# GENETIC STUDIES ON SEED YIELD OF SQUASH *CUCURBITA PEPO* L.

Nagwa M. Etman[1], Ahmed R. Aggour[2], Lotfy A. Badr[2], and Abd-El-Monsef A. Kamooh[1]

[1] Vegetable Research Departments, Horticultural Research Institute, Agricultural Research Center
[2] Department of Horticulture, Faculty of Agriculture, Benha University

## ABSTRACT

Eight inbred lines of squash (*Cucurbita pepo* L.) were used in making half diallel set of crosses to determine some of the genetic parameters which are necessary in breeding programs to improve seed yield as well as seed oil and protein content. The results showed significant general and specific combining ability effects for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds indicating the presence of additive and non-additive gene effects in the inheritance of these characters. However, the calculated ratio GCA/SCA was more than unity, which indicates that the additive genetic variance component is the larger component comparing to other types of genetic variance components. The broad sense heritability values were 88.84%, 86.38%, 67.22%, 81.89%, and 97.28%, while the narrow sense heritability values were 2.00%, 66.60%, 47.08%, 29.63%, and 35.07%, for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds, respectively. These results indicate the influence of the environmental factors and non-additive type of gene action on the expression and inheritance of this character.

## INTRODUCTION

Squash *Cucurbita pepo* is considered one of the popular vegetable crops in many parts of the world including Egypt. Recently many people become amore of the high nutriaus value of squash seeds. Squash seeds are utilized directly for human consumption as a snack Milan *et al.* (2007) which give high economic profit to people who are working in this business. It can be mentioned that *Cucurbita*

*pepo* seeds have an important role in human diet due to its high content of oil (Hamid *et al.*, 1988; Undina *et al.*, 1991; Lee *et al.*, 1994; Idouraine *et al.*, 1996; Murkovic *et al.*, 1999; Stevenson *et al.*, 2007) and protein (Idouraine *et al.*, 1996). Undina *et al.* (1991) reported that seed fat content is around 50% in *C. pepo*. Hamid *et al.* (1988) reported that seeds of pumpkin (*C. pepo*) contained 40% oil. In addition, Idouraine *et al.* (1996) evaluated seeds from 8 lines of naked seeds squash (*C. pepo*) and found that protein values were significantly different among seed types and ranged from 37.1±0.45% to 44.4±0.45%, while oil content was high in all seed and varied from 34.5±0.42% to 43.6±0.06%.

Significant differences among *C. pepo* genotypes concerning seed yield have been reported (Borghi *et al.*, 1973; Doijode *et al.*, 1983; Metwally *et al.*, 1988; Warid *et al.*, 1993; Idouraine *et al.*, 1996; Nerson *et al.*, 2000; Nurgul and Rana, 2003; Nerson, 2005; El-Tahawy, 2007). Warid *et al.* (1993) evaluated selfed progeny of naked seed squash and found that weight\fruit was 1.49 to 64.1g averaging 18.2g. In addition, Nerson and Paris (2000) and Nerson *et al.* (2000) reported that squash produced 19-54g of seeds\fruit. Better parent heterosis has been reported for 100-seed weight (Metwally *et al.*, 1988). In addition, Xu *et al.* (2006) reported heterosis for seed yield/fruit in pumpkin. El-Tahawy (2007) reported the presence of both the additive and non-additive gene effects for the inheritance of 100-seeds weight. The non-additive gene effects were more important than additive gene effects in the inheritance of seed yield and 100-seeds weight in squash (Hamid *et al.*, 1988). In addition, Doijode *et al.* (1983) found that the additive gene action was predominant for seed weight/fruit in pumpkin (*C. moschata*). However, it was found that the non-additive gene effects were more important than additive gene effects in squash (Metwally *et al.*, 1988) and pumpkin (Xu *et al.*, 2006). Moreover, Borghi *et al.* (1973) reported complete dominance for seed weight per plant in *C. pepo*. In addition, El-Tahawy (2007) mentioned that, 100-seeds weight character showed dominance gene action and was controlled by one gene pair. Metwally *et al.* (1988) recorded high broad sense heritability for seed yield in squash but the narrow sense heritability was low. In addition, Lakshmi *et al.* (2002) recorded broad sense heritability of 77.65% for 1000-seeds weight in pumpkin.

Use of *Cucurbita* spp. seed in developing countries could provide a concentrated food source, high in protein and energy value (Loy, 2004; Milan *et al.*, 2007; Ebubekir, 2008). This indicates the importance of genetic improvement of seed yield and its nutrional value. No report has been found concerning the genetics and inheritance of seed oil and protein contents in *C. pepo*.

The objective of this study was to determine some of the genetic parameters which are necessary in breeding programs to improve seed yield as well as seed oil and protein content.

# MATERIALS AND METHODS

The study was conducted in the Experimental Farm of Horticulture Department, Faculty of Agriculture, Moshtohor, Benha University, Kalubia Governorate, and the greenhouse and laboratory of the Department of Cross Pollinated, Vegetable Research Department, Horticultural Research Institute, Agricultural Research Center; during summer and fall seasons of 2004 to 2007.

