Original Research Article

performance evaluation and identification of adaptable new highland quality protein maize in bred lines in Ethiopia

Abstract

Background*: Maize plays a critical role in meeting high food demand. It is globally one of the most widely adopted and cultivated crops. Hybrid and open-pollinated varieties development from fixed inbred lines is one of the strategies for the improvement of maize production. Compared with the world average, the national average maize yield in Ethiopia is low. According to this development and selection of promising germplasm has indispensable value for developing high-yielding maize varieties. The trial consisted of 21Quality Protein Maize (QPM) lines, two QPM testers lines, and one Conventional Maize (CM) line check (FS67) was evaluated in two replications laid out using RCBD at Ambo and Arsi-Negele. The objective of this study was to identify new lines with good performance compared with released QPM checks and CM lines.*

Result: *In this line trial, from the total of 28 traits, 21 of them showed a significant difference between lines at Ambo and 24 traits at Arsi-Negele. In combined mean performance analysis, the highest yielding line (L8) exceeded the mean of all line checks, mean QPM checks, CM line check (FS67), and best QPM line check (CML144) by 34.89%, 54.80%, 7.30%, and 25.31%, respectively for GY. The value of EPP ranged from 0.91 (L14) to 1.85 (L3) with an overall mean of 1.19 (Table 4). The highest yielding line (L8) had the 2nd highest EPP (1.63), (Table 4). Mean EPP of the top five QPM lines was less by 5.45%, 4.96%, 22.41%, and 6.41% compared with a mean of all line checks, mean of QPM line checks, best QPM check, and CM line check, respectively. The high yielder line (L8) had a higher mean value than the mean of lines checks (CML144, CML159, and FS67), mean of QPM lines checks, best QPM check (CML144), and FS67 by 25.71%, 26.36%, 3.16% and 24.43%, respectively.*

Conclusion: *In general, the study confirmed the existence of promising new QPM parental lines like L8 which showed better performance compared with the new lines. This indicates there was a promising line that can be used as source material in the breeding program for further research work.*

Keywords: Quality protein maize, conventional maize, maize

1. INTRODUCTION

Maize (*Zea mays* L. *2n = 20*) belongs to the family Gramineae, and the tribe Maydeae (Andropogoneae) (Norman *et al.*, 1995). Maize is a very productive, adaptable, versatile, and most important food security crop in Sub Saharan Africa (SSA); Eastern and Southern Africa use 85% of maize produced as food while Africa as a whole use 95% as food (Bekele *et al.*, 2011). In 2017, worldwide production of maize was around 1042.4 MT. Its' production took 40% share of all cereals and 25% of the land allocated for cereals (FAO, 2017). The largest share, 37% (384.8 MT) was held by the USA and continued to be the largest maize producing country in the world. Africa contributes 7.6% of the global maize production area; Nigeria, Egypt, Ethiopia, and South Africa are the front-runner countries in order of importance (FAO, 2015). Ethiopia is the third leading country for the production of maize in Africa next to South Africa and Nigeria (FAO, 2017).

Despite its importance, maize yield in sub-Saharan Africa has stagnated at less than 2 t ha^{-1} compared to the world average of more than 5 t ha^{-1}. In Ethiopia, too, the national average maize yield is low compared to the world average grain yield (5.85 t ha^{-1}) (FAO, 2017). This is due to several biotic and abiotic stresses that limit maize productivity across countries in sub-Saharan Africa (Badu-Apraku *et al.*, 2011). Among abiotic stresses, drought and low soil fertility are the most important stresses that affect maize production (Mosisa *et al.*, 2007; Lobell *et al.*, 2011; Weber *et al.*, 2012).

Maize is one of the five strategic crops for food security in Ethiopia. In 2018, maize grew on 21% of the total cereals area and it ranked 2nd following teff (30%) in terms of total production contributing 31% of the total cereals grain produced in the country. About 8.4 MT of maize is produced from 2.1 million hectares with an average yield of 3.94 t ha^{-1} (CSA, 2018). Of all the smallholder cereals framers in the country, 70% grow maize in variable scales (CSA, 2018).

The maize crop is an important source of protein, although its protein is low in essential amino acids such as Lysine (Lys) and Tryptophan (Trp) (Mbuya *et al.*, 2011; Gudeta *et al.*, 2015). It is also a source of minerals, vitamin B, iron, and carbohydrate (Rouf Shah *et al.*,

2016). While millions of people worldwide are overly dependent on maize as a staple food, this nutritional deficiency caused for kwashiorkor is a concern in areas where maize is a staple food, particularly for people with high protein requirements (Bain *et al*., 2013; Morley, 2016). The nutritional superiority of Quality Protein Maize (QPM) to Conventional Maize (CM) has been amply demonstrated in rats (Bressani *et al*., 1969; Gupta *et al.*, 1970), pigs (Lopez-Pereira, 1992; Osei *et al.*, 1994a, and Atlin *et al.*, 2011), infants and small children (Bressani, 1995; Atlin *et al.*, 2011 and Tekeba, 2017) as well as adults (Bressani,1992), dairy cattle (Glover, 1992), pregnant or lactating women, and the ill (Tekeba, 2017) in countries where maize is a staple and is the main protein source. The term QPM refers to maize genotypes whose Lys and Trp levels in the endosperm of the kernels are about twice higher than in CM varieties (Bressani, 1992). QPM has a nutritional advantage over CM. QPM contains the *o2* mutation, which alters the protein composition of the maize endosperm, resulting in increased concentrations of Lys and Trp (Mertz *et al.*, 1964). Consumption of QPM may help alleviate human malnutrition problems in regions with maize-based diets (Bressani, 199; Mertz, 1992) because of the 60 to 100% increase in concentration Lys and Trp (Bressani, 1992).

In Sub-Saharan Africa, where maize is the major source of calories and the existence of malnutrition, emphasis has been given to the introduction and development of QPM varieties as a means to solve malnutrition caused due to heavy dependence on maize as a source of protein. In Africa or elsewhere the most followed QPM breeding strategy relies on the conversion of existing adapted genotypes to QPM (CIMMYT, 2004b, and Krivanek *et al.*, 2007). Adapted CM genotypes that resist major biotic and abiotic stresses are converted to QPM mostly following backcrossing or modified backcross breeding methods (Adefris *et al.*, 2015).

