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Assessment of Heterosis, Combining Ability and Genetic Variance for some Economical Traits in Melon (*Cucumis melo*, L.).

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ABSTRACT

Five genotypes of melon were obtained from Cornell University named, Line 00-1107 (P₁); Line 00-1102 (P₂); Line 00-1107 (P₃); Line 00-1109A (P₄) and Line 00-1113 (P₅) which crossed in a half diallel mating design in Kaha Research Farm, Horticultural Research Institute, Agriculture Research Centre in the Kalyobiya Governorate, Egypt, during the planting summer seasons 2021 and all genotypes were evaluated during 2022 season. The results indicated that the genotypes in the study possessed high variability for all the studied traits. There were high differences between the crosses for mid parent and better parent heterosis in all the studied traits. F₁ hybrids (P₃×P₄) and (P₄×P₅) gave the highest means for yield and yield attributes. The magnitudes of GCA and SCA effects were significantly which indicated the presence of both additive and dominance gene effect in governing all the studied traits. The GCA/SCA ratio was more than one which indicates that additive gene effect was more important in the inheritance of the studied traits. General combining ability analysis exhibited that P₃ and P₄ could be considered as promising parents in breeding programs to produce melon hybrids. Heritability in the broad sense was larger in values than their corresponding heritability in narrow sense, which indicates the large effects of the genetic variance on the expression of these traits. The obtained results of heritability evaluation presented additional evidence about predominance of dominance gene effect in the inheritance of the studied traits. Therefore, hybridization program could be used for producing superior promising melon hybrids.

Keywords: melon, heterosis, combining ability, gene actions and heritability.

INTRODUCTION

In developing countries, the majority of the population depends on agriculture to meet their food needs. Melon is one of the good crops and is rich in different essential minerals making it of large medicinal value. The cultivated area of melon in 2020 according to the Ministry of Agriculture statistics, reached about 4778 feddan which produces 37546 tons with an average of 7.858 tons/fed. Melon (*Cucumis melo*, L. 2n = 24.) is one of the most important dessert cucurbits of Egypt, which is grown in Egypt as the most important vegetable crops for local consumption and exportation to many countries where it occupied an important position between the exported agricultural crops in many countries. Melons are nutrient dense and provide a wide variety of important minerals and vitamins (Anonymous, 2002). Recent crop genetic development programs may usually have the great objective of increasing yield and quality, to be able to feed the 21st century population. The estimates of different genetic parameters are very advantageous in understanding the nature and value of genetic variability in the breeding material (Ansari et al., 2020). Although Egypt has favorable melon genetic sources, most of the commercially grown varieties are produced by foreign seeds companies. Also, some of the imported varieties are not well adapted to consumer tastes and local environmental conditions (Glala et al., 2010). Good understanding of the components of genetic variance and its effects on economical traits. In addition, it is used in understanding the nature of gene effects involved in the expression of quantitative characters (Shivaji et al., 2018; Suzy et al., 2020). Heterosis or hybrid vigor is the genetic expression of the distinction of a hybrid in relation to its parents; the term heterosis has been suggested to

describe the increased performance of the hybrid versus the best parent (Shashikumar and Pitchaimuthu 2016). Developing heterogenous population through heterosis between the desired genotypes was always the optimum tool for melon breeder to improve yield and quality. This procedure was used in Egypt to produce high yielding melon varieties with desired horticulture traits (Mohammadi et al., 2014). Heterosis expressed in terms of mid parent or versus better parent or versus economical hybrid with respect to horticultural desirable traits; basic concept of heterosis has been discussed by Napolitano et al. (2020). In addition, heterosis (hybrid vigor) is modified by the interaction among environment and genotypes (Simranpreet et al., 2022). Diallel crosses mating designs have been used in vegetable breeding research to obtain data on genetic actions estimate the different and major genetic components; i.e., additive genetic variance, non-additive genetic variance, combining abilities and heritability of the parents and cross combinations (Hallauer, 2007). The knowledge of GCA and SCA would be of crucial role to cucurbits breeders, as it provides information about possibilities and methods of development for different horticultural traits. Both GCA and SCA effects have been defined as the performance of a genotype in hybrids and plays a crucial role in selecting excellent genotypes for hybrid combinations and inheritance of yield and quality traits (Alabboud et al., 2020). Also, GCA is involving additive gene actions, representing the mean parental lines performance in hybrids, at the same time, the SCA is involving dominance gene actions. Analysis of variance for general and specific combining ability effects in melon has been determined by several authors; (Singh and Vashisy, 2018; El-Sayed et al., 2019; Badami et al., 2020). Barros et al. (2011) found that TSS, number of fruits, total yield traits was

* Corresponding author. E-mail address: dalaaagri@yahoo.com DOI: 10.21608/jpp.2023.184617.1204 controlled by additive and dominance effects, on the other side, fruit flesh thickness, fruit diameter and average fruit weight traits were governed by additive effects. Hatem et al. (2014) reported that additive and non-additive gene effect was involved while the additive gene effect expressed to play the major role in the inheritance of studied traits. Chaudhary et al. (2017) found that, with genetic analysis of total yield and related traits by the diallel mating design on melons and exhibited the characters of fruit flesh thickness, fruit length and average fruit weight. Genes are governed by the influences of relative non - additive, while total yield traits are governed by the effect of non - additive. In another study, Hussein and selim (2014) observed that additive gene actions were important with respect to days to maturity for fruits, fruit flesh thickness, TSS and average fruit weight, while genetic dominance actions mainly governed total yield. Several researchers studied gene effects of the yield and associated traits and estimated that additive $(\sigma^2 A)$ and dominance $(\sigma^2 D)$ variance components are major in the genetic control of yield and related characters in melon (Shamel, 2013). Badami et al. (2020) showed that the majority of the characters were governed by non-additive gene effect, verifying that the aforementioned breeding material could be efficiently used for the production of cross combinations on the basis of heterotic effects. In a study by El Sayed et al. (2019) recorded that GCA/SCA ratio ranged from 4.40 to 57.80, none of the parental lines were reported to be a good combiner for all studied traits. In melon, Sunil et al. (2018) estimated the gene effect of yield and related traits and found that the general and specific combining ability effects were highly significant for most studied traits. Mohammadi et al. (2014) reported that analysis of variance indicated high significant differences between the genotypes for total soluble solids in Cantaloupe. They noticed the additive $(\sigma^2 A)$, genetic variance and heritability in narrow-sense were significant for the same trait. Heritability coefficient is an index of the transmission of traits from parents to their offspring and it plays a major role in the selection process in vegetable breeding (Taha et al., 2007). Abo Sedera et al. (2016) reported that very high the heritability in broad-sense 95%, 99% and 99%, while the magnitudes of heritability (in narrow-sense) were 22%, 41% and 61% for total sugars, total soluble solids content and total carotenoids, consequently, which indicate the high effects of the genetic variance on the expression of aforementioned traits. In addition, the additive variance components are relatively high compared to the other types of genetic variation components. The estimates of heritability (broad-sense) were larger than their corresponding the heritability (narrow sense) for studied traits (Abd El-Hadi et al., 2020). Recently, Esmaeili et al. (2022) found that high the heritability in narrow-sense for number of fruit per plant, fruit flesh firmness and total yield per plant indicated less environmental effect for aforementioned traits and the important role of additive genetic effects, they reported that the role of dominance genetic effects of genes in controlling fruit flesh firmness and total yield traits was higher than additive genetic effects. Therefore, the aims of this present study were to: (i) assess performance, heterosis, combining ability and heritability percentages for five inbred lines and their hybrids, using a half diallel mating design for agronomic, yield and related traits, (ii) identify desirable parents and cross combinations for further breeding studies on improving melon.

