

Combining ability study of QMM inbred lines for endosperm modification score and tryptophan content under low and optimum soil nitrogen environments

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The nutritional benefit of quality protein maize is more demonstrated on children who live under nutritional insecurity and also children suffering from a severe disease (Kwashiorkor) which is due to protein deficiency. To determine the effects of soil nitrogen on combining ability of tryptophan, endosperm modification score, protein and protein Quality Index (QI), 121 genotypes with five checks were sib-mated to generate F₂ grains under low and optimum N environments. Hereafter 100 grains of each F₂ generation were used for endosperm modification scores and tryptophan and protein concentration analysis in maize kernel endosperm. The results of the study indicated contribution of General Combining Ability (GCA), Specific Combining Ability (SCA) and reciprocal effects were important for all measured traits under both environments indicating quality traits

inheritance were controlled by both additive and non-additive gene action. Inbred lines TL156579, TL156583, and VL05128 had good potential for endosperm modification score and inbred lines TL147078 and VL05128 had good potential for tryptophan, protein and protein quality index under low N environment. Under optimum N environment, parental lines TL156579, TL156583 and VL05128 had good potential for endosperm modification whereas parental lines TL156591 had good potential for tryptophan and protein concentration in grain and quality index. Hybrids TL155932 x VL05128 TL148288 x TL147078, TL155932 x TL156612, TL156612 x VL05128 and TL156579 x TL156591 had significant differences between F₁ hybrids and their F₁ reciprocals for grain yield under low N environment. Under both low and optimum N environments, the importance of reciprocal effects was also identified for endosperm modification score, tryptophan, protein, and quality index.

Key Words: Protein quality index; Reciprocal effects; Tryptophan; Endosperm

INTRODUCTION

Maize is deficient in lysine, methionine and tryptophan relative to the dietary needs of monogastric animals including humans. Deficiencies in these amino acids result in poor utilization of maize protein. In humans feed, these deficiencies are corrected by dietary supplementation with other protein sources or synthetic amino acids, but this adds to the cost of the diet [1] especially for farmers in Sub-Saharan Africa countries. In mature maize kernel, high concentration of protein is found in the endosperm and the germ. The maize kernel endosperm contains a high protein in quantity but low in quality, while the germ maize kernel contains a low level of protein in quantity with high in quality. However, the major portion of the maize kernel comprises of endosperm and contributes as much as 80% of the total grain protein [2]. The deficiencies of essential amino acids in maize kernel endosperm are due to the major seed storage proteins, the zeins. The levels of essential amino acids tryptophan and lysine in the maize kernel endosperm are altered by mutation opaque-2 due to a reduced content of zeins [3]. However, kernels carrying these mutations tend to have a number of pleiotropic effects that reduce their agronomic adaptability (soft kernel endosperm, which makes them susceptible to mechanical damage).

Under stress and non-stress environments, both quantity and quality of maize endosperm protein are altered due to genetic variability of the crop and severity of the stress. Mosisa et al., [4] reported that under low N, the protein, tryptophan and lysine concentration in the grain endosperm of both non-QPM and QPM maize genotypes were low. A recent study revealed that Protein Quality-Index (PQI) was higher under low N environments than optimum N environments due to the concentration of QPM maize grain protein, which was more sensitive to low N than optimum N environments. The percentage of tryptophan in the QPM maize kernel was higher under low N environment than non-QPM maize kernel grown under optimum N environments [5].

Endosperm modification is quantitatively inherited with greater importance

of additive gene action in kernel modification. General combining ability for kernel virtuousness and kernel hardness was positively correlated with an accumulation of dominant kernel modifiers but due to the complex genetic control of kernel modification and lack of reliable molecular markers linked to endosperm modifier genes, the effective approach is to physically screen the kernels using a 'light box' for identification of promising QPM genotypes with desirable kernel modification scores [6]. Also, since the QPM germplasm has to now compete with the normal-endosperm maize, information regarding combining ability of the QPM inbred lines coupled with important characters such as kernel modification scores, tryptophan, protein and protein quality index under low and optimum soil nitrogen environments is required for breeders to utilize this germplasm more effectively in the breeding programmes [6].

