

Inheritance of some Fruit Quality Characteristics of Melon

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ABSTRACT

Nine genotypes of melon (*Cucumis melo* L.) were crossed in a half diallel pattern crosses. The parents and their thirty six F₁ hybrids were evaluated in a complete randomized block design with three replicates for some fruit quality characters to estimate the general and specific combining ability, heterosis and heritability. There were highly significant differences among all parental genotypes and their hybrids for all studied characters. The values of general and specific combining ability effects were highly significant which indicate the presence of both additive and non-additive types of gene action in controlling flesh color, total soluble solids content, total sugars content and total carotenoids. Moreover, the calculated ratio of GCA/SCA was more than unity which indicate that additive type of gene action was more important in the inheritance of all studied characters. There was high variation among hybrids for mid and better-parent heterosis in all studied characters. The additive component (D) and dominant components (H₁) and (H₂) were highly significant, suggesting the importance of both additive and non-additive effects in the determination of the studied characters. The results indicate that the nine parents used in the present study carried more dominant than recessive alleles for the studied characters. There were very high broad sense heritability (99, 95, 99 and 99%), while the values of narrow sense heritability were 51, 41, 22 and 61 %, for flesh color, total soluble solids content, total sugars and total carotenoids, respectively, which indicate the large influences of the genetic variance on the expression of these characters. Furthermore, the additive genetic variance components is relatively large comparing to the other types of genetic variance components.

Key words: *Cucumis melo*, melon, variability, combining ability, heterosis, heritability, gene action.

Introduction

Melon (*Cucumis melo* L.; $2n = 2x = 24$) is an important horticultural crop worldwide. *Cucumis melo* is one of the most economically important species of the cucurbitaceae family, it is the most diversified species of the genus *Cucumis*, and this variability is reflected at the morphological, physiological, biochemical (Burger *et al.*, 2003; Kirkbride, 1993; Whitaker and Davis, 1962), and molecular (Akashi *et al.*, 2002; Mliki *et al.*, 2001; Monforte *et al.*, 2003; Stepansky *et al.*, 1999) levels. The origin of melon was in Africa, new data suggest that melon may probably be of Asian origin (Sebastiana *et al.*, 2010), but the distribution of wild and cultivated melon types currently is worldwide (Pitrat *et al.*, 2000). Melon fruit is one of the most valued summer fruits because of its high nutritive and medicinal value, musky flavor, sweetness and aroma.

There are several types or botanical varieties of melon. Considering the great diversity of melon, breeding programs should focus on more than one melon type. A good genotype must have a high yield, market-standard size, good flesh thickness, small internal cavity, high flesh firmness and high soluble solids content (Nunes *et al.*, 2005). In this sense, the choice of the best population in a study also depends on the goal of the program (Barros *et al.*, 2011). On the other hand, it is known that in melon improvement of many traits are to be taken into consideration for selection.

Knowledge of the mechanisms that control the main agronomic traits of a species is fundamental to genetic improvement and can be acquired through diallel cross. Among the methodologies used to choose the parents and segregating populations, the diallel analysis deserves consideration. It uses information about the performance of parents and their hybrids. From the diallel crosses the general

combining ability (GCA) and specific combining ability (SCA) can be estimated, variance components and heritability for a population from randomly chosen parental lines. GCA is related to additive effects, representing the average parental performance in hybrid combinations, while SCA is related to non-additive effects, traitizing the deviations of hybrid combinations from the average parental performance. According to Cruz and Vencovsky (1989), the breeder must choose a cross with high SCA and with at least one parent with a high GCA estimate. The idea is to join great variability and high frequency of favorable alleles, important properties of a good segregating population. These traits allow the selection of lines with good performance. In addition, the cross mean and the mean of each parent are important to choose the best hybrid combination. Moreover, heterosis, as a function of performance, is often related to degree of genetic relatedness and is dramatically influenced by growing environment. The presence of genetic variation in the breeding material at hand determines the success or failure of any breeding or bioengineering program. Therefore, the measurement of genetic variation and understanding of mode of inheritance of quantitative traits are essential steps in any crop improvement program (Ibrahim 2012). Knowledge on the trait inheritance is useful to define the strategy of a breeding program (Feyzian *et al.*, 2009).

