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Genetic Advance, Heritability and Correlation Estimate in Some Melon Genotypes for Yield Improvement

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Abstract: Four melon genotypes P_1 (Line 00-1108), P_2 (Line 00-1103), P_3 (Line 00-1118) and P_4 (Line 00-1110) were collected from Cornell University and crossed in a partial diallel mating fashion at Kaha Research Farm, Horticultural Research Institute, Agriculture Research Centre, Kalyobiya Governorate, Egypt, during the summer seasons of year 2021, and all genotypes (4 parents and 6 crosses) were evaluated during 2022 summer season. The results exhibited that the mean square for all genotypes had extremely significant influence on all examined characteristics. P_3 and P_4 had the greatest means for most characters, whereas $P_3 \times P_4$ and $P_1 \times P_4$ had the highest means. The values of the GCA and SCA effects were significantly, indicating that both additive and dominant gene actions controlled all of the examined attributes. Higher GCA/SCA ratio than one was found for all traits expect for early yield, fruit length and diameter traits. None of the parents were discovered to be suitable combiners for all characters. Overall, the two parents P_3 and P_4 were the good combiners for breeding to most characteristics. $P_3 \times P_4$ and $P_1 \times P_4$ had substantial SCA effects for most characteristics. Heritability in the broad sense was greater than heritability in the narrow sense. In all analyzed characteristics except early yield, fruit diameter, number of fruits, and total yield, the degree of dominance was more than one. Early yield, number of fruits, fruit weight and total yield demonstrated a high heritability paired with high genetic advance. The magnitudes of the correlation coefficients between the various pairings of attributes were positive or negative and extremely significant.

Key words: Melon genotypes, Genetic advance, Heritability, Correlation, Yield, Fruit quality.

1. Introduction

Melon (*Cucumis melo* L.) belongs to the *Cucurbitaceae* family and chromosome number of $2n = 2x = 24$, which comprises around 118 genera and over 825 species, highly polymorphic, with several botanical and horticultural differences (**Abdeldaym *et al.*, 2014**). Melon is cultivated in Egypt as one of the most significant vegetable crops for both local consumption and exports to various nations, where it ranks highly among exported agricultural crops. High yield, early maturity, consistent fruit shape and size, and outstanding quality are significant goals for fruit number and fruit weight (**Zalapa**

***et al.*, 2008**). The fruits are widely valued for their appealing flavor and sweetness, as well as their high vitamin, mineral, carbohydrate and fiber content (**Shashikumar and Pitchaimuthu, 2016**). Vegetable crop improvement necessitates approaches for enhancing quality as well as the inherent capability of yield and its components. *Cucurbitaceous* plants can be enhanced by using heterosis breeding and combining ability estimations (**Napolitano *et al.*, 2020**). Heterosis breeding has shown to be the most successful strategy among the different technical choices accessible to plant breeders for increasing crop output. Despite not being completely understood genetically, this phenomenon has allowed plant scientists to increase the performance of numerous economic traits (**Davoodi *et al.*, 2021**). Genetic analysis is regarded as a guideline for assessing the relative breeding ability of parents or identifying the best combiners in crops, which might be used to exploit heterosis in F_1 or to collect desirable genes to generate new varieties. Selection of parents based only on historical performance may not always produce the desired results (**Golabadi *et al.*, 2015 and Naroui Rad *et al.*, 2023**). For planned hybridization, parental lines selection must be based on absolute genetic information and probable parent predominance (**Indraja *et al.*, 2020**). The selection of suitable parents in a breeding program is regarded a critical aspect in developing vigor hybrids to make hybrids competitive with hybrids produced by private seed firms, suitable parents must be selected from novel inbred lines and excellent germplasm banks. F_1 hybrids are crucial for improving melon production because of their early maturity, higher quality, high yield potential, and resistance to disease and insect pests (**Mohammadi *et al.*, 2014**). Furthermore, developing F_1hybrids is the quickest approach to improve critical economic features and the simplest means to introduce disease resistance controlled by dominant genes. One of the most significant responsibilities for vegetable breeders is to select parents that will produce hybrids with the required features. The conventional strategy of selecting parents based on their inherent performance may not always result in good hybrids. Diallel mating design suggested by **Griffing (1956)** is an ideal to produce maximum cross combinations from a given number of parental lines. Diallel analysis is one of the primary methodologies employed, this method estimates data on the general combining ability, which is related to concentration of predominantly additive genetic effect and the specific combining ability which is related to gene centration with a non additive genetic action (dominance and epistasis). Heterosis breeding is important in genetically enhancing any crop in terms of production and quality attributes (**Singh *et al.*, 2014**). Diallel mating design is commonly used in plant breeding research to acquire data on genetic effects for a given set of parents or to estimate general combining ability, specific combining ability and variance components for a population using randomly selected parents. The primary benefit of a half diallel design is that each parent is crossed with the other in all feasible combinations (excluding reciprocals). It generates data on the performance of parents and their crosses. In melon, **Monir *et al.* (2022)** discovered that additive and non - additive effects controlled number of fruits per plant and total yield, whereas additive actions controlled fruit weight, fruit length and diameter. Additive gene effects were most relevant in terms of fruit weight and early yield, but genetic dominance actions dominated overall yield. **Hatem *et al.* (2014) and Javanmard *et al.* (2018)** recorded that heterosis breeding is important for efficient melon breeding programs. Total yield is connected with various factors, including non additive genetic effect. **El-Shoura *et al.* (2023)** discovered that both additive and non additive gene effects were present in melon; with additive gene effects appearing play the key part in the inheritance of all investigated traits. None of the parents proved to be effective combiners for all traits. In a research by **El Sayed *et al.* (2019) and Akshita *et al.* (2025)**, the GCA/SCA (ratio) varied from 4.40 to 57.80, and none of the parental lines were shown to be a best combiner for all investigated traits. **Nahla and Shaban (2021)** assessed the gene influence of yield and associated qualities in melon and discovered that the general and specific combining abilities effects were extremely significant for the majority of attributes investigated. Many researchers found that additive ($\sigma^2 A$) and dominance ($\sigma^2 D$) variance components play a significant role in the genetic regulation of yield and related variables in melon (**Esmaeili *et al.*, 2022; Shafin *et al.*, 2022 and Naroui Rad *et al.*, 2023**). **Abo Sedera *et al.* (2016)** exhibited that broad sense heritability were 95, 99 and 99% for number of fruits, average fruit weight and total yield, while the heritability in narrow sense were 22, 41 and 61% for plant length, number of leaves and fruit length, respectively, indicating the high effects of genetic variance on the expression of the aforementioned traits. In addition to, additive variance components are quite high when compared to other forms of genetic variation components. For examined traits, broad sense heritability estimates were higher than narrow sense heritability estimates (**Abd El-Hadi *et al.*, 2020**).