Because of the laboratory cost in lysine and tryptophan concentration analysis in the maize kernel endosperm, reports on effects of stress and non-stress soil nitrogen for the lysine, tryptophan, protein, and kernel endosperm modification as well as combining ability effects of QPM inbred lines are limited in Ethiopia. Objectives of this study were to

(i) determine the combining abilities of QPM inbred lines for kernel modification score, tryptophan and protein contents, and (ii) determine reciprocal effects on quality traits and grain yield.

MATERIALS AND METHODS

Planting materials

The 121 genotypes developed from complete diallel crosses of 11 QPM inbred lines with five checks were used for this study. For endosperm modification scores and tryptophan analysis, two plants for F₁ hybrids were sib-mated to have F₂ grains for all 126 genotypes. The sib-mated F₂ grains were shelled and a uniform size of 100 seeds for each genotype from each plot was taken for endosperm modification scores and tryptophan analysis both under low and optimum N environments.

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Data collection

Endosperm modification scores: For all genotypes evaluated both under low and optimum N environments, endosperm modification scores were done at Ambo Research laboratory using the light table. The kernels were scored from 1 to 5, where 1=completely modified; 2=75% modified; 3=50% modified; 4=25% modified; and 5=completely opaque but only grains with score 2-3 which were modified as hard endosperm could be considered as QPM grains” [7,8].

Tryptophan and protein analysis: Protein and tryptophan concentration for each genotype both under low and optimum N environments were analyzed at the Ethiopian Institute of Agricultural Research Quality laboratory using Near-Infrared Reflectance Spectroscopy (NIRS 6500). The 100 equal size F₂ grain samples for each genotype were ground in an electronic grinder (Foss cyclonic 1093, USA) with a mesh size of 0.5 mm. The protein and tryptophan concentrations in grain sample were expressed as a percentage (%) in the grain sample. “Lysine concentration was not measured because the procedure is more expensive than tryptophan analysis and also lysine and tryptophan concentrations in the protein of o2 endosperm are highly correlated (r=0.85***)” (Hernandez and Bates, 1969; Vivek et al., 2008). Protein Quality Index (PQI) was calculated from the ratio of tryptophan to protein concentration in grain kernel of maize, which expressed in percentage.

Data analysis: Analysis of Variance (ANOVA) per environment was performed for tryptophan and other quality traits for all the genotypes both under low and optimum N environments using PROC GLM procedure of SAS software, version 9.4 (SAS Institute, 2012). The Pearson correlation coefficient was performed using PROC CORR in SAS.

Combining ability analysis: Analysis of variance for a complete diallel crosses excluding checks was done using Analysis of Genetic Designs with R (AGD-R version 5.0 [9]. Griffing’s method I (parents, F₁s, and F₁’s reciprocals were included) and model I (fixed effect) of diallel analysis was used for computing GCA effects of the parents, SCA and reciprocal effects of the crosses. Analysis of variance was done for individual environment, and combined analyses of variance over low N, Optimum N and across all N environments were done for those traits showed significant genotypes mean squares in individual environment. The mean squares for ENV and crosses were tested against the mean squares for ENV x crosses as mean square of error, while ENV x crosses interactions mean squares were tested against pooled error. The significance of GCA, SCA and reciprocal source of variations were tested against F-tests while the significance of GCA, SCA and reciprocal effects were tested against t-test, with standard error of GCA, SCA and reciprocal effects [10,11]. The linear model for combining ability analysis for Griffing’s method-I of the complete diallel cross for a single environment was computed as [11]:

$$Y_{ij} = \mu + g_i + g_j + r_{ij} + s_{ij} + \frac{1}{bc} \sum_k \sum_l e_{ijkl}$$