MATERIALS AND METHODS

The present study entitled "Assessment of heterosis, combining ability and genetic variance for some economical

traits in melon (*Cucumis melo*, L.). Crosses among the selected best performer inbred lines melon in Kaha Research Farm, Horticultural Research Institute, (HRI), Agriculture Research Centre (ARC) in the Kalyobiya Governorate, Egypt., during the planting seasons 2021and 2022.

Collection of planting materials

Seeds of the five inbred lines of melon used were obtained from Cornell University named, Line 00-1107 (P₁), Line 00-1102(P₂), Line 00-1117 (P₃), Line 00-1109A (P₄) and Line 00-1113 (P₅). Selection plants were based on yield and yield related traits. Crosses were made to produce 10 cross combinations, following the half diallel mating design during the 2021 planting summer season. The seeds of the 16 melon genotypes; 5 parents and their 10 F₁hybrids beside the commercial hybrid named Galia 96 were sown in the open field on 20th of March 2022 season using the Randomized Complete Block Design, with three replications. The plot area was 7.5 m² which consisted of one ridge 5 m long and 1.5 m wide with spacing 0.50 m among the growing plants., all practices such as fertilization, irrigation, pest, disease control and weed removal were applied in compliance with those traditionally adopted in Egypt during crop growth period. Data were calculated on five plants in each plot for measuring the growth traits of melon. The data were statistically analyzed of variance (ANOVA) using the Co-STAT software programme.

Data Collection

Observations were calculated for all genotypes under the study on the following traits; plant length (P.L., cm), number of branches per plant (No.B./P.), days to maturity (D.M., Days); samples of five random ripening fruits per plot were randomly taken to estimate the fruits traits such as; fruit shape index (F.Sh.I.), fruit firmness (F.F., g/cm²), flesh thickness (F.Th., cm), total soluble solid of melon juice using a hand refractometer (TSS %), all fruits of each plant were counted and weighted to estimate average fruit weight (A.F.W., kg), number of fruits per plant (No.F./P.) and total yield per feddan (T.Y/F., ton) were calculated for the whole season and then calculated as ton per feddan.

Statistical analysis:

The main goal of the present study was to estimate of heterosis, combining ability and genetic variance for some economical traits in melon (*Cucumis melo*, L.) and identify suitable parents and cross combinations for further breeding studies on improving melon yield.

The amount of heterosis (hybrid vigor) was recorded as follows:

$$H_{MP.}\% = ((F_{1-}((P_{1} + P_{2})/2) / ((P_{1} + P_{2})/2)) \times 100$$
 $H_{BP.}\% = ((F_{1-}B.P.) / B.P.) \times 100$
 $H_{CH.}\% = F_{1-}C.H / C.H \times 100.$
 $SE_{BMCP} = (3Me/2r)^{0.5}, SE_{BEP} = (2Me/r)^{0.5}$

Potence ratio was estimated according to Smith (1952) to measure the degree of dominance as:

$$PR = F_1 - M.P / 0.5 (P_2 - P_1).$$

Analyses of general and specific combining ability: General and specific combining ability effects were recorded, according to Griffing (1956); model two of method II. From the (E.M.S.) indicated in Table 1, the determination of

variance components of GCA ($\sigma^2 gca$) and SCA ($\sigma^2 sca$) were recorded as follows:

$$\sigma^2 g c a = (M_g - M_s) / (n + 2), \ \sigma^2 s \ s c a = M_s - M_e$$

Evaluation of GCA effects (gi) and SCA effects (sij) were calculated as follows:

GCA effect (gi) =
$$1/n+2 \left[\sum (Y_i + Y_{ii}) - 2/n Y_i \right]$$
.

SCA effect
$$(x_{ij}) = Y_{ij} - 1/n + 2(Y_i + Y_{ij} + Y_{ij} + Y_{ij}) + 2/(n+1)(n+2)Y_{ij}$$

Estimation of the standard errors (*S.E.*) of the evaluated general combining ability and specific combining ability effects were calculated as follows:

SE value of GCA
$$(\underline{n}-\underline{n}) = [(2/(n+2))]^{1/2}$$
. SE value of SCA $(\underline{n}) = [n(n-1)/(n+1)(n+2)]^{1/2}$.

Additive $(\sigma^2 A)$ and non-additive $(\sigma^2 D)$ genetic variances were calculated as suggested by Matzinger and Kempthorne (1956).

Determination of heritability: Broad ($h^2_{b.s}$ %) and narrow sense ($h^2_{n.s}$ %) heritability for all the genotypes under the study were counted from the genetic components according to the following formula produced by Mather and Jinks (1982).

$$h^{2}_{b_{2}}\% = \{\sigma^{2}A + \sigma^{2}D / \sigma^{2}A + \sigma^{2}D + \sigma^{2}E\} \times 100; h^{2}_{b_{2}}\% = \{\sigma^{2}A / \sigma^{2}A + \sigma^{2}D + \sigma^{2}E\} \times 100.$$

Table 1. Analysis of variance for the determinations of general combining ability and specific combining ability components.

| S.O.V | D.F | M.S. | E.M.S. |
|--------|------------|---------|--|
| G.C.A. | n – 1 | M_{g} | σ^2 e + σ^2 sca + (n + 2) σ^2 gca |
| S.C.A. | n(n-1)/2 | M_s | $\sigma^2 e + \sigma^2 sca$ |
| Error | (r-1)(p-1) | M_{e} | $\sigma^2 e$ |

 $Mg = Mean \ square \ of \ GCA; \ Ms = mean \ square \ of \ SCA; \ Me = mean \ square \ of \ error; \ r = number \ of \ replicates; \ p = number \ of \ populations \ and \ n = number \ of \ parents.$

RESULTS AND DISCUSSION

Analysis of variance:

The results in Table 2 observed that the highly significant differences among melon genotypes (five parental genotypes + 10 F₁ hybrids + commercial hybrid (Galia 96)) for plant length, days to maturity, fruit shape index, fruit firmness, flesh thickness, TSS, average fruit weight, number of fruits / plant and total yield, revealing a great amount of variability between them. The significant differences between all genotypes are the first required to complete the investigation and predict the improvement between these parents and their crosses in breeding programme. Mean square magnitudes of parents vs. hybrids (as an indicator of average heterosis over F₁ hybrid) were highly significant for aforementioned traits. The genotypes represent high yielding, it's a general melon average yield in Egypt returned in the heterosis in cross combinations; these results indicated that they use these genotypes in breeding programs to improve the yield and quality. The obtained results indicate that genotypic variation between entries was present. The obtained results could be used as indication to mean heterosis overall hybrids and therefore could be used through breeding programs to improve traits. The variation between mean square magnitudes for parents versus crosses were highly significant for all studied traits, reporting that; dominance or epistasis genetic effects were of great role in the inheritance of these traits. Similar results were obtained by Pouyesh et al. (2017); Javanmard et al. (2018) and Suzy et al. (2020).