### Parental genotypes and crosses

Eight inbred lines of squash (*Cucurbita pepo* L.) i.e. inbred line TQ-1, derived from population of Table Queen cultivar (winter squash), inbred lines derived from population of Eskandrani ecotype i.e. Mosh15-27S-19, Mosh11-5S-34, Mosh2-10S, Mosh2-7S-18 and Mosh33-27-13 and two inbred lines#1 and #2, were used in the crosses. Seeds of Line#1 and Line#2 were developed by Prof. Dr. Abd-El-Monsef at the Department of Cross Pollinated, Vegetable Research Department, Horticultural Research Institute, Agricultural Research Center. Seeds of TQ-1 were kindly obtained from Department of Agronomy and Horticulture; University of Nebraska-Lincoln; U.S.A. Seeds of other genotypes were obtained from the Germplasm Preservation Laboratory; Faculty of Agriculture at Moshtohor, Benha University, Kalubia, Egypt.

Plants of each genotype were previously selfed for two generations before starting the present study. The previously mentioned parental genotypes were chosen to be used in the present study based on the relatively wide variation in the different characters observed among these genotypes. The following half diallel set of crosses was made:

## Table (A) The different crosses of parental genotypes in half diallel set mating design (Method 2).

| ♀ \ ♂ | TQ-1 | Mosh.15-27S-19 | Mosh.11-5S-34 | Mosh.2-10S | Line#2 | Mosh.2-7S-18 | Line#1 | Mosh.33-27-13 |
|---|---|---|---|---|---|---|---|---|
| TQ-1 | S | X | X | X | X | X | X | X |
| Mosh.15-27S-19 | | S | X | X | X | X | X | X |
| Mosh.11-5S-34 | | | S | X | X | X | X | X |
| Mosh.2-10S | | | | S | X | X | X | X |
| Line#2 | | | | | S | X | X | X |
| Mosh.2-7S-18 | | | | | | S | X | X |
| Line#1 | | | | | | | S | X |
| Mosh.33-27-13 | | | | | | | | S |

S = Self pollinated.  X = Cross pollinated.

The seeds of the different parental genotypes and their $F_1$ seeds were planted in the field on April 26, 2005. Each experimental plot consisted of 3 ridges which were assigned to study marketable fruit yield characters and 3 other ridges to study seed yield. Each ridge was 5m length and 80cm width. Individual seeds were sown in holes with distance of 50cm a part from each other on the same ridge. A randomized complete block design with four replicates was utilized in conducting this experiment. All agricultural practices and the control of disease and insects were done according to the recommendations of Ministry of Agriculture, Agricultural Research Center.

## Measurements:

1. Seed yield/plant (g.)

2. 1000-seeds weight.

3. Seed net weight (%) = (Core seeds weight / Total seeds weight) X100.

4. Percentage of total oils in seeds: Total oils were extracted by hexane according to the method of Khater et al. (1992) and calculated as percentage.

5. Percentage of total proteins in seeds: It was determined according to the method described by Hafez and Mikkelsen (1981) and calculated using the following equation described in A.O.A.C. (1990):

**Protein (%)** = Total nitrogen (%) X 6.25.

### Genetic statistical analysis

The data obtained for the different traits were analyzed on individual plant mean basis. The correlation coefficient was calculated for all pairs of characters according to Steel and Torrie (1980) using character means of all genotypes. The analysis of variance (ANOVA) was performed using the method described by Gomez and Gomez (1984).

### Heterosis

Estimates of heterosis percentage was calculated according to Singh and Khanna (1975) as following equation:

**Better parent heterosis (%)** $= [(\overline{F_1} - \overline{BP}) / \overline{BP}] \times 100$.

Where:

$\overline{F_1}$ = Mean of $F_1$ generations.          $\overline{B.P.}$ = Mean of better parent.

### Griffing Diallel Analysis

Sum of squares for genotypes was partitioned according to Griffing's (1956) (method 2 model 1) into sources of variations due to general and specific combining ability (GCA and SCA).

### Heritability

The broad and narrow sense heritability values were calculated according to the method described by Pandey and Gritton (1975) using the general and specific combining ability components.

a) Broad sense heritability $(h^2_{bs}) = \dfrac{2\delta^2 gca + \delta^2 sca}{2\delta^2 gca + \delta^2 sca + \delta^2 e} \times 100$

b) Narrow sense heritability $(h^2_{ns}) = \dfrac{2\delta^2 gca}{2\delta^2 gca + \delta^2 sca + \delta^2 e} \times 100$

Where:

$$\delta^2 gca = \frac{2}{n+2} (M_g - M_s)$$

$$\delta^2 sca = M_s - M_e$$

$$\delta^2 e = M_e$$

Where $M_g$ and $M_s$ are mean square for general and specific combining abilities, respectively.