Mohammdi *et al.* (2014) recorded that analysis of variance indicated highly significant differences among genotypes for TSS in Cantaloupe (*Cucumis melo* L. subsp. *melo* var. *cantalupensis* Naudin). The additive genetic variance components (V_A) was significant for TSS and the dominance variance (V_D) was also significant. The significant narrow sense heritability was obtained for TSS. Favorable heterosis was not obtained over the mid- and better parent for TSS. Moreover, Abou kamer *et al.* (2015) calculated the broad sense and narrow sense heritability for fruit chemical characters [fruit TSS, β -carotene content, and total sugars (%)] in five parental lines of sweet melon [line *koozassal* (P_1), line *Matrouh* (P_2), line *orange* (P_3), line *green* (P_4) and line *ideal* (P_5)]. For TSS, the broad sense heritability value for all the crosses ranged from 32.79% to 81.39%. On the other hand, for total sugars, only one cross exhibited moderate value (50.71%) for the broad sense heritability but the other crosses gave low values. For the narrow sense heritability, all the crosses showed low values where it ranged from 0.15% to 8.38%. For β -carotene, only two crosses showed moderate value (42.66% and 37.21%) for the broad sense heritability. But for the narrow sense heritability all the crosses recorded low values.

Whereas, Shashikumar and pitchaimuthu (2016) showed that no parent exhibited superior GCA for fruit TSS content indicating random genetic variability among the parents. Positive GCA effects are preferred for this trait. High, significant and positive SCA effects for total soluble solids was detected in seven from thirty crosses. The magnitude of GCA variance was higher than SCA variance for this trait which indicated predominance of additive gene effects. Data on economic heterosis effects of selected five F_1 hybrids showed that estimates for total soluble solids was significant and positive for these five hybrids.

The aims of this study were to through light on the genetic behavior and combining ability for some of fruit nutrient quality traits in a set of nine parents in half diallel crosses of melon cultivars.

Materials and Methods

The present study was conducted in the Experimental Farm and Laboratory of Horticulture Department, Faculty of Agriculture at Moshtohor, Benha University, Kalubia governorate, Egypt, during the summer seasons of 2012 to 2014 to study the genetic behavior of some nutrient traits for nine melon cultivars.

Plant materials:

Nine parental genotypes of melon (*Cucumis melo* L.) (one of them was foreign and the others were collected from different locations of Egypt) were used in making non-reciprocal diallel pattern of crosses (Table 1 and Figures 1 and 2) during the summer seasons of 2012 and 2013. Seeds of local varieties were obtained from Vegetables Crop Research Dept., Horticultural Research Institute; Agricultural Research Centre.

Individual plants from each of these cultivars were selfed for two successive generations during summer and fall seasons of 2012 in the open field to obtain uniform inbred lines for crossing.

The nine inbred lines were crossed during summer season of 2013 to produce a non-reciprocal diallel set of F₁ hybrids, i.e., 36 single crosses.

Table 1: Parental Genotypes.

Genotype name	Parental number
Ananas	P ₁
Ananas El Dokki	P ₂
Sohag1	P ₃
El Behaira 4	P ₄
Aswan	P ₅
Beni Swif 1	P ₆
El Behaira 1	P ₇
Ismailawi	P ₈
Fayoum	P ₉