Table2. Analysis of variance and mean squares for all studied traits of melon.

| Traits Para. | df | P.L. (cm) | No. B./P. | D.M. (days) | F.Sh.I. (cm) | F.F. (g/cm ²) | F.Th. (cm) | TSS % | A.F.W. (kg) | No. F./ P | T.Y./F (ton) |
|-----------------|----|--------------|--------------|----------------|-----------------|------------------------------|-------------|-------------|----------------|--------------|-----------------|
| Replications | 2 | 4.68 | 1.35 | 2.15 | 0.001 | 0.02 | 0.02 | 0.01 | 0.006 | 0.02 | 0.80 |
| genotypes | 14 | 963.25** | 15.28** | 10.95** | 6.05^{**} | 2.99** | 0.90^{**} | 2.12^{**} | 0.071** | 0.10^{**} | 22.38** |
| Error | 28 | 6.78 | 1.14 | 0.58 | 0.001 | 0.06 | 0.01 | 0.07 | 0.01 | 0.01 | 0.27 |

P.L.: plant length, No. B/P.: number of branches per plant, D.M.: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F./P.: number of fruits per plant and T.Y./F.: total yield per feddan. **: significant at 0.01 levels of probability.

Mean performance:

Mean performance for the ten traits among the genotypes for all traits are listed in Table 3. Regarding the obtained results, there were highly significant differences between genotypes for all the studied traits. Large range of variation was found between the selected inbred lines. These results exhibited variations for plant length in the evaluated melon genotypes. The parental lines ranged from 186.67 cm (P_2) to 241.33cm (P_4) , while the plant length of the F_1 hybrids ranged from 193.67cm ($P_1 \times P_2$) to 233.67cm ($P_1 \times P_4$). Among parents, the highest parents were P₄ and P₃ for plant length, meanwhile P₂ was the shortest. Among F₁hybrid, cross $(P_1 \times P_4)$ had the highest plants. Contrarily, $(P_1 \times P_2)$ had the lowest plants for this trait. Regarding number of branches among parents ranged from 11.00 (P2) to 17.00 (P4), cross $(P_1 \times P_4)$ gave the highest number of branches while F_1 cross $(P_4 \times P_5)$ gave the lowest number of branches / plant. In respect of days to maturity were ranged from 83.00 (P₃) to 87.33 (P₁). The F_1 hybrid ranged from 81.33 ($P_1 \times P_2$) to 87.33 ($P_1 \times P_3$). As well as, the F_1 hybrid $(P_1 \times P_2)$ had the highest significantly days to maturity among all estimated genotypes compared

with the check hybrid. The parental range of fruit shape index was from 0.70 (P_2) to 1.02 (P_4). The fruit shape index of the crosses varied from 0.90 (P₁×P₂) to 1.16 (P₃×P₄). These results are in a accordance to (El-Sayed et al., 2019; Alabboud et al., (2020). Concerning fruit firmness, P₅ gave the highest means while (P_1) gave the lowest value. The cross $(P_1 \times P_4)$ gave the smallest value; on the other hand, $(P_3 \times P_5)$ was the largest value. The obtained data in table 3 exhibited that fruit flesh thickness where P₄ recorded the highest means while (P₂) recorded the lowest value. As well as, the F₁hybrid $(P_3 \times P_4)$ gave the highest value but $P_1 \times P_2$ gave the lowest value. The greatest TSS was noticed by the F_1 hybrid ($P_3 \times P_4$) and it was different significantly from all other estimated genotypes. The F_1 hybrid ($P_2 \times P3$) gave the lowest TSS compared with the Galia 96 hybrid. The obtained results showed that parental variety P4 recorded the highest magnitude for average fruit weight, while parental variety (P5) gave the highest magnitude for number of fruits / plant traits, in the same time F_1 hybrids (P_3xP_4) recorded the highest value for average fruit weight and number of fruits / plant. The total yield per feddan trait was very important for vegetable

breeders and farmers, the parent P_4 recorded the greatest value over all evaluated genotypes. In the same time F_1 hybrid $(P_3 \times P_4)$ and $(P_4 \times P_5)$ gave the highest means, Therefore, these hybrids could be used in melon production. In addition, F_1

cross (P_1xP_2) recorded the smallest magnitude for this trait. These results agreed with those of Abd-Elwanis and Mahmoud (2016); Selim (2019); Badami *et al.* (2020) and Napolitano *et al.* (2020).

Table3. Mean performances of the five parental lines and their cross combinations for studied traits of melon.

| Traits | P.L. | No. B/P. | D.M. | F.Sh.I. | F.F. | F.F.Th. | TSS | A.F.W. | No. | T.Y./F |
|---------------------------------|--------|----------|--------|---------|----------------------|---------|-------|--------|------|--------|
| Geno. | (cm) | NO. D/P. | (days) | (cm) | (g/cm ²) | (cm) | % | (kg) | F./P | (ton) |
| $\overline{\mathbf{P}_1}$ | 192.00 | 11.67 | 87.33 | 1.00 | 9.71 | 2.87 | 9.37 | 0.638 | 1.39 | 7.09 |
| P_2 | 186.67 | 11.00 | 83.67 | 0.70 | 9.10 | 3.42 | 7.70 | 0.687 | 1.50 | 8.24 |
| P_3 | 210.00 | 12.00 | 83.00 | 0.81 | 11.45 | 3.80 | 9.67 | 1.003 | 1.52 | 12.20 |
| P_4 | 241.33 | 17.00 | 83.67 | 1.02 | 10.35 | 4.00 | 8.80 | 1.109 | 1.41 | 12.51 |
| P_5 | 197.00 | 11.33 | 83.67 | 0.97 | 12.10 | 2.33 | 10.82 | 0.876 | 1.56 | 10.93 |
| $P_1X P_2$ | 193.67 | 11.67 | 81.33 | 0.90 | 9.62 | 2.98 | 10.33 | 0.709 | 1.38 | 7.85 |
| $P_1X P_3$ | 200.33 | 13.67 | 87.33 | 0.99 | 11.48 | 3.77 | 9.30 | 0.974 | 1.79 | 13.95 |
| $P_1X P_4$ | 233.67 | 17.67 | 83.33 | 1.13 | 9.93 | 2.77 | 9.66 | 1.070 | 1.60 | 13.70 |
| $P_1X P_5$ | 197.67 | 13.33 | 87.33 | 1.05 | 11.76 | 3.50 | 10.53 | 0.830 | 1.71 | 11.34 |
| $P_2X P_3$ | 212.00 | 14.67 | 83.33 | 0.97 | 10.63 | 3.80 | 8.80 | 0.943 | 1.88 | 14.18 |
| $P_2X P_4$ | 229.33 | 12.33 | 83.00 | 1.15 | 10.09 | 3.02 | 9.40 | 0.991 | 1.81 | 14.36 |
| $P_2X P_5$ | 195.00 | 14.33 | 82.67 | 0.98 | 11.17 | 3.77 | 8.87 | 0.874 | 1.81 | 12.66 |
| $P_3X P_4$ | 217.67 | 17.67 | 83.00 | 1.16 | 10.91 | 4.33 | 10.90 | 1.120 | 1.89 | 16.93 |
| $P_3X P_5$ | 202.00 | 12.33 | 82.00 | 0.98 | 12.10 | 3.20 | 9.80 | 0.993 | 1.64 | 13.07 |
| P ₄ X P ₅ | 229.00 | 11.67 | 83.33 | 1.11 | 11.68 | 3.03 | 9.70 | 1.108 | 1.76 | 15.60 |
| Galia 96 | 190.13 | 12.88 | 85.67 | 1.00 | 11.00 | 4.18 | 10.00 | 0.799 | 1.75 | 11.19 |
| LSD at 5 % | 4.35 | 1.79 | 1.28 | 0.05 | 0.42 | 0.17 | 0.44 | 0.04 | 0.13 | 0.87 |
| LSD at 1 % | 5.70 | 2.41 | 1.72 | 0.07 | 0.62 | 0.23 | 0.59 | 0.06 | 0.18 | 1.19 |