Elite QPM inbred lines well adapted to eastern and southern African regions are being developed by CIMMYT-Zimbabwe, CIMMYT-Kenya, and CIMMYT-Ethiopia (at Ambo, EIAR). Dagne (2008) and Adefris *et al.* (2015) pointed out that as converted QPM inbred lines, OPVs and hybrids can be available to national research programs, and other private and public research organizations from CYMMYT, and other parts of the world. So that,

using this genetic resource, QPM hybrid development efforts can be fruitful in developing nutritionally balanced maize varieties to contribute to solutions to the problem of food and nutrition insecurity. Although currently available elite QPM inbred lines have been tested in hybrid combinations with selected lines and testers, the adaptation and performance evaluation of the new lines also critical for the specific agroecology in addition to a systematic study aimed at classifying the continuously introduced lines into different heterotic groups has not been conducted. Line's information regarding mode of gene action, combining abilities, heritability and heterosis would be useful in the development of inbred lines and essential for the selection of suitable lines for hybridization, identification of promising hybrids, and the development of stable improved maize hybrids and open-pollinated synthetic varieties with high yield for diverse agro-ecologies (Abebe *et al.*, 2004).

Highland maize breeding program in collaboration with CIMMYT has developed a large number of highland elite maize inbred lines. The effort is aimed at identifying better combining inbred lines for the development of hybrids for highland areas of the country. To initiate an effective hybrid breeding program, information on the combining ability of inbred lines and identifying the lines' heterotic group is an essential and critical factor. Recently 21 new elite QPM inbred lines have been developed by the highland maize improvement section at Ambo-EIAR. These lines have been evaluated at the nursery level but not in an organized way in trial form. So, the objective of this study was to assess the *per se* performance of new QPM lines and their level of tolerance to biotic stresses in comparison with the well-known QPM and CM line checks.

2. Materials and Methods

2.1. Description of Experimental Sites

The study was conducted at two locations in the highland agroecology of Ethiopia including; Ambo and Arsi-Negele (transition highland) Agriculture Research Centers during the 2017 main cropping season.

Ambo Agriculture Research Center is located at 8^{o} 57' N latitude, 38^{o} 07' E longitude at an altitude of 2225 masl. It represents the highland sub-humid maize growing agroecology of

Ethiopia. The soil type is heavy clay (vertisol) with a pH of 7.8 for most topsoil (0 - 30 cm) (Demissew, 2014). The long-term total annual rainfall is 1115 mm, and average minimum and maximum temperatures are 11.7^{o}C and, 25.5^{o}C, respectively with an average value of 18.6 ^{o}C.

Arsi-Negele is located at 7^{o}19' N latitude and 38^{o} 39' E longitude at an altitude of 1960 masl. The long-term annual rainfall is 886 mm with erratic and uneven distribution. The site had mean minimum and maximum temperatures of 9.1 ^{o}C and 26 ^{o}C, respectively with an average value of 17.6 ^{o}C. The soil texture is clay loam with a pH of 6.5-7.5 (Etagegnehu and Amare, 2016).

2.2. Experimental Materials

Twenty-one highlands new QPM inbred lines, named hereafter as lines (L1 to L21) and two elite QPM inbred lines checks (CML159 and CML144), named hereafter as QPM checks (T1 and T2, respectively), and one elite CM highland inbred line (FS67) check was tested (Table 1).

2.3 Experimental Design and Crop Husbandry

The trial was laid out using a randomized complete block design (RCBD) consisting of one-row plots replicated twice. Each plot consisted of a 5.25 m long row with 0.75 and 0.25 cm inter-row and intra-row spacing. The plot was hand-planted with two seeds per hill and later was thinned to one plant per hill to attain the final plant density of 53,333 plants per hectare. Diammonium phosphate (DAP) fertilizer was applied all at planting at the rate of 150 kg ha^{-1} while 200 kg ha^{-1} of urea was applied in partition 1/3 at planting, 1/3 at knee height, and 1/3 at flowering at Ambo. At Arsi-Negele, 100 kg ha^{-1} DAP and 150 kg ha^{-1} urea fertilizer were applied based on the site recommendation following the same time of application mentioned for Ambo above.

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2.4. Data Collected

Data on morphological, phenological, yield, and related yield traits were recorded on plot and individual plant basis at each location as specified below.

Days to tasseling (DT), Days to silking (DS) Anthesis silking interval (ASI) Days to maturity (MD), Plant aspect (PAS) Disease score: gray leaf spot (GLS), turcicum leaf blight (TLB), and common leaf rust (CLR), Ear aspect (EAS), Number of ears per plant (EPP), Kernel Modification (MOD) Grain yield (GY), Number of leaves per plant (LFPP), Number of leaves above uppermost ear per plant (LFAE), Number of leaves bellow uppermost ear per plant (LFBE), Leaf angle (LFANG), Leaf length (LL), Leaf width (LW), Leaf area (LFAR), Plant height (PH), ear height (EH), ear length (EL), Ear diameter (ED), Number of kernel rows (NKR), Number of kernels per row (KPR), Thousand seed weight (TSW), Biomass (BIOM) and Harvest index (HI).

Grain yield (t ha^{-1}) = $\frac{fresh\ cob\ weight\ x(100-MC)\ 0.8\ x10}{87.5\ x\ 2.81}$

Where, fresh ear weight = fresh weight of the cob from the plot in kg, 0.8 = shelling percentage, 87.5 = standard value of grain at a moisture content of 12.5% from the total grain mass, MC = grain moisture content (%) at harvest, 2.81 = plot area harvested in meter square (m2).

2.5 Data Analysis

The data obtained from field measurements were organized and analyzed using SAS statistical package (SAS, 2002). Accordingly, to testify to the presence of variation among inbred lines for the trait in question variance for analysis was carried out for individual locations and across locations.

2.5.1. Analysis of variance

Before data analysis, the anthesis-silking interval (ASI) was normalized using ln (ASI +10) as suggested by Bolaños and Edmeades (1996). Individual and across locations data were subjected to analysis of variance using PROC GLM procedure in SAS software version 9.0 (SAS, 2002). In the analysis, treatments were used as fixed factors while replications and locations were considered as random factors. This was specified using the RANDOM statement in the PROC GLM model. A mean separation test was done for traits that expressed differences among treatments using LSD. Combined analysis was done for the significant traits that showed significant differences in each location analysis and testing

homogeneity of error variances. Whenever traits were found to be significant at two locations combined based on the ratio of error (Gomez and Gomez, 1984). In the combined analysis, the variation among genotypes and checks effects were tested against their respective interaction effect with a location. The interaction effect of each source of variation by location was tested as per the expected mean square (MS) of the error estimate.

Table 1. List of parental inbred lines and standard checks used.