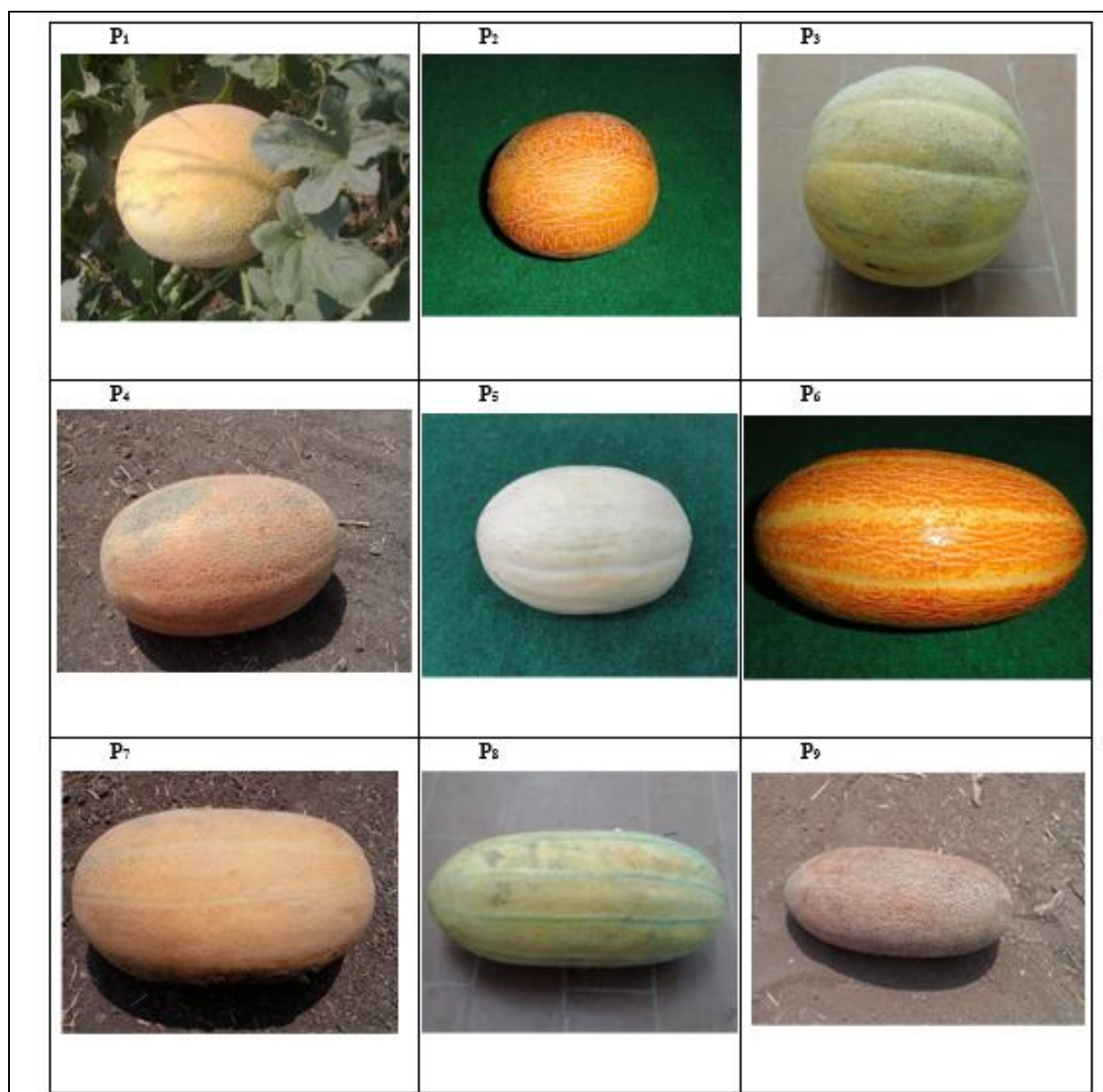


Fig. 1: Fruit shape, skin color and skin netting differences of the parental melon genotypes.

[P₁: Ananas; P₂: Ananas El Dokki; P₃: Sohag1; P₄: El Behaira 4, P₅: Aswan; P₆: Beni Swif 1; P₇: El Behaira 1; P₈: Ismailawi and P₉: Fayoum]



Fig. 2: Fruit flesh color and thickness differences of the parental melon genotypes.

[P₁: Ananas; P₂: Ananas El Dokki; P₃: Sohag1; P₄: El Behaira 4, P₅: Aswan; P₆: Beni Swif 1; P₇: El Behaire 1; P₈: Ismailawi and P₉: Fayoum]

The male and female flower buds that were expected to open in the next morning were covered by small paper bags in the day before, where crossing was usually made 7.00 – 10.00 o'clock at morning. The pollinated flowers were covered with small paper bags and tagged.

On March 20th, 2014, seeds of each parental genotype and their 36 single crosses were planted in the experimental farm to estimate the inheritance and combining ability of some chemical constituents of melon fruits.

Experimental design:

The experimental design was randomized complete blocks with three replicates; each replicate consisted of forty-five plots (nine parents and thirty six hybrids). Each experimental plot was one ridge of 4 meters in length and 1.5 meter in width, therefore, the plot area was 6.0 m².

Treatments in each replicate (parents + F₁s) were randomly assigned to plots. Seeds were sown in hills and the distance between hills was 40 cm apart. Therefore, each ridge consisted of 10 hills. The seeds were sown at the rate of three seeds /hill in the north side of the row. After full germination, plants were thinned to one plant / hill.

All the cultural practices were done as recommended for melon and the control of diseases and insects was practiced according to the recommendation of ministry of agriculture.

Measurements:

In the middle of the harvesting season, three to five fruits/plot, at the same physiological age, from each of parental lines and F₁ hybrids were taken to determine:

Flesh color:

It was determined as the flesh color graded from one to six (1 = cream, 2 = green cream, 3 = pale orange, 4 = light orange, 5 = green orange, 6 = orange).

Fruit total soluble solids (TSS %):

It was measured using a hand refractometer for three ripe fruits from each plot, and averaged.

