24	CKH-08024	KB08A-0A51-19/20
2	CKH-08002:	KB08B-0B20-21/22	25	CKH-08025	KB08A-0A51-21/22
3	CKH-08003	KB08B-0B20-23/24	26	CKH-08026	KB08A-0A51-29/30
4	CKH-08004	KB08B-0B20-27/28	27	CKH-08027	KB08A-0A51-31/32
5	CKH-08005	KB08B-0B20-31/32	28	CKH-08028	KB08A-0A51-35/36
6	CKH-08006	KB08B-0B20-33/34	29	CKH-08029	KB08A-0A51-37/38
7	CKH-08007	KB08B-0B20-35/36	30	CKH-08030	KB08A-0A51-43/44
8	CKH-08008	KB08B-0B20-39/40	31	CKH-08031	KB08A-0A51-51/52
9	CKH-08009	KB08B-0B20-41/42	32	CKH-08032	KB08A-0A51-53/54
10	CKH-08010	KB08B-0B20-45/46	33	CKH-08033	KB08A-0A49-9/10
11	CKH-08011	KB08B-0B20-47/48	34	CKH-08034	KB08A-0A49-17/18
12	CKH-08012	KB08B-0B20-49/50	35	CKH-08035	KB08A-0A49-21/22
13	CKH-08013	KB08B-0B20-51/52	36	CKH-08036	KB08A-0A49-23/24
14	CKH-08014	KB08B-0B20-55/56	37	CKH-08037	KB08A-0A49-25/26
15	CKH-08015	KB08B-0B20-59/60	38	CKH-08038	KB08A-0A49-41/42
16	CKH-08016	KB08B-0B20-61/62	39	CKH-08039	KB08A-0A49-43/44
17	CKH-08017	KB08A-0A51-1/2	40	CKH-08040	KB08A-0A49-27/28
18	CKH-08018	KB08A-0A51-3/4	41	QPMHYB1	KB07B-0B37-1/2
19	CKH-08019	KB08A-0A51-5/6	42	QPMHYB2	KB07B-0B35-1/2
20	CKH-08020	KB08A-0A51-9/10	43	QPMHYB3	KB08B-0B20-71/71
21	CKH-08021	KB08A-0A51-13/14	44	WH403(Local check)	WS
22	CKH-08022	KB08A-0A51-15/16	45	BH-660(commercial)	
23	CKH-08023	KB08A-0A51-17/18			

Table 1: List of QPM hybrids used in the Study.

Where h^2 is Broad Sense Heritability; δ^2g is Genotypic Variance; and δ^2p is Phenotypic Variance.

Results and Discussion

The analysis of variance showed highly significant variation among the genotypes ($p < 0.01$) for characters such as days to 50% tasseling, ear height, plant count and yield (Table 2). This indicates that further mean separation is required for these characters to know which particular genotype is contributing for the differences observed (Table 2).

Mean comparison for characters studied

The mean values for studied character are given in Table 3. Detail and specific information about each character is given below.

Days to 50% tasseling: Days to 50% tasseling ranged from 70 to 86 days, the earliest and latest genotypes being CKH-08019 and BH-660, respectively.

The mean value for days to 50% tasseling was 77.37 days. Only 22 genotypes had shorter days to 50% tasseling than the mean value. Two hybrids (CKH-08016 and CKH-08019) showed significant difference with the commercial standard check (WH403) developed by CIMMYT. However, all the test genotypes tasseled earlier than the local check (BH-660). This is not, in fact, surprising as the test genotypes were developed for moisture-stressed and short rainy season ecologies while BH-660 is a late maturing hybrid developed for high rain fall areas. Thus, the 22 genotypes can be suitable for many agro-ecologies in Ethiopia with moisture-stress and/or short rainy season where BH-660 cannot perform well. Also, the genotypes have lysine and tryptophan contents higher than the local check; thereby fulfill the high protein requirements. Findings of earlier researchers revealed that there are significant differences between late maturing local checks and QPM hybrids in days to 50% tasseling [19-21].

