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COMBINING ABILITIES OF NEWLY-DEVELOPED QUALITY PROTEIN AND HIGH-OIL MAIZE INBREDS AND THEIR TESTCROSSES

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ABSTRACT

Adoption and development of quality protein (QPM) and high-oil maize (Zea mays L.) would increase the nutritional value of food and feed maize products in Egypt. Nineteen newly-developed inbred lines isolated from QPM pools and high-oil populations were crossed to four testers (two local normal and two QPM inbred lines) and 76 testcrosses were produced in 2005 season. The parents and testcrosses as well as the commercial single cross SC10 were evaluated in a lattice 10 × 10 design with 3 replications in 2006 season. There were highly significant differences among parents and among testcrosses for grain protein and oil contents. Mean grain protein content ranged from 6.14 to 10.5% for parents and from 5.5 to 15.98% for testcrosses. Mean grain oil content ranged from 3.16 to 8.95% for parents and from 4.19 to 8.05% for testcrosses. For protein content the best parents were L-10, L-9, L-5, L-6, L-17 and L-4 in mean per se performance and L-4, L-6, L-8, L-1, L-7, L-18 and L-5 for GCA effects and the best testcrosses were L-4 × Gz 639, L-7 × Gz 639, L-8 × Gz639 and L-18 × L-21 for mean per se performance, SCA effects and heterobeltiosis and L-6 × Gz 639 and L-2 × Sd 63 for heterobeltiosis and SCA effects. For oil content, the best parents were L-18, L-2, L-1 and L-9 for mean per se performance and L-6, L-4, L-8, L-9 and L-18 for GCA effects and the testcross L-12 × L-21 for the 3 parameters and L-6 × Gz 639, L-1 × L-20 and L-18 × L-21 for per se performance and SCA effects. Estimates of GCA and SCA variances were significant and positive, suggesting that both heterosis breeding and selection procedures could be efficient for improving protein and oil contents. Dominance was larger than additive variance in magnitude and degree of dominance was overdominance for the two characters. Narrow-sense heritability was 16.19% for protein and 13.46% for oil content. Predicted selection gain, based on 10% selection intensity was 21.82% for protein and 14.68% for oil content.

Key words: ***Quality protein maize, QPM, Combining ability, Heterobeltiosis, Protein content, High-oil.***

INTRODUCTION

Some of the most important traits of interest in the maize (*Zea mays* L.) market are those related to the nutritional quality of the grain, especially protein and oil content (Mittelmann *et al* 2003).

The CIMMYT has developed quality protein maize (QPM) that has improved kernel quality characteristics by introducing modifier genes for denser and more vitreous endosperm (Rodrigues and Chaves 2002). The biological value of the common maize protein is equivalent to approximately 40% of the biological value of milk protein, while for QPM maize this value is 90% (National Research Council 1998). The CIMMYT QPM populations, pools, inbreds and hybrids adapted to subtropical and tropical environments are widely used in the development of high-lysine maize in Brazil, China, Ghana, India and several Latin American countries (Vasal 2001).

Despite the nutritional quality advantages and improved abiotic and biotic stress tolerance of exotic QPM germplasm, very little effort has been made to characterize and introgress exotic QPM into maize germplasm of Egypt. Before incorporation of exotic QPM germplasm into Egyptian germplasm, an initial evaluation of exotic germplasm is useful to determine their breeding potential. Information about how elite QPM inbreds combine and perform in hybrids will facilitate the selection of parents and breeding strategies for hybrid development (Bhatnagar *et al* 2004).

The line × tester analysis developed by Kempthorne (1957) is widely used for evaluating the potential of new inbred lines by crossing them with common testers and evaluating the performance of their testcrosses (Singh and Narayanan 2000). This scheme of evaluation allows progeny comparisons as far as their combining ability with testers. Therefore, our objectives were to (i) estimate GCA effects for grain protein and oil content of newly-developed inbreds isolated from QPM pools (from CIMMYT) and high-oil populations (from Thailand) and identify the best *per se* ones and the best general combiners, (ii) estimate SCA effects and indentify best hybrid combinations and (iii) obtain information on type of gene action controlling the expression of these grain quality traits.

MATERIALS AND METHODS

Material

Nineteen newly-developed maize inbred lines chosen from 86 inbreds that were isolated from QPM pools and high-oil populations based on an evaluation in 2004 season at Giza Res. Sta. of the ARC for their clear differences in grain protein and/or grain oil content. The designation, pedigree and origin of these 19 inbreds are presented in Table (1). These inbreds were topcrossed to four testers (two of them were commercial normal inbreds, i.e. Sd 63 and Gz 639 and two were QPM inbred lines i.e. L-20 and L-21) (Table 1) and 76 testcrosses were produced.

Making the testcrosses

The 19 inbred lines (16 QPM and 3 high-oil) and the four testers were planted at the field of Giza Res. Sta. of the ARC in 2005 season at two planting dates of 12-day interval. Pollen grains from each tester were used

Table 1. Origin and pedigree of QPM inbred lines and four testers used in this study.