Esmaeili *et al.* (2022) discovered that high heritability in narrow sense ($h^2_{n.s.}$) for number of fruit plant^{-1}, fruit and total yield plant^{-1}, indicated less environmental effect for the aforementioned traits, Moreover, the significance of additive genetic effects. They reported that dominance genetic actions of genes played a greater role in controlling number of fruits and fruit yield traits than additive genetic effects.

The correlation between various horticultural qualities is critical to developing an effective breeding program. As a result, employing the phenotypic correlation coefficient is major tools for vegetable breeders to assist them choose and identify difficult to measure characters by selecting easier to measure characters. As a result, some authors assessed the correlation between the various pairs of examined traits, such as **(Naik *et al.*, 2015; Walled *et al.*, 2018 and Naroui Rad *et al.*, 2023**). They determined that there were substantial connections between pairs of numerous economic characters of cabbage that were useful in cabbage selection.

The aim of this investigation was to quantify the GCA, SCA, heritability, genetic advance, and correlation in several melon genotypes for yield enhancement gained by partial diallel mating, in order to identify suitable hybrid combinations.

2. Materials and methods

The current study was conducted over two consecutive seasons of year 2021 and 2022, with four melon genotypes used as experimental material under field conditions at Kaha Research Farm, Horticultural Research Institute, Agriculture Research Centre in the Kalyobiya Governorate, Egypt. Cornell University provided seeds of the four melon genotypes: Line 00-1108 (P1), Line 00-1103 (P2), Line 00-1118 (P3), and Line 00-1110 (P4). The advanced experimental genotypes were employed as parental lines in half diallel mating designs to produce 6 hybrids. The F_1seeds from the six hybrids were generated by hand pollination. After harvesting the mature fruits, the seeds were removed and stored for use in the following season. The four genotypes were planted in the field on the 10th of March 2021, and all potential crossings to cross combinations (F_1hybrids) were made, with no reciprocals. The seeds of all genotypes (four genotypes and six F_1hybrids) were planted on March 10th, 2022, to evaluate the various attributes. The seeds from six hybrids and four parents were sown. The experiment was set out in a randomized complete block design (RCBD), with replicated thrice and ten plants per replication to estimate ten genotypes (four parents and six cross combinations). Each plot was planted in a two rows, 5 meters long and 1.5 meters wide. Seeds were placed in hills 50 cm apart inside the same row. Four weeks later, the seedlings were trimmed to one plant per hill. All practice activities, including fertilization, irrigation, gap filling, weeding, and plant protection, were carried out in line with field melon production. The following characteristics were recorded: vine length (cm), number of leaves plant^{-1}, chlorophyll content in leaves (%), early yield plant^{-1}, fruit length (cm), fruit diameter (cm), number of fruits plant^{-1}, fruit weight (kg), and total yield plant^{-1} (kg). The Co- Stat Statistical Software was used to conduct a variance analysis on the analyzed characteristics. The diallel crossings were evaluated using **Griffings' (1956)** technique II and model II.

The general and specific combining abilities were assessed using the **Cochran and Cox (1950)** t-test.

Estimation of gca effects:

As (g_i) = $1/n+2\ [(\Sigma\ (Yi. + Yii) - 2/n\ Y..)]$.

Estimation of gca effects:

As (s_{ij}**)** $= Yij - 1/ n+2\ (Yi. + Yii + Y.j + Yjj) + 2 / (n+1)\ (n+2)\ Y.$

Estimation of standard errors:

S.E.(g_i**)** $= [(n-1)\ \sigma^2 e/ n(n+2)]^{1/2}$.

S.E.($g_i - g_j$**)** $= [2\ \sigma^2\ e/ (n+2)]^{1/2}$.

$\mathbf{S.E.(s_{ii})} = [(n^2+n+2)\ \sigma^2 e\ /\ (n + 1)\ (n + 2)]^{1/2}$.

$\mathbf{S.E.(s_{ij})} = [2\ (n - 1)\ \sigma^2 e\ /\ (n + 1)\ (n + 2)]^{1/2}$.