# RESULTS AND DISCUSSION

## 1. Seed yield/plant

The results presented in Table 1 and 2 indicate significant differences among different parental genotypes and hybrids concerning seed yield/plant. Plants of line Mosh.15-27S-19 had the highest seed yield/plant (39.03 g) followed by Mosh.2-7S-18 (31.60 g) and Mosh.2-10S (28.27 g). Differences among *C. pepo* genptypes concerning seed yield have been reported (Borghi *et al.*, 1973; Doijode *et al.*, 1983; Metwally *et al.*, 1988; Warid *et al.*, 1993; Idouraine *et al.*, 1996; Nerson *et al.*, 2000; Nurgul and Rana, 2003; Nerson, 2005; El-Tahawy, 2007). The $F_1$ hybrids TQ-1 X Line#2 (56.28 g) and TQ-1 X Mosh.15-27S-19 (47.13 g) had significant higher yield than the higher parental line Mosh.15-27S-19 which indicate the potential of producing $F_1$ hybrids with high seed yield. Xu *et al.* (2006) reported heterosis for seed yield/fruit in pumpkin.

The results presented in Table 2 show significant general and specific combining ability effects indicating the presence of additive and non-additive gene effects. However, the calculated ratio of GCA/SCA was 1.05, i.e., slightly more than one, which indicates that the additive genetic variance component is slightly larger component comparing to other types of genetic variance components. Doijode *et al.* (1983) found that the additive gene action was predominant for seed weight/fruit in pumpkin (*C. moschata*).

The highest value of general combining ability effect was associated with the parental lines Mosh.2-10S (4.52) and Mosh.15-27S-19 (3.49). Based on these results, the parental lines Mosh.2-10S and Mosh.15-27S-19 will be good combiners to form hybrids with high seed yield/plant (Table 3).

Table (1): Means of seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds for different parental genotypes and its $F_1$ hybrids evaluated in field.

| Genotypes | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total proteins (%) |
|---|---|---|---|---|---|
| TQ-1 | 15.33 | 57.92 | 77.44 | 37.95 | 42.80 |
| TQ-1 X Mosh.15-27S-19 | 47.13 | 96.92 | 78.92 | 42.64 | 37.73 |
| TQ-1 X Mosh.11-5S-34 | 37.63 | 107.58 | 81.72 | 40.42 | 44.95 |
| TQ-1 X Mosh.2-10S | 42.40 | 110.17 | 77.19 | 40.22 | 45.40 |
| TQ-1 X Line#2 | 56.28 | 124.58 | 79.25 | 41.39 | 39.23 |
| TQ-1 X Mosh.2-7S-18 | 25.13 | 114.17 | 80.77 | 43.82 | 38.78 |
| TQ-1 X Line#1 | 43.70 | 92.92 | 76.20 | 38.02 | 40.83 |
| TQ-1 X Mosh.33-27-13 | 22.18 | 82.79 | 76.61 | 36.13 | 45.60 |
| Mosh.15-27S-19 | 39.03 | 178.50 | 81.16 | 41.34 | 39.58 |
| Mosh.15-27S-19 X Mosh.11-5S-34 | 37.00 | 142.08 | 81.09 | 37.47 | 45.96 |
| Mosh.15-27S-19 X Mosh.2-10S | 44.13 | 115.67 | 77.52 | 37.60 | 43.00 |
| Mosh.15-27S-19 X Line#2 | 29.60 | 114.09 | 79.98 | 39.07 | 42.35 |
| Mosh.15-27S-19 X Mosh.2-7S-18 | 33.20 | 156.25 | 80.43 | 40.52 | 37.81 |
| Mosh.15-27S-19 X Line#1 | 27.63 | 113.83 | 79.39 | 38.76 | 42.23 |
| Mosh.15-27S-19 X Mosh.33-27-13 | 24.73 | 111.08 | 82.44 | 38.74 | 40.37 |
| Mosh.11-5S-34 | 22.63 | 122.92 | 79.08 | 39.55 | 38.27 |
| Mosh.11-5S-34 X Mosh.2-10S | 32.50 | 103.25 | 77.63 | 41.43 | 33.03 |
| Mosh.11-5S-34 X Line#2 | 22.35 | 132.67 | 81.16 | 40.74 | 40.59 |
| Mosh.11-5S-34 X Mosh.2-7S-18 | 33.55 | 139.09 | 78.22 | 41.61 | 36.80 |
| Mosh.11-5S-34 X Line#1 | 23.73 | 122.83 | 78.28 | 39.31 | 38.95 |
| Mosh.11-5S-34 X Mosh.33-27-13 | 23.38 | 121.00 | 79.40 | 40.09 | 37.93 |
| Mosh.2-10S | 28.27 | 140.84 | 81.16 | 41.24 | 34.65 |
| Mosh.2-10S X Line#2 | 34.90 | 128.58 | 80.22 | 41.60 | 39.52 |
| Mosh.2-10S X Mosh.2-7S-18 | 38.25 | 170.67 | 80.19 | 41.53 | 34.97 |
| Mosh.2-10S X Line#1 | 44.63 | 137.09 | 75.42 | 39.17 | 33.90 |
| Mosh.2-10S X Mosh.33-27-13 | 38.25 | 134.50 | 77.98 | 42.24 | 32.60 |
| Line#2 | 15.05 | 99.75 | 80.51 | 39.28 | 33.74 |
| Line#2 X Mosh.2-7S-18 | 39.23 | 129.00 | 79.56 | 44.42 | 39.27 |
| Line#2 X Line#1 | 43.50 | 115.09 | 80.83 | 41.42 | 37.22 |
| Line#2 X Mosh.33-27-13 | 26.18 | 103.42 | 79.90 | 41.66 | 32.44 |
| Mosh.2-7S-18 | 31.60 | 124.25 | 80.63 | 42.84 | 38.46 |
| Mosh.2-7S-18 X Line#1 | 30.43 | 117.33 | 78.68 | 44.26 | 37.41 |
| Mosh.2-7S-18 X Mosh.33-27-13 | 24.60 | 141.59 | 81.39 | 39.08 | 40.12 |
| Line#1 | 12.98 | 99.08 | 75.54 | 40.43 | 34.87 |
| Line#1 X Mosh.33-27-13 | 42.63 | 114.84 | 77.76 | 40.96 | 41.36 |
| Mosh.33-27-13 | 14.60 | 90.67 | 74.31 | 39.72 | 39.62 |
| L.S.D 5% | 10.16 | 29.67 | 3.62 | 2.49 | 1.89 |
| L.S.D 1% | 13.46 | 39.31 | 4.79 | 3.31 | 2.51 |