The linear model for combining ability analysis for the method I of the complete diallel cross for across environments were computed as [12,13]:

$$Y_{ijk} = \mu + \alpha_1 + b_{ki} + v_{ij} + (\alpha v)_{ij} + e_{ijk}$$

$$v_{ij} = g_i + g_j + s_{ij} + r_{ij}$$

$$r_{ij} = m_i + m_j + n_{ij}$$

Where, Y_{ijkl} is observed trait value from each environmental unit, μ is the population mean, α₁ is location (environment) effects, b_{ki} is block or replication effect within each location, v_{ij} is the hybrid effect=g_i+g_j+s_{ij} (where g_i=GCA effect for the ith parent with

$$\sum_j g_j = 0$$

g_j=GCA effect of jth parent with $\sum_j g_j = 0$

S_{ij} is the SCA for the ijth F₁ hybrid with S_{ij}=S_{ji} and $\sum_{i,j} s_{ij} = 0$

(αv)_{ij} is interaction effect between ijth F₁ hybrid and location, e_{ijkl} is a random residual effect, r_{ij} is Reciprocal of ijth cross with r_{ij} = - r_{ji}, m_i is maternal effect (MAT) of ith parental line with $\sum_j m_j = 0$

$$\sum_j m_j = 0$$

m_i is MAT of jth parental line with $\sum_j m_j = 0$

$$\sum_j m_j = 0$$

n_{ij} is a NonMaternal effect (NMAT) of the cross between the ith and jth parental lines with $\sum_{i,j} n_{ij} = 0$

$$\sum_{i,j} n_{ij} = 0$$

and is an environmental effect associated with individual observation.

RESULTS

General combining ability effects of inbred lines for tryptophan and other traits

Under low N environment, inbred lines TL156579, TL156583 and VL05128 had positive significant GCA effects for endosperm modification score while TL148288, TL148287, TL116960, TL155932, TL147078 and TL156612 had negative significant GCA effects for endosperm modification score. Negative significant GCA effects were observed in TL156583, TL148288 and TL148287 inbred lines whereas positive significant GCA effects in TL147078 and VL05128 inbred lines for protein and tryptophan content in the grain and quality index, and inbred line TL156591 had a negative and non-significant GCA effect for endosperm modification score and protein content under low N environment. Under optimum N environment, inbred lines TL156579, TL156583 and VL05128 had positive and significant GCA effects while TL156591, TL148287, TL155932, TL147078, TL156612 and TL155976 had negative and significant effects for endosperm modification score. Of the three inbred lines with positive GCA effect for endosperm modification score, only inbred TL156579 had positive and significant GCA effects for protein and tryptophan concentration. Inbred TL116960 had positive GCA effects for all four traits but was significant only for tryptophan and protein content. Inbred lines TL156591 and TL147078 had positive and significant GCA effects for tryptophan and protein concentration in the grain and protein quality index while negative significant GCA effects for endosperm modification score were detected. Inbred lines TL156579, TL156583, and VL05128 had positive and significant GCA effects for endosperm modification scores across N environments. Among the three inbred lines, only VL05128 had significant positive GCA effects for tryptophan concentration and protein quality index. Inbred lines TL148288 and TL148287 had negative and significant GCA effects for all quality traits and quality index across N environments. Inbred lines TL156583, TL148288 and TL148287 showed negative and highly significant GCA effects across N environments for all quality traits except kernel modification score, whereas inbred lines TL156591 and TL147078 had positive and highly significant GCA effects for protein and tryptophan concentration in the grain and quality index across N environments (Table 1).

TABLE 1

General combining ability (GCA) effects of 11 QPM inbred lines for quality traits under low, optimum and across N environment

Line	Low N environment				Optimum N environment				Across N environments			
	EMS(1-5) GCA	TRP (%) GCA	PRO (%) GCA	QI (%) GCA	EMS(1-5) GCA	TRP (%) GCA	PRO (%) GCA	QI (%) GCA	EMS(1-5) GCA	TRP (%) GCA	PRO (%) GCA	QI (%) GCA
TL156579	1.00430**	-0.00027**	0.00444	-0.00169	0.73163**	0.0010**	0.19261**	-0.00758*	0.86796**	0.00036	0.09853**	-0.00464
TL156583	0.69657**	-0.00801**	-0.58210**	-0.03656**	0.54777**	-0.0049**	-0.47751**	-0.00926**	0.62217**	-0.00644**	-0.52981**	-0.02291**