$\mathbf{S.E.\ (s_{ii} - s_{jj})} = [2\ (n - 2)\ \sigma^2 e\ /\ (n + 2)]^{1/2}$.

The connection *GCA/SCA* was studied to determine the contribution of additive (σ^2A) and non-additive (σ^2D) effects for all characteristics under consideration. According to **Matzinger and Kempthorne (1956),** σ^2A and σ^2D were recorded with agreement. $\sigma^2D = \sigma^2s,\ \sigma^2A = 2\ \sigma^2g$.

The following equations were used to calculate heritability estimates in both the broad sense ($h^2_{b.s}$) and the narrow sense ($h^2_{n.s}$):

$h^2_{b.s}\ \% = \{\sigma^2A + \sigma^2D\ /\ \sigma^2A + \sigma^2D + \sigma^2E\}\ x\ 100.$

$h^2_{n.s}\ \% = \{\sigma^2A\ /\ \sigma^2A + \sigma^2D + \sigma^2E\}\ x\ 100.$

Estimation of Degree of dominance:

$$D.d= \sqrt{\frac{\sigma 2D}{\sigma 2A}}$$

If: *D.d* = zero indicates no dominance, *D.d* = < 1 indicates partial dominance, *D.d* = 1 indicates complete dominance, *D.d* > 1 indicates over dominance.

Expected genetic advance:

Expected Genetic Advance (EGA) = (K) $\sqrt{\boldsymbol{Vp}}\ \boldsymbol{X}\ \boldsymbol{h^2}_{\mathbf{n.s}}$

EGAM = (EGA/X) x 100

Where:

EGA: Expected genetic advanced

K: intensity of selection (which equals 1.76 when 10% of plants are selected

σ²P: phenotypic deviation

Singh and Chaudhary (1985) estimated the phenotypic correlation coefficient (r_{ph}) and genotypic correlation coefficient (r_g) between pairs of the examined traits using the formulae shown below.

The significance of the r_{ph} and r_g were tested by **Cochran and Cox (1957).**

$r_g = cov.g_{1.2}\ /\ (\sigma^2_{g1}.\ \sigma^2_{g2})^{1/2}$, $r_{ph} = cov.ph_{1.2}\ /\ (\sigma^2_{ph1}.\ \sigma^2_{ph2})^{1/2}$

3. Results and Discussion

The analysis of variance for the experimental design for nine traits *viz.*, vine length, number of leaves plant^{-1}, chlorophyll content in leaves (%), early yield plant^{-1}, fruit length and diameter, number of fruits plant^{-1}, fruit weight and total yield traits (Table 1) showed that the mean squares due to all genotypes (parents and F_1hybrids) were highly significant for all the examined variables, indicate potential genetic genotypes (parental lines and F_1crosses). The examined characteristics accounted for the majority of the observed genetic variability between accessions, viewing that the F_1hybrids and their parents varied from each other (**Abd El-Hadi *et al.*, 2020**). The significance of genotypes mean squares exhibited indicated the expected comparisons for identifying the pattern of variation and establishing the level of heterosis for these variables were valid and could be used (**El-Tahawey *et al.*, 2015 and Marxmathi *et al.*, 2018)**. Enormous genetic variations between the accessions are needed for effective and successful selection effort (**Monir *et al.*, 2022)**. Part of the genetic variation to its components could be made through the analysis of the half diallel crosses mating model. This investigation was backed by the findings of **Badr *et al.* (2021**), who discovered extremely significant variations in the mean squares of the examined variables in F_1 hybrids of squash genotypes.

Table (1). Analysis of variance and mean squares for (parents and crosses) for all studied traits of melon genotypes

Source of variation	**Replications**	**Genotypes**	**Error**
df	2	9	18
Vine length (cm)	4.13^{ns}	1158.58^{**}	7.57
Number of leaves plant^{-1}.	0.23^{ns}	135.83^{**}	0.86
Chlorophyll content in leaves (%)	0.99^{ns}	74.65^{**}	0.54
Early yield (kg)	0.02^{ns}	0.96^{**}	0.01
Fruit length (cm)	0.06^{ns}	1.73^{**}	0.03
Fruit diameter (cm)	0.04^{ns}	1.78^{**}	0.06
Number of fruits plant^{-1}.	0.40^{ns}	2.29^{**}	1.18
Fruit weight (kg)	0.001^{ns}	0.86^{**}	0.88
Total yield plant^{-1}(kg)	0.09^{ns}	19.63^{**}	16.49