Table (2): Mean square values of seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds of the different genotypes, and ratio of general to specific combining ability (GCA/SCA).

| Sources of Variance | d.f | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total proteins (%) |
|---|---|---|---|---|---|---|
| Genotypes | 35 | 424.04** | 2195.13** | 15.50** | 11.00** | 40.92** |
| Parents | 7 | 299.59** | 5245.62** | 28.64** | 6.80* | 28.78** |
| Hybrids | 27 | 322.04** | 1441.18** | 12.44** | 12.47** | 43.92** |
| Parents Vs hybrids | 1 | 4049.38** | 1198.44 | 5.92 | 0.95* | 44.91** |
| Error | 105 | 52.55 | 448.41 | 6.66 | 2.34 | 1.34 |
| General combining ability (GCA) | 7 | 442.69** | 1644.74** | 8.64** | 6.22** | 25.24** |
| Specific Combining ability (SCA) | 28 | 421.18** | 274.79** | 2.68** | 3.03** | 10.74** |
| Error | 105 | 47.95 | 112.10 | 1.66 | 0.78 | 0.45 |
| GCA/SCA | | 1.05 | 5.99 | 3.22 | 2.05 | 2.35 |

** Significant at 1% level of significance

* Significant at 5% level of significance

Table (3): General combining ability effects ($g_i$) of the different parental genotypes for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds.

| Genotypes | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total proteins (%) |
|---|---|---|---|---|---|
| TQ-1 | 1.64 | -23.18 | -0.64 | -0.56 | 2.75 |
| Mosh.15-27S-19 | 3.49 | 13.02 | 1.01 | -0.67 | 1.80 |
| Mosh.11-5S-34 | -3.33 | 3.76 | 0.37 | -0.40 | 0.42 |
| Mosh.2-10S | 4.52 | 10.48 | -0.35 | 0.21 | -1.89 |
| Line# 2 | -0.44 | -2.98 | 0.99 | 0.47 | -1.25 |
| Mosh.2-7S-18 | 0.10 | 13.99 | 0.84 | 1.67 | -0.85 |
| Line# 1 | -0.44 | -6.47 | -1.43 | -0.14 | -0.90 |
| Mosh.33-27-13 | -5.54 | -8.61 | -0.79 | -0.58 | -0.09 |
| L.S.D 5% | 2.12 | 6.21 | 0.76 | 0.52 | 0.39 |
| L.S.D 1% | 2.81 | 8.22 | 1.00 | 0.96 | 0.52 |

Table (4): Specific combining ability effects ($S_{ij}$) of the different $F_1$ hybrids for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds.