Fruit total sugars content:

Total sugars content in the fruit of experimental plot expressed as mg/100g dry weight were determined colorimetrically according to the method described by Flood and Priestly (1973).

Fruit total carotenoids content:

Total carotenoids content in the fruit of experimental plot was determined colorimetrically in fruit as described in the AOAC (1990).

Statistical analysis:

The data obtained for the different traits were analyzed. The analysis of variance was performed for the parents and F₁ hybrids according to the model presented in Table 2, using the method described by Gomez and Gomez (1984).

Table 2: Source of variation, degrees of freedom and expected mean square.

Sources of Variation	d.f.	Expected mean squares
Blocks	(b-1)	$\sigma^2_e + g\sigma^2_b$
Genotypes	(g-1)	$\sigma^2_e + b\sigma^2_g$
Parents	(p-1)	$\sigma^2_e + b\sigma^2_p$
Hybrids	(c-1)	$\sigma^2_e + b\sigma^2_c$
Parent vs. hybrids	1	$\sigma^2_e + b\sigma^2_h$
Error	(g-1)(b-1)	σ^2_e

Where:

- b= Blocks
- g= Genotypes (parents + hybrids)
- p= Parents
- c= Hybrids
- h= Average of heterosis
- σ^2 = Variance
- e= Error

Heterosis:

Heterosis percentage was determined for individual crosses as the deviation of the F₁ mean over the average of the mid parent (MP) or above the better parent (BP). There for, the value of heterosis could be estimated from the following equations:

- a) Heterosis over the mid-parent (M.P)% = $\frac{F_1 - \overline{M.P.}}{\overline{M.P.}} \times 100$
 b) Heterosis over the better-parent (B.P)% = $\frac{F_1 - \overline{B.P.}}{\overline{B.P.}} \times 100$

Griffing diallel analysis:

General and specific combining ability were estimated by performing the Griffing's diallel cross analysis (Method 2), according to the method described by Griffing (1956).

Jinks- Hayman diallel analysis:

Data from parents and the related F₁ generation were analyzed using the diallel cross method of Jinks (1954) and Hayman (1954).

The method involve the computation of the following statistics:

- 1) Variance of parent means (VP) = V₀L₀
- 2) Variance of the component of each array = V_r
- 3) Covariance of the parents with their offspring in each array = W_r
- 4) Mean of array variance = V₁L₁
- 5) Variance of the mean of arrays = V₀ L₁
- 6) Mean of array covariance = W₀L₀₁

The analysis of homogeneity of W_r-V_r over arrays was performed to test the validity of the assumption required for Jinks- Hayman analysis.

The genetic component estimated under this analysis were:

(H₁ / D)^{1/2} = Average degree of dominance.

H₂ / 4H₁ = Measures the proportion of genes with positive and negative effects in the parents.

((4DH₁)^{1/2} + F) / ((4DH₁)^{1/2} - F) = the ratio of the total number of dominant to recessive genes in all the parents.

Where:

D = Component of variation due to the additive effects of genes.

H₁ = Component of variation due to the dominance effects of genes.

H₂ = H₁ [1 - (u - v)²]

Where:

u = Proportion of positive genes in the parents.

v = Proportion of negative genes in the parents.

F = the covariance of dominance and additive effects in a single array.

The previously mentioned estimates were obtained from the variance and covariance by removing the environmental variance (E) which, in this experiment, was estimated from the parent and F₁ block differences.

Heritability:

Narrow and broad-sense heritabilities for the genotypes used in the present study were calculated from the genetic components according to the formula proposed by Mather and Jinks (1971). However, in case where the assumptions required for Jinks-Hayman analysis were not valid, the broad and narrow sense heritability values were calculated according to the method described by Pandey and Gritton (1975) using the general and specific combining ability components as follows:

- a) Broad sense heritability (h²_{bs}) = $\frac{2\sigma^2_{gca} + \sigma^2_{sca}}{2\sigma^2_{gca} + \sigma^2_{sca} + \sigma^2_e} \times 100$
 b) Narrow sense heritability (h²_{ns}) = $\frac{2\sigma^2_{gca}}{2\sigma^2_{gca} + \sigma^2_{sca} + \sigma^2_e} \times 100$

Where:

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

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

$$\sigma^2 e = M_e$$

Where M_g and M_s are mean squares for general and specific combining abilities respectively.