Inbreds	Source	Pedigree	Country of origin	Quality
Lines:				
L-1	Pool 70	5-1-2-1-2-1-3-B-2	CIMMYT - Mexico	QPM
L-2	Pool 29	18-1-1-1-2-4-2-2-1	CIMMYT - Mexico	QPM
L-3	Pool 70	29-2-2-1-3-3-2-1-1	CIMMYT - Mexico	QPM
L-4	Pool 70	8-2-2-1-3-3-2-1-2	CIMMYT - Mexico	QPM
L-5	Pool 70	8-1-1-1-1-1-1-1-2	CIMMYT - Mexico	QPM
L-6	Pool 70	8-3-1-1-3-1-2-2-4	CIMMYT - Mexico	QPM
L-7	Pool 70	29-1-2-1-2-1-2-1-1	CIMMYT - Mexico	QPM
L-8	Pool 70	29-2-1-1-1-1-1-1-1	CIMMYT - Mexico	QPM
L-9	Pool 70	29-2-1-1-1-1-1-2-2	CIMMYT - Mexico	QPM
L-10	Pool 70	29-2-1-1-2-2-1-1-2	CIMMYT - Mexico	QPM
L-11	Pool 70	33-2-1-1-1-1-5-3-2	CIMMYT - Mexico	QPM
L-12	Pool 29 × Pool 70	6-1-1-1-2-2-1-1-1	CIMMYT - Mexico	QPM
L-13	Pop 59	20-1-4-1-1-2-1-1-1	Thailand	High-oil
L-14	Pool 70	32-2-1-1-1-1-7-3-2	CIMMYT - Mexico	QPM
L-15	Pool 70	32-2-1-1-1-2-1-1-2	CIMMYT - Mexico	QPM
L-16	Pool 29	15-1-1-1-3-1-1-1-1	CIMMYT - Mexico	QPM
L-17	Pool 29 × Pool 70	6-1-1-1-2-3-2-1-1	CIMMYT - Mexico	QPM
L-18	Pop 59	37-1-1-1-1-2-1-1-1	Thailand	High-oil
L-19	Pop 59	41-1-1-1-1-1-1-1-1	Thailand	High-oil
Testers:				
T-1 (Sd 63)	Tep-5	Commercial	ARC – Egypt	Normal
T-2 (Gz 639)	B73 × Sd 62	Commercial	ARC – Egypt	Normal
T-3 (L-20)	Pool 29	20-1-1-2-1-1-1-B-1	CIMMYT - Mexico	QPM
T-4 (L-21)	Pool 70	8-2-2-1-1-1-1-1-2	CIMMYT - Mexico	QPM

to pollinate silks of all the 19 inbred lines, so seeds of 76 F_1 testcrosses were obtained. Selfing of all parental inbreds was done at the same season to increase the seeds of parents, so enough quantities of seeds were available for evaluation in the next season.

Evaluation of QPM and high-oil inbreds, testers and testcrosses

In 2006 season, a field experiment was carried out at Giza Res. Sta., to evaluate 100 genotypes, namely 19 inbred lines, 4 testers, 76 testcrosses and the commercial single cross SC 10 as a check. The experimental design used was 10 × 10 lattice with three replicates. The date of planting was the 15th of May. The experimental plot was one row of 6 m length and 0.8 m width, with a distance of 25 cm between hills. All recommended agricultural practices were followed. Sibbing was carried out in each entry for the purpose of determining the grain contents of protein and oil.

The Zeltex ZX-800 Near-Infrared (NIR) non-destruction whole grain analyzer manufactured by Zeltex Inc., Maryland, USA was used for determination of grain protein and oil contents.

Biometrical and genetic analysis

Because the relative efficiency of randomized complete block (RCB) design was higher than that of the lattice design, collected data on grain protein and oil contents were submitted to analysis of variance of RCB design and LSD test according to Snedecor and Cochran (1989). Data were further submitted to the line × tester analysis developed by Kempthorne (1957), to estimate combining ability variances and effects. Additive and non-additive genetic components were calculated according to Comstock and Robinson (1952) and Cockerham (1956). Average degree of dominance "a" was calculated as follows: "a" = $(2\delta^2_D/\delta^2_A)^{½}$, where δ^2_D= dominance variance and δ^2_A= additive variance ("a"= 0 indicated no dominance, "a" < ±1 indicated positive or negative partial dominance, a = ±1 indicated positive or negative complete dominance and a > ±1 indicated positive or negative overdominance). Broad- (h^2_b) and narrow - (h^2_n) sense heritabilities were calculated according to Hallauer and Miranda (1981). Genetic advance (GA) from selection was calculated according to Becker (1984) based on 10% selection intensity. Heterosis relative to the higher parent was calculated as follows: Heterosis = $[(F_1\text{-HP})/\text{HP}] \times 100$, where F_1 and HP are the means of F_1 and the higher parent, respectively. The significance of heterosis was tested according to Singh and Narayanan (2000).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance (Table 2) indicated that mean squares due to replications were highly significant for protein and oil contents, suggesting that replicates differed significantly in environmental conditions.

