Evaluation of Some Maize Genotypes for Some Yield Components, High Protein and Amino Acids Content

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ABSTRACT: The current filed experiments were conducted at Nubaria Region, El- Behira Governorate, Egypt during 2018 and 2019 seasons, to evaluate some maize genotypes for high protein and amino acids content. In this respect, in the first season, six maize single hybrids were planted in two group to granted flowering matching. The crossing had been done to get fifteen hybrids by half diallel design with enough grain for two years. Then, in the next season, the obtained hybrids grains were planted in blocks to determine the heterosis percentage (H %) based on mid and better parents for yield, yield components, protein and amino acids content. The results revealed that the 6 genotypes and 15 hybrid differed significantly in yield, its components, protein % and amino acids (%), where SC3062 X SC3737, SC444 X SC3737 recorded the highest values followed by (SC3062 X SC3737) and (SC3062 X SC444) then (SC2066 X SC3737) and (SC2066 X SC444). The results showed positive values of heterosis percentage between all the obtained hybrids that refer to the successful of hybridization. Amino acids values also showed significant variations between the maize hybrids.

Key words: maize hybrids, heterosis, yield components, protein, amino acids.

INTRODUCTION

Maize (*Zea mays* L.) is the third most important staple food crop in terms of area and production after wheat and rice in Egypt. Worldwide, it is one of the important cereal crops after wheat and rice**.** Maize grain is used for human consumption, animal and poultry feeding and industrial purposes. *Zea mays* L. belonged to Family *Poaceae*; Genus *Zea.* Maize is one of the five species in Genus *Zea*, the others being *Z. diploperennis* HH, *Z. luxurians, Z. nicaraguensis* HH, and *Z. perennis* (USDA, 2005). The species of *Zea* have chromosome number of 2n=20; except *Z. perennis* with 2n=40 (Ellneskog-Staam *et al*., 2007).

Based on the field evaluation, although the local check out performed all the test materials, genotypes such as CKH-08005, CKH-08016, CKH-08020, CKH-08023, CKH-08024, CKH-08031, CKH-08038 and CKH-08040 had better performance than the others in terms of grain yield. The lower yield of the tested materials was due to the fact that the genotypes were early maturing and are primarily developed for moisture stress areas and are not expected to outperform the local check which is a late maturing hybrid (Aman *et al.,* 2016).

The genetic system that confers high levels of lysine and tryptophan in maize endosperm protein is the recessive allele of the Opaque-2 gene mapped to short arm of chromosome 7 of maize (Mertz *et al.*, 1964). The improved protein quality of maize mutants is due to repression of zein synthesis thus increase in non-zein fraction yielding increased lysine and tryptophan (Sofi *et al.*, 2009).

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Hence, though this mutant aroused tremendous interest and enthusiasm for its possible use in developing maize with superior protein quality, the pleiotropic effects of such mutations began to be recognized. The trait was found to be closely associated with several undesirable ones. The Opaque-2 maize kernels were dull and chalky, had 15-20% less grain weight and were more susceptible to several diseases and insects (Ignjatovic *et al.,* 2008) leading to the loss of interest towards it among scientists. Fortunate enough, few international researchers had continued their systematic research activities on refining the original Opaque-2 variety with the aim of maintaining its nutritional quality while making it competitive with conventional varieties of improved maize. And over time, breeders in the International Maize and Wheat Improvement Center (CIMMYT) found modifier genes that restored the desirable hard endosperm phenotype in materials containing the recessive Opaque-2 mutation. These agronomically acceptable and nutritionally enhanced materials later came to be known as quality protein maize (QPM) (Vasal *et al*., 1984; Bjarnason and Vasal, 1992). Quality protein maize (QPM) contains nearly twice as much usable protein as other maize grown in the tropics and yields 10% more grain than traditional varieties of maize (Vasal, 2000). Breeding for high quality protein maize needs yet another, distinctive genetic system included of minor modifying loci and these modifiers/enhancers confer higher lysine/tryptophan contents in corn (Vivek *et al*., 2008). The genotypes like Obatanpa followed by S99TLWQ-B and S01SIYQ gave the highest grain yield under coordinated varietal trials and genotypes namely S99TLYQ-B followed by S01SIWQ-3 and Poshilo Makai-1 produced the highest grain yield (Shrestha, 2016).