Code	Pedigree	Remark
L1	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-1-B-B-B-#	QPM
L2	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-2-6-B-B-#	QPM
L3	(CLQRCWQ50/CML312SR)-2-2-1-BB-1-B-B-B-#	QPM
L4	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-1-B-B-B-#	QPM
L5	([NAW5867/P49SR(S2#)//NAW5867] F#-48-2-2-B*/CML511) F2)-B-B-39-1-B-#	QPM
L6	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-9-1-B-#	QPM
L7	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-35-2-B-#	QPM
L8	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB) F2)-B-B-44-2-B-#	QPM
L9	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-18-2-B-#	QPM
L10	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-30-1-B-#	QPM
L11	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB) F2)-B-B-35-2-B-#	QPM
L12	(CML395/(CML395/[NAW5867/P49SR(S2#)//NAW5867] F#-48-2-2-B*4) F2)-B-B-30-1-B-#	QPM
L13	[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5-2-6-B-B-#	QPM
L14	(CML395/(CML395/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2)-B-B-46-1-B-#	QPM
L15	(CML395/(CML395/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2)-B-B-50-1-B-#	QPM
L16	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-10-3-B-#	QPM
L17	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-14-1-B-#	QPM
L18	(CML395/(CML395/S99TLWQ-B-8-1-B*4-1-B) F2)-B-B-29-1-B-#	QPM
L19	(CML395/(CML395/CML511) F2)-B-B-7-2-B-#	QPM
L20	(CML395/(CML395/CML511) F2)-B-B-11-2-B-#	QPM
L21	(CML395/(CML395/CML511) F2)-B-B-37-1-B-#	QPM
T1	CML144-Check1	QPM
T2	CML159-Check2	QPM
	FS67-Check3	CM

3. RESULT AND DISCUSSION

3.1. Analysis of variance

Individual location ANOVA of the line trial which include 21 new QPM lines and two QPM line checks and one CM line FS67 showed significant difference among genotypes for all traits at both locations except for GLS, CLR, PAS, NKR, and KPR at Ambo and MOD and

TLB at Arsi-Negele (Table 2). The difference between the 24 lines was non-significant for MD and HI at both locations. In the combined analysis, only HI showed a non-significant difference among genotypes (Table 2). In the combined analysis, the difference between 21 QPM lines was significant for GY, DT, DS, ASI, PH, EH, TLB, EL, KPR, ED, LFPP, and LFBE. Regarding QPM checks, the difference was significant in combined analysis for DT, DS, ASI, EH, CLR, EPP, EL ED, TSW, and LW but for the rest of the traits the difference was non-significant (Table 2). Similarly, Demissew (2014) reported significant differences in grain yield and yield-related and phenological traits among QPM inbred lines. Dagne *et al.* (2008) also reported significant MS for PH, MD, and GY.

The Genotype by Location interaction was significant for GY, DT, DS, GLS, CLR, TLB, EAS, TSW, LFANG, LFPP, and LFAE and non-significant for the remaining traits. This indicates that with the traits with a significant difference in interaction, the performance was unstable across the location. Berhanu (2009) also reported similar findings for grain yield, grain yield-related, and other agronomic traits. Gudeta *et al.* (2015) also reported significant GxL interaction for GY. The result in this study contradicted to significance MS difference reported for TSW among the genotypes and the non-significant difference for DT and PH (Gudeta *et al.*, 2015).

Table 2.MS due to genotype (lines) and error for grain yield and other traits of maize evaluated at Ambo and Arsi-Negele Agricultural Research Centers, 2017.

Trait	Mean Square									
	Ambo		Arsi-Negele		Across locations Ambo and Aris-Negele)					
	Genotype (DF=23)	Error (DF=23)	Genotype (DF=23)	Error (DF=23)	Location (DF=1)	Genotype (DF=23)	G X L (DF=23)	Error (DF=46)	QPM line (DF=20)	QPM check (DF=1)
GY	1.19**	0.32	1.60***	0.23	14.23*	2.28***	0.53*	0.28	13.59*	6.00
DT	35.77***	3.00	17.39***	5.30	5265.84*	44.30***	8.86*	4.15	62.59*	1102.1***
DS	41.59***	6.65	18.08***	4.26	4401.04**	45.72***	13.95**	5.45	50.74*	644.48***
ASI	5.39*	2.04	4.38*	1.96	38.76	6.30***	3.48	2.00	5.78*	61.01***
MD	5.91	3.25	7.74	3.87	19238.34***	8.28**	5.37	3.56	11.82	2.29
PH	506.02***	57.86	567.20***	55.78	6600.17	998.58***	74.64	56.82	3092.17***	682.12
EH	380.83***	48.34	347.82***	47.33	2223.38	684.75***	43.92	47.84	1641.54***	4484.00**
MOD	0.69**	0.25	0.59	0.48	5.27	0.77*	0.51	0.36	0.73	0.40
GLS	0.01	0.01	0.11*	0.05	3.56*	0.06*	0.06*	0.03	0.04	0.05
CLR	0.09	0.09	0.92**	0.25	64.19**	0.68***	0.34*	0.17	0.63	5.43**
TLB	0.15*	0.08	0.21	0.14	15.84*	0.16	0.20*	0.11	0.16*	0.12
EAS	0.42*	0.17	0.88***	0.21	3.76	0.96***	0.35*	0.19	0.46	1.83
PAS	0.24	0.13	0.51*	0.19	1.76*	0.56***	0.19	0.16	0.38	1.08
EPP	0.15**	0.05	0.08***	0.02	0.60	0.20***	0.04	0.03	0.18	5.99***
EL	4.21**	1.16	4.21*	1.59	5.59	6.93***	1.49	1.38	24.65**	61.01**
NKR	2.35	1.54	4.83**	1.30	0.51	5.49***	1.68	1.42	3.44	4.59
KPR	17.81	13.31	28.84**	7.97	59.38	34.69***	11.96	10.64	95.06**	4.15
ED	0.28***	0.05	0.22***	0.03	0.09	0.46***	0.05	0.04	0.62*	4.81***

Table 2 (Continued)