Table 2. Analysis of variance for maize grain protein and oil content of 19 lines, 4 testers and their 76 testcrosses evaluated in 2006.

S.O.V.	d.f.	Mean squares	
		Protein%	Oil%
Replications	2	40.36**	16.71**
Genotypes	98	13.42**	4.94**
Parents (P)	22	11.19**	12.75**
Crosses (C)	75	14.20**	2.45**
P vs C	1	3.68**	19.88**
Error	196	0.196	0.099
C.V.(%)		5.36	5.63

** indicate significance at 0.01 probability level.

Mean squares due to genotypes and their components, *i.e.* parents and testcrosses were highly significant, suggesting that studied genotypes, parental inbreds and testcrosses differed significantly at 1% level of probability for grain protein and grain oil contents. Moreover, mean squares due to parents *vs.* crosses were highly significant for both traits (grain protein and grain oil content), indicating the significant role of heterosis for these grain quality traits in maize.

Mean grain protein and oil content

Means of grain protein and oil contents of the studied QPM and high-oil inbred lines, testers and their testcrosses is presented in Table (3). Mean grain protein content of the 19 inbred lines (8.53%) was higher than that of the testers (5.84%). It ranged for the inbred lines from 6.14% to 10.5%. The highest mean protein content was exhibited by L-10 followed by L-9, L-5, L-6, L-17, L-4 and L-14. On the other hand, the lowest mean protein content among inbred lines was shown by L-11, L-12 and L-13.

The existence of genetic variability for protein content in maize has been demonstrated in several studies (Dudley 1977, Dudley and Lambert 1992 and Micu *et al* 1995). This indicates that protein content in maize could be improved by conventional breeding programs.

In general, mean grain protein content across all testcrosses was lower than that across parental inbreds, but the highest mean grain protein content of nine testcrosses was higher than that of the inbreds.

Mean grain protein content of testcrosses ranged from 5.55 to 15.98%. The highest mean protein content was exhibited by the cross L-9 × Gz 639 (15.98 %) followed by L-4 × Gz 639 (14.85%), L-7 × Gz639 (13.60%), L-8 × Gz 639 (13.37%), L-1 × L-20 (12.47%) and L-18 × L-21 (12.47%). On the contrary, the lowest mean grain protein content was shown by the crosses L-3 × Sd 63 (5.55%), L-19 × Sd 63 (5.78%), L-19 × L-21 (5.78%), L-11 × Sd 63 (5.89%) and L-9 × Gz 639 (5.89%). It is interesting to record that the inbred L-4 followed by L-8, L-6, L-7 and L-18 showed the highest mean grain protein content across their crosses with the four testers. Moreover, the tester Gz 639 showed the highest mean protein content across all inbred lines.

Mean grain oil content of studied inbred lines (5.86%) was lower than that of the testers (7.06%) (Table 3). It ranged from 3.16 % to 8.95 % for the inbred lines. The highest mean grain oil content was shown by the inbred line L-18 (8.95 %) followed by L-2 (8.79 %), the tester Sd 63 (8.34 %) and the inbred L-1 (8.21%). On the contrary, the lowest mean grain oil content was shown by L-8, L-15, L-13 and the tester L-21.

Mean grain oil content of the testcrosses ranged from 4.19 to 8.05 %. The highest mean oil content was obtained by the cross L-9 × Gz 639 (8.05 %) followed by L-1 × L-20 (7.59 %), L-12 × L-21 (7.25 %, L-18 × L-21

Table 3. Mean grain protein and oil content of 19 QPM and high-oil inbred lines, 4 testers and 76 topcrosses evaluated in 2006.

