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Diallel Analysis of Maize Inbreds for Grain Yield, Protein and Tryptophan Content

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ADOPTION of quality protein maize in Egyptian maize breeding programs would maximize the nutritional value of maize products. However, the assessment of adaptability of exotic quality protein maize germplasms is an important step before incorporating them in breeding programs. The current studies consisted of two experiments including a preliminary evaluation of some exotic quality protein maize inbreds and combine eight adapted elite inbreds into a half-diallel cross. The current study revealed that CML158 exhibited the highest significant general combining ability effect with an average grain yield/plant of 53.0g. While CML492 contained the highest percentages of both protein (14.5%) and tryptophan (1.02%) with the highest values of general combining ability effects. Based on specific combining ability, the best parental combination for grain yield/plant was CML182×CML184, which yielded 239g and exceeded the average grain yield/plant of all hybrids (201.5g). It seems that CML143 possesses favorable alleles for increasing the percentage of protein (CML143×CML557) and tryptophan (CML158×CML491 and CML143×CML182) because it was a common parent in the best parental combinations for both traits. Mid-parent heterosis % varied from trait to trait; however, the highest amount of heterosis was detected in grain yield/plant due to its polygenic state. In conclusion, superior hybrids in yield and quality were detected. These hybrids need further evaluations across years and locations to assess stability. These hybrids can be considered as a cheap and sustainable source of high protein and tryptophan content for human consumption, which might play a magnificent role in food security in Egypt.

Keywords: Quality protein maize, General combining ability, Specific combining ability, Heterosis.

Introduction

Maize is the main cereal crop in many parts of the world. Its production is estimated to increase by 161 million ton to 1.2 billion ton by 2027 (OECD-FAO, 2018). Maize play a major economic role in both food manufacturing and fresh consumption. As the world population increases, the desire of development of high yielding hybrids resulted in reduction in the nutritional value (e.g., proteins and essential amino acids) caused by the adverse association with yield (Zhang et al., 2008; Bueno et al., 2009). Maize bread is a staple food in most urban and rural areas in Egypt (Galal, 2002). However, maize proteins lack to essential amino acids e.g. tryptophan (Bantte & Prasanna, 2004). Due to the expensive cost of the supplementary essential amino acids, it is paramount to develop genetically enhanced maize hybrids with high content of protein and essential amino acids.

Mertz et al. (1964) discovered the *opaque-2* mutant gene and its relationship with increase the content of tryptophan in maize, which resulted in developing quality protein maize (QPM). This mutant was transferred to normal maize lines via normal breeding strategies, which led to double the content of tryptophan in maize endosperm (Chaudhary et al., 2014). In addition, the percentages of proteins in QPM lines are higher than non-QPM lines (Prasanna et al., 2001). However, QPM breeding materials are 10-15% lower in grain yield comparing to non-QPM materials (Vasal, 2014); this is due to different reasons as revealed by Prasanna et al. (2001) and Vasal (2002). Nevertheless, this reduction in grain

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yield in QPM materials can be lessened down via breeding strategies of selection e.g. recurrent selection (Vasal, 2002).

CIMMYT as well as other maize breeding programs worldwide (Brazil, China, USA and India) have adopted the discovery of opaque-2 (Vasal, 2001; Bhatnagar et al., 2004); that unlocked new vistas and effectively participated in food security for humans, and improved growth of farm animals. Lodha (2014) discussed examples of the positive effect of QPM on both animals and humans. For example, animals that were fed on QPM products gained double weight (g) compared to those that were fed on non-QPM (Lodha et al., 1976), in addition, in India, the weight and height of children fed on QPM improved by 25% and 29%, respectively, compared to those who fed on non-QPM (Singh et al., 1980). Because QPM contains 60–100% more of tryptophan and lysine comparing to non-QPM, the biological value of QPM is 80% while non-QPM is 40–57% (Bressani, 1992).

Screening and adaptability of exotic QPM inbreds and the efficient introducing of such adapted inbreds into breeding programs might increase protein quality and increase genetic variability for selection efficacy (Bhatnagar et al., 2004). Further emphasizes was reported on the importance of exotic QPM inbreds to create genetic variation of maize genetic materials in USA by Goodman et al. (2000).

As Egypt is lagging behind other countries in development of QPM hybrids, the current study is the first trial to adopt QPM and open new vistas to improve Egyptian maize materials and increase nutritional value of maize for both humans and animal. Therefore, it is not only vital to introduce QPM inbred lines into the Egyptian maize germplasm to broaden the genetic base of nutritional value of Egyptian germplasm, but also enhance the adaptability of new hybrids to the Egyptian climatic and edaphic conditions. Consequently, the assessment of combining ability of these QPM inbred lines on grain yield and quality is paramount.

The initial evaluation of exotic QPM inbreds is a vital step to conclude their breeding potential (Geadelmann, 1984). Diallel crosses between adapted elite exotic QPM inbred plays an important role in determining the heterotic interactions among QPM inbreds, which leads to identify the best hybrids (Bhatnagar et al., 2004). Griffing's diallel analysis (Griffing, 1956) partitioned the sum of squares of genotypes (parents and their F_1 crosses) into sum of squares due to general combining ability (GCA), which represents the additive effect and sum of squares due to the specific combing ability (SCA), which symbolizes to the non-additive constitute. This elucidates the genetic control of traits of interest (Werle et al., 2014). Therefore, the objectives of the present study were to: i) evaluate exotic QPM inbreds under Egyptian environmental conditions as an initial step to ensure adaptability, high productivity and quality, ii) assess GCA effects for grain yield and quality as well as other agronomic traits, and iii) estimate SCA effects to recognize the superior hybrids combinations.

Materials and Methods

Plant materials and growing conditions

A set of 49 white maize inbred lines obtained from CIMMYT including 40 QPM inbred lines and nine non-QPM inbred lines (Table 1) were assessed during the summer seasons of two years (2016 and 2017) at Assiut University Agricultural Research Station (AUARS). Eight elite QPM inbred lines were chosen and their non-reciprocal F_1 hybrids were produced during late season of 2017. During the summer season of 2018, the eight elite parental QPM inbred lines and their non-reciprocal F_1 hybrids (half-diallel) were evaluated at AUARS. The current study was performed in a clay soil. Irrigation, fertilization and other cultural practices were carried out as recommended for optimum maize production.

The preliminary experiment of 49 QPM inbred lines for the two growing seasons and the half-diallel experiment were evaluated in a complete randomized block design with three replications. Each inbred line or F_1 hybrid was sown in a 6-meter long row with inter-row space of 0.6m and the distance among plants was 0.20m.

Studied traits

Flowering traits

Days to 50% anthesis (DA; days) were calculated as number of days from sowing until 50% of the plants in each row showing at least one anther from the tassel. Days to 50% silking (DS; days) were calculated as number of days from sowing until 50% of plants in each row showing silks. Anthesis-silking interval (ASI; days) computed as the difference between days to 50% anthesis and silking.