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TL148288	-0.23775**	-0.00277**	-0.12406**	-0.02030**	-0.397	-0.0009*	-0.15731**	0.00469	-0.31738**	-0.00182**	-0.14068**	-0.00781**
TL156591	-0.02434	0.00295**	-0.00763	0.03160**	-0.04291**	0.0047**	0.08156**	0.03996**	-0.03363	0.00381**	0.03697**	0.03578**
TL148287	-0.13684**	-0.00254**	-0.15440**	-0.01310**	-0.20269**	-0.0027**	-0.17891**	-0.01236**	-0.16976**	-0.00261**	-0.16666**	-0.01273**
TL116960	-0.15684**	0.00091*	-0.06536**	0.01346**	0.01163	0.0011**	0.03669*	0.00843	-0.07260*	0.00102**	-0.01434	0.01094**
TL155932	-0.70275**	-0.00449**	-0.00644	-0.04484**	-0.55655**	-0.0020**	0.23938**	-0.03794**	-0.62965**	-0.00325**	0.11647**	-0.04139**
TL147078	-0.34002**	0.00922**	0.85085**	0.02239**	-0.09746**	0.0063**	0.42656**	0.02704**	-0.21874**	0.00777**	0.63870**	0.02471**
TL156612	-0.89616**	0.00358**	0.48724**	-0.0015	-0.86950**	-0.0002	0.33689**	-0.03039**	-0.88283**	0.00167**	0.41206**	-0.01594**
TL155976	-0.01138	-0.00104*	-0.21734**	0.00781*	-0.07928**	-0.0030**	-0.21127**	-0.01397**	-0.04533	-0.00204**	-0.21431**	-0.00308
VL05128	0.80521**	0.00245**	-0.18520**	0.04273**	0.95436**	0.0006	-0.28868**	0.03139**	0.87978**	0.00152**	-0.23694**	0.03706**
SE (gi)	0.04534	0.00037	0.01608	0.00346	0.023	0.0003	0.01304	0.00301	0.02546	0.00025	0.01035	0.0023

Note: EMS=Endosperm Modification Score; TRYP=Tryptophan; PRO=Protein; QI=Quality Index; *= significant at 0.05 level of significance; **=highly significant at 0.01 level of significance.

Specific combining ability and reciprocal effects of hybrids for tryptophan

The results of SCA and reciprocal effects of hybrids for tryptophan concentration in the grain across N environments are presented in Supplementary Table 1. Fifteen hybrids had positive significant (P<0.01) SCA effects for tryptophan concentration out of which 11 hybrids exhibited positive highly significant reciprocal effects. Positive and highly significant effects of both SCA and reciprocal were found between TL156579 x TL148288, TL156579 x TL148287, TL156579 x TL155932, TL156583 x TL155932, TL148288 x TL156591, TL148288 x VL05128, TL156591 x TL155976, TL156591 x VL05128, TL116960 x TL147078, TL155932 x TL155976, TL155932 x VL05128 hybrids for tryptophan concentration in the grain. Positive and significant SCA effects with negative and significant reciprocal effects were found for hybrids TL156579 x TL156583, TL156591 x TL116960 and TL147078 x TL156612. Negative and significant SCA effects with positive and significant reciprocal effects were found between TL156579 x TL116960, TL156579 x TL155976, TL156579 x VL05128 and TL116960 x TL155976 hybrids (Supplementary Table 1).