| Genotypes | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total proteins (%) |
|---|---|---|---|---|---|
| TQ-1 X Mosh.15-27S-19 | 10.16 | -12.56 | -0.56 | 3.41 | -5.78 |
| TQ-1 X Mosh.11-5S-34 | 5.31 | 7.36 | 2.89 | 0.92 | 2.83 |
| TQ-1 X Mosh.2-10S | 4.41 | 3.22 | -0.93 | 0.11 | 5.58 |
| TQ-1 X Line#2 | 23.24 | 31.11 | -0.20 | 1.02 | -1.23 |
| TQ-1 X Mosh.2-7S-18 | -8.45 | 3.72 | 1.46 | 2.24 | -2.07 |
| TQ-1 X Line#1 | 10.66 | 2.92 | -0.83 | -1.74 | 0.02 |
| TQ-1 X Mosh.33-27-13 | -5.76 | -5.05 | -1.01 | -3.19 | 3.98 |
| Mosh.15-27S-19 X Mosh.11-5S-34 | 5.00 | 5.67 | 0.60 | -1.92 | 4.79 |
| Mosh.15-27S-19 X Mosh.2-10S | 4.28 | -27.48 | -2.25 | -2.40 | 4.14 |
| Mosh.15-27S-19 X Line#2 | -5.29 | -15.59 | -1.12 | -1.20 | 2.85 |
| Mosh.15-27S-19 X Mosh.2-7S-18 | -2.23 | 9.61 | -0.54 | -0.95 | -2.10 |
| Mosh.15-27S-19 X Line#1 | -7.27 | -12.36 | 0.70 | -0.90 | 2.37 |
| Mosh.15-27S-19 X Mosh.33-27-13 | -5.06 | -12.96 | 3.11 | -0.47 | -0.30 |
| Mosh.11-5S-34 X Mosh.2-10S | -0.52 | -30.63 | -1.50 | 1.16 | -4.46 |
| Mosh.11-5S-34 X Line#2 | -5.71 | 12.25 | 0.70 | 0.21 | 2.47 |
| Mosh.11-5S-34 X Mosh.2-7S-18 | 4.94 | 1.70 | -2.10 | -0.13 | -1.72 |
| Mosh.11-5S-34 X Line#1 | -4.34 | 5.90 | 0.24 | -0.62 | 0.47 |
| Mosh.11-5S-34 X Mosh.33-27-13 | -0.41 | 6.24 | 0.71 | 0.61 | -1.35 |
| Mosh.2-10S X Line#2 | -1.01 | 1.44 | 0.48 | 0.46 | 3.70 |
| Mosh.2-10S X Mosh.2-7S-18 | 1.79 | 26.56 | 0.59 | -0.82 | -1.25 |
| Mosh.2-10S X Line#1 | 8.71 | 13.43 | -1.91 | -1.37 | -2.27 |
| Mosh.2-10S X Mosh.33-27-13 | 7.44 | 12.99 | 0.01 | 2.15 | -4.37 |
| Line#2 X Mosh.2-7S-18 | 7.73 | -1.64 | -1.48 | 1.81 | 2.42 |
| Line#2 X Line#1 | 12.54 | 4.90 | 2.17 | 0.63 | 0.41 |
| Line#2 X Mosh.33-27-13 | 0.32 | -4.60 | 0.59 | 1.31 | -5.17 |
| Mosh.2-7S-18 X Line#1 | -1.08 | -9.82 | 0.16 | 2.26 | 0.20 |
| Mosh.2-7S-18 X Mosh.33-27-13 | -1.80 | 16.58 | 2.24 | -2.47 | 2.11 |
| Line#1 X Mosh.33-27-13 | 16.77 | 10.28 | 0.87 | 1.22 | 3.39 |
| L.S.D 5% | 6.51 | 19.03 | 0.76 | 1.60 | 1.21 |
| L.S.D 1% | 8.63 | 25.20 | 1.00 | 2.12 | 1.61 |

**Table (5): Better parent heterosis (%) of the different $F_1$ hybrids for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds.**

| Genotypes | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total proteins (%) |
|---|---|---|---|---|---|
| TQ-1 X Mosh.15-27S-19 | 20.74 | -45.70 | -2.76 | -11.85 | 3.14 |
| TQ-1 X Mosh.11-5S-34 | 66.26 | -12.48 | 3.34 | 5.02 | 2.21 |
| TQ-1 X Mosh.2-10S | 49.98 | -21.78 | -4.90 | 6.06 | -2.45 |
| TQ-1 X Line#2 | 267.09 | 24.89 | -1.57 | -8.34 | 5.37 |
| TQ-1 X Mosh.2-7S-18 | -20.49 | -8.11 | 0.17 | -9.38 | 2.29 |
| TQ-1 X Line#1 | 185.06 | -6.22 | -1.59 | -4.61 | -5.98 |
| TQ-1 X Mosh.33-27-13 | 51.88 | -8.68 | -1.07 | 6.54 | -9.03 |
| Mosh.15-27S-19 X Mosh.11-5S-34 | -5.20 | -20.40 | -0.09 | 16.13 | -9.36 |
| Mosh.15-27S-19 X Mosh.2-10S | 13.05 | -35.20 | -4.48 | 8.66 | -9.03 |
| Mosh.15-27S-19 X Line#2 | -24.16 | -36.09 | -1.45 | 7.02 | -549 |
| Mosh.15-27S-19 X Mosh.2-7S-18 | 0.51 | -12.46 | -0.90 | -4.46 | -5.40 |
| Mosh.15-27S-19 X Line#1 | -29.22 | -36.23 | -2.18 | 6.71 | -6.25 |
| Mosh.15-27S-19 X Mosh.33-27-13 | -36.65 | -37.77 | 1.58 | 1.89 | -6.30 |
| Mosh.11-5S-34 X Mosh.2-10S | 14.96 | -26.69 | -4.35 | -13.72 | 0.46 |
| Mosh.11-5S-34 X Line#2 | -1.24 | 7.93 | 0.81 | 6.04 | 3.03 |
| Mosh.11-5S-34 X Mosh.2-7S-18 | 6.17 | 11.94 | -2.98 | -4.32 | -2.87 |
| Mosh.11-5S-34 X Line#1 | 4.84 | -0.07 | -1.01 | 1.75 | -2.79 |
| Mosh.11-5S-34 X Mosh.33-27-13 | 3.29 | -1.56 | 0.41 | -4.25 | 0.94 |
| Mosh.2-10S X Line#2 | 23.54 | -8.70 | -1.16 | 14.05 | 0.89 |
| Mosh.2-10S X Mosh.2-7S-18 | 21.04 | 21.18 | -1.20 | -9.08 | -3.06 |
| Mosh.2-10S X Line#1 | 57.85 | -2.66 | -7.08 | -2.79 | -5.02 |
| Mosh.2-10S X Mosh.33-27-13 | 35.30 | -4.50 | -3.92 | -17.71 | 2.43 |
| Line#2 X Mosh.2-7S-18 | 24.13 | 3.82 | -1.45 | 2.11 | 3.70 |
| Line#2 X Line#1 | 189.04 | 15.37 | 0.39 | 6.75 | 2.44 |
| Line#2 X Mosh.33-27-13 | 73.92 | 3.67 | -0.77 | -18.12 | 4.89 |
| Mosh.2-7S-18 X Line#1 | -3.72 | -5.57 | -2.42 | -2.74 | 3.32 |
| Mosh.2-7S-18 X Mosh.33-27-13 | -22.15 | 13.95 | 0.94 | 1.28 | -8.77 |
| Line#1 X Mosh.33-27-13 | 191.95 | 15.90 | 2.94 | 4.40 | 1.31 |
| L.S.D 5% | 8.80 | 25.70 | 3.13 | 1.63 | 2.16 |
| L.S.D 1% | 11.65 | 34.04 | 4.15 | 2.17 | 2.87 |