TABLE 1. The original pedigree of the inbred lines used in the current study.

CML No.	Original pedigree	CML No.	Original pedigree
140	Pob62c3HC87-2-1-#-#-1-B-#-B	177	G32MH84-2-2-1-1-B-B
141	Pob62c5HC24-5-3-2-1-B-B-2-B-B-#	178	G32MH12-3-1-B-1-B-B
142	Pob62c5HC93-5-6-1-3-B-B-B-7-B-B-#	179	G32MH85-2-1-B-2-B-B
143	Pob62c6HC88-1-1-B-B-B-10-B-B-#	180	(G32Q/EV8444SRBC4)#-B-#-B-B-21-2-BB
144	Pob62c5HC182-2-1-2-B-B-3-1-#-#	181	UWO417-B-2-1-1-B-B
145	Pob63c0HC181-3-2-1-4#-2-B-B-B-B-#-#	182	WOMTA1-B-1-1-1-B-B
146	AC8563MH35-3-1-B-2-1-B-B-1-B-B-#	184	G32QMH30-2-2-B-1-B-B
147	Pob63c2HC53-1-1-B-B-B-9-B-B-#	186	Pob67C2HC26-1-2-1-B-B
148	G23QMH19-1-1-B-1-2-B-B-B-B-#	490	P63C2HC161-1-3-BB-2-BB-2-B
149	G24QMH159-2-2-2-B-2-B-B-B-#-B	491	(6207QB/6207QA)-1-4-#-2-2-B-B
150	G24QMH169-2-1-B-3-1-1-B-B-3-B-#-#-B	492	P62C3HC163-3-3-3-2-#-1-1-2-BB
151	S8662Q-1-4-4-1-B-#	541†	ZEWB-C1-F2-216-2-2-B
152	S8662Q-1-4-4-5-B-#	544†	[(CML395/CML444)-B-4-1-3-1-B/CML444//[[TUXPSEQ]C1F2/P49-SR]F2-45-7-1-2-B]-2-1-2-2-B
153	S8662Q-28-4-B-B-B-#	545†	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-B]-1-2-1-1-2-B
154	[EV8762-SR]-17-1-B-B-#	547†	DRB-F2-60-1-1-1-B
155	Pob62c3HC163-2-1-3#-1-1-1-1-B-1-B-B-#	550†	P25 (HSRRS) C1-246-3-1-2-1-B-B-B-1
156	Pob62c3HC163-3-1-3-1-B-1-3-B-3-1-1-B-#	552†	(CML495xCML401)-B-6-B-1-B
157	Pob62c1HC24-5-3-2-1-B-2-1-1-B-#	553†	(CML264 x CLRCW41)-B-17-1-B-B-B-1-B
158	[EV8762-SR]-2-1-B-1-B-#	554	(CML491xCLQ-RCWQ13)-B-18-1-B-1-1-B
159	Pob63c2HC5-1-3-1-B-2-1-1-B-#	555	H132-28-B-45-1-1-B
160	Pob63c2HC6-2-1-1-B-2-1-B-#	556	(CML502/CLQRCWQ26)-B-39-2-2-B
173	Pob68C1HC180-1-3-1-1-B-2-B-B	557	(CML-176/CML264)-13-1-1-1-BBBB-10-B
174	Pob68C1HC249-1-4-4-2-B-B	558†	[POOL9Ac7-SR(BC2)]FS89-1-2-4-2-1-1-1
175	Pob68C0HC77-2-3-7-B-2-3-1-B-1-B-B	560†	(CML311/MBRC3-F1)//CML311//CML311)-95- B-1-1-2-B
176	(P63-12-2-1/P67-5-1-1)-1-2-B-B		

†Non-QPM inbred lines.

Morphological traits

Plant height (PH; cm) was measured as the distance from the soil surface to the top of tassel. Ear height (EH; cm) was measured as the distance from the soil surface to the main ear bearing node.

Grain yield per plant (GYP; g) was recorded at harvest by dividing the grain yield of each row by the number of plants per row.

Quality traits

Protein content (mg/100 mg flour): the total protein content in endosperm of grains was assessed using Micro-Kjeldahl digestion (AOAC, 1965). The protein content in the endosperm was estimated based on the nitrogen percentage as per Moro et al. (1996) and Kassahun (2001).

Tryptophan content in protein (mg/ 100mg protein): the tryptophan content was estimated using the colorimetric method as per Herbabdes & Bates (1969).

Statistical analyses

Separate and combined analysis of variance over two growing seasons of the preliminary experiment of assessing 49 inbred lines were accomplished using PROC GLM procedure (SAS v9.0, SAS Institute Inc., Cary, NC, USA, 2003). The 28 F_1 hybrids were analyzed using Griffing's method 4 (Griffing, 1956) via AGDR-R version 4 (Rodríguez et al., 2015).

Both broad-sense heritability ($h_b = \frac{\sigma_g^2}{\sigma_p^2}$) and narrow-sense heritability ($h_n = \frac{\sigma_a^2}{\sigma_p^2}$) were estimated as per Zhang & Kang (1997) assuming no epistasis. Where, $\sigma_g^2 = 2\sigma_{gca}^2 + \sigma_{sca}^2$, and

$$\sigma_p^2 = 2\sigma_{gca}^2 + \sigma_{sca}^2 + \sigma_{error}^2 \; \sigma_a^2 = 2\sigma_{gca}^2$$

Mid-parent Heterosis % for each F_1 hybrid was calculated as the difference between the F_1 hybrid mean ($\overline{F}_1$) and the average of the two parental inbred lines (MP) as the following:

$$\text{Heterosis} = \frac{\overline{F}_1 - MP}{MP} \times 100$$

Results

Mean performance of inbreds

Mean performance of all traits based on separated years and combined overall years are presented in Tables 2 and 3. In general, QPM inbreds were superior over non-QPM inbreds on their content of both protein and tryptophan. Eight elite QPM inbred were selected based on their performance over two years to develop half-diallel F_1 hybrids. These inbreds included CML # 143, 155, 158, 182, 184, 491, 492 and 557.

Based on analyses of variance for the preliminary experiment, inbred lines showed significant differences for all traits in both separated and combined analyses (Tables 4 and 5). Similarly, the interaction between inbred lines and years was significant except for DS and ASI. Years had significant effect on only three traits (EH, protein and tryptophan).

The mean performance of all traits for parental inbreds and their 28 F_1 hybrids are presented in Table 6.

Mean square estimates

Significant differences were observed among F_1 hybrids for all traits (Table 7). The means of DA and DS of F_1 hybrids were 6.49 and 6.21 days, respectively, earlier than the mean of parental inbreds. The mean of PH and EH of F_1 hybrids exceeded the mean of parental inbreds with 93.42 and 57.39 cm. The mean GYP for F_1 hybrids was more than triple of mean of parental inbreds. Nevertheless, the mean protein percentage of F_1 hybrids did not exceed the mean of parental inbreds unlike tryptophan percentage. Significant differences among both GCA and SCA effects were detected for all traits. In addition, the mean square values of GCA were higher than SCA for all traits.