**: Significant at 0.01 probabilities.

Mean performance of parent lines and cross combinations for the Studied Traits

The per se performance of all genotypes exhibited that the parents were genetically unique and had potential breeding magnitudes. The mean performance of 6 crosses with their parents listed in Table 2. The mean magnitudes revealed that no single parent outperformed all other parents for all assessed attributes. Among the parents, vine length diverged from 186.67 (P_2) to 241.33 cm (P_4), while the F_1hybrids varied from 193.67(P_1xP_2) to 239.67(P_1xP_4). On the other side, number of leaves per plant ranged from 38.90(P_2) to 61.03(P_4) for the parents, whereas the F_1hybrids varied from 48.70(P_1xP_2) to 59.55(P_3xP_4). Also, chlorophyll content in leaves (%) ranged between 36.33(P_1) and 48.46(P_4) among the parents, whereas the F_1hybrids varied from 37.54(P_2xP_3) to 49.12(P_1xP_4). For early yield plant^{-1} varied from 2.87(P_2) to 3.08 kg (P_3) amid the parental genotypes, while the F_1hybrids ranged from 3.09(P_1xP_2) to 4.33kg (P_3xP_4) (Table2). For fruit characteristics, fruit length exhibited a broad range of variance, from 8.43(P_4) to 10.85cm (P_3) among the parents, but the F_1hybrids ranged from 10.30(P_1xP_2) to 11.93cm (P_2xP_3), also, fruit diameter demonstrated a broad range of variance, from 8.02 (P_4) to 10.27cm (P_3) among the parents, but the F_1hybrids ranged from 10.40 (P_1xP_2) to 12.33 cm (P_2xP_3). The best performing F_1hybrids, P_3xP_4 (5.11), yield substantially more fruits per plant than the top-performing parents, P_3 (3.95). These findings were more or less comparable to the reported magnitudes of **Areej *et al.* (2023)**. These might be due to genetic and environmental constitutes of the genotypes. In a melon hybridization program, the most important aspect is the yield potential, which is directly related to fruit weight **(Abd El-Hadi *et al.*, 2020)**. In this experiment, parent (Line 00-1110) is the high performer for fruit weight (1.55 kg) and total yield plant^{-1} (5.43 kg) and the F_1hybrids (P_3xP_4) produced significantly higher magnitudes for fruit weight (2.09 kg) and total yield plant^{-1} (10.67 kg) for the F_1hybrids. Melon hybrids with fruit weight and yield plant^{-1} varying from 1.11 to 2.09 kg and 4.11 to 10.67 kg, consequently, were reported by (**Abd-Elwanis and Mahmoud, 2016; Nahla and Shaban, 2021 and Naroui Rad *et al.*, 2023**). Overall, the study found that the F_1hybrid mean outperformed the parents' mean, which might be attributed to the occurrence of heterosis. These findings suggested that crosses were selected as superior genetic resources for melon genotype improvement. Heterosis is the superior performance of crosses over the superior parent, the parents' mean, or the usual check, based on the accumulation of desired dominant genes into the cross combination population that originated from both female and male parents (**Kumar *et al.*, 2018**). The results illustrated that the magnitudes of the means of the F_1hybrids were similar to each other for most examined traits. These results were agreement to **Badami *et al.* (2020) and Esmaeili *et al.* (2022).**

Table (2). Mean performances of 4 parents, 6 cross combinations for studied variables of melon

Traits Geno.	Vine length (cm)	Number of leaves plant^{-1}	Chlorophyll content in leaves (%)	Early yield (kg)	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant^{-1}	Fruit weight (kg)	Total yield plant^{-1}(kg)
Parents									
P_1	192.00	46.80	36.33	3.03	9.13	9.17	2.39	0.64	1.53
P_2	186.67	38.90	39.71	2.87	9.33	9.63	3.60	0.75	2.70
P_3	210.00	51.60	43.64	3.08	10.85	10.27	3.95	1.25	4.94
P_4	241.33	61.03 61.03	48.46	2.99	8.43	8.62	3.50	1.55	5.43
F_1 hybrids									
P_1 x P_2	193.67	48.7	40.54	3.09	10.3	10.4	3.70	1.11	4.11
P_1 x P_3	200.33	55.66	44.40	3.75	11.8	10.99	4.00	1.70	6.80
P_1 x P_4	239.67	50.5	49.12	4.22	10.8	10.79	2.60	2.07	5.38
P_2 x P_3	217.67	49.77	37.54	3.91	11.93	12.23	5.00	1.10	5.50
P_2 x P_4	229.33	58.21	47.99	3.96	10.63	11.7	4.10	1.99	8.16
P_3 x P_4	217.67 217.66	59.55	40.61	4.33	9.77	10.76	5.11	2.09	10.67
LSD at 5 %	4.72	1.59	1.26	0.19	0.30	0.44	1.77	1.62	2.06
LSD at 1 %	6.46	2.18	1.73	0.26	0.41	0.60	2.42	2.21	2.54

P1: Line 00-1108, P2: Line 00-1103, P3: Line 00-1118, and P4: Line 00-1110.

Analyses of variance owing to general and specific combining abilities

Highly significant differences were found for the general and specific combining abilities, for the characters under study (Table 3). The extremely significant mean squares for general and specific combining ability reported in all characteristics, suggest that dominance and additive genetic variation play a vital role in heritable effect. These results are substantiated with author also reported significant mean squares of GCA, and SCA in *Cucurbitaceae*. General combining ability mean squares were larger than specific combining ability means squared for all traits expect for early yield, fruit length and fruit diameter, demonstrating that hybridization may increase such features due to the predominance of additive gene effect. The GCA/SCA (ratio) in this experiment ranged from 0.29 (early yield) to 7.60 (vine length). The results exhibited that the GCA / SCA (ratio) were higher than one, a higher GCA / SCA ratio than one were found for vine length (7.60), number of leaves (5.25), chlorophyll content (4.65), number of fruits plant^{-1} (2.68), fruit weight (1.70), and total yield plant^{-1} (2.86), indicating that the inheritance of these examined traits was mostly governed by additive gene actions. While the other traits were less than one which means that non additive gene actions mainly control the inheritance of these traits, which is compatible with **El- Sayed *et al.* (2019). Baker (1987)** reached a similar conclusion, indicating that when the GCA/SCA (ratio) was around one, additive gene action predominated in the transmission of those traits, however, when it was less than one, non additive gene action predominated. Furthermore, a breeder should consider a trait's heritability, since it shows the scope and potential for improvement that selection offers. It examines the link between parents and offspring while also recommending the direction of selection ability to be used for a characteristic during selection (**Naroui Rad *et al.*, 2023**).