Effect of reciprocal crosses on quality traits and grain yield of maize hybrids

Under low N environment, 15 hybrids showed significant differences between F₁ hybrids and their F₁ reciprocal for endosperm modification scores of which only four hybrids showed significant differences between F₁ hybrids and their F₁ reciprocal for tryptophan and protein concentration in the grain. Hybrids TL155932 x VL05128 TL148288 x TL147078, TL155932 x TL156612, TL156612 x VL05128 and TL156579 x TL156591 had significant differences between F₁ hybrids and their F₁ reciprocals for grain yield under low N environment (Table 2). Twenty-seven hybrids showed highly significant differences between F₁ hybrids and their F₁ reciprocals for endosperm modification score of which six hybrids showed highly significant differences between F₁ hybrids and their F₁ reciprocals for tryptophan and protein concentration in the grain under optimum N environment. Hybrids TL156579 x TL156612, TL156579 x VL05128, TL156583 x TL148287, TL156583 x TL116960, TL156583 x TL155932, TL156591 x VL05128, TL148287 x TL147078, TL148287 x VL05128, TL116960 x TL147078, TL147078 x VL05128 and TL148288 x TL148287 had significant differences between F₁ hybrids and their F₁ reciprocals for grain yield under optimum N environment (Table 3).

TABLE 2
The reciprocal effects in complete diallel crosses of 11 QPM parental lines for quality traits and grain yield under low N environment

Hybrids	Quality traits				
	EMS (1–5) ↑Rec. effect	TRYP (%) ↑Rec. effect	PRO (%) ↑Rec. effect	QI (%) ↑Rec. effect	GY (t ha ⁻¹) ↑Rec. effect
TL156579 x TL156583	0.085	0	0.465**	0.055*	0.13
TL156579 x TL148288	0.31	0.015**	1.160**	0.050*	0.42
TL156579 x TL156591	0.55	0.005	0.385**	0.090**	0.850**
TL156579 x TL148287	0.005	0.005	0.285*	0.03	0.41
TL156579 x TL116960	0.455	0.010*	1.165**	0.090**	0.57
TL156579 x TL155932	0.04	0.010*	0.615**	0.005	0.405
TL156579 x TL147078	2.665**	0.015**	1.430**	0.025	0.305
TL156579 x TL156612	0.425	0.005	1.325**	0.01	0.2
TL156579 x TL155976	0.695**	0.005	0.095	0.02	0.06
TL156579 x VL05128	0.25	0.005	0.430**	0.055*	0.125
TL156583 x TL148288	0.625**	0.010*	0.700**	0	0.075
TL156583 x TL156591	0.595*	0.015**	2.060**	0.005	0.41
TL156583 x TL148287	1.500**	0.005	0.125	0.055*	0.275
TL156583 x TL116960	0.165	0.010*	0.280*	0.045	0.265
TL156583 x TL155932	0.065	0.010*	0.795**	0.065**	0.18
TL156583 x TL147078	2.035**	0.010*	1.085**	0.01	0.215
TL156583 x TL156612	0.22	0	0.815**	0.03	0.475
TL156583 x TL155976	0.07	0.005	0.19	0.015	0.2
TL156583 x VL05128	0	0.010*	0.185	0.100**	0.25
TL148288 x TL156591	0.23	0.005	0.710**	0.03	0.03
TL148288 x TL148287	1.030**	0.015**	1.350**	0.055*	0.21
TL148288 x TL116960	0.575	0.010*	0.535**	0.025	0.295
TL148288 x TL147078	1.350**	0.015**	1.130**	0.03	0.885**
TL148288 x TL156612	0.095	0.020*	2.335**	0.02	0.38
TL148288 x TL155976	0.245	0.010**	0.420**	0.015	0.11
TL148288 x VL05128	1.310**	0.010*	0.840**	0.045	0.515
TL156591 x TL148287	0.59	0.010*	1.455**	0.01	0.2
TL156591 x TL116960	1.205**	0.015**	1.055**	0.080**	0.135