Heritability

Broad-sense heritability values were high for all traits except ASI; whereas, narrow-sense heritability showed poor value for ASI, moderately low values for PH, EH, GYP and tryptophan, and high for the rest of traits. More details about heritabilities can be found in Table 7.

General combining ability (GCA) effects

The GCA effects are shown in Table 8. The GCA effects showed significant differences for all parental inbreds for DA except for CML158. CML557 and CML182 showed the highest and the smallest GCA effect, respectively, for DA. Regarding DS, all parental inbreds showed significant differences for their GCA effects except for CML143, 155 and 158. CML182 showed the smallest GCA effect unlike CML557. Only three parental inbreds (CML155, 184 and 557) showed significant differences for ASI. The desirable negative effect of GCA effect was found in CML182 indicating its earliness of flowering. For PH, all parental inbreds showed effects of their GCA effects except CML155, 182, 184 and 491. CML158 showed the highest GCA effect, whereas CML557 showed the smallest GCA effect. In addition, for EH, all parental inbreds showed significant GCA effects except for CML182 and 557. The CML184 showed the highest significant effect of GCA unlike CML143. For GYP, all parental inbreds showed significant differences for their GCA effect. CML158 showed the highest GCA effect while CML143 showed the smallest GCA effect. Regarding the grain quality traits, the GCA effects for all parental inbreds were significant for percentage of protein, where CML492 showed the highest GCA effect while CML155 showed the smallest GCA effect. For percentage of tryptophan, CML492 showed the highest GCA effect unlike CML158.

TABLE 2. Mean performance of 49 maize inbreds for studied traits separated by growing seasons (Y1= 2016 and Y2= 2017).

CML No.	DA		DS		ASI		PH		EH		GYP		Protein		Tryptophan	
	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2
140	90.00	90.67	91.33	92.00	1.33	1.33	152.33	156.67	75.00	70.00	46.00	51.33	10.53	10.77	1.05	1.00
141	75.33	76.00	76.00	77.00	0.67	1.00	140.00	150.00	65.00	65.67	68.67	76.00	8.73	9.00	1.05	1.05
142	65.33	67.67	66.67	68.33	1.33	0.67	110.67	128.33	55.00	60.00	65.33	75.33	10.10	10.03	1.02	1.08
143	59.00	61.00	60.00	62.67	1.00	1.67	130.00	130.00	65.00	60.00	30.67	24.67	10.60	10.50	0.91	0.95
144	62.00	63.00	62.33	64.33	0.33	1.33	159.33	153.33	65.00	60.00	50.00	42.00	10.50	10.63	1.04	1.05
145	64.00	63.00	65.33	65.00	1.33	2.00	153.67	160.00	66.00	63.33	49.33	55.33	9.15	9.25	0.87	0.90
146	87.00	89.00	88.67	90.00	1.67	1.00	165.00	158.33	79.33	65.00	46.67	56.00	9.15	9.02	1.11	1.02
147	64.00	65.00	65.67	65.67	1.67	0.67	169.67	167.00	78.67	66.67	50.00	60.00	10.90	10.57	1.02	0.97
148	60.33	60.00	61.67	61.00	1.33	1.00	151.67	170.00	76.67	65.00	51.33	60.67	8.80	8.23	0.96	1.05
149	74.00	73.00	74.67	74.00	0.67	1.00	148.33	155.00	65.00	60.00	45.33	60.00	9.40	9.80	0.83	0.95
150	89.67	90.67	91.00	91.67	1.33	1.00	160.00	165.00	63.67	64.00	52.00	42.00	8.47	9.02	0.95	1.02
151	85.33	85.33	86.67	86.67	1.33	1.33	160.00	165.00	65.00	60.00	36.67	42.00	9.60	9.10	1.02	0.92
152	93.67	91.00	94.00	92.33	0.33	1.33	163.67	155.00	65.67	61.67	50.00	58.00	9.60	10.02	1.02	1.06
153	71.00	72.00	72.33	73.00	1.33	1.00	148.33	155.00	65.67	60.00	50.00	58.00	12.06	12.60	0.92	1.00
154	65.33	65.67	66.67	67.00	1.33	1.33	152.33	158.33	55.00	64.00	56.00	45.33	9.70	9.10	0.87	0.82
155	92.33	92.33	93.33	93.33	1.00	1.00	165.00	160.00	73.33	65.00	36.67	25.33	9.90	10.07	0.93	0.99
156	75.33	75.33	76.00	76.00	0.67	0.67	147.33	155.00	61.67	55.00	56.00	47.33	9.05	9.60	0.91	1.00
157	75.33	75.67	76.33	77.33	1.00	1.67	158.33	155.00	66.33	57.00	54.67	40.67	8.50	9.05	0.84	0.92
158	65.33	66.00	66.33	67.00	1.00	1.00	151.67	156.67	61.67	64.67	28.67	31.33	9.10	9.57	0.72	0.82
159	91.00	91.67	92.33	92.67	1.33	1.00	160.00	165.00	65.00	61.67	49.33	58.00	8.40	8.06	0.99	0.92
160	70.67	72.00	72.00	73.00	1.33	1.00	165.00	163.33	61.00	61.67	68.67	76.00	10.63	10.40	1.00	0.94
173	91.67	93.00	93.00	93.67	1.33	0.67	128.33	138.33	50.00	45.00	51.33	42.00	8.30	8.70	0.83	0.90
174	85.33	86.33	86.33	87.67	1.00	1.33	164.33	160.00	74.33	65.00	62.67	67.33	9.05	8.95	0.99	0.92
175	66.33	67.00	67.67	68.00	1.33	1.00	164.33	161.67	67.33	60.00	65.33	61.33	8.57	8.80	0.92	0.97
176	75.00	75.33	76.33	76.67	1.33	1.33	168.33	160.00	80.33	60.00	56.00	63.33	7.43	7.70	1.01	1.02
177	93.67	93.33	94.67	94.33	1.00	1.00	165.00	155.00	64.33	58.33	53.33	45.33	10.40	10.50	0.84	0.87

TABLE 2. Cont.