Table (3). Analysis of variance for general and specific combining ability and the mean squares of crosses for various traits of melon

Source of variation	GCA	SCA	Error	GCA / SCA
d.f	**3**	**6**	**18**	
Vine length (cm)	2751.37**	362.18**	130.20	7.60
Number of leaves plant^{-1}	295.08**	56.21**	0.80	5.25
Chlorophyll content in leaves (%)	156.62**	33.67**	0.54	4.65
Early yield (kg)	0.36**	1.26**	0.01	0.29
Fruit length (cm)	1.19**	1.99**	0.05	0.60
Fruit diameter (cm)	1.69**	1.82**	0.06	0.93
Number of fruits plant^{-1}	4.07**	1.52**	1.18	2.68
Fruit weight (kg)	27.05**	15.92**	0.88	1.70
Total yield plant^{-1}	0.86**	0.30**	0.003	2.86

**: Significant at 0.01 probabilities

General combining ability effect of parental lines and specific combining ability effect of cross combinations

As a result, vegetable breeders usually use parents and hybrids when generating high yielding cultivars. A parent is considered a competent general combiner if it has more significant favorable general combining ability impacts (**Singh and Vashisht 2018; Shafin *et al.*, 2022 and Akshita *et al.*, 2025**). The general combining ability factor is frequently caused by additive genetic variance, and the decisions made by each parent are greatly affected by this variation. General combining ability effect of parents and specific combining ability effect of crosses for the studied traits are showed in Table 4. For the vine length, the general combining ability effect varied from -0.8.83(P_2) to 18.00 (P_4). In this study, the parent (Line 00-1110) fashioned a higher general combining ability magnitude for vine length trait. On the other side, the indicted specific combining ability effect for this trait ranged from – 10.71 (P_3xP_4) to 16.68 (P_1xP_4). Three F_1hybrids had highly significant positive specific combining ability effects and the F_1hybrid (P_1xP_4) was found as the best specific combiner, followed by the F_1hybrid (P_2xP_3), for vine length plant^{-1}. The general combining ability effect for number of leaves varied from -4.31(P_2) to 1.30 (P_3). Moreover, five F1hybrids exhibited extremely positive significant specific combining ability results for this trait, which varied from -4.58 (P_1xP_4) to 5.46 (P_2xP_4). In this study, the parental line P_4 presented the highest general combining ability value for chlorophyll content in leaves. The general combining ability effect varied from -2.20 (P_2) to 4.16 (P_4) for chlorophyll content trait. For this trait, the parents P_4, had a highly significant positive general combining ability effect and were deemed as good combiners. While, the indicated specific combining ability effect for this trait ranged from -4.03 (P_2xP_3) to 3.21 (P_1xP_4) and five F_1hybrids showed highly significant and positive magnitudes of SCA effect for this character. The parent P_4 showed highly significant and positive GCA effect, with the general combining ability effect for early yield plant^{-1} ranging from -0.15 to 0.15. The attributes' estimated specific combining ability effects varied from -0.20 (P_1xP_2) to 0.63 (P_1xP_4), were desirable as the best specific combiners for early yield plant^{-1}. Four crosses showed extremely significant and positive SCA effect for early yield plant^{-1}. Higher SCA impacts for early yield were recorded by **(Naroui Rad *et al.*, 2023)**. **Alabboud *et al.* (2020) and Monir *et al.* (2023)** noticed similar significant results for early yield in melon genotypes**.** The general combining ability effect for fruit length ranged from -0.33 (P_1) to 0.29 (P_3). The estimated specific combining ability effects for this trait varied from -0.66 (P_1xP_2) to 1.36 (P_2xP_4). Regarding SCA effect, the F_1hybrid P_2xP_4 was the best combiner for fruit length. Also, the varied of the GCA effect for fruit diameter was from -0.39 (P_1) to 0.31 (P_3), while considerable GCA effect was significantly beneficial for the parent (P_3).

Table (4). Displays the estimations of GCA and SCA effects of four parental lines and their F_1 hybrids for variables of melon

Traits **Geno.**	**Vine length (cm))**	**Number of leaves plant^{-1}**	**Chlorophyll content in leaves**	**Early yield (kg)**	**Fruit length (cm)**	**Fruit diameter (cm)**	**Number of fruits plant^{-1}**	**Fruit weight (kg)**	**Total yield plant^{-1}(kg)**
GCA									
P_1	-7.28**	-1.98**	-1.99**	-0.08	-0.33**	-0.39**	-0.62**	-0.39**	-1.49**
P_2	-8.83**	-4.31**	-2.20**	-0.15**	0.06	0.17**	0.09	-0.46**	-0.41
P_3	-1.89	1.30**	0.03	0.09	0.29**	0.31**	0.003	0.13	0.54
P_4	18.00**	-1.98**	4.16**	0.15**	-0.02	-0.09**	0.53**	0.72**	1.35**
SE(gi)	0.65	0.18	0.15	0.01	0.03	0.05	0.22	0.19	0.82
SE(gi – gj)	0.91	0.30	0.24	0.03	0.05	0.08	0.36	0.31	1.30
SCA									
P_1 x P_2	-2.49**	2.92**	1.00**	-0.20*	-0.66**	-0.70**	0.47*	0.26	1.15*
P_1 x P_3	-2.77**	4.27**	2.63**	0.22*	-0.39**	-0.34**	0.33*	-0.33*	1.56*
P_1 x P_4	16.68**	-4.58**	3.21**	0.63**	-0.08	-0.14*	-0.54**	0.64**	-0.67
P_2 x P_3	10.46**	0.71**	-4.03**	0.45**	-0.65**	-0.56**	0.62**	-0.85**	0.51
P_2 x P_4	7.90**	5.46**	2.29**	0.44**	1.36**	1.31**	0.25	0.63**	2.35**
P_3 x P_4	-10.71**	1.18**	1.69**	0.58**	0.26*	0.23*	0.81**	-0.45	2.59**
SE(Sii)	1.36	0.453	0.363	0.046	0.085	0.12	0.53	0.46	2.00
SE(Sij)	0.70	0.23	0.18	0.02	0.04	0.06	0.27	0.24	1.04
SE(Sii-Sij)	1.29	0.43	0.34	0.04	0.08	0.11	0.50	0.43	1.90