Results and Discussion

Flesh color:

Mean performance, analysis of variance, combining ability and heterosis:

The mean performance of the tested nine melon genotypes and their 36 F_1 hybrids are presented in Table 3. The results presented in Tables 3 and 4 indicate highly significant differences among parents and their F_1 hybrids concerning flesh color. The parents El Behaira 4 (P_4) and Fayoum (P_9) had the highest mean performance for flesh color (6, orange), meanwhile the cultivars Ananas (P_1), Sohag 1 (P_3) and Aswan (P_5) had the lowest values (2, green cream) (Table 3). Significant differences concerning flesh color among melon genotypes had been recorded (Abou kamer *et al.*, 2015; Clayberg, 1992; Cuevas *et al.*, 2010; Glala *et al.*, 2010 and 2012; Monforte *et al.*, 2004).

None of the hybrids exceeded the cultivar with the highest value, i.e., Behaira 4 (P_4) and Fayoum (P_9). Meanwhile, the hybrids Ananas (P_1) \times Behaira 4 (P_4), Ananas (P_1) \times Fayoum (P_9), Ananas El Dokki (P_2) \times Beni Swif 1 (P_6), Behaira 4 (P_4) \times Fayoum (P_9), Aswan (P_5) \times Fayoum (P_9) and Beni Swif 1 (P_6) \times Fayoum (P_9) were not significantly different from the highest parent concerning flesh color (Table 3), while, the hybrids, Ananas (P_1) \times Ananas El Dokki (P_2), Ananas (P_1) \times Sohag1 (P_3), Ananas (P_1) \times El Behaira 1 (P_7), Ananas (P_1) \times Ismailawi (P_8), Ananas El Dokki (P_2) \times El Behaira 1 (P_7), Ananas El Dokki (P_2) \times Ismailawi (P_8), Sohag1 (P_3) \times Beni Swif 1 (P_6), El Behaira 4 (P_4) \times Aswan (P_5) and Aswan (P_5) \times Ismailawi (P_8) recorded values less than the cultivar with the lowest value (2, green cream) (Table 3).

Analysis of variance for general and specific combining ability for flesh color are presented in Table 4. The results indicate highly significant general and specific combining ability effects which indicate the presence of both additive and non-additive types of gene action in controlling flesh color in melon. Moreover, the calculated ratio of GCA/SCA was 4.64, i.e., more than unity, which indicates that additive type of gene action was more important in the inheritance of flesh color. Many investigators working on the inheritance of melon flesh color among them Monforte *et al.* (2004) and Cuevas *et al.* (2010).

Estimates of general combining ability effects of the parental genotypes indicate that the genotypes Fayoum (P_9), El Behaira 4 (P_4) and Beni Swif 1 (P_6) had highly significant positive GCA, the highest value of general combining ability associated with cultivar Fayoum (P_9) followed by El Behaira 4 (P_4) and Beni Swif 1 (P_6) without significant differences among them (Table 5), while six genotypes recorded highly significant negative values, the lowest value was associated with the parental cultivars Sohag1 (P_3). Based on these results, the parental cultivars Fayoum (P_9), El Behaira 4 (P_4) and Beni Swif 1 (P_6) will be good combiners for development of hybrids with orange flesh color, while the rest genotypes will be good combiners for development of hybrids with cream flesh color.

Concerning specific combining ability effects of the crosses, the results presented in Table 6 indicate that 15 of 36 hybrids had highly significant positive SCA, the highest positive value was associated with hybrid Ananas (P_1) \times El Behaira 4 (P_4) and the lowest positive value (0.25) associated with hybrids Sohag1 (P_3) \times Aswan (P_5), Sohag1 (P_3) \times Ismailawi (P_8) and Beni Swif 1 (P_6) \times El Behaira 1 (P_7). On the other hand, 16 hybrids had highly significant negative SCA, the lowest SCA effects were associated with the F_1 hybrids El Behaira 4 (P_4) \times Aswan (P_5), Sohag1 (P_3) \times Beni Swif 1 (P_6) and El Behaira 4 (P_4) \times El Behaira 1 (P_7). Such F_1 hybrids will give fruits with cream flesh.

With regard to heterosis, highly significant mean squares for parental genotypes vs. F_1 hybrids were detected as an indication of average heterosis for flesh color (Table 4). Estimates of mid and better-parent heterosis of crosses presented in Table 7 indicate that 7 hybrids had highly significant

positive mid-parent heterosis, the highest value was associated with the hybrid Ananas El Dokki (P₂) × Aswan (P₅) followed by the hybrids Ananas (P₁) × El Behaira 4 (P₄), Ananas (P₁) × Fayoum (P₉),

Table 3: The genotypes mean performance for some fruit chemical contents of 45 genotypes of melon.