CML No.	DA		DS		ASI		PH		EH		GYP		Protein		Tryptophan	
	Y1	Y2	Y1	Y2	Y1	Y2	Y1	Y2		Y1	Y2	Y1	Y2	Y1	Y2	Y1
178	88.33	87.67	89.67	89.67	1.33	2.00	165.00	158.33	75.00	58.33	56.00	54.67	10.05	9.95	0.85	0.90
179	67.00	67.67	69.00	68.67	2.00	1.00	160.00	165.00	60.00	61.67	54.67	62.00	10.12	10.40	0.84	0.90
180	70.33	70.33	71.00	71.67	0.67	1.33	153.33	165.00	63.00	65.00	85.33	79.33	9.20	9.40	0.94	0.92
181	75.00	75.00	76.33	76.33	1.33	1.33	165.00	165.00	65.00	60.00	85.33	84.00	8.60	8.30	0.92	0.93
182	64.67	64.67	65.67	65.67	1.00	1.00	133.33	125.00	50.00	45.00	92.67	96.00	10.30	10.20	0.87	0.87
184	75.00	74.67	75.33	75.67	0.33	1.00	158.33	161.67	65.00	60.00	49.33	56.67	12.20	12.37	0.84	0.87
186	89.33	88.67	90.67	90.00	1.33	1.33	175.67	171.67	90.00	71.67	62.00	74.67	8.18	8.10	1.03	1.01
490	61.33	61.67	61.67	62.33	0.33	0.67	165.33	171.33	65.00	67.33	66.47	76.00	12.30	12.20	0.94	0.95
491	60.73	61.33	62.00	62.33	1.27	1.00	160.67	150.00	75.67	55.00	76.69	80.00	12.35	12.40	0.85	0.86
492	59.67	60.33	60.67	61.33	1.00	1.00	165.33	160.00	67.67	61.67	69.00	78.00	14.62	14.60	1.06	1.03
541†	66.00	65.33	66.67	66.67	0.67	1.33	158.67	160.00	69.33	55.00	56.67	44.67	9.30	9.10	0.13	0.14
544†	72.33	71.33	73.09	73.00	0.76	1.67	134.10	150.00	62.27	55.00	48.76	58.00	8.10	8.05	0.65	0.60
545†	66.00	66.67	67.00	67.67	1.00	1.00	143.52	151.67	65.24	59.00	83.40	79.33	10.40	10.23	0.63	0.62
547†	71.67	70.00	73.08	71.00	1.41	1.00	154.10	155.00	67.77	60.00	37.98	34.00	7.53	7.60	0.63	0.61
550†	91.33	91.33	92.40	93.00	1.07	1.67	128.33	148.33	45.67	53.33	94.00	88.67	10.15	10.03	0.15	0.13
552†	93.00	91.33	94.67	92.33	1.67	1.00	153.67	160.00	58.33	60.00	76.67	82.00	11.05	11.08	0.14	0.15
553†	92.67	92.33	93.67	93.33	1.00	1.00	163.00	158.33	61.67	58.33	51.33	60.00	9.10	9.30	0.09	0.10
554	94.67	94.00	95.67	95.33	1.00	1.33	160.00	165.00	62.33	65.00	64.00	72.67	11.30	11.40	0.87	0.90
555	92.43	91.00	93.90	92.67	1.47	1.67	153.67	155.00	65.33	55.00	75.87	62.00	12.70	12.50	0.85	0.92
556	93.50	93.33	94.17	94.33	0.67	1.00	155.33	165.00	55.33	63.33	81.20	89.33	10.70	10.60	0.88	0.92
557	93.50	93.33	94.33	94.33	0.83	1.00	155.33	160.00	61.00	60.00	74.67	80.00	12.42	12.70	1.10	1.06
558†	95.33	95.00	96.67	97.00	1.33	2.00	165.00	165.00	78.33	65.00	78.67	82.00	8.15	8.15	0.08	0.11
560†	70.00	70.33	71.67	71.67	1.67	1.33	145.00	160.00	64.33	61.67	79.33	80.00	9.05	9.07	0.08	0.12
Mean	77.38	77.52	78.5	78.7	1.11	1.18	154.58	157.21	65.8	60.71	59.81	61.61	9.89	9.93	0.82	0.83
Revised $LSD_{0.05}$ inbred	1.07	1.31	1.29	1.52	1.84	2.00	7.69	9.65	7.82	9.62	8.16	5.08	0.19	0.20	0.05	0.05

- †Non-QPM inbred lines.
- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 3. Mean performance of 49 maize inbres for studied traits over the two growing seasons (2016 and 2017).

CML No.	DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
140	90.33	91.67	1.33	154.50	72.50	48.67	10.65	1.03
141	75.67	76.50	0.83	145.00	65.33	72.33	8.87	1.05
142	66.50	67.50	1.00	119.50	57.50	70.33	10.06	1.05
143	60.00	61.33	1.33	130.00	62.50	27.67	10.55	0.93
144	62.50	63.33	0.83	156.33	62.50	46.00	10.57	1.05
145	63.50	65.17	1.67	156.83	64.67	52.33	9.20	0.89
146	88.00	89.33	1.33	161.67	72.17	51.33	9.09	1.07
147	64.50	65.67	1.17	168.33	72.67	55.00	10.73	0.99
148	60.17	61.33	1.17	160.83	70.83	56.00	8.52	1.00
149	73.50	74.33	0.83	151.67	62.50	52.67	9.60	0.89
150	90.17	91.33	1.17	162.50	63.83	47.00	8.75	0.98
151	85.33	86.67	1.33	162.50	62.50	39.33	9.35	0.97
152	92.33	93.17	0.83	159.33	63.67	54.00	9.81	1.04
153	71.50	72.67	1.17	151.67	62.83	54.00	12.33	0.96
154	65.50	66.83	1.33	155.33	59.50	50.67	9.40	0.85
155	92.33	93.33	1.00	162.50	69.17	31.00	9.99	0.96
156	75.33	76.00	0.67	151.17	58.33	51.67	9.33	0.96
157	75.50	76.83	1.33	156.67	61.67	47.67	8.78	0.88
158	65.67	66.67	1.00	154.17	63.17	30.00	9.33	0.77
159	91.33	92.50	1.17	162.50	63.33	53.67	8.23	0.95
160	71.33	72.50	1.17	164.17	61.33	72.33	10.52	0.97
173	92.33	93.33	1.00	133.33	47.50	46.67	8.50	0.86
174	85.83	87.00	1.17	162.17	69.67	65.00	9.00	0.96
175	66.67	67.83	1.17	163.00	63.67	63.33	8.68	0.95
176	75.17	76.50	1.33	164.17	70.17	59.67	7.57	1.02
177	93.50	94.50	1.00	160.00	61.33	49.33	10.45	0.86
178	88.00	89.67	1.67	161.67	66.67	55.33	10.00	0.88
179	67.33	68.83	1.50	162.50	60.83	58.33	10.26	0.87
180	70.33	71.33	1.00	159.17	64.00	82.33	9.30	0.93
181	75.00	76.33	1.33	165.00	62.50	84.67	8.45	0.93
182	64.67	65.67	1.00	129.17	47.50	94.33	10.25	0.87
184	74.83	75.50	0.67	160.00	62.50	53.00	12.28	0.85
186	89.00	90.33	1.33	173.67	80.83	68.33	8.14	1.02
490	61.50	62.00	0.50	168.33	66.17	71.23	12.25	0.95
491	61.03	62.17	1.13	155.33	65.33	78.34	12.38	0.86
492	60.00	61.00	1.00	162.67	64.67	73.50	14.61	1.05
541†	65.67	66.67	1.00	159.33	62.17	50.67	9.20	0.13
544†	71.83	73.05	1.21	142.05	58.64	53.38	8.08	0.63
545†	66.33	67.33	1.00	147.59	62.12	81.36	10.32	0.62
547†	70.83	72.04	1.21	154.55	63.89	35.99	7.57	0.62
550†	91.33	92.70	1.37	138.33	49.50	91.33	10.09	0.14

TABLE 3. Cont.