Many previous publications defined the heterosis as the superiority of F_1 hybrids over their inbred parents; is expressed by increased biomass, growth rate, and fertility, resistance to diseases and insects as well as tolerance to abiotic factors; as advantageous quantitative and qualitative traits of off springs over their parents; heterosis is the phenomenon in which progeny of crosses between inbred lines or pure bred populations are better than the average of the two populations manifested that heterosis depended on the genetic divergence of two parental varieties; also, genetic divergence of the parents was inferred from the heterotic patterns manifested in a series of cross combination (Hallauer and Miranda, 1988, Li *et al.*, 2001 and Zsubori *et al.*, 2002). Sharief *et al*. (2009) reported that heterosis, or hybrid vigor, is the better performance of a hybrid relative to the parents and is the outcome of the genetic and phenotypic variation. Heterosis can be divided into two broad categories, true heterosis and pseudoheterosis. They showed that, in case of true heterosis, there is an increase in general vigor, yield and adaptation. In instance of pseudoheterosis, the F_1 hybrid exhibits rise in growth only. It states to the superiority of F_1 over the standard commercial check variety. So, it is also called economic heterosis or superiority over checks. They showed that general combining ability refers to the average performance of the genotype in a series of hybrid combinations and is a measure of additive gene action whereas; specific combining ability is the performance of a parent in a specific cross in relation to general combining ability. Birchler *et al.* (2010) reported

that heterosis refers to the phenomenon that progeny of diverse varieties of a species or crosses between species exhibit greater biomass, speed of development, and fertility than both parents. They reviewed that the various models have been posited to explain heterosis, including dominance, overdominance, and pseudo-overdominance. In this perspective, they consider that it might be useful to the field to abandon these terms that by their nature constrain data interpretation and instead attempt a progression to a quantitative genetic framework involving interactions in hierarchical networks. Izhar and Chakraborty (2013) explained that heterosis and combining ability are prerequisite for formulating hybrid breeding programmes and for developing a good economically viable hybrid maize variety. Combining ability analysis is useful to assess the potential inbred lines and to identify the nature of gene action involved in various quantitative characters. Shrestha *et al*. (2018) reported that determination of heterosis in maize hybrids is necessary for their commercial exploitation. Many authors stated that the F_1 hybrids showed range of heterosis with negative and positive values which indicated the potential for developing hybrids superior to their better parent for earliness, plant height, grain yield and 1000-gram weight (Ali, 2000, Prabhakar, 2001; Al-Naggar *et al*., 2002; Abd-El-Halim, 2003; Abd-El-Mottaleb, 2004; Hovny *et al*., 2005; Abo-Zaid, 2007; Mahmoud 2007; Abd-El-Mottaleb, 2009; Mahoumed and Ahmed, 2010). Keeping in view the importance of high yielding and quality of maize hybrids, the study was conducted to find out the high yielding, protein and amino acid of maize hybrid.

MATERIALS AND METHODS

Filed experiments were conducted at a Farm in Nubaria Region, El- Beheira Governorate, Egypt during 2018 and 2019 seasons, to evaluate some maize genotypes for high grain yield, protein and amino acids content. The preceding crop was Egyptian clover (berseem) in the two seasons. Soil texture was sandy clay loam. The grains of the maize hybrids were obtained from Maize Research, Section Agriculture Research Center, Ministry of Agriculture. The grains were sown on May 15th and 10th of 2018 and 2019 seasons, respectively.

In the first season, six hybrids (SC 2066= (SC 66), SC 3062= (SC 3062), SC 2088 = (SC 2088), SC 2055 = (SC 2055), SC 444 = (SC 444) and SC 3737 = (SC 3737) were planted into two group to granted flowering matching. The crosses had been done to get 15 hybrids by half diallel program with enough grain for two years according to the equation n(n-1) /2 with enough seed for two years (Griffing, 1956). In the second season, the obtained 15 hybrids + six parents were planted in blocks to determine the heterosis %, yield, yield components, protein and amino acids content in grains of maize hybrids. Each plot included 5 ridges each 3 m in length and 0.70 m in width with the distance between hills (20 cm). All agricultural practice according to the recommendation of Ministry of Agriculture and Land Reclamation were carried out.

Grain yield and yield components as number of grains/row, number of grains/ear, ear weight, 100- grain weight (g), grain yield (t/ha), straw yield (t/ha) were measurements as an average of 2 ridges from mid of each plot. Protein percentage was determined by estimating the total nitrogen in the grains multiplied by 6.25 to obtain the percentage according of grains protein percentage to AOAC (1990). Free amino acids were analyzed by using Beckman amino hydrolysis (4h) of maize parents and their hybrids samples, according to the method described by Newkirk *et al*. (2003).

The formula used for estimating heterosis was as follows
Hmp = ($^{F1-MP}/_{MP}$) x 100,
Hmp = Heterosis relative mid parental value,
F1 = Mean hybrid performance, and MP = Mid parental value
Heterosis was calculated at the superiority of hybrid from the better parent as follows:
Hbp = ($^{F1-BP}/_{BP}$) x 100,
Hbp: Heterosis relative to better parent,
BP = Average performance of better parent.