*: Significant at 0.05 probabilities.
**: Significant at 0.01 probabilities.

These obtained results suggested that the parent Line 00-1118 (P_3) is the best to improve fruit diameter. The indicated SCA effect for this trait varied from -0.70 (P_1xP_2) to 1.31 (P_2xP_4). For number of fruits plant^{-1}, the GCA effect varied from -0.62 (P_1) to 0.53 (P_4), while the SCA effect for this trait varied from -0.54 (P_1xP_4) to 0.81 (P_3xP_4), and five crosses showed positive and significantly SCA effects. Identical results were reported for total number of fruits plant^{-1} by (**Shashikumar and Pitchaimuthu, 2016; El- Sayed *et al.*, 2019 and Napolitano *et al.*, 2020**). The range of the GCA effect of fruit weight - 0.46 (P_1) to 0.72 (P_4). In the intended orientation, the parent P_4 is followed by the parent P_3, had a favorable general combining ability effect. The result exhibited that none of the parents were the good general combiner for all examined traits. Similar results were discovered by **Shamel *et al.* (2013) and El Gazzar *et al.* (2015)**, who showed that no parents outperformed for all studied traits. The parent (P_4) performed with highest general combining ability value on fruit weight trait. According to our obtained results, The SCA effect of this trait was ranged from -0.85 (P_2xP_3) to

0.64 (P_1xP_4). The cross P_1xP_4 was noted as the best specific combiners. The GCA effect for total yield plant^{-1} varied from -1.49 (P_1) to 1.35 (P_4) and the parent (P_3) exhibited highly positive significant effects. The recorded SCA effect for this trait varied from -0.67 (P_1xP_4) to 2.59 (P_3xP_4). Five crosses had extremely significant positive specific effects on this characteristic, and the best specific combiner for total yield plant^{-1}, exhibited that the highest positively significant specific combining ability effect may be caused by additive by additive gene effect. The creation of high performing crosses necessitated crossings with greater SCA effects. This might be because they included parents who had low x low, high x low and high x high GCA effects, consequently, which suggested the existence of dominance, additive and epistatic gene actions for controlling the characters. This finding exhibited that parental lines (P_4) is responsible for increased vine length, chlorophyll content in leaves, early yield, fruit number, fruit weight and total yield traits. **Choudhary *et al.* (2003)** documented that parent DMDR-1 had the best combining ability for total fruit yield plant^{-1}, number of fruits plant-1and fruit weight. In according to **Vashisht *et al.* (2010**), the parent Hara Madhu was an excellent general combiner in terms of fruit quantity, weight, and yield plant^{-1}. Several researchers proposed considerable SCA impacts on total fruit output **Glala *et al.* (2010), Tak, (2017), Shivaji *et al.* (2018), Simranpreet *et al.* (2022), Monir *et al.* (2022) and Simranpreet *et al.* (2022).**