CML No.	DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
552†	92.17	93.50	1.33	156.83	59.17	79.33	11.06	0.15
553†	92.50	93.50	1.00	160.67	60.00	55.67	9.20	0.10
554	94.33	95.50	1.17	162.50	63.67	68.33	11.35	0.88
555	91.72	93.28	1.57	154.33	60.17	68.93	12.60	0.89
556	93.42	94.25	0.83	160.17	59.33	85.27	10.65	0.90
557	93.42	94.33	0.92	157.67	60.50	77.33	12.56	1.08
558†	95.17	96.83	1.67	165.00	71.67	80.33	8.15	0.10
560†	70.17	71.67	1.50	152.50	63.00	79.67	9.06	0.10
Mean	77.45	78.60	1.15	155.90	63.26	60.71	9.91	0.82
Revised $LSD_{0.05}$ inbred	1.20	1.41	1.86	8.39	8.43	6.72	0.19	0.05

- †Non-QPM inbred lines.
- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 4. Mean squares of variance for studied traits separated by growing seasons 2016 and 2017.

Source	DF	Mean Squares							
		DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
		2016/2017							
Rep.	2	0.615	1.532	0.326	860.107	21.499	6.68	0.007	0.001
Line	48	463.870***	465.963***	0.441	488.681***	207.572***	23.960***	6.712***	0.248***
Error	96	0.56	0.806	0.355	27.673	26.823	31.152	0.018	0.001
Source	DF	2017/2018							
Rep.	2	0.68	0.333	0.061	100.905	23.286	20.762	0.001	0.001
Line	48	442.515***	446.323***	0.348	290.912***	77.931***	920.829***	6.748***	0.246***
Error	96	0.84	1.132	0.388	37.53	29.216	12.623	0.016	0.001

- *** Significant at 0.001 probability level.
- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 5. Mean squares of variance for studied traits combined over the two growing seasons.

Source	DF	MS							
		DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
Year	1	1.294	3.077	0.38	509.069	1902.287***	236.919	0.159**	0.014*
Rep. (Year)	4	0.648	0.933	0.193	480.506***	22.392	114.395***	0.004	0.001
Line	48	904.956***	911.051***	0.413	689.612***	213.648***	1571.374***	13.337***	0.490***
Line×Year	48	1.429***	1.235	0.376	89.981***	71.854***	95.840***	0.123***	0.004***
Error	192	0.7	0.969	0.371	32.601	28.02	21.888	0.017	0.001

- *,**,*** Significant at 0.05, 0.01 and 0.001 probability levels, respectively.
- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 6. Mean performance for studied traits in parental inbreds and their 28 single-cross hybrids in maize.

CML/F_1 hybrid	DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
143	61.00	62.33	1.67	135.00	65.00	34.67	10.47	0.92
143×155	70.33	71.67	1.33	230.10	110.07	183.73	9.77	1.05
143×158	61.00	63.00	2.00	255.63	124.13	210.83	10.15	0.77
143×182	65.00	66.33	1.33	251.70	119.90	177.43	9.47	1.03
143×184	62.33	64.00	1.67	255.33	126.80	191.97	10.20	1.05
143×491	58.33	59.67	1.33	231.80	115.73	183.10	10.10	0.87
143×492	64.00	65.00	1.00	259.00	125.50	192.77	12.63	1.15
143×557	72.00	73.67	1.67	232.47	110.33	184.30	14.00	0.93
155	91.00	92.00	1.00	165.40	70.60	39.80	10.05	0.98
155×158	70.33	72.00	1.67	248.83	122.83	220.07	8.47	1.04
155×182	61.00	62.00	1.00	242.23	116.07	190.63	8.67	0.86
155×184	61.67	63.00	1.33	255.47	123.30	205.90	11.27	1.06
155×491	58.33	60.00	1.67	252.60	122.37	182.50	10.04	0.95
155×492	58.33	59.00	0.67	265.10	119.33	201.93	12.30	1.10
155×557	74.67	76.33	1.67	242.73	119.93	205.97	8.90	1.01
158	65.67	67.00	1.33	156.03	66.00	39.00	9.53	0.77
158×182	60.33	61.33	1.00	257.33	120.50	209.13	9.83	0.88
158×184	61.67	63.33	1.67	256.37	122.03	235.67	9.34	0.95
158×491	64.00	65.33	1.33	265.60	126.27	196.67	11.10	1.06
158×492	60.33	61.67	1.33	265.80	124.73	208.40	12.20	1.08
158×557	73.67	76.33	2.67	267.33	122.67	230.67	9.90	0.91
182	65.00	66.00	1.00	140.00	54.33	98.67	10.43	0.92
182×184	60.33	63.00	2.67	254.33	122.67	239.03	11.53	0.89
182×491	58.67	60.33	1.67	256.67	123.33	215.33	10.48	1.05
182×492	60.33	61.67	1.33	248.73	124.33	166.33	12.65	1.13
182×557	68.33	69.67	1.33	225.33	123.67	177.07	9.93	0.98
184	74.33	75.67	1.33	160.33	66.00	55.00	12.60	0.93
184×491	65.33	66.67	1.33	261.00	129.33	191.70	11.30	0.98
184×492	60.33	62.00	1.67	245.33	123.33	190.67	12.63	1.05
184×557	68.33	70.33	2.00	230.33	119.67	215.60	11.32	1.05
491	60.33	61.67	1.33	160.33	66.33	71.00	12.63	0.92
491×492	62.00	63.33	1.33	236.00	123.33	215.10	13.76	0.99
491×557	75.00	76.67	1.67	226.00	121.53	211.13	12.05	1.08
492	60.33	61.67	1.33	167.33	66.00	70.33	14.47	1.02
492×557	70.33	73.00	2.67	256.67	125.60	207.27	13.91	1.08
557	90.33	92.00	1.67	161.33	60.67	74.33	12.60	1.05
Mean parental inbreds	71.00	72.29	1.33	155.72	64.37	60.35	11.60	0.94
Mean F_1 hybrid	64.51	66.08	1.57	249.14	121.76	201.46	11.00	1.00

- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 7. Mean squares for studied traits in eight parents half-diallel hybrids in maize.