Genotype \ Trait	Flesh color	Total soluble solids content (brix°)	Total sugars content (mg/100 g d.w.)	Total carotenoids (mg/100 g f.W.)
Ananas (P ₁)	2.00	7.67	8.15	5.04
Ananas El Dokki (P ₂)	3.00	8.33	8.13	8.96
Sohag1 (P ₃)	2.00	8.00	8.10	5.70
El Behaira 4 (P ₄)	6.00	6.67	8.16	33.71
Aswan (P ₅)	2.00	5.33	5.31	6.05
Beni Swif 1 (P ₆)	5.00	6.00	8.11	36.29
El Behaira 1 (P ₇)	5.00	5.00	5.37	8.43
Ismailawi (P ₈)	4.00	6.33	5.96	12.86
Fayoum (P ₉)	6.00	6.33	4.82	38.55
P ₁ × P ₂	1.00	6.00	8.12	3.17
P ₁ × P ₃	1.00	8.67	7.50	4.58
P ₁ × P ₄	6.00	4.67	8.07	17.02
P ₁ × P ₅	2.00	6.67	7.35	8.12
P ₁ × P ₆	2.00	7.33	9.23	9.86
P ₁ × P ₇	1.00	6.00	5.27	4.41
P ₁ × P ₈	1.00	7.33	8.07	3.66
P ₁ × P ₉	6.00	8.33	7.70	34.45
P ₂ × P ₃	2.00	8.67	8.07	6.15
P ₂ × P ₄	4.00	8.33	6.13	10.01
P ₂ × P ₅	4.00	6.67	8.16	9.73
P ₂ × P ₆	6.00	6.00	7.60	33.33
P ₂ × P ₇	1.00	6.67	7.30	5.54
P ₂ × P ₈	1.00	6.33	7.35	5.44
P ₂ × P ₉	3.00	8.33	7.81	9.65
P ₃ × P ₄	3.00	7.33	8.07	9.25
P ₃ × P ₅	2.00	5.33	8.05	6.10
P ₃ × P ₆	1.00	5.67	8.07	5.27
P ₃ × P ₇	2.00	7.33	8.20	6.46
P ₃ × P ₈	2.00	7.67	4.47	6.18
P ₃ × P ₉	4.00	8.33	8.20	10.65
P ₄ × P ₅	1.00	6.33	8.16	5.02
P ₄ × P ₆	3.00	7.33	8.02	9.39
P ₄ × P ₇	2.00	6.00	7.54	6.63
P ₄ × P ₈	3.00	6.33	8.16	8.57
P ₄ × P ₉	6.00	6.67	8.08	41.80
P ₅ × P ₆	4.00	7.33	7.53	10.94
P ₅ × P ₇	3.00	4.33	8.30	8.96
P ₅ × P ₈	1.00	4.67	4.07	5.63
P ₅ × P ₉	6.00	9.33	8.12	32.36
P ₆ × P ₇	4.00	4.33	8.14	11.73
P ₆ × P ₈	4.00	6.33	8.03	10.36
P ₆ × P ₉	6.00	6.67	8.03	44.16
P ₇ × P ₈	3.00	5.67	6.74	9.01
P ₇ × P ₉	4.00	5.33	7.21	13.13
P ₈ × P ₉	4.00	6.00	8.14	14.99
LSD 5%	0.24	0.85	0.30	0.97
LSD 1%	0.32	1.13	0.39	1.29

Table 4: Mean squares for 45 genotypes, general (GCA) and specific (SCA) combining ability for some fruit quality characters.

S.O.V	d.f.	Flesh color	Total soluble solids	Total sugars content	Total carotenoids content
Rep.	2	0.02	0.16	0.01	0.60
Genotypes	44	9.08 **	4.62 **	4.09 **	402.02 **
Parents (P)	8	8.58 **	4.04 **	6.62 **	622.68 **
Crosses (C)	35	9.00 **	4.89 **	3.35 **	347.53 **
P vs C	1	16.02 **	0.05	10.08 **	543.91 **
Error	88	0.02	0.28	0.03	0.36
GCA	8	8.45 **	3.79 **	2.04 **	465.28 **
SCA	36	1.82 **	1.04 **	1.21 **	60.39 **
Error	88	0.01	0.09	0.01	0.12
GCA/SCA		4.64	3.64	1.68	7.70

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 5: Estimates of general combining ability effects for some fruit chemical contents of nine parentals melon genotypes.