Trait	Mean Square									
	Ambo		Arsi-Negele		Across Locations Ambo and Arsi-Negele)					
	Genotype (DF=23)	Error (DF=23)	Genotype (DF=23)	Error (DF=23)	Location (DF=1)	Genotype (DF=23)	G X L (DF=23)	Error (DF=46)	QPM line (DF=20)	QPM check (DF=1)
TSW	7613.35***	1425.51	5446.06***	610.3	51666.65	10306.21***	2753.21**	1017.91	10496.97	234328.2**
BIOM	9.83*	4.48	6.37*	2.68	13.77	10.72***	5.5	3.58	30.86	44.84
HI	143.51	160.28	97.84	89.69	4220.75	119.83	121.51	124.98	221.59	0.63
LANG	81.19***	13.7	220.03***	16.09	580.17	243.68***	57.55***	14.9	23.08	2.61
LL	118.70***	4.69	157.11***	34.52	4842.67*	244.21***	31.6	19.61	85.97	1.59
LW	1.76***	0.3	2.08**	0.63	126.42***	2.89***	0.96*	0.47	0.39	3.14*
LFAR	8076.17***	1715.4	14656.32**	4851.32	1198421.01**	18097.12***	4635.38	3283.36	7006.99	15019.4
LFPP	1.99***	0.33	1.32*	0.55	9.17	2.39***	0.92*	0.44	2.32*	0.37
LFAE	0.72***	0.1	0.64***	0.08	0.12	1.19***	0.18*	0.09	0.29	0.02
LFBE	1.33***	0.33	1.15**	0.31	7.22	2.01***	0.48	0.32	1.67**	0.37

= significant at 0.05 probability level, **= significant at 0.01probabilty level and * = significant at 0.001probabilty level, DF = Degree of freedom, GxL= Genotype by location interaction, GY = Grain yield (t/ha), DT = Days to tasseling (days), DS = Days to silking (days), ASI = Anthesis Silking Interval (days), MD = Days to Maturity (days), PH = Plant Height (cm), EH = Ear Height (cm), MOD = Kernel Modification (1-5 scoring), GLS = Gray Leaf Spot (1-5 scoring), CLR = Common Leaf Rust (1-5 scoring), TLB = Turcicum Leaf Blight (1-5 scoring), EAS = Ear Aspect (1-5 scoring), PAS = Plant Aspect (1-5 scoring), EPP = Ear Per Plant (number), EL= Ear Length (cm), NKR = Number of Kernel Rows (number), KPR = Kernel Per Row (number), ED = Ear Diameter (cm), TSW = Thousand Seed Weight (gram), BIOM = Biomass yield (t/ha), HI = Harvest Index (%), LFANG = Leaf Angle (degree), LL = Leaf Length (cm), LW = Leaf Width (cm), LFAR = Leaf Area (cm^2), LFPP =Leaf Per Plant (number), LFAE = Leaf above upper most ear (number), LFBE = Leaf bellow upper most ear (number).*

3.2. Sum Square Contribution

Percent sum contribution of the genotype (G), the Location (L), and GxL interaction to the total sum of the square of treatment for various traits are presented in the following (Table 3). When the total sum of squares for the trial is partitioned to its various sources, the sum square due to location constitutes a preponderance amount for DT, DS, GLS, CLR, and TLB and followed by Genotype for DT, DS, GLS, and TLB. The sum square contribution to the total sum square contribution was higher for GY, EAS, TSW, LFAG, LPFPP, and LFAE. The effect of GxL was far less than location and genotype for DT and DS. Except for GY, DT, and CLR, the sum of squares due to genotype was the 2nd most important contributor to the total sum of squares (Table 3).

Table 3**.** Percent sum square contribution by genotype, GxL interaction, location, rep (location), and error in combined analysis for traits showed a significant GxL effect in the line trials.

Source of variation	DF	GY	DT	DS	GLS	CLR	TLB	EAS	TSW	LFANG	LFPP	LFAE
Genotype	23	56.37	14.94	17.27	17.87	16.15	12.33	51.34	58.01	67.20	50.83	76.38
Genotype*location	23	13.07	2.99	5.27	17.87	8.04	15.70	18.51	15.50	15.87	19.44	11.79
Location	1	15.32	77.19	72.28	46.42	66.61	52.46	8.71	12.64	6.96	8.46	0.32
Rep (location)	2	1.62	2.09	1.05	1.70	1.11	1.76	1.21	2.39	1.76	2.44	0.17
Model	49	86.37	97.20	95.88	83.86	91.90	83.20	79.77	88.54	91.78	81.18	88.67
Error	46	13.63	2.80	4.12	16.21	8.10	16.79	20.23	11.46	8.22	18.82	11.33
Total	95	100.00	100.00	100.00	100.06	100.00	99.99	99.99	100.00	100.00	100.00	100.00

3.3. Mean comparison in combined data analysis

In the combined line trial analysis, GY ranged from 2.10 to 5.0 t ha^{-1} with an overall mean value of 3.04 t ha^{-1} (Table 4). The mean of the top five lines had higher mean performance over the means of all checks (CML144, CML159, and FS67) and the mean of QPM checks (CML 144 and CML 159) by 5.32% and 20.87%, respectively. The mean of the top five QPM lines had an inferior performance by 2.16% and 16.22% over the best QPM line check (CML144) and CM line check (FS67), respectively. The highest yielding line (L8) exceeded the mean of all line checks, mean QPM checks, CM line check (FS67), and best QPM line check (CML144) by 34.89%, 54.80%, 7.30%, and 25.31%, respectively for GY.

The value of EPP ranged from 0.91 (L14) to 1.85 (L3) with an overall mean of 1.19 (Table 4). The highest yielding QPM line (L8) had the 2nd highest EPP (1.63) (Table 4). The mean EPP of the top five QPM lines was less by 5.45%, 4.96%, 22.41%, and 6.41% compared with the mean of all line checks, mean of QPM line checks, best QPM check, and CM line check, respectively. The high yielder line (L8) had a higher mean value than the mean of lines checks (CML144, CML159, and FS67), mean of QPM lines checks, best QPM check (CML144), and FS67 by 25.71%, 26.36%, 3.16%, and 24.43%, respectively. This indicates there was a promising line that can be used as source material in the breeding program for further research.

For EL the value ranged from 9.17 g (L13) to 14.50 cm (L10) (Table 4). The mean of new QPM lines and mean of QPM line checks had almost equal EL values of 11.29 and 11.27 cm, respectively. For ED, the values were ranged from 2.91g (L3) to 4.41 cm (L13). Like that of the value for EL, the mean of QPM line checks and QPM line checks had almost equal performance (Table 4).

At Ambo, considering the new QPM lines for TSW the highest and lowest value was obtained from L3 (139.23 g) and L17 (318.55 g) but from the overall genotypes tested, the highest value was obtained from FS67 with values of 364.16 g and 410.99 g at Ambo and Arsi-Negele, respectively (Table 5 and 6). The mean of new QPM lines and the overall mean showed almost equal values in magnitude. From the new QPM lines, the highest value (353.50 g) was obtained from L18 at Arsi-Negele (Table 6). For NKR and KPR, the highest value was obtained from L15 with the value of 14 and 31.83, respectively (Table 6). This line was also good for grain yield 2nd in grain yielding ability highlighting the existence of an association of these traits with GY (Table 6).