Data obtained was exposed to the proper method of statistical analysis of variance as described by Gomez and Gomez (1984). The treatment means were compared using the least significant differences test (L.S.D.) at 5% level of probability by using the RCBD model as obtained by CoStat 6.311 (2005) statistical program.

RESULTS AND DISCUSSIONS

A- Yield, yield components and protein (%):
Table (1) showed the analysis of variances of 21 hybrids during 2019 for yield and its component**.** There were highly significant differences between the studied genotypes for yield and its component. Also, genotypes showed the wide diversity between the parental materials used under this investigation. Results also showed that mean square due to parents were significant for the all studied traits.

Table (1). Mean square of twenty-one corn genotypes for yield and yield components characters during season 2019

SOV	df	Number of grains/row	Number of grains/ear	Ear weight (g)	100- grain weight (g)	Grain yield (t/ha)	Straw yield (t/ha)	Protein (%)
Rep	2	3.86ns	1306.35ns	78.81ns	8.75ns	0.79ns	1.53ns	0.17ns
Geno	20	125.11 **	26756.20 **	6806.40 **	142.30 **	4.30 **	3.98 **	2.41 **
Error	40	3.77	1467.97	501.25	19.72	0.29	0.28	0.39

ns: not significant difference ,** highly significant differences at 0.01 level of probability were significantly.

The presented results in Table (2) revealed that the studied genotypes differed in their mean performance in yield and its components during 2019 season. The grain yield mean performance of six parental genotypes of maize is shown in Table (2), the crosses of (SC 3062 x SC 3737), (SC 444 x SC 3737) and (SC 3062 x SC 444) recorded the highest values followed by (SC 2066 X SC 444) and (SC 2066 X SC 3737) for number of grains/row.

For the number of grains/ear (SC 3062 x SC 3737), (SC 3062 x SC 444), (SC2066 x SC444), (SC 444 x SC 3737) and (SC 2066 x SC 3737) crosses gave the highest values followed by the cross (SC 3062 x SC 444) and SC 2055 X SC 3737) (SC 2066 x SC 3737), (SC 2066 x SC444), (SC 2066 x SC 444) and (SC 3062 x SC 444) recorded the highest values of ear weight. The highest mean values of 100- grain weight (g) were obtained by (SC 444 x SC 3737), (SC 3062 x SC444), and (SC 3062 x SC 3737).

For grain yield, (SC 2066 x SC 3737) and (SC 3062 x SC 444) followed by (SC 444 x SC 3737), (SC 2088 x SC 444), and (SC 2088 x SC 3737) which recorded the highest mean values of this trait in comparison with the other genotypes.

The crosses (SC 444 x SC 3737), (SC 3062 x SC 444), (SC 2066 x SC 3737) and (SC 3062 x SC 2055) gave the highest mean values of straw yield in evaluation season 2019 as compared with the others genotypes and parents which recorded the lowest mean values of these traits.

Regarding the protein (%), it can be noticed from Table (2) that the crosses (SC 2066 x SC 3737), (SC 3062 x SC 3737), and (SC 444 x SC 3737), (SC 3062 x SC 444) and (SC 3062 x SC 2055) revealed the highest values than the remain crosses.

These results indicated that it could be used these crosses in breeding programs for getting the highest values of yield, its components, and proteins.

These results are in the same trend with those obtained by Upadhyay *et al.* (2009) they reported that out of 11 genotypes evaluated including 7 genotypes and 4 checks maize, the genotype S99 TLWQ-HG-AB produced the highest grain yield and its components followed by Population 45 C10 and Manakamana-3 enhanced check (normal maize). These genotypes were statistically at par with improved check and significantly superior to the Farmers' Local Check variety. However all the tested genotypes were significantly higher grain yield than the Farmers' Local Variety. Also, Prasai *et al.* (2015) indicated similar results.

Table (2). Mean performance of twenty one corn genotypes for yield, its components and protein content during 2019 season.