P.L.: plant length, No.B/P.: number of branches per plant, D.M.: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F. /P.: number of fruits per plant and T.Y./F.: total yield per feddan.

Magnitude of heterosis:

The obtained results presented in Table 4 revealed the most of cross combinations manifested positive significantly heterosis over mid parents and better parents for all studied traits. The results revealed that the highest positive heterosis effect for plant length gave by hybrid $P_1 \times P_4$ (7.85%) versus mid and P₃ x P₅ (6.92%) better parents. F₁ hybrids P₂ x P₃ (31.33%) over mid and (29.48%) better parents for the same cross were highest positive heterosis effect for number of branches. Moreover, the highest positive heterosis effect for days of maturity was recorded by P₁ x P₃ (2.54%) over mid and (5.22%) better parents for the same hybrid. Similarly, for four crosses gave negative and significant heterosis which is a favorable trend of heterosis for this trait. The highest positive heterosis effect for shape index was noticed by F₁ hybrid P₃ x P₄ (4.12 %) over mid and better parents. For fruit firmness trait hybrid P_{1 X}P₃ (8.30 %) over mid and (7.40 %) better parents were noticed positive heterosis. The highest positive heterosis effect for fruit flesh thickness was reported in $P_{1 X} P_{3}$ (12.88) and $P_{3X} P_{5}$ (6.92%) over mid parents and better parents, respectively. For TSS, P_{1 X} P₂ (21.11%) and (10.25%) versus mid and better parents, consequently was showed the highest positive heterosis. The highest positive heterosis effect for average fruit weight was reported in P₁ x P₄ (27.00%) over mid and (21.24%) better parents for the same hybrid. For number of fruits / plant, P₃ x P₄ (28.57%) over mid and (24.34%) better parents were showed the highest positive heterosis for the same hybrid. Finally, the highest positive heterosis effect of total yield F₁ hybrid P₁ x P₄ (43.68%) versus mid parent and (37.51 %) better parent for the same hybrid, which is consistent with Greish et al. (2005) and Luan et al. (2010)

The maximum positive and significant mid parent heterosis are observed in F_1 hybrids $P_3 \times P_4$ and $P_1 \times P_4$ (12.44% and 8.69%), (19.84% and 9.46%) for both plant length and number of leaves / plant respectively. While, F_1 hybrids $P_3 \times P_4$ and $P_2 \times P_4$ exhibited the best desirable heterotic effect for days to maturity and total yield / feddan,

respectively. The same conclusion are reached in the case of negative mid-parent heterotic magnitudes recorded in days to maturity in all the crosses except crosses (P₁xP₂), (P₁xP₃) and (P₂ xP₃) Negative heterosis in days to maturity has been reported by (Chaudhary et al., 2018; Costa et al., 2019). Besides, significant positive mid parent heterosis for fruit length and fruit shape index for crosses P₂ x P₄ and P₃ x P₄ 20.20%, 7.93% and 40.78% and 32.17%, respectively. The results are confirmed by Abou Kamer et al. (2015); Abd-Elwanis and Mohmoud (2016) and Selim (2019). On the other side, the F_1 hybrids $P_4 \times P_5$ and $P_3 \times P_4$ have a significant positive mid parent heterosis for average fruit weight (20.06 and 17.59%) while, the F_1 hybrids $P_2 \times P_3$ and $P_3 \times P_4$ had significant positive mid parents heterosis for number of fruits / plant. P₁ x P₂ and P₃xP₄ were the most promising cross combinations with the high desirable heterosis values of total yield versus mid parent and bitter parent. Heterosis was recorded by many authors for the economical traits in melon (EL-Sayed et al., 2019; Macro et al., 2020; Suzy et al., 2020; Nahla and Shaban 2021 and Esmaeili et al., 2022).

The obtained potence ratio (P.R.) values for these crosses (Table 5) supported the existence of this gene reaction and elucidate that most of F_1 hybrids had positive magnitudes for most traits suggesting dominance towards the largest parent in the traits (partial, complete and over dominance). These obtained results reflected various degrees of dominance which were involved in the inheritance of these traits. When the potence ratio magnitudes were more than one, this indicated dominance control in inheriting these traits. While, the potence ratio magnitude was less than one, indicating that partial dominance influential these traits. On the contrary, the recorded magnitudes of potence ratio in most F₁ hybrids were negative for most traits. Estimates of potence ratio supported the results on heterosis (hybrid vigor). Negative recorded magnitudes of potence ratio indicated the presence of different degrees of recessiveness. These results are consistent with those obtained by Hatem et al. (2014); Mohammadi et al. (2014); Abd-Elwanis and Mahmoud (2016); Tak, (2017); Sunil et al. (2018); Abd El-Hadi et al. (2020) and Simranpreet et al. (2022).

Table 4. Percentage of heterosis versus mid parents, better parents and commercial hybrid for crosses of studied melon traits,