ASI ranged from 1.25 to 6.75 with a mean value of 3.4 days. The highest yielding line (L8) performed consistently across locations had a reasonable ASI (2.5 days) (Table 4). Low ASI was shown by L1 (1.75), L13 (1.25), and T1 (1.75 days). L1 is among the top 10 higher-yielding lines and T1 also recorded a high GY (Table 4). Lower ASI is a preferred trait to correspond to male and female flowering for better fertilization.

L8 had the highest BIOM of 10.59 t ha^{-1} and followed by FS67 (10.55 t ha^{-1}). The lowest BIOM (4.84 t ha^{-1}) was obtained from L11 compared with an overall mean of 6.90 t ha^{-1}. The mean of BIOM obtained in this study was relatively smaller than the mean performance of QPM lines tested by Berhanu (2009) and Beyene (2016). They reported 8.37 t ha^{-1} and 10.8 t ha^{-1}, respectively. Out of the 21 new QPM lines tested, 52.38 % had higher BIOM than the mean of the QPM checks indicating that the new coming lines had higher performance in converting inputs into different sinks which finally contribute to the total biomass (Table 4). The mean BIOM of new QPM lines (6.73 t ha^{-1}) was almost equal to the mean of the QPM line checks (6.87 t ha^{-1}) (Table 4). The line which was superior for BIOM (L8) also had a high GY in the combined analysis (Table 4).

Among new QPM lines, L15 attained the maximum PH (156.25 cm) while L13 was the shortest (95.75 cm) (Table 4). EH mean value ranged from 36.25 to 89.50 cm with a mean value of 62.06 cm. The mean of QPM new lines and the mean of QPM line checks were almost equal in value for both PH and EH (Table 4).

For LFBE, the lowest (6.08) was recorded by L13, and the highest (8.83) was obtained from L8 with an overall mean value of 7.34 for LFBE (Table 4). LL ranged from 53.83 cm (FS67) to 90.75 cm (L5) with an overall mean value of 71.95 cm. For LFAR the mean value of lines ranged from 408.94 cm^2 (FS67) to 654.4 cm2 (L5) with an overall mean value of 538.62 cm^2. These lowest and highest LFAR scored QPM line and CM line check also had relatively high GY. The L8 which had the highest GY at both locations and in the combined analysis ((Tables 4, 5, and 6)) showed relatively high LFAR (530.68 cm^2) in the combined analysis (Table 4).

Table 4. Mean of each line for traits combined over two locations Ambo and Arsi-Negele Agricultural Research Centers, in 2017.

Code	GY	ASI	PH	EH	EPP	EL	ED	BIOM	LL	LFAR	LFBE
L1	2.88	1.75	111.75	52.75	1.02	10.75	4.02	7.15	69.92	595.95	7.25
L2	2.52	2.75	104.00	41.75	1.04	9.83	3.74	5.41	68.92	554.43	6.83
L3	2.58	2.75	144.50	73.25	1.85	11.08	2.91	7.81	79.25	513.28	6.50
L4	2.74	3.00	106.25	47.25	1.13	10.00	3.91	5.81	70.08	579.82	6.75
L5	3.58	2.75	131.75	59.50	1.11	11.46	3.89	7.54	90.75	654.40	7.75
L6	3.62	4.25	137.50	74.00	1.23	11.92	3.51	9.27	76.00	527.73	7.25
L7	3.03	4.50	131.25	62.75	1.29	11.50	3.55	6.17	76.58	500.95	7.08
L8	5.00	2.50	151.75	89.50	1.63	12.58	3.63	10.59	75.83	530.68	8.83
L9	2.87	3.25	143.75	75.25	1.24	13.08	3.43	7.23	72.17	490.43	7.92
L10	2.76	3.50	131.25	64.50	1.25	14.50	3.66	5.97	72.33	514.23	6.83
L11	2.44	4.50	130.25	59.25	1.17	11.08	3.87	4.84	70.25	461.59	6.67
L12	3.19	2.75	152.00	69.75	0.94	10.17	4.40	8.60	82.67	651.02	7.42
L13	2.33	1.25	95.75	36.25	1.09	9.17	3.72	5.01	68.92	569.13	6.08
L14	2.46	6.75	143.00	68.50	0.91	9.33	4.41	6.19	80.58	598.61	7.83
L15	3.86	2.75	156.25	80.25	1.08	12.25	4.19	7.82	73.00	621.16	8.33
L16	3.46	4.50	120.25	50.50	1.08	11.42	4.21	6.14	64.83	478.71	6.50
L17	2.53	4.25	123.25	53.50	1.03	10.58	4.25	5.21	65.42	485.98	7.50
L18	2.62	3.00	135.50	68.00	1.29	12.08	3.76	6.44	56.71	434.15	8.33
L19	2.10	4.00	138.75	50.25	1.27	13.17	3.51	6.58	73.17	540.36	6.67
L20	2.24	5.25	132.25	63.00	1.01	10.13	4.11	5.35	75.50	580.73	7.67
L21	2.91	4.25	118.50	59.75	1.09	11.00	3.83	6.25	66.25	494.01	8.00
T1	3.99	1.75	130.75	60.00	1.58	11.17	3.82	8.34	75.42	642.69	7.58
T2	2.47	3.75	119.50	49.25	1.00	11.38	3.62	5.40	68.42	497.84	6.50
FS67	4.66	2.00	145.25	80.75	1.31	13.17	3.64	10.55	53.83	408.94	8.00
Grand Mean	3.04	3.41	130.63	62.06	1.19	11.37	3.81	6.90	71.95	538.62	7.34
CV (%)	17.28	41.51	5.77	11.14	15.49	10.32	5.21	27.42	6.15	10.64	7.69
F-Test	***	**	***	***	***	***	***	**	**	***	***
LSD	0.75	2.01	10.73	9.84	0.26	1.67	0.28	2.69	6.30	81.56	0.80
Minimum (QPM line)	2.10	1.25	95.75	36.25	0.91	9.17	2.91	4.84	56.71	434.15	6.08
Maximum (QPM line)	5.00	6.75	156.25	89.50	1.85	14.50	4.41	10.59	90.75	654.40	8.83
Mean (QPM lines)	2.94	3.54	130.45	61.88	1.18	11.29	3.83	6.73	72.82	541.78	7.33
Mean (QPM checks)	3.23	2.75	125.13	54.63	1.29	11.27	3.72	6.87	71.92	570.27	7.04

Table 5. Mean of each line for yield, yield-related parameters, phenological, disease, and morphological traits evaluated and significant only at Ambo, 2017.