Table (6): Estimates of heritability in broad ($h^2_{bs}\%$) and narrow ($h^2_{ns}\%$) sense for seed yield/plant, 1000-seeds weight, seed net weight percentage, and total oils and protein percentage of seeds.

| Heritability (%) | Seed yield/plant (g) | 1000-seeds weight (g) | Seed net weight (%) | Total oils (%) | Total protein (%) |
|---|---|---|---|---|---|
| Broad sense heritability ($h^2_{bs}\%$) | 88.84 | 86.38 | 67.22 | 81.89 | 97.28 |
| Narrow sense heritability ($h^2_{ns}\%$) | 2.00 | 66.60 | 47.08 | 29.63 | 35.07 |

The highest value of specific combining ability effect was associated with the $F_1$ hybrids TQ-1 X Line#2 (23.24) and Line#1 X Mosh.33-27-13 (16.77). These $F_1$ hybrids will give plants with high seed yield/plant (Table 4).

The results presented in Table 5 show, that the highest value of better parent heterosis was associated with the $F_1$ hybrids TQ-1 X Line#2 (267.09%), which indicates that this hybrid had high seed yield/plant. The potentiality of producing hybrids with high seed yield has been reported by Metwally et al. (1988).

The results presented in Table 6 show that, the broad sense heritability was (88.84%) while the narrow sense heritability was (2.00%), which indicates that selection in the segregating generation of squash crosses should be performed on family mean basis to achieve progress in the genetic important of this character. These results were close to those reported by Metwally et al. (1988) who recorded high broad sense heritability and low narrow sense heritability for seed yield in squash.

## 2. 1000-seeds weight (g)

The results presented in Table 1 and 2 indicate significant differences among different parental genotypes and hybrids concerning weight of 1000-seeds. Plants of line Mosh.15-27S-19 had the highest 1000-seeds weight (178.50 g). None of the hybrids exceeded the high parent i.e. Mosh.15-27S-19. Warid et al. (1993) recorded variation among lines of naked seed squash concerning seed weight. However, the $F_1$ hybrids Mosh.2-10S X Mosh.2-7S-18 (170.67g/1000-seeds) and Mosh.15-27S-19 X Mosh.2-7S-18 (156.25g/1000-seeds) were not significantly different from the highest

parent. This result agreed with that of Metwally *et al.* (1988) who recorded non-significant between parent heterosis for 100-seed weight.

The results presented in Table 2 show significant general and specific combining ability effects, which indicate the presence of both the additive and non-additive gene effects in the inheritance of this character. Metwally *et al.* (1988) and El-Tahawy (2007) reported the involvement of both additive and non-additive gene action in the inheritance of 100-seeds weight in squash. .However, the calculated ratio GCA/SCA was 5.99, i.e., more than unity, which indicates that the additive type of gene action was more important in the inheritance of this character. This result agreed with that of El-Tahawy (2007) who recorded the predominance of the additive gene action in inheritance of the seed weight in squash. However, Metwally *et al.* (1988) reported that the non-additive gene action was more important in the inheritance of this character in squash. This discrepancy could be due to differences in the genetic background of the parental genotypes used in the different experiments. This conclusion can be supported by the findings of Warid *et al.* (1993); Nerson and Paris (2000) and Nerson *et al.* (2000) who reported a wide range of variation in seed weight among squash germplasm.