Genotypes	Number of grains/row	Number of grains/ear	Ear weight (g)	100- grain weight (g)	Grain yield (t/ha)	Straw yield (t/ha)	Protein (%)
SC2066	31.00	372.00	271.00	35.33	4.53	5.67	7.30
SC3062	43.00	503.67	348.33	42.00	4.93	6.57	8.73
SC2088	38.67	392.00	311.20	36.33	4.03	6.20	7.97
SC2055	33.67	430.00	258.00	37.33	4.17	5.67	7.90
SC444	43.00	603.67	320.00	43.67	5.07	6.70	8.92
SC3737	42.33	574.00	339.00	44.00	5.50	6.83	9.00
SC2066×SC3062	46.33	529.00	353.67	45.00	5.47	7.30	10.13
SC2066×SC2088	49.87	526.00	357.00	46.33	5.70	7.55	9.30
SC2066×SC2055	45.67	532.33	389.50	46.33	6.03	7.75	9.67
SC2066×SC444	51.67	680.33	411.67	50.00	6.07	7.82	9.67
SC2066×SC3737	50.10	654.00	422.00	51.00	7.00	8.67	10.87
SC 3062×SC2088	45.67	484.33	383.50	45.00	6.13	7.57	9.10
SC 3062×SC2055	46.00	507.00	393.40	45.67	6.03	8.46	10.17
SC 3062×SC444	53.60	643.67	401.33	58.01	6.70	9.16	10.10
SC 3062×SC3737	55.34	681.33	410.00	56.20	6.20	8.40	10.33
SC2088×SC2055	42.67	491.33	295.17	48.60	5.30	7.98	9.87
SC2088×SC444	45.00	575.00	246.17	47.00	6.23	8.20	9.87
SC2088×SC3737	44.00	484.67	224.50	50.00	6.19	7.98	9.56
SC2055×SC444	44.67	569.00	251.50	44.33	6.08	7.65	9.30
SC2055×SC3737	44.00	596.00	277.17	46.33	5.86	8.16	9.93
SC444×SC3737	55.33	666.00	415.67	58.67	6.60	9.26	10.33
L.S.D at 0.05	3.21	63.23	36.95	7.33	0.88	0.87	1.03

- SC= single cross

B- Heterosis percentage (H %):

Heterosis, or hybrid vigor, is the better performance of a hybrid relative to the parents and is the outcome of the genetic and phenotypic variation. The heterosis values were measured based on mid parents (Hmp) and better parents (Hbp) values.

Data presented in Table (3) showed high positive heterosis relative to mid parent and better parent, and indicated that the cross (SC 2066 x SC 2088)recorded the desirable values of both heterosis type for number of grains/row, number of rows/ear and number of grains/ear. These values were (43.16, 28.97 %), (44.44, 44.44 %) and (37.70 , 34.18 %) for the above mentioned traits, respectively, as well as (SC 2066 x SC 444) crosses for the three traits in addition ear weight (39.31, 28.65 %). On the contrary, the crosses (SC 2088 x SC 3737) gave the lowest values in heterosis relative to both mid – parents and better parent for number of grains/row, number of rows/ear and number of grains/ear.

The fine parents' characters have the main role in their hybrids, this fact was translated in the heterosis percentage which was high in the 100- grain weight (g) for the hybrids SC2066 x SC 2088 (29.30% and 27.52%) for Hmp and Hbp, in respect as presented in Table (3), the lowest values were 9.47% and 1.53% for

both Hmp and Hbp in (SC 2055 x SC 444) cross. The results also indicated that the maize hybrid SC444 x Sc3737 record high values of heterosis for 100 grains weight (g) were 33.84% and 33.33% for Hmp and Hbp. Concerning to grain yield (t/ha) in Table (4), (SC 2066 x SC 3737) and (SC 2066 x SC 2055) maize hybrids detect the high values of heterosis (Hmp) were 38.87% and 38.70%, while (SC 2066 x SC 2055) and (SC 3062 x SC 444) recorded high Hbp (32.24%), (33.09 and 32.24 %) as found in Table (4). A total of 7 maize hybrids from 15 showed more that 30% increase in straw yield (t/ha) for Hmp were SC2066 x SC2055, (SC 2066 x SC 3737), (SC 3062 x SC 2055), (SC 3062 x SC444), (SC 2088 x SC 2055), (SC 2055 x SC 3737) and (SC 444 x SC 3737) by the following values 36.76%, 38.67%, 38.42%, 38.19%, 34.55%, 30.67% and 36.95%, respectively as found in Table (4). While, (SC 2066 x SC 2055), (SC 3062 x SC 444) and (SC 444 x SC 3737) recorded more than 36% of Hbp. According to the data in Table (4) for protein percentage (%) showed that (SC 2066 x SC 3737) gave the high Hmp (33.33 %). From these data the maize parent SC2066 have great effect on the heterosis values of the pervious studied characters.