Source	DF	MS							
		DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
REP	2	0.58	1.08	1.00	191.93	103.86	847.23	0.12	0.004
F_1 hybrids	27	85.91***	92.34***	0.71**	493.78***	58.26***	994.57***	7.55***	0.03***
GCA	7	241.58***	263.74***	1.03**	832.88***	102.65***	1741.11***	21.28***	0.04***
SCA	20	31.43***	32.34***	0.60*	375.10***	42.72**	733.28***	2.73***	0.02***
Residuals	54	0.60	0.80	0.32	48.77	18.08	23.68	0.02	0.002
Mean parents		71.00	72.29	1.33	155.72	64.37	60.35	11.60	0.94
Mean F_1 hybrids		64.51	66.08	1.57	249.14	121.76	201.46	11.00	1.00
Revised $LSD_{0.05}$ F_1 hybrids		1.10	1.28	1.22	11.00	7.92	6.95	0.18	0.06
GCA component		13.39	14.61	0.04	43.56	4.70	95.41	1.18	0.002
SCA component		10.28	10.52	0.09	108.78	8.21	236.53	0.91	0.01
GCA-SCA ratio		1.30	1.39	0.42	0.40	0.57	0.40	1.30	0.28
Phenotypic Variance		37.65	40.53	0.49	244.67	35.69	451.04	3.29	0.01
$h_n^{\dagger}$		0.71	0.72	0.16	0.36	0.26	0.42	0.72	0.31
$h_b^{\ddagger}$		0.98	0.98	0.35	0.80	0.49	0.95	0.99	0.87

- *,**,*** Significant at 0.05, 0.01 and 0.001 probability levels, respectively.

- †Narrow-sense heritability.

- ‡Broad-sense heritability.

- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

TABLE 8. Estimate of general combining ability (GCA) effects (g_i) of parents for studied traits in eight parent half-diallel hybrids in maize.

CML No.	gi	DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
143	1	0.24	0.13	-0.11	-4.64**	-3.31**	-14.35***	-0.11***	-0.03**
155	2	0.51**	0.24	-0.28*	-1.15	-3.07**	-3.25**	-1.26***	0.01
158	3	-0.04	0.07	0.11	12.16***	1.81*	16.87***	-1.00***	-0.05***
182	4	-2.93***	-3.04***	-0.11	-1.27	-0.31	-5.88***	-0.74***	-0.03*
184	5	-1.93***	-1.71***	0.22*	2.37	2.47**	10.05***	0.10***	0.004
491	6	-1.65***	-1.76***	-0.11	-2.38	1.60*	-2.45*	0.31***	-0.01
492	7	-2.65***	-2.82***	-0.17	5.45**	2.31*	-4.63***	2.19***	0.10***
557	8	8.46***	8.90***	0.44**	-10.52***	-1.49	3.63***	0.50***	0.01**

- *, **, *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively.

- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Aanthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

Specific combining ability (SCA) effects

The detailed SCA effects of F_1 hybrids for all traits are shown in Tables 9-12. Briefly, the earliest F_1 hybrid based on anthesis was CML155×CML491 (58 days) with the smallest significant SCA effect (SCA= -5.04), while CML143×CML491 was the earliest F_1 hybrid to silk (SCA= -4.78) with 59 days followed by CML155×CML491. The maximum significant SCA effect for ASI was found in CML182×CML184 (SCA= 0.98). Hybrid CML158×CML557 showed the highest significant SCA effect for PH (SCA= 16.55), while hybrid CML143×CML184 exhibited the highest significant SCA for EH (SCA= 5.88). For GYP, CML182×CML184 showed the highest significant positive SCA effect (SCA= 33.40) with highest GYP (239g) which was higher than the average GYP for all F_1 hybrids (201.5g). In general, GYP showed the highest SCA effects among studied traits. For percentage of protein, CML143×CML557 showed the highest SCA effects (SCA= 2.61) with 14%, which exceeded the mean percentage of protein (11%) for all F_1 hybrids. While CML158×CML491showed the highest SCA effect (SCA= 0.11) with percentage of tryptophan= 1.06%. In addition, the second most promising hybrid in terms of percentage of tryptophan was CML143×CML182 (SCA= 0.09) with 1.03%. Both hybrids exceeded the mean percentage of tryptophan (1%) for all hybrids. The presence of CML143 in the best hybrids in terms of percentages of protein and tryptophan showed that this parental inbred possessed favorable alleles for increasing both protein and tryptophan.

TABLE 9. Estimates of specific combining ability (SCA) effects of days to 50% anthesis (DA; days) and days to 50% silking (DS; days) for 28 maize F_1 hybrids.

Hybrid	Days to 50% anthesis			Days to 50% silking		
	SCA	P value	Rank	SCA	P value	Rank
143×155	5.071429	1.73E-11	2	5.222222	1.42E-10	2
143×158	-3.70635	4.14E-09	25	-3.27778	3.03E-07	25
155×158	5.349206	6.55E-12	1	5.611111	3.95E-11	1
143×182	3.18254	4.95E-08	5	3.166667	5.06E-07	5
155×182	-1.09524	0.008693	17	-1.27778	0.0083	18
158×182	-1.20635	0.004463	18	-1.77778	0.00059	22
143×184	-0.48413	0.213298	15	-0.5	0.265288	15
155×184	-1.42857	0.00114	21	-1.61111	0.001441	20
158×184	-0.87302	0.031152	16	-1.11111	0.019206	17
182×184	0.68254	0.08497	12	1.666667	0.001071	7
143×491	-4.7619	5.37E-11	27	-4.77778	6.72E-10	28
155×491	-5.03968	1.94E-11	28	-4.55556	1.52E-09	27
158×491	1.18254	0.005154	10	0.944444	0.042671	12
182×491	-1.2619	0.003183	20	-0.94444	0.042671	16
184×491	4.404762	2.14E-10	3	4.055556	1.06E-08	3
143×492	1.904762	6.02E-05	6	1.611111	0.001441	8
155×492	-4.03968	9.6E-10	26	-4.5	1.87E-09	26
158×492	-1.48413	0.000808	22	-1.66667	0.001071	21
182×492	1.404762	0.001321	8	1.444444	0.003488	9
184×492	0.404762	0.295271	13	0.444444	0.320491	14
491×492	1.793651	0.000119	7	1.833333	0.000438	6
143×557	-1.20635	0.004463	19	-1.44444	0.003488	19
155×557	1.18254	0.005154	9	1.111111	0.019206	11
158×557	0.738095	0.064092	11	1.277778	0.0083	10
182×557	-1.70635	0.000204	23	-2.27778	4.14E-05	23
184×557	-2.70635	5.87E-07	24	-2.94444	1.45E-06	24
491×557	3.68254	4.61E-09	4	3.444444	1.43E-07	4
492×557	0.015873	0.966799	14	0.833333	0.070561	13

TABLE 10. Estimates of SCA effects of days to anthesis-silking interval (ASI; days) and plant height (PH; cm) for 28 maize F_1 hybrids.