| Tuble with the contained of inevertibles with building better parents and commercially britarior erospes of studied inevertible | | | | | | | | | | | | | | | |
|---|-------------|---------|--------------|--------------|--------------|---------|-------------|----------|---------|-------------|-------------|--------------|-------------|-------------|-------------------------|
| Traits | | P.L.(cn | n) | | No. B./P | | D | . M.(day | rs) | F | Sh.I. (cr | n) | F | .F. (g/cm | 1 ²) |
| Hybrids | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. |
| $P_1 \times P_2$ | 2.29** | 0.88 | 1.86 | 2.94** | 0.00 | -9.39** | -4.88** | -2.80** | -5.07** | 0.00 | -1.00** | -10.00** | 2.23** | -0.93** | -12.55** |
| $P_1 \times P_3$ | -0.33 | -4.61** | 5.36* | 18.87** | 17.14^{**} | 6.13** | 2.54^{**} | 5.22** | 1.94 | -1.00** | -1.00** | -1.00 | 8.30^{**} | 0.00 | 4.36* |
| $P_1 \times P_4$ | 7.85** | -3.18** | 22.90^{**} | 23.31** | 3.94** | 37.19** | -2.54** | -0.41 | -2.73* | 1.00^{**} | 1.00^{**} | 13.00** | -1.00** | -4.06 | -9.73** |
| $P_1 \times P_5$ | 1.63 | 0.34 | 3.97 | 15.91** | 14.22^{**} | 3.49 | 2.14^{**} | 4.37** | 1.93 | -2.02** | -0.30** | 5.00^{*} | 7.79** | -2.81** | 6.09^{**} |
| $P_2 \times P_3$ | 6.90^{**} | 0.95 | 11.50** | 31.33** | 29.48^{**} | 13.90** | -0.01 | 0.40 | -2.73* | -1.02** | -2.02** | -3.00 | 3.30 | 7.40^{**} | -3.36 |
| $P_2 \times P_4$ | 7.17^{**} | -4.97** | 20.62** | -11.93** | -27.47** | -4.27* | -0.80 | -0.80 | -3.12** | 0.00 | -1.00** | 15.00^{**} | 3.70 | -2.51** | -8.27** |
| $P_2 \times P_5$ | 1.65 | -1.02 | 2.56 | 28.29^{**} | 26.48** | 11.26** | -1.20* | -1.20 | -3.50** | 4.12^{**} | 4.12^{**} | -2.00 | 5.38 | -2.70** | 1.55 |
| $P_3 \times P_4$ | -3.54** | -9.80** | 14.48** | 24.70^{**} | 3.94** | 37.19** | -0.41 | 0.00 | -3.11** | 0.00 | 0.00 | 16.00^{**} | -0.09 | -4.97** | -0.82 |
| $P_3 \times P_5$ | | -3.80** | 6.24^{*} | 8.83** | 8.83** | -4.27* | -1.61* | -1.20 | -4.28** | 0.00 | -1.01** | -2.00 | 2.63 | 0.00 | 10.00^{**} |
| P ₄ x P ₅ | 4.49^{**} | -5.11** | 20.44** | -17.64** | -31.35** | -9.39** | -0.80 | -0.80 | -2.73* | 0.00 | -1.00** | 11.00^{**} | 4.01 | -3.47** | 6.18^{**} |

P.L.: plant length, No. B./ P.: number of branches per plant, D.M.: days to maturity, F.Sh. I: fruit shape index, F.F.: fruit firmness, *, ***: significant at 0.05 and 0.01 levels of probability, respectively, M.P. and B.P.; heterosis versus mid and better parents and C.H.: commercial hybrid

Table 4.Continu.....

| Traits | F. Th. (cm) | | | TSS % | | A | .F.W. (k | (g) |] | No. F./ P | | T.Y./F. (ton) | | | |
|---------------------------------|--------------|-------------|----------|-------------|-------------|-------------|-------------|-------------|------------|-----------|---------|---------------|---------|---------|----------|
| Hybrids | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. | M.P | B.P | C.H. |
| $P_1 \times P_2$ | -5.40** | -12.87** | -28.71** | 21.11** | 10.25** | 3.30** | 7.31** | 7.12** | -11.26** | -4.83** | -8.00** | 21.14** | 2.11** | 0.46 | -29.85** |
| $P_1 \times P_3$ | 12.88** | -0.80** | -9.81** | -2.31** | -3.83** | -7.00** | 0.66^{**} | 0.09 | 21.90** | 22.60** | 17.76** | 2.29 | 22.26** | 17.39** | 24.66** |
| $P_1 \times P_4$ | 6.55** | -3.48** | -33.73** | 6.30^{**} | 3.10^{**} | -3.40** | 27.00** | 21.24** | 33.92** | 14.29** | 13.48** | -8.57** | 43.68** | 37.51** | 16.09** |
| $P_1 \times P_5$ | 1.16** | -13.58** | -16.27** | 7.93** | 0.74^{**} | 5.30** | -3.45** | -3.97 | 3.88 | 15.54** | 9.62** | -2.29 | 10.47** | 4.75** | 1.34 |
| $P_2 \times P_3$ | 5.26** | 0.00 | -9.09** | 1.40** | -8.99** | -12.00** | 6.25** | 5.46** | 18.02** | 24.50** | 23.68** | 7.43** | 31.61** | 29.57** | 26.72** |
| $P_2 \times P_4$ | 4.86^{**} | -11.70 | -27.75** | 10.91** | 6.82^{**} | -6.00** | -3.20** | -7.76** | 24.03** | 23.97** | 20.67** | 3.43^{*} | 20.63** | 18.37** | 28.33** |
| $P_2 \times P_5$ | 0.80 | -6.91** | -9.81** | -4.21** | -18.02** | -11.30** | 5.77** | 5.01** | 9.39^{*} | 18.30** | 16.03** | 3.43* | 25.75** | 22.22** | 13.14** |
| $P_3 \times P_4$ | 4.23** | -15.79** | 0.04 | 14.10** | 8.90** | 9.00^{**} | 5.96** | 1.70^{*} | 40.18** | 28.57** | 24.34** | 8.00 | 36.09** | 35.64** | 51.30** |
| $P_3 \times P_5$ | 10.18^{**} | 6.92^{**} | -23.44** | -4.39** | -9.43** | -2.00 | 0.11 | 0.09 | 24.28** | 6.49** | 5.13** | -6.29** | 16.72** | 15.21** | 16.80** |
| P ₄ x P ₅ | -5.02** | -25.19** | -27.51** | -1.12** | -10.35** | -3.00* | -4.17** | -8.05** | 38.67** | 18.12** | 12.82** | 0.57 | 13.83** | 12.73** | 39.41** |

F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F. /P.: number of fruits per plant, and T.Y./F.: Total yield per feddan. *, **: significant at 0.05 and 0.01 levels of probability, consequently, M.P. and B.P.; heterosis versus mid and better parents and C.H.: commercial hybrid

Table 5. Potence ratios of cross combinations for some studied melon traits.

| Traits crosses | P.L. (cm) | No. B./P. | D.M. (days) | F.Sh.I. (cm) | F.F. (g/cm ²) | F. Th. (cm) | TSS % | A.F.W. (kg) | No. F./P. | T.Y./F. (ton) |
|-------------------|--------------|-----------|----------------|-----------------|------------------------------|----------------|-------|----------------|-----------|------------------|
| $P_1 \times P_2$ | -1.62 | -0.97 | -26.47 | 0.00 | -0.68 | -0.61 | -2.13 | 0.02 | -1.67 | 0.40 |
| $P_1 \times P_3$ | -0.07 | -12.76 | -0.99 | 0.20 | 0.99 | 0.91 | -1.47 | 0.84 | 4.71 | 1.31 |
| $P_1 \times P_4$ | 0.69 | 2.31 | -12.76 | 0.00 | -0.31 | -0.63 | -1.97 | 0.83 | 20.00 | 1.48 |
| $P_1 \times P_5$ | 1.27 | -10.76 | 10.76 | 0.40 | 0.71 | 0.07 | 1.10 | 0.61 | 2.56 | 1.20 |
| $P_2 \times P_3$ | 1.17 | 20.59 | -0.03 | -1.00 | 0.29 | 1.27 | 0.11 | 0.62 | 37.00 | 1.86 |
| $P_2 \times P_4$ | 0.56 | -0.56 | 0.00 | 0.00 | 0.57 | -0.25 | 2.09 | 0.44 | -7.00 | 1.94 |
| $P_2 \times P_5$ | 0.61 | 18.59 | 0.00 | 0.00 | 0.38 | 0.09 | -0.25 | 0.49 | 9.33 | 1.78 |
| $P_3 \times P_4$ | -0.51 | 1.23 | -1.10 | 0.00 | 0.02 | 0.18 | -2.93 | 0.55 | -7.00 | 39.00 |
| $P_3 \times P_5$ | 0.23 | 0.00 | 0.00 | 0.00 | 1.00 | 3.08 | -0.78 | -0.33 | 5.00 | 2.34 |
| $P_4 \times P_5$ | -0.44 | 0.88 | 0.00 | 0.00 | 0.51 | -0.19 | -0.11 | -0.96 | 3.38 | -5.13 |

P.L.: plant length, No. B/P.: number of branches per plant, D.M.: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F/P.: number of fruits per plant and T.Y/F: total yield per feddan.