Genotype		Sd 63	Gz 639	L-20	L-21	Mean
			Protein%			
	Per se	5.60	5.62	5.71	6.43	5.84
L-1	9.97	8.95	10.09	12.47	8.05	9.89
L-2	7.65	10.99	8.39	7.14	8.05	8.64
L-3	6.23	5.55	6.91	6.57	8.05	6.77
L-4	10.16	9.07	14.85	11.33	9.86	11.28
L-5	10.28	9.29	7.59	10.65	9.97	9.38
L-6	10.21	11.33	15.98	9.63	7.93	11.22
L-7	9.91	7.48	13.60	9.97	7.82	9.72
L-8	8.55	6.91	13.37	9.63	10.99	10.23
L-9	10.42	7.37	5.89	7.03	6.12	6.60
L-10	10.50	6.01	6.23	7.14	7.14	6.63
L-11	6.14	5.89	6.46	6.91	7.37	6.66
L-12	6.22	8.05	7.14	6.35	8.39	7.48
L-13	6.22	6.35	8.50	8.27	6.23	7.34
L-14	10.13	7.93	6.46	7.48	6.46	7.08
L-15	6.28	6.46	6.46	7.48	6.69	6.77
L-16	8.23	7.93	7.37	7.59	7.93	7.71
L-17	10.21	7.71	8.39	7.37	7.48	7.74
L-18	6.37	8.27	9.97	7.37	12.47	9.52
L-19	8.46	5.78	6.80	7.37	5.78	6.43
Mean	8.53	7.75	8.97	8.30	8.04	8.27
LSD $_{0.05}$	Lines = 0.349,	Testers = 0.286,	Lines *vs* Testers = 0.328,		Crosses = 0.511	
			Oil%			
	Per se	8.34	7.74	8.60	3.55	7.06
L-1	8.21	4.76	5.78	7.59	4.42	5.64
L-2	8.79	4.99	5.67	4.76	4.87	5.07
L-3	4.11	4.19	3.85	4.76	5.10	4.48
L-4	5.83	5.78	6.91	6.57	5.55	6.20
L-5	7.46	6.01	5.10	5.89	6.01	5.75
L-6	7.37	6.01	8.05	6.01	5.78	6.46
L-7	4.30	5.21	6.91	5.67	6.01	5.95
L-8	3.16	4.53	5.78	6.23	6.23	5.69
L-9	7.22	4.76	6.57	5.44	5.21	5.50
L-10	7.62	5.10	5.44	5.33	6.80	5.67
L-11	7.12	3.97	5.89	4.76	4.65	4.82
L-12	4.68	4.87	5.33	5.44	7.25	5.72
L-13	3.55	5.89	6.12	5.33	4.99	5.58
L-14	4.29	4.76	4.65	4.87	6.69	5.24
L-15	3.37	4.99	5.21	4.53	5.55	5.07
L-16	3.68	5.10	4.76	5.21	4.31	4.85
L-17	4.40	4.65	5.55	5.67	3.85	4.93
L-18	8.95	5.55	4.08	6.35	7.14	5.78
L-19	7.24	5.10	5.89	5.78	5.10	5.47
Mean	5.86	5.06	5.66	5.59	5.55	5.47
LSD $_{0.05}$	Lines = 0.223,	Testers = 0.951,	Lines *vs* Testers = 0.370,		Crosses = 0.365	

(7.14 %), L-7 × Gz 639 (6.91 %) and L-4 × Gz 639(6.91%). On the contrary, the lowest mean oil content was shown by L-3 × Gz 639 (3.85 %), L-17 × L-21 (3.85 %) and L-11 × Sd 63 (3.97 %). Across the four testers, crosses with L-6 followed by L-4 and L-7 showed the highest average oil content as compared with other inbreds. Moreover the crosses with the tester Gz 639 showed the highest average oil content as compared with other testers.

The existence of genotypic differences and the prospect of selection for maize oil content was reported in several studies (Misevic and Alexander 1989, Dudley and Lambert 1992 and Song *et al* 1999).

It is interesting to report that testcrosses of the inbred lines L-4, L-6, L-18 and the tester Gz 639 followed by L-20 showed the highest means for both protein and oil contents.

Heterosis for grain protein and oil contents

In general, average heterosis relative to the higher parent (heterobeltiosis) across all studied 76 testcrosses (Table 4) was in the negative direction (-0.47 % for protein and -24.5 % for oil content). This indicates average dominance of the alleles for both low oil and low protein contents. This negative average heterosis was previously confirmed by Mittelmann e*t al* (2006) for oil content and Oliveira *et al* (2007) for protein content. However, some hybrid combinations with positive heterosis relative to the higher parent were observed, especially for protein content.

Table 4. Heterosis (%) relative to the higher parent for grain protein and oil content of 76 topcrosses evaluated in 2006.

	Protein%				Oil%			
	Sd 63	Gz 639	L-20	L-21	Sd 63	Gz 639	L-20	L-21
L-1	-10.20**	1.17	25.04**	-19.29**	-42.95**	-29.60**	-11.71*	-46.16**
L-2	43.64**	9.58	-6.71	5.14	-43.23**	-35.49**	-45.85**	-44.60**
L-3	-10.81**	11.03*	5.57	25.14**	-49.78**	-50.28**	-44.63**	24.09**
L-4	-10.76**	46.13**	11.55*	-2.95	-30.72**	-10.76*	-23.58**	-4.80
L-5	-9.63	-26.16**	3.60	-3.01	-27.97**	-34.14**	-31.49**	-19.44**
L-6	11.00*	56.51**	-5.65	-22.30**	-27.97**	3.96	-30.09**	-21.57**
L-7	-24.52**	37.24**	0.64	-21.09**	-37.55**	-10.76*	-34.04**	39.77**
L-8	-19.11**	56.47**	12.71*	28.63**	-45.71**	-25.36**	-27.53**	75.49**
L-9	-29.28**	-43.42**	-32.54**	-41.25**	-42.95**	-15.15*	-36.72**	-27.81**
L-10	-42.79**	-40.63**	-32.00**	-32.00**	-38.87**	-29.75**	-38.00**	-10.76*
L-11	-4.07	5.15	12.53*	14.57*	-52.42**	-23.93**	-44.63**	-34.72**
L-12	29.30**	14.73*	1.98	30.43**	-41.63**	-31.17**	-36.72**	54.91**
L-13	1.98	36.58**	32.94**	-3.06	-29.40**	-20.96**	-38.00**	40.56**
L-14	-21.71**	-36.25**	-26.18**	-36.25**	-42.95**	-39.95**	-43.35**	55.82**
L-15	2.87	2.87	19.11**	3.99	-40.19**	-32.72**	-47.31**	56.34**
L-16	-3.60	-10.49*	-7.74	-3.60	-38.87**	-38.53**	-39.40**	17.12*
L-17	-24.52**	-17.86*	-27.85**	-26.74**	-44.27**	-28.33**	-34.04**	-12.43*
L-18	29.95**	56.65**	15.71*	93.88**	-37.97**	-54.40**	-29.02**	-20.19**
L-19	-31.68**	-19.62**	-12.92*	-31.68**	-38.87**	-23.93**	-32.76**	-29.56**
Average	-0.47				-24.50			