Plant height: Plant height ranges from 156.8 to 261.4 cm (mean 189.7 cm), the tallest genotype being the local check while the shortest genotype being CKH-08001. Of all the genotypes, 19 of them were taller than the mean height whereas the rest were shorter. Interestingly, the height of the local check was statistically significantly greater than the other genotypes ($p \leq 0.01$; Table 3). XX QPM test genotypes yielded plant height greater than 2 meters.

Ear height: The mean ear height of the genotypes in this study was 84.2 cm, the tallest being the local check (147.2 cm) and the shortest being CKH-08001 (58.4 cm). The study revealed high correlation between the plant height and ear height. This finding contradicts the report by where QPM hybrids were taller and had higher ear placement than non-QPM hybrids [22] (Table 3).

Plant count: The mean number of plants per plot stands at 13.52

(SD=1.64), the highest being 24 for BH-660 and the lowest being 10 for CKH-08031. Twenty five genotypes tested in the study have yielded plants per plot below the mean value. The local check yielded mean plant count (24.0) statistically significantly greater than that of all other genotypes ($p \leq 0.05$). The mean values of three genotypes with highest plant count per plot, namely CKH-08008, CKH-08025 and CKH-08005 are statistically significantly highest than the three genotypes with lowest plant count per plot, namely CKH-08031, CKH-08026 and CKH-08035. The analyses revealed weak correlation between plant count and grain yield as the genotype with the lowest grain yield (CKH-08001) had higher number of plant count.

Grain yield: Grain yield per hectare ranged from the 20.8 (CKH-08001) to 106.76 (BH-660) quintals. The overall mean grain yield per hectare was 36.48 quintals. Mean grain yields of majority of the genotypes were much lower than the overall yield per hectare; and the local check yielded statistically significantly greater mean yield than all entries. This finding is similar to the findings of Tulu et al. and Wannows et al. [23,24]. As indicated earlier, the QPM hybrids were early maturing and are not expected to perform like the plants of the late maturing check that exploits the full growing season. Interestingly, there were early flowering genotypes such as CKH-08005, CKH-08016, CKH-08020, CKH-08023, CKH-08024, CKH-08031, CKH-08038, and CKH-08040 that yielded better mean grain yield compared to others including the commercial check. As stated earlier, the genotypes are primarily developed for moisture-stressed and short rainy season agro ecologies, thus were not able to exploit their full potential. Hence, it is difficult to underestimate their yielding ability. And yet, they are readily available sources of essential proteins for households and communities consuming maize as their principal daily food for economic and cultural reasons. The QPM varieties can also help farmers meet their food needs during a period of food shortage before the late maturing varieties were ready for harvest.

Hundred grains weight: The study revealed that the overall mean value for hundred grains weight was 27.64 g, the highest mean hundred grains weight recorded for BH-660 (42.9 g) and the smallest for CKH-08003 and CKH-08014 (22.0 g). Of all the genotypes, 25 of them yielded mean hundred grains weight less than the overall mean. All early maturing genotypes with higher grain yield per hectare except CKH-08005 were found to have higher hundred grains weight than most genotypes. This, furthermore, gives some additional clue that these genotypes have to be privileged in further studies.

Number of kernel rows per ear: The mean number of kernel rows per year was 14.3, the highest mean number kernel rows per ear being 16.8 for CKH-08007 the lowest being 12.8 for CKH-08034. Majority of the genotypes had 14 mean number kernel rows per ear. All genotypes with higher grain yield had lesser mean number of kernel rows per ear than the overall mean with the exception of CKH-08038 that

Source of Variation	df	t – Values (p Values)							
		TS	PH	EH	PC	NRE	NGR	HGWt	Yield
Replication	1	6.068 (0.325)	1078.828 (0.054)	481.636 (0.017)	1.877 (0.412)	0.171 (0.674)	9.501 (0.345)	8.403 (0.450)	7.85 (0.802)
Block	16	19.197 (0.000)	609.886 (0.027)	232.786 (0.004)	2.620 (0.512)	0.895 (0.532)	22.124 (0.039)	17.053 (0.331)	130.580 (0.423)
Entry	44	15.038 (0.004)	335.534 (0.264)	220.605 (0.002)	6.789 (0.006)	0.951 (0.503)	13.218 (0.248)	23.137 (0.089)	297.890 (0.007)
Error	28	5.642	267.079	74.889	2.703	0.944	10.251	14.284	121.870
Total	89								
CV		3.07	8.62	10.28	12.16	6.78	9.70	13.67	30.26

TS: Days to 50% Tasseling; PH: Plant Height; EH: Ear Height; PC: Plant Count; NRE: Number of Kernel-Rows per Ear; NKR: Number of Kernels per Row; HGWt: Hundred Grains Weight; Numbers in Parenthesis indicate the Probability Values.