Analysis of variance for combining ability:

Analysis of variance for combining abilities and components of variance listed in Table 6. Analysis of variance for general combining ability and specific combining ability of traits for all genotypes under the study showed highly significant for GCA variance for all studied traits. The recorded significant positive GCA magnitudes are desirable for all studied traits. Golabadi et al. (2015) reported that significant magnitudes of GCA for all traits adverting that selection and due to the accumulation of desirable genes of the two inbred lines in the resulting genotype, hybridization methods would result in an engaging genetic development of these traits. The obtained results exhibited that highly significant for specific combining ability variance was observed in all traits. Highly significant for mean squares of GCA and SCA noticed in all traits, propose the important role of dominance genetic variances ($\sigma^2 D$) and additive ($\sigma^2 A$) of heritable effect and which are accountable for diversity found in all studied traits. The obtained results illustrated that the GCA variance was higher in magnitudes than the specific combining ability (SCA) variance for all traits. These means play a great part of additive and additive by additive types of gene effect are involve in controlling these traits. Estimation of GCA / SCA ratios is higher than one for all traits under the

study, showing the predominance of non-additive gene effect in the inheritance of these characters. The obtained results were in accordance to Suzy et al. (2020) that evaluated varying ratios, larger than unity in plant length; fruit flesh thickness; TSS; fruit weight; number of fruits per plant and total yield per feddan. The GCA variance $(\sigma^2 g)$ was lesser than the SCA variance $(\sigma^2 s)$ for all studied traits expect for plant length and total yield / feddan traits. These obtained results were found to agreement to those reported by Pouyesh et al. (2017), El-Sayed et al. (2019) and Abd El-Hadi et al. (2020). In addition, Alabboud et al. (2020) reported that important role for $(\sigma^2 g)$ in fruit weight and total yield/feddan among all studied traits, indicating that additive genes had higher effect on the genetic control of these characters. In accordance with our results, Varinder and Vashisht. (2018) and Esmaeili et al. (2022) they found higher of general combining ability variance magnitudes compared with specific combining ability variances resulted in higher magnitudes of GCA / SCA ratio in melon. The GCA / SCA ratio for all traits was higher than one, which indicates the higher role of additive gene effects in the inheritance and controlling of these traits, which is compatible with Walled et al. (2018) in melon. The less magnitude of $\sigma^2 g / \sigma^2 s$ ratio was reported for all studied traits expect for plant length and total

yield / feddan traits. Furthermore, in melon, Bamadi *et al.* (2020) and Simranpreet *et al.* (2022) reported that association of additive and dominance genetic variances of heritable variance for fruit shape index, average fruit weight, number of fruits per plant and total yield per feddan, these traits

exhibited significant variances for specific combining ability had been proposed to be improved heterosis which adverts the predominance of dominance gene action, while general combining ability has been suggestive of selection as the good development programs.

Table 6. Estimates of various components of the total variance for the studied traits of five parental lines of melon.

| Traits | df | P.L. | No. | D.M. | F.Sh. I. | F.F. | F.Th. | TSS | A.F.W | No. | T.Y./F. |
|-----------------------------|----|--------|--------------|--------|----------|----------------------|-------|-------|-------|--------|---------|
| Parameters | uı | (cm) | B./P. | (days) | (cm) | (g/cm ²) | (cm) | % | (kg) | F./ P. | (ton) |
| GCA | 4 | 898.79 | 8.360 | 5.80 | 1.53 | 190.67 | 19.28 | 1.30 | 0.070 | 4.882 | 11.27 |
| SCA | 10 | 90.01 | 4.411 | 2.78 | 0.613 | 74.872 | 7.294 | 0.47 | 0.05 | 1.953 | 0.79 |
| GCA/SCA | | 9.99 | 1.89 | 1.90 | 2.49 | 2.55 | 2.64 | 2.77 | 1.4 | 2.50 | 14.27 |
| Error | 28 | 2.26 | 0.380 | 0.19 | 0.003 | 0.021 | 0.003 | 0.023 | 0.002 | 0.002 | 0.082 |
| | | | | | | Componen | its | | | | _ |
| $\sigma^2 g$ | 1 | 15.54 | 0.56 | 0.43 | 0.13 | 16.35 | 1.71 | 0.12 | 0.02 | 0.42 | 1.50 |
| σ^2 s | 8 | 37.75 | 4.03 | 2.59 | 0.61 | 76.19 | 7.29 | 0.45 | 0.05 | 1.95 | 0.67 |
| σ^2 g / σ^2 s | | 1.32 | 0.14 | 0.17 | 0.22 | 0.21 | 0.23 | 0.26 | 0.42 | 0.21 | 2.24 |

P.L.: plant length, No. B./P.: number of branches per plant, D.M.: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F. /P.: number of fruits per plant and T.Y./F: total yield per feddan.

Estimates of general and specific combining ability:

The estimates of GCA and SCA effects the traits under the study are listed in Tables 7 and 8. The determines of general combining ability (GCA) exhibited that none of the genotypes was a best general combiner for all the traits generally; Parent (P₄) was the good combiner for plant length, number of branches per plant, fruit shape index, fruit firmness, average fruit weight and total yield / feddan, thus P₄ may be desirable in breeding programs intentness to increase total yield. While parent (P₃) was the good combiner for number of fruits per plant. P2 was the good combiner for earliness since it revealed the highest negative magnitudes for days to maturity. In addition, (P₅) was the good combiner for fruit flesh thickness and TSS %. So, it could be suggested that P₄, and P₃ posse the desirable genes for improving cross combinations and could be utilized in a breeding programme for improving aforementioned traits. In the contrary, (P_1) was the lowest general combiner for most characters while, P₂ was the lowest general combiner for plant length, fruit firmness, TSS and average fruit weight traits respectively. P₅ was the poorest general combiner for number of branches per plant and fruit shape index. In case of the aim is not for the vegetable breeder to achievement great fruits, which is getting a lot of attention today, choosing the character of having more number of fruits per plant will lead to increasing total yield. To short-term breeding aims of melon fruits, the low and average fruit weight along with more number of fruits per plant and high TSS in the fruit should be significant.