**** indicate significance at 0.01 probability level.**

Out of 76 testcrosses, percentages of heterobeltiosis were significant and positive (favorable) in 24 testcrosses for maize protein content and eight testcrosses for maize oil content (Table 4). The highest significant positive heterobeltiosis percentage for protein content was obtained from the testcross L-18 × L-21 (93.88%) followed by L-18 × Gz 639 (56.65 %), L-6 × Gz 639 (56.51 %), L-8 × Gz 639 (56.47 %), L-4 × Gz 639 (46.13 %) and L-2 × Sd 63 (43.64 %); most of them included Gz 639 as a common parent.

For grain oil content, the highest significant positive heterobeltiosis estimate was exhibited by the testcross L8 × L-21 (75.49 %) followed by L-15 × L-21 (56.34 %), L-14 × L-21 (55.82 %), L-12 × L-21 (54.92%) and L-13 × L-21 (40.56 %); all included L-21 as a common parent.

These results indicated the possibility of obtaining useful heterosis in a large number of F_1 testcrosses for protein content and a few number of F_1 testcrosses for oil content of the maize grain. The previous results demonstrate the existence of bidirectional dominance of loci with dominance for reduction of oil and protein content (Oliveira *et al* 2007). In a program targeting hybrids, the strategy would be to select combinations with positive heterosis. This situation would indicate parent pairs that are divergent precisely in the loci with dominance for high oil and/or protein content. It is worthnoting that the best hybrids for their *per se* performance and specific heterosis were L-18 × L-21, L-8 × Gz 639 and L-4 × Gz 639 for protein content and L-12 × L-21 for oil content. These crosses could therefore be considered promising for the respective traits (protein or oil content) improvement.

Combining ability of QPM and high-oil inbreds and their testcrosses

Combining ability variance

Partitioning of mean squares due to the tested F_1 crosses into their components, *i.e.* lines, testers and line × tester interaction for protein and oil content is presented in Table (5). Mean squares due to males and females in their respective crosses were highly significant for both studied grain quality characters. This indicates that estimates of GCA effects were significant ($P \leq 0.01$) for both QPM and high-oil inbreds and testers for both traits.

Variation due to line × tester interaction was also highly significant for both studied traits. This suggests that SCA effects were also significant at the 0.01 probability level for both traits (protein and oil contents).

Contribution of the variation due to lines, testers and line × tester crosses to the total variation for grain protein and oil contents is presented in Table (6). Contribution of the variation due to lines × testers interaction (SCA variance) to the total variation was greater than 50% (*i.e.* greater than GCA variance) for oil content, suggesting that SCA variance was more important than GCA variance in the inheritance of this character.

Table 5. Analysis of variance for maize grain protein and oil content of lines × testers in 2006.

S.O.V.	d.f.	Mean squares	
		Protein%	Oil%
Lines (L)	18	32.25**	3.31**
Testers (T)	3	16.86**	6.22**
L × T	54	8.04**	1.96**
Error	196	0.196	0.099

** indicate significance at 0.01 probability level.

For grain protein content, line × tester interaction variance contributed less than 50% to the total variance, suggesting that SCA variance was less important than GCA variance in the inheritance of this character.

Contribution of variation due to QPM and high-oil inbred lines to the total variation was much greater than the contribution of the variation due to testers for both studied grain quality traits, indicating that most of the total GCA variance was due to QPM and high-oil inbred lines GCA variance for grain protein and oil content.

Table 6. Proportional contribution (%) of lines, testers and line × tester interaction to the total variation for protein and oil content of maize testcrosses in 2006.