Table 2: Analysis of variance for evaluation of QPM hybrids.

Name	TS	PH	EH	PC	NRE	NKR	HGWt	Yield
CKH-08001	82.0 ^{ba}	156.8	58.4 ^l	14.5 ^{cb}	14.0	29.8	24.05	20.80 ^h
CKH-08002	79.0 ^{fbedcg}	173.9	84.8 ^{fkceibhdg}	12.0 ^{cebd}	13.0	31.3	27.15	33.88 ^{foehdg}
CKH-08003	77.5 ^{fbedcg}	174.2	68.0 ^{ij}	12.5 ^{cebd}	14.0	30.3	22.00	26.03 ^{fhg}
CKH-08004	80.5 ^{bedc}	181.8	79.8 ^{fkceibhdg}	14.0 ^{cbd}	14.8	27.9	27.25	27.03 ^{fhg}
CKH-08005	75.5 ^{fbedcg}	198.1	91.3 ^{foebdg}	15.0 ^b	14.2	35.3	26.50	49.95 ^{cebd}
CKH-08006	74.5 ^{fihg}	206.3	93.8 ^{foebd}	14.0 ^{cbd}	13.4	32.2	28.80	35.00 ^{foehdg}
CKH-08007	73.5 ^{ihg}	204.0	96.8 ^{cbd}	14.0 ^{cbd}	16.8	33.6	22.85	37.12 ^{foehdg}
CKH-08008	78.5 ^{fbedcg}	188.1	80.5 ^{fkceibhdg}	15.0 ^b	14.8	34.1	28.25	32.39 ^{foehdg}
CKH-08009	76.5 ^{fbedhcg}	185.5	88.4 ^{foebhdg}	12.5 ^{cebd}	14.6	33.6	26.65	39.86 ^{foehdg}
CKH-08010	79.0 ^{fbedcg}	176.1	68.1 ^{ij}	13.0 ^{cebd}	14.3	35.3	33.95	30.15 ^{fahg}
CKH-08011	78.5 ^{fbedcg}	170.8	70.2 ^{ihg}	12.0 ^{cebd}	14.2	34.5	27.25	27.16 ^{fhg}
CKH-08012	77.5 ^{fbedcg}	192.8	87.3 ^{foebhdg}	12.5 ^{cebd}	14.6	36.5	29.05	39.36 ^{foehdg}
CKH-08013	76.0 ^{fbedhcg}	188.7	77.5 ^{fahg}	14.5 ^{cb}	13.6	34.3	29.55	34.13 ^{foehdg}
CKH-08014	78.5 ^{fbedcg}	187.9	84.8 ^{foebhdg}	13.0 ^{cebd}	14.8	30.3	22.00	24.17 ^{hg}
CKH-08015	77.0 ^{fbedcg}	199.3	88.2 ^{foebhdg}	13.0 ^{foebhd}	14.2	34.2	28.20	35.12 ^{foehdg}
CKH-08016	71.0 ^h	184.2	79.7 ^{fkceibhdg}	14.5 ^{cb}	14.4	32.8	29.35	42.23 ^{foehdg}
CKH-08017	76.0 ^{fbedhcg}	184.2	77.3 ^{fahg}	14.0 ^{cbd}	14.8	33.6	28.75	30.15 ^{fahg}
CKH-08018	78.0 ^{fbedcg}	171.0	70.8 ^{ihg}	13.5 ^{cbd}	15.4	29.6	24.05	29.52 ^{fahg}
CKH-08019	70.0 ⁱ	189.3	83.8 ^{foebhdg}	13.0 ^{cebd}	13.6	34.1	26.65	30.76 ^{foehdg}
CKH-08020	80.0 ^{bedc}	195.6	94.8 ^{cebd}	12.5 ^{cebd}	15.2	33.8	27.05	47.83 ^{foebdg}
CKH-08021	77.0 ^{fbedcg}	192.7	79.5 ^{fkceibhdg}	14.5 ^{cb}	14.0	33.8	29.30	27.77 ^{fahg}
CKH-08022	81.0 ^{bdc}	187.9	79.4 ^{fkceibhdg}	12.0 ^{cebd}	15.0	32.7	26.00	31.76 ^{foehdg}
CKH-08023	75.0 ^{fbedhcg}	196.7	95.5 ^{cebd}	14.0 ^{cebd}	13.6	34.5	34.25	53.18 ^{cb}