Trait \ Parent	Flesh color	Total soluble solids content	Total sugars content	Total carotenoids
Ananas (P ₁)	-0.73**	0.33**	0.28**	-3.40**
Ananas El Dokki (P ₂)	-0.36**	0.64**	0.21**	-2.89**
Sohag1 (P ₃)	-1.00**	0.76**	0.21**	-6.06**
El Behaira 4 (P ₄)	0.73**	-0.03	0.37**	3.85**
Aswan (P ₅)	-0.45**	-0.48**	-0.38**	-3.07**
Beni Swif 1 (P ₆)	0.73**	-0.33**	0.58**	6.81**
El Behaira 1 (P ₇)	-0.18**	-1.00**	-0.46**	-4.54**
Ismailawi (P ₈)	-0.45**	-0.33**	-0.68**	-3.92**
Fayoum (P ₉)	1.73**	0.45**	-0.14**	13.23**
LSD(gi)0.05	0.05	0.17	0.06	0.19
LSD(gi)0.01	0.06	0.23	0.08	0.26
LSD(gi-gj)0.05	0.07	0.26	0.09	0.29
LSD(gi-gj)0.01	0.10	0.34	0.12	0.39

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Ananas El Dokki (P₂) × Beni Swif 1 (P₆) and Aswan (P₅) × Fayoum (P₉) with the same percentage (50.00%), while 25 hybrids recorded highly significant negative mid-parent heterosis, the lowest values were associated with the F₁ hybrids Ananas El Dokki (P₂) × El Behaira 1(P₇) and El Behaira 4 (P₄) × Aswan (P₅) followed by the hybrids Ananas (P₁) × El Behaira 1(P₇), Ananas El Dokki (P₂) × Ismailawi (P₈) and Sohag1 (P₃) × Beni Swif 1(P₆) with the same ratio. Moreover, 2 hybrids recorded highly significant positive heterosis over better-parent, the highest better-parent heterosis was associated with the F₁ hybrid Ananas El Dokki (P₂) × Aswan (P₅), meanwhile 27 hybrids recorded highly significant negative better-parent heterosis, the lowest values was associated with the hybrid Ananas (P₁) × Sohag1 (P₃) (-100.00%). Glala *et al.* (2012) evaluated melon fruit flesh color degree by using a chromameter device and found that there were high hybrid vigour among F₁ plants.

Estimation of genetic components:

The estimates of the genetic components of variation in Table 8 show that the additive component (D) and dominant components (H₁) and (H₂) were highly significant, suggesting the importance of both additive and non-additive effects in determination of fruit flesh color.

The regression line of Vr-Wr intersected the Wr axis above the origin (Fig. 3). This indicates the presence of partial dominance. Moreover, the sign of h, which measures the direction of dominance, was positive (+ 2.34), (Table 8). This result indicates that dominance acted in the direction of parents that give fruits with orange flesh. In addition, the degree of dominance averaged over all loci,

measured by $(H_1 / D)^{1/2}$ was 1.65 (Table 8). This can be considered that the over-dominance was toward the parents that give fruits with orange flesh.

The relative values of the Vr and Wr showed that the parental cultivars Fayoum (P₉), Ananas El Dokki (P₂), Aswan (P₅) and Sohag1 (P₃) had the lowest values which indicate that these cultivars contained the most dominant genes concerning fruit flesh color. On the other hand, the parental cultivars Ananas (P₁), El Behaira 1(P₇) and Ismailawi (P₈) had the highest values of Vr and Wr and hence, contained the most recessive genes.

Table 6: Specific combining ability effects for some fruit chemical contents of 36 melon F₁ hybrids.