The estimates of specific combining ability (SCA) exhibited that F_1 hybrid $P_3 \times P_4$ had the highest positive estimated magnitudes of SCA for TSS % (1.22), number of fruits / plant (0.33) and total yield /fed., It was noticed that the good hybrid combination in terms of specific combining ability effects always related one or both high general

combiners as parents, while P₁xP₄ had the highest positive estimated magnitudes of SCA for plant length. Also, F₁ hybrid P₁xP₅ reflected earliness of maturity, since they exhibited that the highest negative estimates for days to maturity. P₄xP₅ had the highest positive magnitudes of SCA for fruit flesh thickness. It was noticed that the good cross combination in terms of specific combining ability effects always related one or both high general combiners as parents. However, most F₁ hybrids with high specific combining ability effects interested at least one of the three high general combining genotypes P₁, P₃ and P₄. For instance, the lowest general combiner such as P3 or P4 sometimes revealed good hybrid when they were crossed with high general combiners. Alabboud et al. (2020) suggested that when genotype (parental line) with large GCA cross another with low GCA, the poor parental line could throw up favourable transgressive segregates giving rise to favorable population. This is only feasible if the additive genetic effect present in the best general combiner and the complementary epistasis action present in the cross combinations act in a complementary model to maximize favorable plant attributions which could be exploited for further breeding. Finally, the present obtained data are in agreement with the findings of Esmaeili et al. (2022) they obtained hybrids of melon with high SCA effects from parental lines having either high \times low or high \times high GCA actions. So, it cannot be generalized that the lines with high GCA effects could only produce good crosses. These results indicated that no cross combinations consistently best for all studied traits. These results align with the findings of Tak, (2017); Varinder and Vashisht (2018) and Simranpreet et al. (2022) they found high GCA and positive SCA for fruit weight, number of fruits / plant and total yield in melon.

Table 7. Estimates of general combining ability effects on the studied traits of five parental lines of melon.

| Traits | P.L. | No. | D.M. | F.Sh. I. | F.F. | F.Th. | TSS | A.F.W | No. | T.Y./F. |
|---------------------------|-------|--------------|--------|----------|----------------------|--------|------|--------|---------------|---------|
| Parents | (cm) | B./P. | (days) | (cm) | (g/cm ²) | (cm) | % | (kg) | F./ P. | (ton) |
| $\overline{\mathbf{P}_1}$ | -6.51 | -0.141 | 1.559 | 0.004 | -0.376 | -0.214 | 2.56 | -0.10 | -0.005 | -1.77 |
| P_2 | -7.37 | -0.810 | -0.771 | -0.005 | -0.733 | 0.022 | 1.68 | - 0.10 | 0.083 | -1.22 |
| P_3 | -0.42 | 0.047 | -0.201 | -0.001 | 0.462 | 0.349 | 2.39 | 0.06 | 0.135 | 1.34 |
| P_4 | 19.66 | 1.810 | -0.485 | 0.009 | -0.219 | -0.511 | 2.26 | 0.13 | -0.118 | 1.60 |
| P_5 | -5.32 | -0.907 | -0.103 | -0.006 | 0.867 | 0.353 | 2.84 | 0.001 | 0.106 | 0.08 |
| SE(gi) | 4.45 | 0.208 | 0.149 | 0.019 | 0.049 | 0.019 | 0.08 | 0.024 | 0.015 | 0.16 |
| SE(gi-gj) | 0.80 | 0.330 | 0.236 | 0.029 | 0.077 | 0.029 | 0.44 | 0.132 | 0.024 | 0.863 |

P.L.: plant length, No. B./P.: number of branches per plant, D.M: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F. /P: number of fruits per plant and T.Y./F: total yield per feddan.

Table 8. Estimates of specific combining ability effects on the studied traits of ten F₁hybrids, derived from all possible combinations of the five parental lines of melon.

| Traits | P.L. | No. | D.M. | F.Sh. I. | F.F. | F.Th. | TSS | A.F.W | No. | T.Y./F. |
|---------------------------------|--------|-------|--------|----------|----------------------|-------|-------|--------|--------|---------|
| Hybrid | (cm) | B./P. | (days) | (cm) | (g/cm ²) | (cm) | % | (kg) | F./ P. | (ton) |
| P ₁ X P ₂ | -1.60 | -0.82 | -3.30 | 0.01 | 2.93 | -0.20 | 1.00 | -0.02 | -0.24 | -1.09 |
| $P_1X P_3$ | -1.89 | 0.32 | 2.13 | -0.02 | 0.59 | 0.26 | -0.52 | 0.09 | 0.12 | 1.15 |
| $P_1X P_4$ | 11.40 | 2.56 | -1.58 | 0.01 | -0.28 | 0.12 | -0.03 | 0.11 | 0.18 | 1.85 |
| $P_1X P_5$ | 0.35 | 0.94 | 2.03 | -0.02 | 0.47 | -0.01 | 0.65 | 0.003 | 0.07 | 1.03 |
| $P_2X P_3$ | 10.64 | 1.99 | 0.46 | -0.03 | 0.10 | 0.06 | -0.40 | 0.048 | 0.12 | 1.9 |
| $P_2X P_4$ | 7.93 | -2.11 | 0.42 | -0.04 | 0.24 | 0.14 | 0.60 | 0.029 | 0.30 | 1.56 |
| $P_2X P_5$ | -1.45 | 2.61 | -0.30 | 0.04 | 0.13 | 0.02 | -1.40 | 0.042 | 0.08 | 0.87 |
| $P_3X P_4$ | -10.60 | 2.37 | -0.15 | -0.01 | -0.14 | -0.01 | 1.22 | -0.035 | 0.33 | 6.69 |
| $P_3X P_5$ | -1.40 | -0.26 | -1.54 | -0.03 | -0.03 | 0.26 | -0.30 | 0.03 | -0.15 | 0.11 |
| P ₄ X P ₅ | 6.55 | -2.67 | -0.25 | -0.06 | 0.23 | 0.84 | -0.27 | 0.05 | 0.23 | 1.07 |
| SE(Sij) | 1.31 | 0.538 | 0.385 | 0.048 | 0.126 | 0.048 | 0.07 | 0.019 | 0.039 | 0.13 |
| SE(Sii-Sij) | 0.80 | 0.571 | 0.409 | 0.051 | 0.134 | 0.051 | 0.13 | 0.039 | 0.041 | 0.25 |

P. L.: plant length, No. B./ P.: number of branches per plant, D.M.: days to maturity, F.Sh.L.: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F./P: number of fruits per plant and T.Y./F.: total yield per feddan.