CKH-08024	76.5 ^{fbedhcg}	206.2	99.9 ^b	12.5 ^b	14.4	31.6	28.20	43.97 ^{foebdg}
CKH-08025	76.5 ^{fbedhcg}	187.8	85.6 ^{foebhdg}	15.0 ^b	14.6	32.3	27.50	29.39 ^{fahg}
CKH-08026	76.5 ^{fbedhcg}	196.6	89.4 ^{foebhdg}	11.0 ^{cebd}	14.8	29.5	23.40	33.01 ^{foehdg}
CKH-08027	77.5 ^{fbedcg}	199.4	85.2 ^{foebdg}	14.5 ^{cb}	14.0	34.7	29.15	37.87 ^{foehdg}
CKH-08028	76.0 ^{fbedhcg}	199.1	88.3 ^{foebdg}	12.0 ^{cebd}	14.0	31.5	24.85	36.62 ^{foehdg}
CKH-08029	81.5 ^{bac}	182.6	76.2 ^{fahg}	12.5 ^{cebd}	14.4	37.7	26.65	31.89 ^{foehdg}
CKH-08030	81.0 ^{bdc}	184.7	78.6 ^{foebhdg}	12.5 ^{cebd}	14.6	35.4	26.15	37.87 ^{foehdg}
CKH-08031	77.5 ^{fbedcg}	186.8	81.2 ^{foebhdg}	10.0 ^b	14.2	34.0	27.60	47.71 ^{foebdg}
CKH-08032	77.0 ^{fbedcg}	199.2	101.50 ^b	13.5 ^{cbd}	13.4	31.9	30.10	35.88 ^{foehdg}
CKH-08033	80.5 ^{bedc}	163.6	68.30 ^{ih}	13.5 ^{cbd}	13.6	31.9	26.30	24.79 ^{hg}
CKH-08034	78.5 ^{fbedcg}	188	84.0 ^{foebhdg}	13.0 ^{cebd}	12.8	32.3	27.85	26.41 ^{fhg}
CKH-08035	75.5 ^{fiedh}	205.8	82.1 ^{foebhdg}	11.5 ^{ced}	13.6	37.4	28.00	31.39 ^{foehdg}
CKH-08036	76.5 ^{fbedhcg}	202.6	92.5 ^{foebd}	14.5 ^{cb}	14.6	30.9	25.55	33.38 ^{foehdg}
CKH-08037	78.0 ^{fbedcg}	174.8	73.5 ^{ihg}	14.5 ^{cb}	14.8	29.9	23.30	27.41 ^{fahg}
CKH-08038	74.5 ^{fihg}	192.9	88.1 ^{foebdg}	14.0 ^{cebd}	15.6	35.2	29.90	52.44 ^{cbd}
CKH-08039	74.5 ^{fihg}	191.5	78.2 ^{fahg}	12.5 ^{cebd}	13.8	33.4	26.75	34.38 ^{foehdg}
CKH-08040	73.5 ^{ihg}	203.8	95.8 ^{cbd}	13.0 ^{cb}	14.2	34.1	33.00	61.54 ^b
QPMHYB1	77.0 ^{fbedcg}	187.3	77.9 ^{fahg}	14.0 ^{cbd}	14.0	32.3	24.95	26.03 ^{fhg}
QPMHYB2	79.5 ^{fbedcg}	168.7	77.0 ^{fahg}	14.0 ^{cbd}	14.2	34.3	25.50	30.64 ^{foehdg}
QPMHYB3	78.0 ^{fbedcg}	177.5	74.5 ^{fahg}	14.0 ^{cbd}	14.4	30.3	28.90	24.54 ^{hg}
WH403	77.5 ^{fbedcg}	188.2	83.9 ^{foebhdg}	13.0 ^{cebd}	14.4	34.7	28.45	42.10 ^{foebhdg}
BH-660	86.5 ^a	261.4	147.2 ^a	24.0 ^a	.	.	42.90	106.76 ^a
Mean	77.37	189.7	84.17	13.52	14.31	37.7	27.64	36.48
CV (%)	3.07	8.62	10.28	12.16	6.78	9.7	13.67	30.26
LSD (0.05)	2.05	NS	17.72	3.368	NS	NS	NS	22.613