The highest value of general combining ability effect was associated with the parental lines Mosh.2-7S-18 (13.99), Mosh.15-27S-19 (13.02) and Mosh.2-10S (10.48). These results indicated that, the parental lines Mosh.2-7S-18, Mosh.15-27S-19 and Mosh.2-10S are expected to be good combiners in forming hybrids with high seed weight (Table 3).

The highest value of specific combining ability effect was associated with the $F_1$ hybrids TQ-1 X Line#2 (31.11) and Mosh.2-10S X Mosh.2-7S-18 (26.56). These $F_1$ hybrids will give plants with high seed weight (Table 4).

The results presented in Table 5 show, the highest values of better parent heterosis were associated with the $F_1$ hybrids TQ-1 X Line#2 (24.89%), Mosh.2-10S X Mosh.2-7S-18 (21.18%), Line#1 X Mosh.33-27-13 (15.90%) and Line#2 X Line#1 (15.37%).These results indicate the potentiality of forming hybrids with high seed weight.

In addition, the results presented in Table 6 show that, the broad sense heritability was high (86.38%). Close value for broad sense

heritability (77.65%) was calculated by Lakshmi *et al.* (2002) for 1000-seeds weight in pumpkin. The narrow sense heritability was relatively high (66.60%), which indicates the potentially of this quantitative character to be genetically imported through hybridization and selection. However, El-Tahawy (2007) reported that 100-seeds weight character in summer squash was controlled by one dominant pair of gene.

### 3. Seed net weight (%)

The results presented in Table 1 and 2 indicate significant differences among different parental genotypes and hybrids concerning seed net weight. Plants of line Mosh.15-27S-19 and Mosh.2-10S had the highest seed net weight (81.16%) followed by Mosh.2-7S-18 (80.63%) and Line#2 (80.51%). The $F_1$ hybrids Mosh.15-27S-19 X Mosh.33-27-13 (82.44%), TQ-1 X Mosh.11-5S-34 (81.72%) and Mosh.2-7S-18 X Mosh.33-27-13 (81.39%) were not significantly different from the highest parents.

The results presented in Table 2 show significant general and specific combining ability effects which indicate the influence of both the additive and non-additive gene effects on the inheritance of seed net weight. However, the additive gene effects were more important since the calculated ratio GCA/SCA was 3.22.

The highest values of general combining ability effect were associated with the parental lines Mosh.15-27S-19 (1.01), Line#2 (0.99) and Mosh.2-7S-18 (0.84) (Table 3). These results indicate that, the parental lines Mosh.15-27S-19, Line#2 and Mosh.2-7S-18 will be good combiners in forming hybrids with high seed net weight.

The highest values of specific combining ability effect were associated with the $F_1$ hybrids Mosh.15-27S-19 X Mosh.33-27-13 (3.11) and TQ-1 X Mosh.11-5S-34 (2.89). These $F_1$ hybrids will give plants with high seed net weight (Table 4).

The results presented in Table 5 show that the highest values of better parent heterosis were associated with the $F_1$ hybrids TQ-1 X Mosh.11-5S-34 (3.34%), Line#1 X Mosh.33-27-13 (2.94%) and Mosh.15-27S-19 X Mosh.33-27-13 (1.58%). These values could be higher in other combinations of parental genotypes.

In addition, the results presented in Table 6 show that, the broad sense heritability was above intermediate (67.22%) while the narrow sense heritability was intermediate (47.08%), which indicates that the

potentiality of this character to be genetically improved. Developing new *C. pepo* genotypes with high seed net-weight will suit the consumption methods of *C. pepo* seeds either for direct human consumption as a nutrious snack (Milan *et al.*, 2007) or for oil extraction which is used in many purposes (Stevenson *et al.*, 2007; Ebubekir, 2008)

### 4. Percentage of total oils in seeds

The results presented in Table 1 and 2 indicate significant differences among different parental genotypes and hybrids concerning total oils. Plants of line Mosh.2-7S-18 had the highest percentage of total oils (42.84%) followed by and Mosh.15-27S-19 (41.34%), Mosh.2-10S (41.24%) and Line#1 (40.43%). Differences among *C. pepo* genotypes concerning seed oil content have been reported (Hamid *et al.*, 1988; Undina *et al.*, 1991; Lee *et al.*, 1994; Idouraine *et al.*, 1996; Murkovic *et al.*, 1999; Milan *et al.*, 2007; Stevenson *et al.*, 2007). Oil contents in seeds of C. pepo cultivars ranged from 31.8 to 51% (Stevenson *et al.*, 2007) .In addition, the $F_1$ hybrid Mosh.2-7S-18 X Line#1 (44.26%), TQ-1 X Mosh.2-7S-18 (43.82%) slightly exceeded the highest parental line i.e., Mosh.2-7S-18 but the differences were not significant.

The results presented in Table 2 show significant general and specific combining ability effects. However, the calculated ratio for GCA/SCA was 2.05, i.e., more than unity. This result indicates that the additive type of gene action was more important in the inheritance of this character.

The highest value of general combining ability effect was associated with the parental lines Mosh.2-7S-18 (1.67). This result indicated that, the parental line Mosh.2-7S-18 will be good combiner in forming hybrids with high total oils seed content (Table 3).