Hybrid	Anthesis-silking interval			Plant height		
	SCA	P value	Rank	SCA	P value	Rank
143×155	0.150794	0.591469	8	-13.2341	0.000924	27
143×158	0.428571	0.13676	5	-1.00635	0.770799	15
155×158	0.261905	0.354753	7	-11.3119	0.00342	24
143×182	-0.01587	0.954783	12.5	8.488095	0.021653	7
155×182	-0.18254	0.516598	16	-4.48413	0.203104	18
158×182	-0.57143	0.051923	28	-2.68968	0.439203	17
143×184	-0.01587	0.954783	12.5	8.48254	0.021729	8
155×184	-0.18254	0.516598	17.5	5.110317	0.149334	12
158×184	-0.2381	0.399306	20.5	-7.29524	0.044795	20
182×184	0.984127	0.001963	1	4.099206	0.243059	13
143×491	-0.01587	0.954783	14	-10.3008	0.006722	22
155×491	0.484127	0.095232	4	6.993651	0.053463	9
158×491	-0.2381	0.399306	20.5	6.688095	0.063753	10
182×491	0.31746	0.264379	6	11.18254	0.003731	5
184×491	-0.34921	0.221055	25	11.87698	0.002333	3
143×492	-0.29365	0.300798	24	9.071429	0.01497	6
155×492	-0.46032	0.111483	26	11.66587	0.002692	4
158×492	-0.18254	0.516598	17.5	-0.93968	0.78557	14
182×492	0.039683	0.887298	9.5	-4.57857	0.194132	19
184×492	0.039683	0.887298	9.5	-11.6175	0.002782	25
491×492	0.039683	0.887298	11	-16.2008	0.000121	28
143×557	-0.2381	0.399306	20.5	-1.50079	0.664366	16
155×557	-0.07143	0.798757	15	5.260317	0.138353	11
158×557	0.539683	0.065059	3	16.55476	9.53E-05	1
182×557	-0.57143	0.051923	27	-12.0175	0.002121	26
184×557	-0.2381	0.399306	23	-10.6563	0.005308	23
491×557	-0.2381	0.399306	20.5	-10.2397	0.006999	21
492×557	0.81746	0.007794	2	12.59921	0.001426	2

Heterosis estimates

The Mid-parent heterosis % of all traits for 28 F_1 hybrids is presented in Table 13. Briefly, the mid-parent heterosis % for DA and DS ranged from 5.49% for hybrid (CML143×CML492) to -25.40% for hybrid (CML155×CML184). For GYP, it ranged from 96.84% in hybrid (CML182×CML492) to 472.39% for hybrid (CML143×CML158). For protein %, it ranged from -21.41% for hybrid (CML155×CML557) to 21.39% for hybrid (CML143×CML557), while for tryptophan%, it ranged from -9.47% for hybrid (CML155×CML182) to 24.87% for hybrid (CML158×CML491).

TABLE 11. Estimates of SCA effects of ear height (EH; cm) and grain yield/plant (GYP; g) for 28 maize F_1 hybrids.

Hybrid	Ear height			Grain yield/plant		
	SCA	P value	Rank	SCA	P value	Rank
143×155	-5.31349	0.018637	27	-0.13016	0.95683	14
143×158	3.875397	0.076522	3	6.853175	0.009132	9
155×158	2.336508	0.273463	8	4.986508	0.048616	11
143×182	1.75873	0.406679	11	-3.80238	0.124982	19
155×182	-2.31349	0.278075	20	-1.70238	0.481702	16
158×182	-2.75794	0.198751	22	-3.31905	0.177492	18
143×184	5.880952	0.010248	1	-5.19683	0.040663	20
155×184	2.142063	0.314223	9	-2.36349	0.331453	17
158×184	-4.00238	0.068051	25	7.286508	0.006061	8
182×184	-1.25238	0.552905	18	33.39762	7.84E-12	1
143×491	-4.31349	0.05071	26	-1.56349	0.51776	15
155×491	2.080952	0.327883	10	-13.2635	1.82E-05	23
158×491	1.103175	0.600808	12	-19.2135	9.77E-08	26
182×491	0.286508	0.891556	15	22.19762	9.7E-09	2
184×491	3.50873	0.106356	5	-17.3635	4.54E-07	25
143×492	4.742063	0.033337	2	10.28095	0.000325	4
155×492	-1.66349	0.432138	19	8.347619	0.002176	7
158×492	-1.14127	0.588386	17	-5.30238	0.037135	21
182×492	0.575397	0.784386	14	-24.6246	1.71E-09	28
184×492	-3.20238	0.138413	24	-16.219	1.22E-06	24
491×492	-2.33016	0.27473	21	20.71429	2.98E-08	3
143×557	-6.63016	0.004544	28	-6.44127	0.013401	22
155×557	2.730952	0.202999	7	4.125397	0.097699	12
158×557	0.586508	0.780337	13	8.70873	0.001528	5
182×557	3.703175	0.08948	4	-22.1468	1.01E-08	27
184×557	-3.0746	0.153977	23	0.45873	0.848759	13
491×557	-0.33571	0.873089	16	8.492063	0.001889	6
492×557	3.019841	0.161073	6	6.803175	0.009571	10

Discussion

As the mean square values of GCA were higher than SCA for all traits, this indicates the importance of additive gene action. These results were consistent with San Vicente et al. (1998) and Bhatnagar et al. (2004) who revealed the importance of gene action in breeding programs. The ratio of additive to non-additive constituents gives an idea about the gene action (Baker, 1978). The additive gene action was predominant in CIMMYT's QPM hybrids that enhanced grain yield (Vasal et al., 1993), which is consistent with the results of the current study. The negative effects of GCA effect for inbred CML492 (60 days; for DA) indicated its earliness of flowering and its adaptability to Egyptian environment. Bhatnagar et al. (2004) detected CML184 as the earliest inbred in flowering traits, while, in the current study, CML184 (≈74 days, DA) showed medium time of flowering. This result is inconsistent with those found by Bhatnagar et al. (2004). This could be due to differences in adaptability between USA and Egypt.

TABLE 12. Estimates of SCA effects of protein content (mg/100mg flour) and tryptophan content in protein (mg/100mg protein) for 28 maize F1 hybrids.