NRE: Number of Kernel-Rows per Ear; NK: Number of Kernels per Row; HGWt: Hundred Grains Weight.

NS: Not Significant; TS: Days to 50% Tasseling; PH: Plant Height; EH: Ear Height; PC: Plant Count.

Table 3: Mean performance QPM hybrids evaluated at Eladalle (Jimma) for different characters.

yielded the second highest mean number of kernel rows per ear. CKH-08016, CKH-08020, CKH-08024, and CKH-08038 had statistically significantly greater mean numbers of kernel rows per ear than that of commercial check.

Number of kernels per row: The overall mean number of kernels per row was 33.02; the maximum mean number of kernels per row being 37.7 for CKH-08029 and the minimum being 27.9 for CKH-8004.

Among the genotypes yielding high grain yield, only CKH-08016 and CKH-08024 had a mean number of kernels below the overall mean, though all variations are non-significant at $p \leq 0.05$.

Phenotypic and genotypic variances and their coefficients of variations

Estimated variance components (phenotypic and genotypic),

Variable	Mean (SD)	GCV (%)	PCV (%)	δ^2p	δ^2g	H ²
TS	77.37 (3.66)	2.25	4.74	13.48	3.028	0.2247
PH	189.67 (13.89)	7.17	10.23	379.61	186.58	0.4915
EH	84.17 (11.50)	12.55	18.55	243.79	111.48	0.4573
PC	13.52 (1.64)	11.62	16.77	5.143	2.470	0.4805
NRE	14.31 (0.69)	15.79	16.57	5.363	4.876	0.9092
NKR	33.02 (1.37)	16.72	17.57	32.112	29.127	0.9071
HGWt	27.64 (2.15)	11.66	13.89	15.601	10.997	0.7049
Yield	37.66 (6.87)	31.38	36.38	186.9	139.66	0.7473

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; δ^2p : Phenotypic Variance; δ^2g : Genotypic Variance; H²: Heritability in Broad Sense.

Table 4: Components of variance, coefficient of variations and heritability of characters.

phenotypic coefficient of variability, genotypic coefficient of variability, broad sense heritability of the characters investigated in the present study are presented in Table 4.

Phenotypic and genotypic variances: Analyses of estimated components of variances showed the highest phenotypic variance in plant height ($\delta^2p=379.61$) followed by ear height ($\delta^2p=243.79$) whereas the minimum phenotypic variance was observed for plant count ($\delta^2p=5.14$). This implies that there is great variation in the test materials with regard to height of plants and ear height. Phenotypic variance is sum total of genotypic variance, environmental variance, and the interaction of effect of the two (G×E). But, as the study was carried out in a single location, the contribution G×E is considered negligible. Thus, genotypes and the environment shall be accountable to the observed phenotypic variations. It can, then, be claimed that the effect of the environment on the total variance in plant height and ear height has to be high as the genotypic variances for the traits are relatively less compared to the phenotypic variation.