Genetic variability parameters and gene action

Table 5 shows an evaluation of the variance components, as well as the degree of dominance (*D.d)*, heritability in broad and narrow senses, and expected genetic advance (*E.G.A.*) for each of the variables evaluated. The obtained findings showed that for the aforementioned qualities, the magnitudes of additive genetic variation were greater than dominant genetic variance, confirming the favorable influence of selection on the breeding of these characters. The results exhibited that additive genetic variance was bigger than dominant genetic variance in these traits, implying that additive genetic effect was more essential in inheritance for all characters (**El-Sayed *et al.*, 2019; Badami *et al.*, 2020 and El-Shoura *et al.*, 2023**). This shows that the environment had a little influence on these features in this experiment. All analyzed characters had a σ^2A/σ^2D (ratio) greater than unity. The degree of dominance is greater than one for number of leaves, chlorophyll content in leaves, fruit length and fruit weight, indicating the presence of an over-dominance gene effect for the aforementioned traits; however, the degree of dominance (*D.d*) is less than one for vine length, early yield, fruit diameter, number of fruits and total yield. The results agree with those of **Abd El-Hadi *et al.* (2020**). Because to epistasis, linkage disequilibrium, and pseudodomination actions, the degree of dominance for number of leaves, chlorophyll content, fruit length, and fruit weight exceeded unity; thus, selecting of these characteristics was successful. Therefore, it is preferable to adopt the hybrid production approach to enhance these characteristics in the examined population. Additional studies that studied the gene effect of many features in melon revealed similar findings (**Abd-Elwanis and Mahmoud 2016; Simranpreet *et al.* 2022**). Furthermore, the degree of dominance ranged from 0.13 (fruit diameter) to 1.27 (chlorophyll content %), indicating the relative or partial dominant gene effect, as well as the significance of both additive and dominance genetic effects in these variables. Thus, selection may be made in early generations (**Varinder and Vashisht 2018; Ene *et al.*, 2019 and Shafin *et al.*, 2022).** Most traits demonstrated a high degree of broad sense heritability. Furthermore, significant narrow sense heritability in several parameters, such as early yield plant^{-1}, fruit weight, and overall yield, suggested that selecting the good individuals based on these qualities might be effective, as the phenotype displays almost the same genotype (**Javanmard *et al.*, 2018**). The broad sense heritability varied from 93.20 (fruit diameter) to 98.41% (total yield plant^{-1}), whereas the narrow sense heritability ranged from 52.21 (fruit diameter) to 67.85% (vine length). In this experiment, the heritability in narrow sense (h^2_{ns}) was reported to be lower than the similar magnitudes of heritability in broad sense for all variables under investigation. The heritability in a broad sense (h^2_{bs}) was highest in all investigated characteristics, ranging from 93.20 (fruit diameter) to 98.41% (total yield), indicating the importance of dominant gene effect in these variables. At the same time, heritability in a narrow sense reported the smallest magnitudes for all traits, ranging from 52.21 to 77.7% for the aforementioned traits, reflecting the lowest part of additive gene action in these traits and indicating the important role of hybridization method in improving them. The results are consistent with those of

Alabboud ***et al.*** **(2020) and Esmaeil** ***et al.*** **(2022)** on melon, which discovered modest levels of heritability for several yield components. The broad sense heritability magnitudes for the characteristics under consideration were more than twice as large as the similar narrow sense heritability magnitudes. These findings conclusively indicated that non additive gene action, as opposed to additive gene action, has a stronger influence on the inheritance of these traits and, as a result, their overall performance. This finding implies that there is much possibility for heterosis breeding to improve these features. This outcome is congruent with **Nahla, and Shaban (2021)** findings, which revealed that the metrics number of fruits, fruit weight, and total yield had poor heritability in the limited meaning of melon. Our narrow and broad sense heritability findings were comparable to those of **Napolitano** ***et al.*** **(2020**), who studied the number of fruits and total yield in melon. These results were comparable with those recorded by **Areej** ***et al.*** **(2023),** who found that the magnitudes of broad and narrow sense heritability were high for fruit weight. This highlights the significance of additive genetic variation in the inheritance of this characteristic. Addition, poor narrow sense heritability in these characteristics indicates that additive variation has a lower influence and selection has a favorable effect on these traits (**Indraja** ***et al.*****, 2020**). The expected genetic advance as a percentage (*EGA%*) was low to medium for all examined variables, with values ranging from 13.02 (vine length) to 44.67% (total yield plant^{-1}). Substantial heritability in the broad sense, as well as expected genetic advance as a percentage of the mean, were observed for early yield, fruit weight, and total yield, suggesting that additive gene action affects prevail in their inheritance. High genetic advance as percentage was found in parental lines and crosses which suggested that improvement of fruit weight and total yield would be effective through phenotypic selection. The results exhibited strong heritability paired with high genetic advance indicating that effective selection might be done for fruit weight and total yield in both the parents and cross combinations. The findings of genetic variability study indicated that environment plays a major role in expressing fruit yield. The drop in genetic advance magnitudes is attributable to the fall in narrow sense heritability magnitudes. These findings are consistent with the results of (**Abo Sedera** ***et al.*****, 2016; Davoodi** ***et al.*** **2021 and Akshita** ***et al.*****, 2025**).

Table (5). Displays the relative values of various genetic parameters and heritability for studied traits

Traits **Gen. Para.**	**Vine length (cm)**	**Number of leaves plant^{-1}**	**Chlorophyll content in leaves**	**Early yield plant^{-1}(kg)**	**Fruit length (cm)**	**Fruit diameter (cm)**	**Number of fruits plant^{-1}**	**Fruit weight (kg)**	**Total yield plant^{-1} (kg)**
σ^2A	265.47	26.54	13.66	0.22	0.52	0.49	0.04	0.02	0.15
σ^2D	118.20	18.45	11.04	0.06	0.40	0.39	0.01	0.01	0.04
σ^2A / σ^2D	2.25	1.44	1.24	3.67	1.30	1.26	4.00	2.00	3.75
σ^2E	7.58	0.86	0.54	0.01	0.03	0.07	0.001	0.001	0.003
σ^2P	368.56	45.81	25.24	0.29	0.94	0.94	0.06	0.03	0.19
D. d	0.94	1.18	1.27	0.74	1.24	0.13	0.71	1.00	0.73
$h^2_{b.s}$ %	98.06	98.12	97.85	95.64	96.69	93.20	97.62	97.94	98.41
$h^2_{n.s}$%	67.85	57.88	54.11	75.46	54.74	52.21	73.11	75.67	77.17
EGA	27.65	8.99	6.50	0.82	1.25	1.23	0.37	0.26	0.67
EGAM	13.02	17.26	14.86	23.30	13.54	13.21	22.98	28.23	44.67

Genotypic and phenotypic correlation coefficients

The results of the genotypic and phenotypic correlation coefficients among various traits of melon studied are shown in Table (6). Genotypic and phenotypic correlations coefficients among the pairs of traits were estimated. Genotypic and phenotypic correlation coefficients magnitudes of the most important traits, *i.e.*, vine length, number of leaves, chlorophyll content in leaves (%), early yield, fruit length, fruit diameter, number of fruits, fruit weight and total yield. It is observed that the genotypic correlation coefficients of all studied traits were higher than the phenotypic correlation coefficients which indicated that the apparent correlation might be due to genetic reason. Similar findings are were recorded by **Areej *et al.* (2023)** who found that the genotypic correlation(r_g) coefficients were greater than the phenotypic correlation (r_{ph}) coefficients for number of fruits per plant, fruit weight and total yield in melon.