The highest value of specific combining ability effects were associated with the $F_1$ hybrids TQ-1 X Mosh.15-27S-19 (3.41), Mosh.2-7S-18 X Line#1 (2.26), TQ-1 X Mosh.2-7S-18 (2.24) and Mosh.2-10S X Mosh.33-27-13 (20.15) (Table 4). These $F_1$ hybrids will give plants with high total oils seed content.

The results presented in Table 5 show, the highest value of better parent heterosis was associated with the $F_1$ hybrids Mosh.15-27S-19 X Mosh.11-5S-34 (16.13%). This result indicates the potentiality of

producing hybrids with high total oils content in seeds which contributes in enhancing the nutritional value of these seeds.

The broad sense heritability was high (81.89%) while the narrow sense heritability was below intermediate, (29.63%) (Table 6). These results indicate the influence of the environmental factors and non-additive type of gene action on the expression and inheritance of this character.

## 5. Percentage of total proteins

The results presented in Table 1 and 2 indicate significant differences among different parental genotypes and hybrids concerning percentage of total proteins. Plants of the inbred line TQ-1 which was derived from the population of cultivar Table Queen had the highest percentage of seed total proteins (42.80%). Such variations among squash genotypes concerning seed protein content are useful in breeding programs to improve this character. Idouraine *et al.* (1996) reported that protein values were significantly different among inbred lines of squash and ranged from 37.1% to 44.4%. The $F_1$ hybrid Mosh.15-27S-19 X Mosh.11-5S-34 (45.96%), TQ-1 X Mosh.2-10S (45.40%), TQ-1 X Mosh.33-27-13 (45.60%) and TQ-1 X Mosh.11-5S-34 (44.95%), significantly exceeded the highest parental line i.e., TQ-1.

The results presented in Table 2 show significant general and specific combining ability effects The calculated ratio GCA/SCA was 2.35, i.e., more than unity, which indicates that the additive type of gene action was more important in the inheritance of this character

The highest value of general combining ability effect was associated with the parental lines TQ-1 (2.75). This result indicated that, the parental line TQ-1 will be good combiner in forming hybrids with high total proteins seed-content (Table 3).

The highest value of specific combining ability effect were associated with the $F_1$ hybrids TQ-1 X Mosh.2-10S (5.58) and Mosh.15-27S-19 X Mosh.11-5S-34 (4.79) (Table 4). These $F_1$ hybrids will give plants with high total proteins seed-content. Seeds of such $F_1$ hybrids will be of great value as a human food (Loy, 2004; Milan *et al.*, 2007).

The results presented in Table 5 show that, the highest values of better parent heterosis were associated with the $F_1$ hybrids TQ-1 X Line#2 (5.37%) and Line#2 X Mosh.33-27-13 (4.89%). These results

indicate that the possibility of obtaining hybrids with high nutritional seeds due to its high total proteins content.

In addition, the results presented in Table 6 show that, the broad sense heritability was too high (97.28%) and the narrow sense heritability was low (35.07%). These results indicate the influence of the environmental factors on this character.

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# دراسات وراثية علي المحصول البذرى في الكوسة

نجوي محمود عثمان [1] ، أحمد رضا عجور [2] ، لطفى عبد الفتاح بدر [2] ، عبد المنصف عبد الرؤوف قموح[1]

1- أقسام بحوث الخضر – معهد بحوث البساتين – مركز البحوث الزراعية

2- قسم البساتين – كلية الزراعة – جامعة بنها

استخدم في هذا البحث ثمانية سلالات مرباة ذاتياً من الكوسة تم التهجين فيما بينهـا بنظام التزاوج النصف دائرى ، وذلك لدراسة بعض المعايير الوراثية الضرورية لبـرامج التربية لتحسين المحصول البذرى وكذلك محتوى البذور من الزيت والبروتين .

وقد أوضحت النتائج التأثير المعنوى للقدرة العامة والخاصة للتوافـق علــى صـفات المحصول البذرى للنبات ، وزن الألف بذرة ، نسبة الوزن الصافى للبذرة ، وكذلك نسبة الزيت والبروتين لها ، مما يدل على وجود تأثير إضافى وغير إضافى للجينات في توريث تلك الصفات . وقد كانت نسبة القدرة العامة إلي القدرة الخاصة علي التــآلف أكبــر مــن الواحد الصحيح مما يشير إلي أن مكونات التأثير الإضافى هـى الأكثـر تـأثير بالنــسبة للمكونات الوراثية الأخرى .

معامل التوريث علي النطـاق الواسـع كـان 88.84% ، 86.38% ، 67.22% ، 81.89% ، 97.28% بينما معامل التوريث علي النطاق الضيق كان 2.0% ، 66.60% ، 47.08% ، 29.63% ، 35.07% لكل من المحصول البذرى للنبات ، وزن الألف بذرة ، نسبة الوزن الصافى للبذرة ، نسبة الزيت والبروتين فى البذور ، على التوالى . أوضـحت تلك النتائج تأثير العوامل البيئية والتأثير الغير إضافي للجين فى وراثة تلك الصفات.