S.O.V.	d.f.	Contribution (%) to total variation	
		Protein%	Oil%
Lines (L)	18	54.50	32.39
Testers (T)	3	4.75	10.15
L × T	54	40.75	57.46

General combining ability effects

Estimates of GCA effects of studied parental lines and testers for grain protein and oil content traits are presented in Table (7). Significant and positive GCA effects were considered favorable for both traits. Out of 19 lines, eight and nine lines showed significant and positive GCA effects for protein and oil content, respectively. The highest significant and positive GCA effects were given by the inbred lines L-4, L-6, L-8, L-1, L-7, L-18 and L-5 in a descending order and the inbred tester Gz 639, indicating that these parents are good general combiners for enhancement of grain protein content of their hybrid combinations.

For grain oil content, the highest significant and positive GCA effects were exhibited by the inbred lines L-6, L-4, L-8, L-9 and L-18 and the testers L-20 and Gz 639, suggesting that these parents are good general combiners for oil content trait.

Table 7. General combining ability effects of studied parental lines and testers for maize grain protein and oil contents in 2006.

Genotype	% Protein content	% Oil content
Lines		
L-1	1.588**	0.211**
L-2	0.504**	-0.540**
L-3	-1.496**	-1.123**
L-4	3.004**	0.711**
L-5	1.088**	0.044
L-6	2.838**	0.877**
L-7	1.421**	0.461**
L-8	1.921**	0.461**
L-9	-1.912**	0.211**
L-10	-1.579**	0.294**
L-11	-1.662**	-0.706**
L-12	-0.662**	0.377**
L-13	-0.746**	-0.040
L-14	-1.162**	-0.290**
L-15	-1.412**	-0.290**
L-16	-0.662**	-0.456**
L-17	-0.496**	-0.540**
L-18	1.338**	0.461**
L-19	-1.912**	-0.123
SE g_i-g_i	0.181	0.129
Testers		
Sd 63	-0.557**	-0.491**
Gz 639	0.724**	0.175**
L-20	0.057	0.211**
L-21	-0.224**	0.105**
SE g_i-g_i	0.083	0.059

**** indicate significance at 0.01 probability level.**

It is interesting to note that the lines L-4, L-6, L-7, L-8 and L-18 and the inbred tester Gz 639 are good general combiners for both protein and oil contents of maize grain. The inbreds L-4 and L-6 were among the best ones in *per se* performance for protein and the inbred L-18 was the best *per se* performing for mean oil content.

Miranda and Chaves (1991) concluded that general combining ability can be a good parameter for the selection of the parents to form a good composite. Inbreds showing significant positive GCA effects for protein and/or oil content in this study would be ideal for initiating a high-protein and/or high-oil composites.

Specific combining ability effects

Estimates of SCA effects of 76 line × tester crosses for grain protein and oil content are presented in Table (8). Significant and positive SCA effects for both studied traits were considered favorable. Out of 76

Table 8. Specific combining ability effects of 76 line × tester crosses for maize grain protein and oil contents in 2006.

	Protein%				Oil%			
	Sd 63	**Gz 639**	**L-20**	**L-21**	**Sd 63**	**Gz 639**	**L-20**	**L-21**
L-1	-0.69**	-0.31	2.36**	-1.36**	0.51**	-0.18	1.79**	-1.11**
L-2	3.06**	-1.22**	-1.56**	-0.28	0.24	0.58**	-0.46**	-0.36**
L-3	-0.61**	-0.89**	-0.22	1.72**	0.16	-0.84**	0.12	0.56**
L-4	-1.44**	2.94**	-0.06	-1.44**	-0.01	0.33**	0.29**	-0.61**
L-5	0.47**	-2.47**	0.86**	1.14**	0.66**	-0.68**	-0.04	0.06
L-6	0.72**	4.11**	-1.56**	-3.28**	-0.18	1.82**	-0.88**	-0.77**
L-7	-1.53**	2.86**	0.53**	-1.86**	0.24	0.58**	-0.46**	-0.36**
L-8	-3.03**	2.36**	-0.64**	1.31**	-0.76**	-0.43**	0.54**	0.65**
L-9	1.81**	-1.47**	0.19	-0.53**	-0.51**	0.83**	-0.21	-0.11
L-10	-0.53**	-0.81**	0.53**	0.81**	-0.26**	-0.26**	-0.29**	0.81**
L-11	-0.44**	-0.72**	-0.06	1.22**	-0.26**	0.74**	-0.29**	-0.19
L-12	1.22**	-1.06**	-1.06**	0.89**	-0.68**	-0.34**	-0.38**	1.40**
L-13	-0.36**	0.36**	0.69**	-0.69**	0.74**	0.08	0.04	-0.86**
L-14	1.06**	-1.22**	0.44**	-0.28	-0.01	-0.68**	-0.71**	1.40**
L-15	0.31	-0.97**	0.69**	-0.03	-0.01	0.33**	-0.71**	0.40**
L-16	0.56**	-0.72**	-0.06	0.22	0.49**	-0.51**	0.46**	-0.44**
L-17	0.39**	-0.22	-0.22	0.06	0.24	0.58**	0.54**	-1.36**
L-18	-0.78**	-0.06	-2.06**	2.89**	0.24	-2.09**	0.54**	1.31**
L-19	-0.19	-0.47**	1.19**	-0.53**	0.16	0.16	0.12	-0.44**
SE $S_{ij}-S_{ik}$	0.256				0.182			
SE $S_{ij}-S_{kl}$	0.362				0.257			

** **indicate significance at 0.01 probability level.**

testcrosses, 28 and 32 crosses showed significant positive (favorable) and significant negative (unfavorable) SCA effects, respectively for grain protein content. However, for grain oil content, 25 and 30 testcrosses exhibited significant positive and significant negative SCA effects, respectively.