Code	GY	DT	DS	MOD	TLB	EAS	TSW	LANG	LW	LFPP	LFAE
L1	2.65	113.00	114.00	1.00	1.00	3.00	270.84	43.33	11.87	13.17	6.33
L2	2.01	111.50	113.50	2.00	1.00	2.75	248.92	31.17	11.58	13.17	6.17
L3	2.15	108.00	110.00	1.00	1.25	4.00	181.49	27.50	9.25	14.33	7.67
L4	2.30	112.00	114.00	1.50	1.50	3.25	210.78	37.50	12.08	12.83	6.00
L5	3.39	114.50	120.00	1.50	1.00	2.75	303.93	30.00	9.83	15.33	6.83
L6	2.92	107.50	111.00	1.00	1.75	3.25	202.88	43.33	10.00	13.33	5.83
L7	2.59	103.50	107.00	1.00	1.00	3.75	139.23	36.67	9.92	13.00	5.67
L8	4.38	107.00	109.00	1.00	1.50	2.25	175.75	45.00	10.08	14.83	6.00
L9	2.71	108.00	111.00	1.00	1.25	3.50	199.58	38.33	9.75	15.00	6.50
L10	2.74	104.00	106.50	2.50	1.00	3.75	160.19	38.33	10.50	13.00	6.00
L11	2.15	104.00	107.50	2.50	1.00	3.50	166.77	40.00	10.33	14.17	6.67
L12	3.18	117.00	119.00	2.00	1.00	2.50	295.69	29.17	11.47	15.50	7.67
L13	2.24	110.00	109.00	1.50	1.00	2.75	216.45	33.33	12.00	13.33	6.83
L14	2.15	111.00	117.00	2.50	1.00	3.00	248.93	28.33	10.92	15.00	6.67
L15	2.20	110.00	112.00	1.00	1.00	3.00	314.17	34.17	12.58	14.67	6.33
L16	3.13	101.00	106.00	2.00	1.75	2.75	220.91	32.50	11.00	12.50	6.33
L17	2.24	112.00	116.00	2.50	1.25	3.25	318.55	30.83	10.67	14.50	6.67
L18	2.52	109.00	111.00	1.00	1.00	2.75	286.89	40.00	12.08	15.67	6.83
L19	1.37	106.00	108.50	1.00	1.75	3.75	295.90	51.67	10.92	14.50	7.67
L20	2.15	110.50	116.00	1.00	1.50	3.00	290.90	40.00	11.83	15.00	6.83
L21	2.62	108.50	112.00	1.00	1.00	3.25	243.50	34.17	10.42	14.00	6.33
T1	3.39	105.00	105.50	2.00	1.00	2.50	164.63	36.67	12.33	15.83	7.33
T2	1.68	107.50	109.50	1.50	1.00	3.50	172.75	30.83	11.08	13.17	6.50
FS67	4.74	99.00	101.00	1.00	1.00	2.75	364.16	47.50	11.67	14.00	5.50
Grand Mean	2.65	108.31	111.08	1.50	1.19	3.10	237.24	36.68	11.01	14.16	6.55
CV %)	21.45	1.60	2.32	33.09	23.23	13.29	15.91	10.09	4.96	4.08	4.80
F-Test	**	***	***	**	*	*	***	***	***	***	***
LSD	1.18	3.58	5.34	1.03	0.57	0.85	78.10	7.66	1.13	1.19	0.65
Minimum (QPM line)	1.37	101.00	106.00	1.00	1.00	2.25	139.23	27.50	9.25	12.50	5.67
Maximum (QPM line)	4.38	117.00	120.00	2.50	1.75	4.00	318.55	51.67	12.58	15.67	7.67
Mean (QPM lines)	2.56	108.95	111.90	1.50	1.21	3.13	237.73	36.44	10.91	14.13	6.56
Mean (QPM checks)	2.53	106.25	107.50	1.75	1.00	3.00	168.69	33.75	11.71	14.50	6.92

Table 6. Mean of each line for yield, yield-related parameters, phenological, agronomic, disease, and morphological traits evaluated and significant at Arsi-Negele, 2017.

Code	GY	DT	DS	GLS	CLR	EAS	PAS	NKR	KPR	TSW	LANG	LW	LFPP	LFAE
L1	3.11	96.50	99.00	1.25	2.50	3.25	2.50	13.00	17.83	310.93	40.83	10.83	14.17	6.50
L2	3.03	95.00	98.50	1.25	2.50	2.50	3.00	13.00	20.83	270.09	35.83	9.58	13.00	6.33
L3	3.01	95.00	98.50	1.25	2.25	3.00	3.00	10.00	20.17	205.75	28.33	7.83	13.50	7.17
L4	3.18	94.50	98.50	1.50	2.00	3.25	2.75	13.00	16.67	324.45	38.33	9.83	13.50	6.83
L5	3.76	99.00	99.00	1.50	2.00	2.75	3.00	14.00	28.83	208.64	27.50	9.33	13.67	6.67
L6	4.33	92.00	97.00	1.75	3.00	2.25	2.75	13.00	22.00	261.00	48.33	8.33	12.83	5.83
L7	3.46	93.00	98.50	1.25	3.50	3.25	3.00	14.00	25.50	187.91	39.17	7.17	12.50	5.67
L8	5.62	95.00	98.00	1.25	3.25	2.00	3.00	12.00	26.67	299.23	53.33	8.50	15.00	6.17
L9	3.03	95.50	99.00	1.00	4.50	3.00	3.50	11.00	25.17	232.62	45.83	8.17	13.83	6.50
L10	2.77	94.50	99.00	1.00	3.50	4.25	3.25	14.00	22.50	256.25	45.83	8.33	12.83	6.17
L11	2.73	91.00	96.50	1.00	3.25	2.50	3.50	14.00	22.00	243.11	61.67	6.58	12.00	6.17
L12	3.19	95.50	99.00	1.50	3.00	1.50	2.25	14.00	25.00	275.81	32.50	9.33	14.67	7.67
L13	2.42	96.00	99.50	1.25	2.50	2.75	3.00	12.00	18.00	287.01	40.83	9.63	12.50	6.83
L14	2.77	95.00	102.50	1.50	1.75	3.25	2.50	13.00	18.50	225.92	30.00	8.83	14.17	6.83
L15	5.52	92.00	95.50	1.75	2.75	1.25	1.75	14.00	31.83	293.77	40.00	10.00	15.33	7.00
L16	3.80	86.50	90.50	1.50	2.00	1.75	2.00	14.00	23.67	316.59	45.83	8.33	13.33	6.50
L17	2.83	92.50	97.00	1.25	3.00	2.50	2.25	11.00	20.67	335.00	39.17	9.00	13.17	6.00
L18	2.72	92.00	96.00	2.00	2.00	3.25	2.50	10.00	20.67	353.50	47.50	7.33	14.00	6.17
L19	2.83	93.50	99.00	1.50	2.00	2.75	2.00	10.00	24.83	319.02	43.33	8.50	13.67	7.17
L20	2.32	94.00	99.00	1.50	3.25	2.50	2.75	12.00	20.33	309.45	40.00	8.17	13.33	6.17
L21	3.21	93.50	98.50	1.50	2.50	2.50	2.00	11.00	23.83	337.00	43.33	9.33	14.33	6.00
T1	4.59	95.50	98.50	1.50	3.25	2.50	1.75	13.00	26.67	266.83	30.83	10.12	13.50	6.83
T2	3.26	91.50	97.00	1.25	2.75	3.50	2.50	13.00	23.00	276.51	28.33	8.00	13.50	7.17
FS67	4.57	85.50	87.50	1.25	1.75	3.00	2.50	9.00	28.33	410.99	71.67	8.00	12.67	5.17
Grand Mean	3.42	93.50	97.54	1.39	2.70	2.71	2.63	12.38	23.06	283.64	41.60	8.71	13.54	6.48
CV %	13.93	2.46	2.12	16.79	18.52	16.89	16.81	9.22	12.24	8.71	9.64	9.14	5.50	4.29
T-Test	***	**	***	*	**	**	*	**	**	***	***	**	*	***
LSD	0.99	4.76	4.27	0.48	1.03	0.95	0.91	2.36	5.84	51.11	8.30	1.65	1.54	0.57
Minimum (QPM line)	2.32	86.50	90.50	1.00	1.75	1.25	1.75	10.00	16.67	187.91	27.50	6.58	12.00	5.67
Maximum (QPM line)	5.62	99.00	102.50	2.00	4.50	4.25	3.50	14.00	31.83	353.50	61.67	10.83	15.33	7.67
Mean (QPM lines)	3.32	93.88	98.00	1.39	2.71	2.67	2.68	12.48	22.64	278.72	41.31	8.71	13.59	6.49
Mean (QPM checks)	3.93	93.50	97.75	1.38	3.00	3.00	2.13	13.00	24.83	271.67	29.58	9.06	13.50	7.00