TL156591 × TL155932	0.145	0.005	0.440**	0.080**	0.52
TL156591 × TL147078	0.285	0.005	0.465**	0	0.04
TL156591 × TL156612	0.005	0.005	0.640**	0.03	0.205
TL156591 × TL155976	0.305	0.005	1.085**	0.025	0.04
TL156591 × VL05128	0.52	0	0.455**	0.01	0.39
TL148287 × TL116960	0.805**	0	0.960**	0.065**	0.015
TL148287 × TL155932	0.18	0.010*	0.785**	0	0.385
TL148287 × TL147078	0.045	0	0.910**	0.03	0.25
2TL148287 × TL156612	0.345	0	0.02	0.02	0.055
TL148287 × TL155976	0.14	0.015**	1.415**	0.050*	0.2
TL148287 × VL05128	0.335	0	0.375**	0.015	0.35
TL116960 × TL155932	0.115	0	0.04	0.005	0.215
TL116960 × TL147078	0.03	0.005	0.910**	0.01	0.640*
TL116960 × TL156612	0.015	0	0.045	0.005	0.215
TL116960 × TL155976	0.860**	0	0.560**	0.035	0.135
TL116960 × VL05128	0.04	0.015**	0.625**	0.130*	0.32
TL155932 × TL147078	0.035	0.020**	0.405**	0.120*	0.415
TL155932 × TL156612	0.075	0.010*	1.410**	0.04	1.020**
TL155932 × TL155976	0.31	0.005	0.055	0	0.395
TL155932 × VL05128	1.615**	0.005	0.185*	0.055*	0.990**
TL147078 × TL156612	0.32	0.010*	1.085**	0.005	0.425
TL147078 × TL155976	1.145**	0	0.22	0.03	0.56
TL147078 × VL05128	1.915**	0.010*	0.675**	0.02	0.07
TL156612 × TL155976	0.05	0	0.18	0.005	0.06
TL156612 × VL05128	0.03	0	0.550**	0.01	1.015**
TL155976 × VL05128	1.095**	0.005	0.495**	0.085**	0.670*
LSD (0.05)	0.5994	0.0085	0.2237	0.0485	0.5897
LSD (0.01)	0.7939	0.0113	0.2962	0.0642	0.781

Note: EMS=Endosperm Modification Score; TRYP=Tryptophan; PRO=Protein; QI=Quality Index; GY=Grain Yield; †Rec. effect=Mean reciprocal effect; *= significant at 0.05 level of significance; **=highly significant at 0.01 level of significance.

TABLE 3

The reciprocal effects in complete diallel crosses of 11 QPM parental lines for quality traits and grain yield under optimum N environment

Hybrids	Quality traits				
	EMS (1–5)	TRYP (%)	PRO (%)	QI (%)	GY (t ha ⁻¹)
	†Rec. effect	†Rec. effect	†Rec. effect	†Rec. effect	†Rec. effect
TL156579 × TL156583	0.460**	0	0.250**	0.05	0.925*
TL156579 × TL148288	0.485*	0.010**	0.105	0.01	0.785
TL156579 × TL156591	1.570**	0.010**	0.760**	0	1.020*
TL156579 × TL148287	0.275	0.005	0.490**	0.035	1.215*
TL156579 × TL116960	1.750**	0	0.05	0.03	0.295
TL156579 × TL155932	0.125	0.020**	1.425**	0.065*	0.885*
TL156579 × TL147078	0.785**	0.005	1.070**	0	0.415
TL156579 × TL156612	0.205	0.005	0.695**	0.035	2.200**
TL156579 × TL155976	0.095	0.020**	1.005**	0.110**	0.495
TL156579 × VL05128	0.155	0	0.550**	0.025	1.250**
TL156583 × TL148288	0.435**	0.010**	0.880**	0.005	0.335
TL156583 × TL156591	1.210**	0.005	0.810**	0.02	0.525
TL156583 × TL148287	0.03	0.010**	0.09	0.055	1.580**
TL156583 × TL116960	2.270**	0.010**	0.335**	0.085**	1.390**
TL156583 × TL155932	0.570**	0.005	0.515**	0.025	1.175**
TL156583 × TL147078	0.900**	0.005	0.03	0.04	0.11
TL156583 × TL156612	0.025	0.010**	0.930**	0.01	1.050*
TL156583 × TL155976	1.450**	0	0.190**	0.03	0.345
TL156583 × VL05128	0.27	0.010**	0.055	0.065*	0.06
TL148288 × TL156591	0.905**	0	0.02	0.01	0.595
TL148288 × TL148287	0.900**	0.010**	0.610**	0.03	1.825**
TL148288 × TL116960	1.110**	0.005	0.795**	0.005	0.145
TL148288 × TL147078	1.075**	0.005	0.310**	0.05	0.51
TL148288 × TL156612	0.035	0.005	0.005	0.015	0.58
TL148288 × TL155976	0.975**	0.005	0.285**	0.015	1.065*
TL148288 × VL05128	0.710**	0	0.295**	0.005	0.12
TL156591 × TL148287	0.960**	0.020**	1.940**	0.005	0.75
TL156591 × TL116960	0.485**	0	0.215*	0.01	0.655