The current research is fundamental and applicable to enchantment the maize growth and productivity. These finding are agree with Flint-Garcia *et al.* (2009) who reported that the application of heterosis is extremely effective for the genetic improvement of different traits and that the concepts of combining ability are the fundamental tools for enhancing productivity of different crops in the form of F_1 hybrids. In addition, Yao *et al.* (2011) concluded that selection for plant height and its components would be effective in early generation and improvement in these traits will be promising to develop new varieties with desirable traits, most importantly lodging resistance. The results of current experiment detected that heterosis increases yield potential and improves adaptation to biotic and a biotic stress in maize; and these results in a line with Araus *et al.* (2010) who reported that the underlying mechanisms of heterosis and combining ability is an important toots to increases yield potential. The analysis of heterosis for several characters in a small set of testcrosses showed that corn hybrids exhibit both Hmp and Hbp for almost all the traits, these finding are agreeing with Flint Garcia *et al.* (2009), who analyzed a large set of hybrid maize for Hbp. The results indicated that there are increase in all morphological characters and heterosis between hybrids and these results at the same trend of Freeman (1919), who reported that there are an advantages of first generation where the plants of F1 generation had all advantages compared to the average of the parents. Also, to development new genotypes with high production capacity that requires genetic distance between parents who participate in the breeding program (Morgan, 1998). Singh *et al.* (2004) also suggested that the heterosis in relation to the better parent could be useful to optimize heterozygous combination. Other studies showed that positive heterosis is desired in the selection for yield and its components (Lamkey and Edwards, 1999). The results are in harmony with Fetahu *et al.* (2015) who evaluated mode of inheritance level of heterosis and heterobeltiosis for plant height and grain weight from parents into the F1 generation, in order to create and develop desired genotypes for particular purposes, for example bread wheat and

food production. High and significant heterosis for grain yield was accompanied by significant heterosis for one or more yield contributing characters. Amiruzzaman *et al.* (2013), Izhar and Chakraborty (2013), Hiremath *et al.* (2013), Kage *et al.* (2013), Kumar *et al.* (2014) and Ruswandi *et al.* (2015) reported positive and significant economic heterosis in maize for grain yield. Rosa *et al.* (2002) also reported similar findings that in their study there was significant level of heterosis for the yield. Gadad (2003) found significant and positive standard heterosis for test weight in inter-varietal crosses of maize. Gurung (2006) indicated that -22 to 63.1% heterosis for grain yield in maize populations. Also, Sharma *et al.* (2016) reported that there was more than 20% standard heterosis in single cross hybrids of maize.

Table (3). Mid parents and better parent heterosis of maize hybrids for number of grains/row number of rows/ears, number of grains/ears, and ear weight

Characters	Number of grains/row		Number of rows/ear		Number of grains/ear		Ear weight(g)	
Crosses	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
SC2066 x SC3062	25.23	07.75	19.05	04.17	20.82	05.03	21.37	7.89
SC2066 x SC2088	43.16	28.97	44.44	44.44	37.70	34.18	28.42	25.26
SC2066 x SC2055	41.24	35.64	07.69	00.00	32.75	23.80	17.66	14.83
SC2066 x SC444	39.64	20.16	28.57	12.50	39.67	12.87	39.31	28.65
SC2066 x SC3737	36.64	18.35	25.58	8.00	38.27	13.25	38.36	24.48
SC3062 x SC2088	11.84	06.20	03.57	09.38	13.14	00.60	21.11	10.10
SC3062 x SC2055	20.00	06.98	06.67	0.00	08.60	00.66	29.76	12.94
SC3062 x SC444	24.65	24.65	12.50	12.50	16.26	06.63	20.10	15.22
SC3062 x SC3737	29.69	28.68	10.20	8.00	26.45	18.70	19.30	17.70
SC2088 x SC2055	17.97	10.34	17.95	9.52	19.63	14.34	16.02	10.53
SC2088 x SC444	10.20	04.65	14.29	0.00	15.62	04.65	12.51	06.35
SC2088 x SC3737	08.64	03.94	16.28	0.00	00.35	15.56	17.41	08.06
SC2055 x SC444	16.52	03.88	06.67	0.00	10.09	05.74	22.61	10.73
SC2055 x SC3737	15.79	03.94	04.35	4.00	18.73	03.83	25.18	10.23
SC444 x SC3737	29.69	28.68	10.20	8.00	13.11	10.33	26.15	22.62
LSD at 0.05	0.13	0.10	0.17	0.10	0.23	0.23	0.16	0.17

* Hmp: Heterosis relative to mid parents, Hbp: Heterosis relative to better parents.

Table (4). Mid parents and better parent heterosis of maize hybrids for 100-grain weight, grain yield (t/ha), straw yield (t/ha) and protein content.