3.4. Comparison of mean of lines with mean of line checks

A. Across locations

Of the total of 28 traits, 13 traits: GY, DT, DS, ASI, MOD, CLR, TLB, EAS, TSW, LANG, LW, LFPP, and LFAE had significant GxL in the line trial and due to this, the contrast analysis conducted for the individual location.

3.4.1. Comparison between the 21 QPM lines and the two QPM checks across locations

In the combined ANOVA, MS of QPM line vs QPM check was significant for DS, MD, EH, TSW, LANG, and LFAE but this orthogonal analysis showed a non-significant difference for GY, DT, ASI, PH, MOD, GLS, CLR, TLB, EAS, PAS, EPP, EL, ED, NKR, KPR, BIOM, HI, LL, LW, LFAR, LFPP, and LFBE. In contrast, Pavan *et al*. (2011) reported significant MS for DT, PH, EH, KPR, NKR, and GY but his report is in line with the finding in this study for TSW, DS, and EL. An overall observation of the combined analysis of this trial showed that QPM lines vs QPM check had a positive magnitude (above zero) for DT, DS, ASI, MD, PH, EH, GLS, TLB, PAS, EL, ED, TSW, LANG, LL, and LFBE. Whereas GY, MOD, EAS, EPP, NKR, KPR, BIOM, HI, LW, LFAR, LFPP, and LFAE had a negative magnitude (below zero).

The orthogonal mean difference between QPM lines had lower GY performance by 0.29 t/ha compared with QPM checks. The mean difference indicates that the mean of QPM lines had less value by 0.14 t ha compared to the mean of QPM checks for BIOM. For EL, the mean of QPM lines mean had almost equal to the mean of QPM checks in magnitude (0.02 cm). QPM lines were taller than QPM checks by 5.33 and 7.26 cm for PH and EH, respectively. QPM lines had a higher value than the mean of QPM checks by 0.90 cm for LL however for LFAR, these new QPM lines had a lower magnitude than the mean of QPM checks by 28.49 cm^2 (Table 7).

3.4.2. Comparison between the 21 QPM lines and the QPM check line FS67 across locations

The MS of the QPM line vs FS67 showed significant MS for GY, DT, DS, ASI, PH, EH, CLR, TLB, EL, NKR, TSW, BIOM, LANG, LL, LFAR, and LFAE ($P<0.001$, $P<0.01$ or $P<0.05$) whereas the MS of MD, MOD, GLS, EAS, PAS, EPP, KPR, ED, HI, LW, LFPP, and LFBE was non-significant (data not shown). For QPM lines vs FS67: DT, DS, ASI, GLS,

CLR, TLB, EAS, NKR, ED, HI, LL, LFAR, LFPP, and LFAE had positive values (above zero) but GY, MD, PH, EH, MOD, PAS, EPP, EL, KPR, TSW, BIOM, LANG, LW and LFBE inferior performance than FS67(data not shown).

The mean of QPM lines had a lower performance by 1.72 t ha^{-1} and 3.82 t ha^{-1} compared with CM FS67 for GY and BIOM, respectively. For EL, the QPM lines mean had shorter by 1.88 cm compared with the value of FS67. Similarly, QPM lines were shorter than FS67 by 14.80 and 18.87 cm for PH and EH, respectively. For LL and LFAR, the mean of QPM lines had a higher value than FS67 by 18.98 cm 132.82 cm^2, respectively. QPM Lines mean had wider days of ASI interval compared with FS67 with the value of 1.54. Based on this, it can be concluded that QPM lines were with the problem of male and female flower synchronization (Table 7) but while considering each line in pairwise comparison, there are QPM lines that had ASI values in the acceptable range.

Table 7. MS of contrast between lines, testers, and CM line check (FS67) and estimated value of mean difference for grain yield and other traits in combined analysis evaluated at Ambo and Arsi-Negele Agricultural Research Centers, 2017.