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TL156591 × TL155932	0.360*	0	0.340**	0.015	1.000*
TL156591 × TL147078	0.055	0.020**	1.495**	0.105	0.22
TL156591 × TL156612	0.11	0.015**	1.210**	0.055	0.03
TL156591 × TL155976	0.14	0	0.125	0.04	0.61
TL156591 × VL05128	0.390*	0.020**	1.080**	0.110**	1.630**
TL148287 × TL116960	0.05	0.010**	0.920**	0	0.925*
TL148287 × TL155932	1.065**	0.005	0.515*8	0.02	0.4
TL148287 × TL147078	0.875**	0	0.135	0.02	2.270**
2TL148287 × TL156612	0.215	0	0.825**	0.055	0.05
TL148287 × TL155976	0.28	0.010**	0.655**	0.005	0.48
TL148287 × VL05128	0.06	0.010**	0.265**	0.075**	1.325**
TL116960 × TL155932	0.505**	0	0.470**	0.055	0.895*
TL116960 × TL147078	0.14	0.005	0.185	0.045	1.170**
TL116960 × TL156612	0.045	0	0.17	0.015	0.59
TL116960 × TL155976	0.015	0	0.210*	0.015	0.705
TL116960 × VL05128	0.015	0	0.17	0.035	0.945*
TL155932 × TL147078	1.050**	0.005	0.620**	0.01	0.21
TL155932 × TL156612	0.02	0	0.085	0.01	0.25
TL155932 × TL155976	0.06	0.010**	0.580**	0.035	0.62
TL155932 × VL05128	2.475**	0.010**	0.960**	0.045	0.775
TL147078 × TL156612	0	0.005	0.02	0.01	0.195
TL147078 × TL155976	0.09	0	0.07	0.015	0.985
TL147078 × VL05128	1.925**	0	0.715**	0.01	2.780**
TL156612 × TL155976	0.04	0.020**	0.870**	0.075**	0.75
TL156612 × VL05128	1.045**	0.005	0.465**	0.01	0.055
TL155976 × VL05128	1.160**	0.005	0.505**	0.02	0.34
LSD (0.05)	0.3125	0.0074	0.1877	0.0581	0.8332
LSD (0.01)	0.4139	0.0098	0.2486	0.077	1.0997

Note: EMS=Endosperm Modification Score; TRYP=Tryptophan; PRO=Protein; QI=Quality Index; GY=Grain Yield; †Rec. effect=Mean reciprocal effect; *= significant at 0.05 level of significance; **=highly significant at 0.01 level of significance.

DISCUSSION

The result of individual and combined complete diallel cross analyses of variances showed that GCA, SCA, Reciprocal, GCA × E, SCA × E, and Reciprocal × E effects were highly significant among genotypes for all traits under two environments. These indicate that GCA, SCA and Reciprocal effects were important in controlling the inheritance of the measured traits in forming variability among genotypes as well as their effects were determined by their interaction with the effects of environmental factors. The significant effects of GCA × E, SCA × E and Reciprocal × E interaction for the measured quality traits indicates that GCA effects of the inbred lines and SCA effects of the crosses as well as reciprocal effects of the crosses were not consistent for the traits both under low and optimum N environments. Significant effects of GCA × E and SCA × E-interaction was reported by Wegary et al. [5] on QPM for endosperm modification under both low and optimum N environments. This finding confirms previous results that quality traits and some quantitative traits performances can be influenced by extra chromosomal inheritance that is involved in gene control of the traits. This is important for plant breeder in determination of parental lines to be used as female or male during hybrid development. Darrigues et al. [14] also reported highly significant effects of reciprocal for tryptophan and methionine concentrations in maize grain under non-stress environment. Uddin et al. [15] reported significant effects of reciprocal cross for maize grain yield, days to silking and tasseling, plant and ear height under managed environment.