Heritability percentage:

The obtained results of Table 9 revealed, generally, that the determinations of heritability percentages in the broad $(h_{bs}^2 \%)$ and narrow sense $(h_{ns}^2 \%)$, for the different studied traits, were found to be within the range of 9.97 % in narrow sense for flesh thickness trait, and up to 99.98 % in broad sense for fruit firmness trait. High heritability magnitudes were recorded for all studied traits; plant length (99.29 %), number of branches plant (93.14 %), days to maturity (94.65%), fruit shape index (99.90%), fruit firmness (99.98%), fruit flesh thickness (99.00%), total soluble solid (96.92%), average fruit weight (97.77%), number of fruits per plant (95.30%) and total yield (97.71%). The obtained results illustrated that evaluate of heritability (broad sense) were higher than their corresponding heritability (narrow sense) for studied traits. Also, the high magnitude of heritability in broad sense which is corresponds with the low magnitudes of heritability in narrow sense indicated that the higher part of the total variance is attributed to the genetic variation and that the non- additive variance represented the greatest part of the total genetic variance. These magnitudes suggest that these traits may generally be governed by additive gene effect and hence the phenotype would provide a fairly reliable measure of the inbred line which provides scope for selection based on the phenotypic performance. Heritability (narrow sense) estimates for plant length, number of fruits / plant and total

yield traits were found to be relatively high; since the evaluated h_{ns}^2 % were found to be 71.96, 75.92 and 79.87%, consequently. The records of h_{ns}^2 % exhibited relatively low or low percentages for the given seven traits number for number of branches, days to maturity, fruit shape index, fruit firmness, flesh thickness, TSS and average fruit weight, which were evaluated by 20.36, 23.60, 30,09, 30.65, 9.97, 31.59 and 44.44%, respectively. According to Badami et al. (2020) found that high heritability indicates less environmental effect on observed variation. While, the moderate and low heritability evaluate obtained for plant length, number of branches / plant and average fruit weight indicated that low progress could be achieved if selection is based on these traits. Also, suggested that heritability coefficient purveys an idea of the extension of genetic control for the expression of a particular trait and the reliability of phenotype in predicting its breeding magnitude. Recently, in melon, Nahla and Shaban (2021) and Esmaeili et al. (2022), they observed the qualification of selection depends not only on the methods of selection but also on the percentage of heritability of various traits in different genotypes. So, these traits can be improved through selection based on phenotypic observations in early segregating generations in melon genotypes. The obtained results are in the same direction with those exhibited by Pouyesh et al. (2017); Alabboud et al. (2020) and Sandeep et al. (2021).

Table 9. The relative magnitudes of the different genetic parameters and heritability for studied traits of melon.

| Traits | P.L. | No. | D.M. | F.Sh.I. | F.F. | F.Th. | TSS | A.F.W | No. | T.Y./F. |
|------------------|--------|-------|--------|---------|----------------------|-------|-------|-------|--------|---------|
| Parameters | (cm) | B./P. | (days) | (cm) | (g/cm ²) | (cm | % | (kg) | F./ P. | (ton) |
| $\sigma^2 A$ | 231.08 | 1.128 | 0.860 | 3.345 | 32.704 | 3.428 | 0.236 | 0.040 | 0.836 | 3.00 |
| $\sigma^2 D$ | 87.75 | 4.031 | 2.59 | 0.61 | 76.19 | 7.291 | 0.488 | 0.048 | 1.951 | 0.67 |
| σ^{2}_{E} | 2.26 | 0.380 | 0.19 | 0.003 | 0.021 | 0.003 | 0.023 | 0.002 | 0.002 | 0.085 |
| $h^2_{bs} \%$ | 99.29 | 93.14 | 94.65 | 99.90 | 99.98 | 99.00 | 96.92 | 97.77 | 95.30 | 97.71 |
| $h^2_{ns} \%$ | 71.96 | 20.36 | 23.60 | 30.09 | 30.65 | 9.97 | 31.59 | 44.44 | 75.92 | 79.87 |

P.L.: plant length, No. B/P.: number of branches per plant, D.M.: days to maturity, F.Sh.I: fruit shape index, F.F.: fruit firmness, F.Th.: flesh thickness, TSS: total soluble solid, A.F.W.: average fruit weight, No. F./P.: number of fruits per plant and T.Y./F.: total yield per feddan.

CONCLUSION

The obtained results demonstrated that considerable variability was found among the inbred lines and cross combinations in this study which assists to select the good lines and their desirable hybrids (crosses) for total yield / feddan contributing traits. The parent P_4 recorded the greatest value over all evaluated genotypes, F_1 hybrid ($P_3 \times P_4$) and ($P_4 \times P_5$) gave the highest means for yield and yield attributes.

Therefore, these hybrids could be used in melon production. The results showed that P_3 and P_4 were good general combiners. Also, the F_1 hybrids results from hybridization (P_1xP_4 and P_3xP_4) were the good specific crosses for total yield and related traits and promising cross combinations. The results illustrated that gene actions are extremely major to melon breeders for the selection of lines for crosses. The obtained results showed the importance of additive and dominance gene effect in the inheritance of most traits. The

heritability (broad sense was larger in values than their corresponding in narrow sense heritability, indicated that the higher part of the total variability is related to the genetic variance and that the dominance gene action represented the greatest part of the total genotypic variance. Therefore, hybridization programs could be utilized for producing superior promising melon hybrids.

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تقدير قوة الهجين والقدرة على التآلف والتباين الوراثى لبعض الصفات الإقتصادية فى الشمام. علاء محمد محمد الشورة ، جيهان زينهم محمد و نورا إبراهيم شفيق.

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الملخص

أجريت هذة الدراسة بمزرعة قها بمحافظة القليوبية خلال الموسم الصيفي لعامي 2021 و 2022 وذلك لتقدير قوة الهجين والقدرة على التآلف والتباين الوراثي بين بعض الصفات كاملة الإقتصادية في الشمام, وقد أستخدمت في هذة الدراسة خمسة سلالات من الشمام وقد أجرى التهجين بين هذة السلالات بنظام التهجين النصف دائرى وذلك باستخدام تصميم قطاعات كاملة العشوائية في ثلاث مكر رات. وقد أشارت النتائج إلى وجود تباين بين السلالات المستخدمة كأباء لكل الصفات التي تمت دراستها. وقد تبين وجود قوة هجين في بعض الهجن بالمقار نة بمتوسط الهجين الأبوين وي بعض الصفة ونفس الهجين الأبوين حيث سجلت أعلى قوة هجين بالمقارنة بأحسن الأباء لنفس الصفة ونفس الهجين الأبوين و P₁ × P₄ بالنسبة لصفة المحصول الكلى / فدان ببينما سجلت أعلى قوة الهجين بالمقارنة بأحسن الأباء لنفس الصفة ونفس الهجين P₁ × P₄ كما أشارت النتائج إلى وجود إختلافات عالية المعنوية لكلاً من القدرة الخاصة على التآلف وذلك لكل الصفات التي تمت دراستها. وأن الأبوين P₁ × P₄ أظهرا تقوقا الهجبياً القدرة العامة على التألف تقوقا الهجن P₁ × P₄ P₁ × P₄ و P₁ P₁ × P₄ المعنوية لكرا معنى القدرة الخاصة على التآلف تقوق الهجن P₁ × P₃ × P₄ , P₁ × P₄ معظم الصفات. كما سجلت النتائج أيضا أن القدرة العامة على التألف القدرة العامة على التألف كثير من الصفات أكبر من نظيرتها في المعنى الضيق وتراوحت قيم معامل التوريث بالمعنى الواسع من 11.99٪ إلى 9.99٪ المعنى الفدرة ما المكلى الفدان. لذلك ، يمكن الشرة المنائدات كأباء في برامج التهجين لإنتاج هجن واعدة من الشمام وذلك من خلال الإنتحاب في الأجيال الإنعز الية المتقدمة.