Characters	100- grain weight (g)		Grain yield (t/ha)		Straw yield (t/ha)		Protein percentage (%)	
Crosses	Hmp	Hbp	Hmp	Hbp	Hmp	Hbp	Hmp	Hbp
SC2066 x SC3062	16.38	07.14	15.49	10.81	19.89	11.68	26.40	16.03
SC2066 x SC2088	29.30	27.52	33.07	25.74	27.25	21.77	21.83	16.74
SC2066 x SC2055	27.52	24.11	38.70	33.09	36.76	36.76	27.19	22.36
SC2066 x SC444	26.58	14.50	26.46	19.80	26.47	16.72	19.18	08.35
SC2066 x Sc3737	28.57	15.91	38.87	26.67	38.67	26.83	33.33	20.74
SC3062 x SC2088	14.89	7.14	36.80	24.32	18.54	16.13	08.98	4.20
SC3062 x SC2055	15.13	08.73	32.60	22.30	38.42	33.53	22.24	00.18
SC3062 x SC444	35.44	32.85	34.00	32.24	38.19	36.82	14.41	13.21
SC3062 x SC3737	30.71	27.73	18.85	12.73	25.37	22.93	16.54	14.81
SC2088 x SC2055	31.95	30.18	29.27	27.20	34.55	31.47	24.37	23.85
SC2088 x SC444	17.50	07.63	36.92	22.96	27.13	22.39	16.85	10.59
SC2088 x SC3737	24.48	13.64	29.86	12.55	22.51	16.83	12.71	6.24
SC2055 x SC444	9.47	01.53	31.70	20.00	23.72	14.18	10.57	04.24
SC2055 x SC3737	13.93	05.30	21.45	06.73	30.67	19.51	17.54	10.36
SC444 x Sc3737	33.84	33.33	24.92	20.00	36.95	36.32	15.33	14.81
LSD at 0.05	0.17	0.03	0.22	0.11	0.09	0.22	0.08	0.05

* Hmp: Heterosis relative to mid parents, Hbp: Heterosis relative to better parents.

C. Amino acids contents:

Results in Table (5) for amino acids content showed high variations between the maize parents and their hybrids, the total content of amino acids in maize parents ranged from (65.44 for SC 2055 to 76.02% for SC 3737). Glutamic acid showed the highest values for all maize parents that ranged from 10.2 % (SC 3062 and SC 444) to 12.40 (SC 2055); Leucine also showed high values ranged from 6.90 % (SC 2055) to 9.15 % (SC 3737); Lysine which consider an important amino acid in maize ranged from 2.0 % (SC 2066) to 4.88 % (SC2088). These data are agree with those obtained by Lošák *et al.* (2010) who studied the effect of nitrogen fertilization on essential and non-essential amino acids on maize grain.

According to the 15 maize crosses the total amino acids ranged from (62.06, 62.74 and 66.85 %) (SC 2066 x SC 2055), (SC 2066 x SC 2088) and (SC 2088 x SC 2055) to 93.49, 96.72 , 96.02 and 98.57 %) recorded to (SC2066 x SC3062, SC3062 x SC444, SC444 x (SC 3737 and SC 2055 x SC 444), respectively as shown in (Table 5). The results in Table (5) showed an increase for the amino acids content in maize hybrids comparing with their parents, for example the amino acid Lycine reached up to ~5 in some maize hybrids such as (SC 2066 x SC 444), (SC 3062 x SC 2088), (SC 3062 x SC 444), (SC 3062 x SC 3737), (SC 2055 x SC 444) and (SC 2055 x SC 3737). These maize hybrids obtained from crossing

between high Lysine parents, so these values indicate the successful of crossing between maize hybrids. Analysis of amino acids is an important tool between maize varieties or hybrids for their important in plant such as Proline is an extensively molecule in the context of plant responses to abiotic stresses (Pavlíková *et al*., 2008). According to Atanasova (2008), an increase in proline and alanine could serve as an indicator of imbalance in nitrogen nutrition. Other study showed the role of alanine (Ala) in plant to response the stress (Pavlík *et al*., 2010). Asparagine is the major compound in the xylem for transport from the roots to the leaves (Lea *et al.,* 2007). The most limiting amino acid in maize grain, with respect to the dietary requirements of monogastric animals, is lysine. Therefore, development of lysine content is a primary objective for improving grain quality. The poor nutritional quality of maize protein is mostly caused by the amino acid composition of endosperm proteins. Maize protein has a lysine content of 2.7%, which is well below the recommendation by FAO for human nutrition, in current results we obtained more than twice of this value as found in Table (5).