Greater GCA sum of squares were higher than SCA sum of squares for endosperm modification score under low, optimum and across N environments. However, SCA sum of squares were higher than GCA sum of squares for protein quality index under low, optimum and across N environments. This indicates that inheritance of the kernel endosperm modification of the genotypes is predominantly controlled by additive gene action than non-additive gene actions under low and optimum N environments, but the protein quality index was more affected by non-additive gene action, which is the effect of environmental factors than additive gene actions. Hossain et al. [6] reported equal contribution of additive and non-additive effects for kernel endosperm modification in QPM under non-stressed environment. Nepir et al. [16] reported higher SCA effects than GCA for kernel endosperm modification and higher GCA

effects than SCA for protein concentration in the grain of QPM under optimum N environments.

Under low N environment, inbred lines TL156579, TL156583 and VL05128 had positive significant GCA effects for endosperm modification scores whereas inbred lines TL147078 and VL05128 had positive significant GCA effects for tryptophan and protein concentration in the grain and quality index. These indicate that inbred lines TL156579, TL156583 and VL05128 can be good combiners for kernel endosperm modification and inbred lines TL147078 and VL05128 can be good combiners for tryptophan and protein concentration in the grain and protein quality index under low N environment. Inbred lines TL156579, TL156583 and VL05128 can be considered as good combiners for endosperm modification whereas TL156591 is considered as good combiner for tryptophan and protein concentrations in the grain, and protein quality index under optimum N environment. Therefore, the inbred lines could be used as donor parents for tryptophan, protein and endosperm modification during QPM hybrid development under specific environments.

From GCA analysis for 11 QPM inbred lines under both low and optimum N environments, parental lines TL156579 and VL05128 were observed as good general combiners for endosperm modification score under both low and optimum N environments, whereas parental line TL147078 was observed as good general combiner for tryptophan and protein concentration in the grain under both low and optimum N environments. The two inbred lines consistently had significant positive GCA effects for modifier under low, optimum and across N environments implying that the inbred lines are good general combiner for endosperm modification and they can be used as a donor parent in a QPM breeding programme.

The mode of inheritance and environmental factors also determined the interrelationship among the measured traits. Increased protein concentration in grain could increase the tryptophan concentration in the grain under low and optimum N environments. A weak negative significant correlation ($r > -0.260$) between grain yield and tryptophan concentration in the grain observed under optimum N environment indicates increased grain yield led to low tryptophan concentration in the grain. Scott et al. [17] reported negative correlation between tryptophan and kernel modification in QPM germplasm.

From the estimates of reciprocal effects on quality traits, reciprocal effect determines the direction of the cross should be made in order to obtain the desired kernel endosperm, which had increased in tryptophan and protein concentration in the kernel endosperm [6,14]. The result of this study showed that many hybrids showed significant differences between direct F_1 hybrids and their reciprocal F_1 s for endosperm modification score, tryptophan and protein and quality index under both low and optimum N environments. This indicates that the performance of the quality traits improved based on whether the parents used was male or female in crosses during hybrid development. Thus, maize breeders should have to identify which parent used to be male or female before hybrid maize development.

CONCLUSION

From the research finding, inbred lines TL156579, TL156583, and VL05128 had good potential for endosperm modification score and inbred lines TL147078 and VL05128 had good potential for tryptophan, protein and protein quality index under low N environment. Under optimum N environment, parental lines TL156579, TL156583 and VL05128 had good potential for endosperm modification whereas parental lines TL156591 had good potential for tryptophan and protein concentration in grain and quality index. Reciprocal effects were significant in some hybrids for endosperm modification scores, tryptophan, protein, quality index and grain yield under both low and optimum N environments, indicating the opportunity to develop QPM hybrids with good kernel endosperm, which have higher tryptophan concentration in the grain than the normal maize hybrids under both environments.

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CONFLICT OF INTEREST

The author has declared no conflict of interest.

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