		MS of Contrast							
Source of Variation	DF	**GY**	**ASI**	**PH**	**EH**	**EL**	**BIOM**	**LL**	**LFAR**
QPM Lines vs QPM checks	1	0.62	4.51	207.3	384.57**	0.001	0.14	5.9	5927.24
QPM Lines vs FS67	1	11.2***	9.00*	836.07**	1359.4***	13.45*	55.69 **	1375.77***	67378.25 **
		Estimate of Mean Difference							
QPM Lines vs QPM checks	1	-0.29	0.79	5.33	7.26**	0.02	-0.14	0.9	-28.49
QPM Lines vs FS67	1	-1.72	1.54*	-14.80**	-18.87***	-1.88*	-3.82**	18.98***	132.84**

B. Individual Location

3.4.3. Comparison between the 21 QPM lines and the two QPM checks at each location

The MS for QPM line vs QPM checks and QPM line vs FS67 and the mean difference of the contrast is presented in (Table 8) for traits considered at an individual location. At Ambo, the mean of QPM lines had a higher value by 0.03 t ha^{-1} than the mean of QPM checks for GY however at Arsi-Negele mean of QPM checks showed higher than the mean of QPM lines by 0.61 t ha^{-1}. But while considering the performance of each line with the checks, some lines had higher performance (Tables 5 and 6). For TSW the mean of QPM lines exceeded the mean of QPM checks by 69.04 and 7.05 g at Ambo and Arsi-Negele, respectively (Table 8). This indicates that the new QPM lines are coming which are better than the QPM checks have developed in the breeding program. So that the breeding program can have the chance to get better new QPM lines after further evaluation to be used in the breeding work. At Arsi-Negele, the mean of QPM lines was delayed by 2.87 days for maturity compared with the

mean of QPM checks (Table 8). For DT and DS, QPM lines were late by 2.70 and 4.4 days compared with QPM checks at Ambo.

At Arsi-Negele, the smaller value of QPM lines compared with QPM checks by 0.29 for CLR indicates that the QPM lines are more tolerant to this disease. The poorness of QPM checks for PAS is manifested by the higher value of 0.55 compared with the mean value of QPM lines (Table 8). The mean of QPM lines had wider LANG ((by 11.73^{o}) and thinner LW (by 0.80 cm) than the mean of QPM checks at Arsi-Negele and Ambo, respectively. Regarding LFAE, QPM lines were also showed higher performance than QPM checks by 0.51 leaves at Arsi-Negele (Table 8).

3.4.4. Comparison between the 21 QPM lines and the CM check line FS67 at each location

At both locations (Ambo and Arsi-Negele), the performance of FS67 was higher by 2.17 t ha^{-1} and 1.26 t ha^{-1} compared with the mean of QPM lines, respectively (Table 8). But while considering each line pairwise there are QPM lines (L8 and L15) that had higher GY than FS67 (Table 6).

Regarding NKR, the mean of QPM lines gave higher than FS67 by 2.31 and 3.48 kernel rows at Ambo and Arsi-Negele, respectively. Regarding TSW, the mean of QPM lines had a lower value of 126.43 and 132.27 g compared with the FS67 at Ambo and Ars-Negele, respectively. The mean of QPM lines was lower by 126.43 g compared with FS67 at Ambo for TSW (Table 8). QPM lines mature earlier by 1.88 days compared with FS67 at Arsi-Negele (Table 8). For DT and DS, QPM lines were late for flowering by 9.95 and 10.90n days compared with FS67 at Ambo, respectively. Similarly, at Arsi-Negele, the mean difference indicates that the mean of QPM lines was late for DT by 8.38 and DS by 10.50 compared with the FS67 CM check (Table 8).

The positive orthogonal mean difference for CLR (0.96) between QPM lines vs FS67 confirms that QPM lines were more attacked by this disease than FS67. Based on the value the higher value (0.18) for PAS cored by FS67, the new QPM lines were good for this trait (Table 8). Regarding LANG, the mean of QPM lines had a narrow-leaf angle than FS67 by 11.06^{o} and 30.36^{o} at Ambo and Arsi-Negele, respectively. For LW the mean of QPM lines was thinner by 0.76 cm than FS67 at Ambo which is more advantageous for crop production in terms of improving photosynthesis. Similarly, Li et al (2015) suggested and confirmed the importance of erect leaf angle and optimum leaf orientation value to allow for more efficient light capture during photosynthesis and better wind circulation under dense planting conditions. Other linked traits like leaf length, leaf width, and leaf area have a role in

photosynthesis. For LFAE, QPM lines had greater by 1.06 and 1.33 than FS67 at Ambo and Arsi-Negele, respectively (Table 8).

Table 8. MS contrast between lines, testers, and CM line check (FS67) and the estimated value of mean difference for traits at Ambo and Arsi-Negele which are not included in the combined analysis, 2017.

						MS of Contrast					
						Ambo					
Source of Variation	DF	GY	DT	DS	NKR	TSW	LANG	LW	LFAE		
QPM Line vs QPM check	1	0.002	26.671**	70.86***	0.13	17406.84***	26.51	2.34*	0.45		
QPM Lines vs FS67	1	9.02***	189.10***	227.017***	10.18*	30516.9***	233.34 ***	1.10***	2.15**		
						Estimate of Mean Difference					
QPM Line vs QPM check	1	0.03	2.70**	4.40***	-0.19	69.04***	2.69	-0.80	-0.35		
QPM Line vs FS67	1	-2.17***	9.95***	10.90***	2.31*	-126.43***	-11.06***	-0.76	1.06		
						MS of Contrast					
						Arsi-Negele					
Source of Variation	DF	GY	DT	DS	MD	CLR	PAS	NKR	TSW	LANG	LFAE
QPM Line vs QPM check	1	1.36	0.53	0.23	30.06***	0.30	1.12*	1.00	181.42	502.19**	0.94*
QPM Line vs FS67	1	3.02*	134.10 ***	210.48***	6.75	1.78*	0.06	23.10**	33399.98***	1759.33***	3.35***
						Estimate of Mean Difference					
QPM Line vs QPM check	1	-0.61	0.38	0.25	2.87***	-0.29	0.55*	-0.52	7.05	11.73**	-0.51*
QPM Line vs FS67	1	-1.26*	8.38***	10.50***	-1.88	0.96*	0.18	3.48**	-132.27***	-30.36**	1.33***

Conclusion

The result of the analysis variance for grain yield, the difference between 24 tested parental lines was significant at each location and in the combined analysis. The significant difference in G*L for grain yield indicates that the performance of the genotypes was not consistent at both locations. Based on the mean performance analysis, in combined analysis and at Arsi-Negele L8 had higher compared with both the QPM checks and CM check (FS67). At Arsi-Negele, L15 was also one of good performed lines than all standard checks and the new QPM lines tested. The orthogonal analysis for DT and DS highlighted that the new lines were relatively late for flowering compared with both QPM and CM checks. In general, the study confirmed the existence of promising new QPM parental lines like L8 which will be used in the breeding program in the future.

Ethics approval and consent to participate

The researchers have obtained permission from funding institutions CIMMYT and EIAR. Accordingly, the information under this article had been developed in collaboration with CIMMY, Ethiopian Institute of agriculture research investigators, and university instructors.

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