Table (5). Constituent amino acids of grain maize parents and their hybrids samples

| Genotypes Maize Parents and crosses | Amino acids (mg/100g) | | | | | | | | | | | | | | | | | | Total |
| | Essential amino acids (E.A.A) | | | | | | | | | | Non - essential amino acids (N.A.A) | | | | | | | | |
	Isoleucine	Leucine	Lysine	Methionine	Cystine	Phenylalnine	Tyrosine	Threonine	Tryptophan	Valine	Arginine	Histidine	Alanine	Aspartic acid	Glutamic acid	Glycine	Proline	Serine	
SC2066	2.10	8.81	2.0	1.66	2.04	3.14	1.62	2.21	1.72	3.15	3.0	2.01	4.93	4.88	11.9	2.52	8.99	2.99	69.67
SC3062	2.63	7.98	2.99	1.99	2.44	2.11	2.25	2.66	1.98	2.89	4.01	2.56	4.88	5.33	10.2	2.96	8.01	3.11	70.98
SC2088	2.72	7.63	4.88	1.84	1.35	3.06	2.15	2.13	1.7	3.17	4.07	2.18	4.62	4.32	10.24	2.79	7.16	2.14	68.15
SC2055	2.00	6.90	3.5	1.4	1.2	2.8	2.7	2.5	1.4	2.81	3.01	1.89	4.1	3.72	12.41	1.88	8.51	2.71	65.44
SC444	2.55	8.22	4.18	1.69	2.33	3.22	3.05	2.74	1.99	3.69	3.23	2.87	4.6	4.5	10.2	2.96	8.5	3.22	73.74
Sc3737	2.44	9.15	4.55	1.89	2.01	3.89	3.21	2.66	1.81	3.88	3.55	2.11	4.18	4.52	12.4	2.56	8.22	2.99	76.02
SC2066 x SC3062	2.99	10.22	4.88	2.5	2.55	3.99	3.65	2.98	2.1	3.91	4.89	3.11	5.89	6.99	15.86	2.79	10.22	3.97	93.49
SC2066 x SC2088	2.01	7.00	3.33	1.4	1.33	2.8	2.5	2.3	1.4	2.81	3.21	1.9	4.22	3.52	10.41	1.98	8.01	2.61	62.74
SC2066 x SC2055	2.11	6.98	3.51	1.41	1.21	2.55	2.3	2.51	1.42	2.66	3.01	1.88	4.12	3.44	11.33	1.81	7.08	2.73	62.06
SC2066 x SC444	3.00	10.0	5.11	2.22	2.6	4.01	3.78	3.05	1.99	3.58	4.91	3.43	5.9	6.55	15.5	2.99	9.5	3.99	92.11
SC2066 x Sc3737	2.99	9.61	4.99	2.21	2.33	3.99	3.66	2.78	2.0	3.99	4.9	3.11	5.99	7.0	15.41	2.91	9.16	3.9	90.93
SC3062 x SC2088	2.79	9.55	5.21	2.11	2.45	3.97	3.58	2.99	1.79	4.00	4.78	3.32	5.97	6.76	15.99	3.01	9.06	4.11	91.44
SC3062 x SC2055	2.67	9.95	4.95	2.11	2.12	3.67	3.55	3.4	1.8	3.69	4.98	3.09	5.69	6.59	16.01	2.99	9.6	3.98	90.84
SC3062 x SC444	2.90	9.49	5.09	2.23	2.05	4.04	3.5	2.93	1.99	3.69	6.2	3.55	6.22	7.11	16.22	4.31	10.0	5.2	96.72
SC3062 x Sc3737	2.91	10.2	5.11	2.31	2.1	3.96	3.44	3.01	1.69	3.99	5.01	3.56	6.0	6.9	15.22	2.98	9.0	3.66	91.05
SC2088 x SC2055	2.11	6.90	3.50	1.78	1.32	2.99	2.99	2.6	1.47	2.9	3.33	1.96	4.1	3.99	12.01	1.92	8.0	2.98	66.85
SC2088 x SC444	2.66	11.0	4.99	2.01	2.98	4.00	3.99	2.98	1.99	3.89	4.81	3.11	5.89	7.0	15.77	2.87	9.56	3.49	92.99
SC2088 x Sc3737	2.78	10.0	4.88	2.00	2.55	3.99	3.78	2.88	1.96	3.99	4.6	3.14	5.9	6.9	15.56	2.79	9.9	3.98	91.58
SC2055 x SC444	3.00	9.93	5.00	2.99	2.77	3.76	3.99	3.22	1.89	4.33	4.55	3.33	6.5	6.88	16.0	3.88	12.0	4.55	98.57
SC2055 x Sc3737	3.00	9.99	5.00	2.00	2.58	3.55	3.66	2.67	1.55	4.0	4.89	3.76	5.55	7.15	15.0	2.99	10.2	4.0	91.54
SC444 x Sc3737	2.91	9.01	4.99	2.22	2.98	5.2	3.43	3.0	2.0	5.22	4.65	3.67	6.2	7.16	16.04	3.0	10.35	3.99	96.02
LSD at 0.05	0.03	0.14	0.04	0.01	0.03	0.05	0.02	0.01	0.04	0.07	0.09	0.11	0.16	0.21	0.12	0.01	0.13	0.03	2.95

CONCLUSIONS

Considering the observed results, the 6 genotypes and 15 hybrid differed significantly in yield, its components, protein % and amino acids (%), where (SC 3062 x SC 3737), and (SC 444 X SC3737 recorded the highest values followed (SC3062 x SC3737) and (SC3062 x SC444) then (SC 2066 x SC 3737) and (SC 2066 x SC 444) recorded the highest mean values of the yield, yield components, protein (%) and amino acids. The results showed positive values of heterosis percentage (%) between all the obtained hybrids that refer to the successful of hybridization. Amino acids values also showed significant variations between the maize hybrids. It could be used this genotypes (F1) in breeding programs for getting the highest values of yield, its components, proteins and amino acids.