Table (6). Genotypic and phenotypic correlation coefficients of various traits studied in melon genotypes

Characters		Vine length (cm)	Number of leaves plant^{-1}	Chlorophyll content in leaves (%)	Early yield (kg)	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant^{-1}	Fruit weight (kg)
Number of leaves plant^{-1}	r_g	0.90^{**}							
	r_{ph}	0.86^{**}							
Chlorophyll content in leaves (%)	r_g	0.71^{**}	0.81^{**}						
	r_{ph}	0.62^{**}	0.79^{**}						
Early yield (kg)	r_g	0.42^{*}	0.70^{**}	0.40^{*}					
	r_{ph}	0.36^{*}	0.78^{**}	0.38					
Fruit length (cm)	r_g	0.58^{**}	-0.59^{**}	-0.33^{**}	0.22				
	r_{ph}	0.52^{**}	-0.48^{**}	-0.22^{**}	0.16				
Fruit diameter (cm)	r_g	0.20	-0.55^{**}	-0.23	-0.12	-0.33			
	r_{ph}	0.17	-0.50^{**}	-0.23	-0.08	-0.30			
Number of fruits plant^{-1}	r_g	0.77^{**}	0.78^{**}	0.73^{**}	0.38^{*}	0.31	-0.22		
	r_{ph}	0.76^{**}	0.75^{**}	0.72^{**}	0.36^{*}	0.30	-0.18		
Fruit weight (kg)	r_g	0.22	0.66^{**}	0.55^{**}	0.11	0.52^{**}	0.52^{**}	-0.65^{**}	
	r_{ph}	0.25	0.60^{**}	0.51^{**}	0.10	0.50^{**}	0.48^{**}	-0.68^{**}	
Total yield plant^{-1} (kg)	r_g	0.73^{**}	0.78^{**}	0.88^{**}	0.28	0.43^{*}	0.88^{**}	0.93^{**}	0.93^{**}
	r_{ph}	0.76^{**}	0.80^{**}	0.87^{**}	0.24^{**}	0.39	0.87^{**}	0.91^{**}	0.90^{**}

*: Significant at 0.05 Probability.
**: Significant at 0.01 Probability.

Regarding genotypic correlation, results exhibited that vine length was significant positively correlated with number of leaves, chlorophyll content in leaves, fruit length, number of fruits plant^{-1}, fruit weight and total yield plant^{-1}traits. Regarding total yield plant^{-1}exhibited the positive and significant correlations to all traits under this study expect for fruit traits (fruit length and diameter). The positive and significant associations between yield component traits make it easier and effective for vegetable breeder to make indirect selection for high yielding hybrids. Whereas, fruit weight recorded the positive and significant coefficients correlation with vine length, number of leaves and chlorophyll content in leaves. These findings are in agreement with **El-Tahawey (2015)** for the positive significant genotypic and phenotypic correlations between fruit yield and number of fruits per plant and average fruit weight. Phenotypic correlation (r_{ph}) among traits indicated significant and positive correlation between vine length plant^{-1} and number of leaves plant^{-1} (r_{ph} = 0.86); chlorophyll content (r_{ph} = 0.62); fruit length (r_{ph} = (0.52); number of fruits (r_{ph} = 0.76) and total yield (r_{ph} = (0.76). Moreover, positive and significant phenotypic correlation was found between number of fruits and total yield. These estimations are a crucial consideration that should be used to create a better selection program. The association between the traits may be caused by either a peliotrophic action of a gene on distinct regions of the plants or the linkage. These results are in accordance with the findings of (**Walled *et al.*, 2018 and Naroui Rad *et al.*, 2023**) on melon. The results indicated the importance of these characters in the improvement of number of fruits, fruit weight and total yield in melon and would be considered in selection program. Similar findings were recorded by **Taha *et al.* (2003)** and **Naik *et al.* (2015)** who reported that higher yield was mainly associated with increased number of fruits plant^{-1} and average fruit weight. Our results are in agreement with those obtained by **El-Shoura *et al.* (2020**) who found that the highest significant positive correlation of fruit yield plant^{-1} with average fruit weight followed by vine length and fruit number per vine.

4. Conclusion

On the basis of results which obtained from the study and it concluded that P_3 and P_4 had the highest means for most characteristics, whereas F_1hybrids $P_3 \times P_4$ and $P_1 \times P_4$ had the highest means for growth and yield parameters. SCA effects were significant for most traits. Heritability in the broad sense was higher than in the narrow sense. For the majority of the attributes investigated, the degree of dominance exceeded one. The correlation coefficients between the different attribute pairs were either positive or negative, and they were quite significant. According to the current findings, it may be advised to use these parental lines into genetic modification melon projects aimed at increasing yield and improving other desirable features.

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