The best cross, with significant positive SCA effects for grain protein content was L-6 × Gz 639 followed by L-2 × Sd 63, L-4 × Gz 639, L-19 × L-21, L-7 × Gz 639, L-8 × Gz 639 and L-1 × L-20.

For grain oil content, the best cross with significant positive SCA effects was L-6 × Gz 639 followed by L-1 × L-20, L-12 × L-21, L-14 × L-21 and L-18 × L-21.

It is interesting to report that the cross L-6 × Gz 639 showed the most favorable SCA effects for both grain protein and oil contents. Moreover, the crosses L-1 × L-20 and L-18 × L-21 exhibited also high positive significant SCA effects for both traits.

It is worthy to note that the testcrosses L-4 × Gz 639, L-8 × Gz 639 and L-18 × L-21 were superior in mean performance, heterobeltiosis and SCA effects and the testcross L-7 × Gz 639 was superior in mean performance and SCA effects for grain protein content. The cross L-12 × L-21 was superior in the three parameters for grain oil content and the crosses L-6 × Gz 639, L-1 × L-20 and L-18 × L-21 were superior in two parameters, *i.e.* mean performance and SCA effects for the same trait. It should be noted that the testcross L-18 × L-21 was superior for both traits (protein and oil contents) in most studied parameters. These crosses could be recommended to maize breeding programs for improving both quality traits.

Variance components, heritability and selection gain

Estimates of the components of variance due to GCA among lines ($\delta^2_{GCA(L)}$) and testers ($\delta^2_{GCA(t)}$) and SCA ($\delta^2_{SCA(l\times t)}$), additive ($\delta^2_A$) and dominance ($\delta^2_D$), degree of dominance (''a''), narrow-sense heritability (h^2_n) and genetic advance (GA %) from selection for grain protein and oil contents are presented in Table (9). Data indicated that all estimates of GCA and SCA variances were positive and significant, suggesting the importance of both additive and non-additive genetic effects for the inheritance of grain protein and oil contents. Our results are in concordance with those reported by Sreeramulu and Bauman (1970), Dudley (1977) and Berke and Rocheford (1995).

Table 9. Estimates of variance due to GCA(δ^2_{GCA}), SCA(δ^2_{SCA}), additive (δ^2_A), dominance (δ^2_D), degree of dominance "a", broad- (h^2_b) and narrow- (h^2_n) sense heritability and expected genetic advance (GA) for maize grain protein and oil contents.

Variance component	% Protein content	% Oil content
$\delta^2_{GCA\ (l)}$	2.018**	0.226**
$\delta^2_{GCA\ (t)}$	0.210**	0.204**
$\delta^2_{GCA\ (Aver.)}$	0.524**	0.104**
$\delta^2_{SCA\ (l\times t)}$	2.615**	0.619**
δ^2_A	1.048	0.208
δ^2_D	5.230	1.238
δ^2_A / δ^2_D	0.200	0.168
''a''	3.159	3.450
h^2_b (%)	96.97	93.59
h^2_n (%)	16.19	13.46
GA%	21.82	14.68

** indicate significance at 0.01 probability level.

Variance component estimates of the testcrosses were appreciably larger for dominance (δ^2_D) than for additive (δ^2_A), suggesting that dominance effects are the major components controlling both studied grain quality traits. This was obvious from the ratio δ^2_A/δ^2_D which was less than the unity for both traits. This indicates that these quality traits could be improved using the heterosis breeding procedure. Our results disagree with those of Bhatnagar *et al* (2004) who reported that for maize grain quality traits GCA effects across environments were more important than SCA effects. This conflict in results could be attributed to the genetic background of the germplasm used in the two studies.

Degree of dominance (a) was overdominance ("a" was exceeding the unity) for both studied traits confirming previous results of Presolska and Kamara (1995) and Angelov and Lalov (1995) for protein content and Mangolin *et al* (2004) for oil content. Heritability in the broad-sense (h^2_b) was very high for both traits (>93%). By contrast narrow-sense heritability (h^2_n) was very low (16.19% for grain protein and 13.46% for grain oil content). Such low h^2_n estimates are mainly due to the small additive genetic variance in comparison to dominance variance. Expected genetic advance from selection (based on 10% selection intensity) was 21.82% for protein content and 14.68% for oil content. This indicates that selection could also be considered an effective breeding program for improving both studied traits, where few cycles of selection practiced in the proposed composite populations resulting from the best general combiners of this study are predicted to increase grain content of both protein and oil. The actual gain achieved from previous selection programs (Dudley 1977, Misevic and Alexander 1989, Dudley and Lambert 1992 and 2004 and Song *et al* 1999 for high oil content) confirmed the reasonably high predicted selection gain calculated in the present study.