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الملخص العربي

تقييم بعض التراكيب الوراثية للذرة الشامية لبعض مكونات المحصول والمحتوى العالي من البروتين والأحماض الأمينية

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اقيمت تجارب حقلية في شمال التحرير – منطقة النوبارية – محافظة البحيرة – مصر في الموسم الصيفي لعامي ٢٠١٨ و ٢٠١٩ في الموسم الأول تم زراعة ٦ تراكيب وراثية ثم عمل التهجينان الممكنة في اتجاه واحد (التوافيق المختلفة بين التراكيب الوراثية) لإنتاج الهجن ثم في الموسم الثاني تم زراعة ٦ أباء و١٥ هجين الناتجة لتقييم الصفات المحصولية ومحتواها من البروتين وأهم الأحماض الأمينية ، في قطاعات عشوائية كاملة في ثلاث مكررات. وكانت الصفات المدروسة هي: عدد الحبوب/صف– عدد الحبوب/كوز وزن الكوز ووزن ١٠٠ حبة ومحصول الحبوب ومحصول القش ومحتوى البروتين في الحبوب – محتوي الحبوب من أهم الأحماض الأمينية وقوة الهجين لبعض التراكيب الوراثية الناتجة.

ولخصت أهم النتائج فيما يلي:

كان التباين الراجع الي التراكيب الوراثية معنويا لكل الصفات تحت الدراسة. وسجلت الهجن (ه. ف. ٤٤٤ x ه.ف. ٣٧٣٧) و(ه. ف. ٣٠٦٢ x ه.ف. ٤٤٤) و(ه. ف. ٢٠٦٦ x ه.ف.٣٧٣٧) و (ه. ف. ٢٠٦٦ x ه.ف.٤٤٤) و(ه. ف. ٣٠٦٢ x ه. ف. ٣٧٣٧) سجلت أعلى القيم لصفات المحصول ومكوناته ومحتوى الحبوب من البروتين وبعض الأحماض الأمينية خلال موسم الدراسة ٢٠١٩ متبوعة بـ (ه. ف. ٢٠٨٨ x ه.ف. ٤٤٤) ثم (ه. ف. ٢٠٨٨ x ه.ف. ٣٧٣٧) و (ه. ف. ٢٠٥٥ x ه.ف. ٤٤٤) مقارنة مع باقي الهجين والآباء خلال موسم الدراسة ٢٠١٩. قوة الهجين سجلت معنوية عالية للهجن حيث أن هذه التهجينان (ه. ف. ٢٠٦٦ x ه.ف.٤٤٤) و (ه. ف. ٢٠٦٦ x ه.ف.٢٠٨٨) و (ه. ف. ٢٠٨٨ x ه.ف.٣٧٣٧) و (ه. ف. ٢٠٦٦ x ه.ف.٣٧٣٧) حققت أعلى قوة هجين في معظم صفات المحصول ومكوناته ونسبة البروتين (%). بالنسبة لمحتوى الحبوب من أهم الأحماض الأمينية وجد أن الهجين المستخدم كأب (ه. ف. ٣٧٣٧) حقق أعلى نسبة مئوية لمجموع الأحماض الأمينية الضرورية. بينما حقق (ه. ف. ٢٠٥٥) أقل القيم. في حين أن التهجينان

الناتجة من (ه. ف. ٢٠٥٥ x ه.ف.٤٤٤) و (ه. ف. ٣٠٦٢ x ه.ف.٤٤٤) و (ه. ف. ٤٤٤ x
ه.ف.٣٧٣٧) سجلت أعلى نسبة مئوية لمحتوي الحبوب من الأحماض الأمينية الضرورية على الترتيب.

يوصي البحث عمل برنامج تربية للتوسع في زراعة هجن الذرة الشامية الناتجة (الجيل الأول) التي حققت أعلى
متوسطات قيم لصفات المحصول ومكوناته ونسبة بروتين في الحبوب وأعلى محتوي من بعض الأحماض الأمينية
تحت ظروف الدراسة بالنوبارية.

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