The contribution of genotypic variance ($\delta^2g=3.03$) in the phenotypic variance ($\delta^2p=13.48$) for days to 50% tasseling was also low, where the contribution of the environment stands at 10.45. Similar findings were reported by Upadhyay et al. [25] based on field evaluation of QPM genotypes under rain-fed conditions. The workers observed lower contributions of genetic variance for the total observable variation with regard to days to 50% tasseling, plant height, and ear height. It was also reported that smaller contribution of genotypic variance to the total phenotypic variance in regard to ear height and plant height [26]. For the rest of traits, the phenotypic variances were largely contributed by the genotypic variances indicating a relatively smaller effect of environmental. Where phenotypic variances are primarily dependent on the genotypes, the selection of varieties with desirable phenotype ensures the selection of better genotype. Genetic variability is the core of plant breeding because proper management of diversity can produce permanent gains in the performance of plants and can buffer against seasonal fluctuations [27,28] (Table 4).

Phenotypic and Genotypic Coefficient of Variations: The levels of variability observed among the genotypes were assessed based on the genetic and phenotypic coefficients of variation (Table 4). PCV for the studied characters ranges from 4.74% (for Days to 50% Tasseling) to 36.38% (for Yield per Hectare) whereas the GCV ranged from 2.25% (for Days to 50% Tasseling) to 31.38% (for Grain Yield per Hectare). The PCV and GCV values were high for Ear Height, Plant Count, Number of Kernel-Rows per Ear, Number of Kernels per Row and Grain Yield per Hectare. These imply the presence of considerable level of observable variations within the genotypes in regard to these traits. Hence, there are good opportunities for improving the traits among the tested genotypes because of wide scope for selection. The highest GCV

for Grain Yield (33.6%) and the lowest for Days to Anthesis (5.2%) on QPM inbred lines and PVC ranging from 5.8% for Days to Anthesis to 43.4% for Grain Yield was reported [29], quite similar to the findings of the present study. Relatively higher estimates of GCV for Grain Yield per Plant, Ear Height, and Grains per Row, Hundred Grains Weight, and Grain Yield showing activities are effective with these traits [30-32].

Broad sense heritability

The Broad Sense Heritability ranged from 0.2247 (for Days to 50% Tasseling) to 0.9092 (for Number of Kernel-Rows per Ear). Traits with moderate Broad Sense Heritability estimates include Plant Height (0.4915), Ear Height (0.4573) and Plant Count (0.480) (Table 4). This observation implies that the profound phenotypic variations are not due the genotype but due to the environment. Hence, as such variations are not heritable the selection of the characters bringing the variations is not efficient because the true performance of the genotypes will not be consistent along successive generations. Lower heritability for Days to 50% Tasseling and Plant Height in double cross hybrids was also reported [33]. Likewise, Rafique et al. [34] reported moderate Broad Sense Heritability (0.396) for Ear Height in 3-way crosses hybrid. As shown in Table 3, we observed higher Broad Sense Heritability for Number of Kernel-Rows per Ear (0.9092), Number of Kernels per Row (0.9071), 100-Grains Weight (0.7049), and Grain Yield (0.7473) implying that these traits are highly heritable and selection would be fairly easy and effective [34,35]. Selection for a character with high Broad Sense Heritability is fairly easy as the effect of the environment on the genotype is believed to be minimal [36]. Values of Broad Sense Heritability alone would not be sufficient parameters in selecting the best individuals [37]. In this regard Mulatu et al. [38] have suggested that genetic coefficients of variation together with heritability estimates would give the best picture of genetic advances in selection. Hence, traits exhibiting high genotypic coefficients of variation and high heritability would be preferred in selection. We observed higher values of GCV and H² for Number of Kernel-Rows per Ear, Number of Kernels per Row, 100-Grains Weight, and Grain Yield. However, the Number of Kernel-Rows per Ear had negative and statistically significant genotypic correlation with Grain Yield while the Number of Kernels per Row had non-significant genotypic correlation with the same trait. Hence, it is safe to suggest the use of 100-Grains Weight as selection criteria in crop improvement studies.

Conclusion

Based on the field evaluation, although the local check outperformed all the test materials, genotypes such as CKH-08005, CKH-08016, CKH-08020, CKH-08023, CKH-08024, CKH-08031, CKH-08038 and CKH-08040 had better performance than the others in terms of

grain yield. The lower yield of the test materials was due to the fact that the genotypes were early maturing and are primarily developed for moisture stress areas and are not expected to outperform the local check which is a late maturing hybrid.

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