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القدرات الإئتلافية لسلالات ذرة شامية مستنبطة حديثاً ذات بروتين عالى الجودة وزيت عالي وهجنها الإختبارية

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إن إستنباط ذرة شامية ذات بروتين عالى الجودة وزيت عالي من الممكن أن يزيد القيمة الغذائية لمنتجات الذرة المستخدمة فى الغذاء والعلف. إن المعلومات عن كيفية الإئتلاف والأداء فى الهجن لسلالات الذرة ذات البروتين عالى الجودة من الأصول المختلفة سوف تسهل اختيار الآباء واستراتيجيات التربية لتطوير الهجن. كانت أهداف هذه الدراسة هى تقدير القدرات الإئتلافية العامة والخاصة لمحتوى الحبوب من البروتين والزيت للسلالات ذات البروتين عالى الجودة وتحديد أفضل التوليفات الهجينية فى هجن هذه السلالات مع مختبرات مختلفة. تم فى موسم ٢٠٠٥ تهجين تسعة عشر سلالة مستنبطة حديثا من عشائر وPools ذات بروتين عالى الجودة مستوردة من الـCIMMYT بالمكسيك ومن تايلاند مع أربعة مختبرات (أثنين منها سلالات تربية داخلية تجارية عادية البروتين Sd 36, Gz 639 والاثنين الآخرين سلالتين ذات بروتين عالي الجودة L-20،L-21) ونتج عن ذلك ٧٦ هجين اختباري. تم فى موسم ٢٠٠٦ تقييم الآباء والهجن الإختبارية فى الحقل بمحطة البحوث التابعة لمركز البحوث الزراعية بالجيزة فى تصميم شبكى بثلاثة مكررات. أوضحت النتائج وجود فروق عالية المعنوية بين الآباء وبين الهجن الإختبارية بالنسبة لمحتوى كل من بروتين وزيت الحبوب. تراوح متوسط محتوى بروتين الحبة من ٦,١٤ إلى ١٠,٥% بالنسبة للآباء ومن ٥,٥٥ إلى ١٥,٩٨ بالنسبة للهجن الإختبارية. وتراوح متوسط محتوى زيت الحبة من ٣,١٦ إلى ٨,٩٥% بالنسبة للآباء ومن ٤,١٩ إلى ٨,٠٥ للهجن. بالنسبة لمحتوى البروتين كانت أحسن الآباء هى L-18، L-9، L-5، L-6، L-17، L-4 من حيث متوسط الأداء وL-4، L-6، L-8، L-1، L-7، L-18، L-8 من حيث تأثيرات القدرة العامة على الإئتلاف وكانت أحسن الهجن هىL-4 × Gz 639، L-7 × Gz 639، L-8 ×Gz 639، L-21 × L-18 من حيث متوسط الأداء وتأثيرات القدرة الخاصة على الإئتلاف وقوة الهجين للأب الأعلى والهجين L-6 × Gz 639، L-2 ×Sd 63 من حيث قوة الهجين للأب الأعلى وتأثيرات القدرة الخاصة على الإئتلاف. بالنسبة لمحتوى الزيت كانت أحسن الآباء هى L-18، L-2، L-1، L-9 من حيث متوسط الأداء و L-6، L-4، L-8، L-9، L-18 من حيث تأثيرات القدرة العامة على الإئتلاف وكانت أحسن الهجن هى L-21 × 12 من حيث المعايير الثلاثة وL-6 × Gz639، L-20× L-1، L-21 × L-18 من حيث متوسط الأداء وتأثيرات القدرة الخاصة على الإئتلاف. كانت تقديرات تباينات القدرة العامة والقدرة الخاصة على الإئتلاف معنوية وموجبة لكلا الصفتين تحت الدراسة وكان تباين السيادة أكبر فى المقدار من التباين المضيف وكانت درجة السيادة هى السيادة الفائقة لكلا الصفتين. وكانت كفاءة التوريث بالمعنى الخاص ١٦,١٩% لمحتوى البروتين و ١٣,٤٦% لمحتوى الزيت. إن السلالات ذات البروتين عالى الجودة وعالية الزيت التى أظهرت تأثيرات مضيفة وهجنها التى أظهرت تأثيرات غيرمضيفة يمكن إدخالها في المادة الوراثية المحلية بعمل هجن أو مركبات Composites وهذه إما أن تستخدم مباشرة أو تكون أساس يبدأ فيها برنامج إنتخاب دوري لزيادة البروتين عالي الجودة وزيادة الزيت والعشائر المحسنة يمكن إستخدامها في عزل السلالات وإستنباط الهجن عالية الزيت وذات بروتين عالي الجودة.

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