Hybrid	Protein			Tryptophan		
	SCA	P value	Rank	SCA	P value	Rank
143×155	0.140317	0.036518	12	0.067302	0.002365	8
143×158	0.260873	0.000476	8	-0.15492	1.15E-07	28
155×158	-0.27135	0.000322	17	0.081746	0.000415	4
143×182	-0.68413	6.98E-10	23	0.086746	0.000227	2
155×182	-0.33302	3.32E-05	19	-0.11992	4.68E-06	27
158×182	0.570873	1.46E-08	5	-0.03548	0.081568	19
143×184	-0.78913	5.68E-11	25	0.068413	0.002071	7
155×184	1.428651	8.88E-16	2	0.045079	0.030359	10
158×184	-0.76413	1.01E-10	24	-0.00048	0.980603	14
182×184	1.170873	3.86E-14	3	-0.08214	0.000395	24
143×491	-1.09746	1.32E-13	27	-0.0977	6.12E-05	25
155×491	-0.00302	0.962058	14	-0.0577	0.007353	23
158×491	0.790873	5.46E-11	4	0.113413	9.79E-06	1
182×491	-0.09079	0.162508	15	0.085079	0.000277	3
184×491	-0.10913	0.096686	16	-0.02325	0.24333	17
143×492	-0.43913	8.35E-07	20	0.080635	0.000474	6
155×492	0.378651	6.52E-06	6	-0.00603	0.758396	15
158×492	0.015873	0.802447	13	0.038413	0.060927	12
182×492	0.204206	0.003905	11	0.060079	0.005568	9
184×492	-0.65079	1.64E-09	22	-0.04825	0.021477	21
491×492	0.270873	0.000328	7	-0.10103	4.12E-05	26
143×557	2.608651	0	1	-0.05048	0.016777	22
155×557	-1.34024	2.89E-15	28	-0.01048	0.594075	16
158×557	-0.60302	5.93E-09	21	-0.0427	0.03913	20
182×557	-0.83802	1.93E-11	26	0.005635	0.773809	13
184×557	-0.28635	0.000184	18	0.040635	0.048544	11
491×557	0.238651	0.001092	9	0.08119	0.000443	5
492×557	0.220317	0.002158	10	-0.02381	0.232635	18

The most promising parental combination for GYP was CML184×CML182. In this regard, the current outcome is consistent with the findings of Bhatnagar et al. (2004) who found that CML184 is one parental line for most yielding F_1 hybrids. In the current study, very high effects of SCA have been detected for GYP; this indicates that potential improvement of GYP can be expected. This is consistent with the conclusions of Glover et al. (2005) when they used adapted exotic germplasm in diallel analyses.

The current results showed high divers amount of heterosis % from trait to trait. This is due to the genetic basis of each trait-dependent (Flint-Garcia et al., 2009). In addition, heterosis for GYP was higher than other traits. Flint-Garcia et al. (2009) found similar results when they compared heterosis of yield and its components. This is because yield and its components are complex traits (Lippman & Zamir, 2007). In their study about heterosis in different maize inbreds, Flint-Garcia et al. (2009) reported positive associations between genetic distance and heterosis. However, Melchinger (1999) indicated that the genetic distance is not a good indicator of heterosis for grain yield. The current study supports latter statement.

TABLE 13. Mid-parent heterosis as % for studied traits in 28 maize single-cross hybrids.

Hybrid	DA	DS	ASI	PH	EH	GYP	Protein	Tryptophan
143×155	-7.46	-7.13	-0.04	53.20	62.34	393.46	-4.79	10.35
143×158	-3.68	-2.58	33.33	75.67	89.52	472.39	1.50	-9.39
143×182	3.17	3.38	-0.04	83.05	100.95	166.15	-9.41	11.77
143×184	-7.88	-7.25	11.13	72.91	93.59	328.18	-11.56	13.01
143×491	-3.85	-3.76	-11.13	56.98	76.24	246.56	-12.55	-5.74
143×492	5.49	4.84	-33.33	71.33	91.60	267.18	1.33	18.56
143×557	-4.85	-4.53	0.00	56.90	75.60	238.17	21.39	-5.73
155×158	-10.21	-9.43	42.91	54.83	79.84	458.55	-13.53	18.86
155×182	-21.79	-21.52	0.00	58.63	85.81	175.35	-15.37	-9.47
155×184	-25.40	-24.85	14.27	56.86	80.53	334.39	-0.51	10.99
155×491	-22.91	-21.91	42.91	55.10	78.73	229.42	-11.45	-0.47
155×492	-22.91	-23.21	-42.82	59.35	74.72	266.71	0.34	10.17
155×557	-17.65	-17.03	25.01	48.58	82.73	260.92	-21.41	-0.79
158×182	-7.65	-7.77	-14.27	73.85	100.28	203.82	-1.50	4.50
158×184	-11.90	-11.22	25.06	62.07	84.90	401.42	-15.63	12.12
158×491	1.59	1.55	0.00	67.91	90.83	257.58	.15	24.87
158×492	-4.23	-4.14	0.00	64.40	88.99	281.22	1.67	21.21
158×557	-5.56	-3.98	77.80	68.47	93.68	307.06	-10.54	0.33
182×184	-13.40	-11.06	128.63	69.37	103.88	211.11	0.14	-3.46
182×491	-6.38	-5.48	42.91	70.92	104.42	153.83	-9.13	13.94
182×492	-3.72	-3.39	14.27	61.87	106.65	96.84	1.61	16.37
182×557	-12.02	-11.81	-0.04	49.56	115.07	104.70	-13.80	-0.20
184×491	-2.97	-2.91	0.00	62.79	95.47	204.29	-10.43	5.45
184×492	-10.40	-9.71	25.06	49.75	86.87	204.26	-6.65	8.17
184×557	-17.00	-16.10	33.33	43.21	88.95	233.40	-10.18	6.36
491×492	2.76	2.70	0.00	44.05	86.40	204.39	1.57	2.06
491×557	-0.44	-0.22	11.13	40.52	91.39	190.55	-4.49	9.78
492×557	-6.64	-4.99	77.80	56.19	98.32	186.55	2.76	4.50
mean	-8.50	-7.98	18.00	60.30	89.58	252.80	-5.37	6.72
Min.	-25.40	-24.85	-42.82	40.52	62.34	96.84	-21.41	-9.47
Max.	5.49	4.84	128.63	83.05	115.07	472.39	21.39	24.87

- DA= Days to 50% anthesis (days), DS= Days to 50% silking (days), ASI= Anthesis siliking interval (days), PH= Plant height (cm), EH= Ear height (cm), GYP= Grain yield per plant (grams), protein= Protein content (mg/100mg flour) and tryptophan= Tryptophan content in protein (mg/100mg protein).

Conclusion

The adoption of incorporation of adapted exotic QPM inbreds from diverse backgrounds in the Egyptian maize breeding programs will lead to develop QPM hybrids. This study aims to unlock doors for new and promising vistas to benefit from exotic QPM germplasm in enhancing the nutritional value of Egyptian maize as cheap and sustainable sources of increasing proteins and essential amino acids, e.g. tryptophan. In the current study, I identified superior hybrids in grain yield and quality. Further evaluation of these hybrids should be performed under different locations across Egypt and for many years to guarantee stability and ensure tolerance to biotic and abiotic stresses.

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