Cross	Flesh color	Total soluble solids content	Total sugars content	Total carotenoids
P ₁ × P ₂	-1.11**	-1.64**	0.18	-3.81**
P ₁ × P ₃	-0.47**	0.91**	-0.45**	0.77*
P ₁ × P ₄	2.80**	-2.30**	-0.04	3.30**
P ₁ × P ₅	-0.02	0.15	-0.01	1.31**
P ₁ × P ₆	-1.20**	0.67*	0.92**	-6.82**
P ₁ × P ₇	-1.29**	0.00	-2.01**	-0.92**
P ₁ × P ₈	-1.02**	0.67*	1.02**	-2.29**
P ₁ × P ₉	1.80**	0.88**	0.11	11.34**
P ₂ × P ₃	0.16	0.61*	0.20*	1.83**
P ₂ × P ₄	0.44**	1.06**	-1.90**	-4.22**
P ₂ × P ₅	1.62**	-0.15	0.87**	2.42**
P ₂ × P ₆	2.44**	-0.97**	-0.64**	16.14**
P ₂ × P ₇	-1.65**	0.36	0.10	-0.30
P ₂ × P ₈	-1.38**	-0.64*	0.37**	-1.02**
P ₂ × P ₉	-1.56**	0.58*	0.29**	-13.96**
P ₃ × P ₄	0.07	-0.06	0.04	-1.82**
P ₃ × P ₅	0.25**	-1.61**	0.76**	1.96**
P ₃ × P ₆	-1.93**	-1.42**	-0.17	-8.75**
P ₃ × P ₇	-0.02	0.91**	1.00**	3.79**
P ₃ × P ₈	0.25**	0.58*	-2.50**	2.89**
P ₃ × P ₉	0.07	0.45	0.67**	-9.79**
P ₄ × P ₅	-2.47**	0.18	0.72**	-9.04**
P ₄ × P ₆	-1.65**	1.03**	-0.38**	-14.55**
P ₄ × P ₇	-1.75**	0.36	0.18	-5.95**
P ₄ × P ₈	-0.47**	0.03	1.03**	-4.63**
P ₄ × P ₉	0.35**	-0.42	0.40**	11.44**
P ₅ × P ₆	0.53**	1.48**	-0.13	-6.07**
P ₅ × P ₇	0.44**	-0.85**	1.69**	3.31**
P ₅ × P ₈	-1.29**	-1.18**	-2.32**	-0.65*
P ₅ × P ₉	1.53**	2.70**	1.19**	8.93**
P ₆ × P ₇	0.25**	-1.00**	0.57**	-3.80**
P ₆ × P ₈	0.53**	0.33	0.68**	-5.80**
P ₆ × P ₉	0.35**	-0.12	0.14	10.85**
P ₇ × P ₈	0.44**	0.33	0.44**	4.21**
P ₇ × P ₉	-0.75**	-0.79**	0.36**	-8.83**
P ₈ × P ₉	-0.47**	-0.79**	1.52**	-7.59**
LSD 0.05 Sij	0.16	0.55	0.20	0.63
LSD 0.01 Sij	0.21	0.73	0.26	0.83
LSD 0.05 Sij-Sik	0.23	0.82	0.29	0.92
LSD 0.01 Sij-Sik	0.31	1.08	0.38	1.23
LSD 0.05 Sij-Skl	0.22	0.77	0.27	0.88
LSD 0.01 Sij-Skl	0.29	1.03	0.36	1.16

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

The ratio H₂ /4H₁, which is used to estimate the average frequency of negative versus positive alleles in the parents, was 0.21 (Table 8). Since this value was less than 0.25, this result indicates the

unequal distribution of alleles which decreased the expression of flesh color and that which increased it over the related loci. In addition, the ratio KD/KR which measures the total number of dominance to recessive alleles in all parents was > 1, i.e., 1.18 (Table 8). This result indicates that the nine parents used in the present study carried more dominant than recessive alleles. This conclusion was supported by the positive value of F, i.e., + 0.77 (Table 8) which indicates that there were more dominant than recessive alleles in the parents used in this study. The negative value of (r) (- 0.18) indicates that the parents are containing the most increasing genes. The value of (r²) (0.03) could suggest the existence of (yr) and (wr ± vr) and hence, prediction on completely dominant and recessive parents is possible.

Table 7: Heterosis of 36 melon hybrids in the F₁ generation over both mid parent (MP) and better parent (BP) for some fruit chemical contents.

Trait Cross	Flesh color		Total soluble solids content		Total sugars content		Total carotenoids	
	MP	BP	MP	BP	MP	BP	MP	BP
P ₁ × P ₂	-60.00**	-66.67**	-25.00**		-0.24	-0.34	-54.67**	-64.60**
P ₁ × P ₃	-50.00**	-	10.64*	-28.00**	-7.74**	-8.03**	-14.69	-76.88**
P ₁ × P ₄	50.00**	0.00	-34.88**	4.17	-1.09	-1.14	-12.12**	-49.49**
P ₁ × P ₅	0.00	0.00	2.56	-39.13**	9.23**	-9.83**	46.46**	34.16**
P ₁ × P ₆	-42.86**	-60.00**	7.32	-13.04*	13.54**	13.24**	-52.30**	-72.84**
P ₁ × P ₇	-71.43**	-80.00**	-5.26	-4.35	-22.09**	-35.39**	-34.51**	-47.70**
P ₁ × P ₈	-66.67**	-75.00**	4.76	-21.74**	14.32**	-1.03	-59.12**	-71.55**
P ₁ × P ₉	50.00**	0.00	19.05**	-4.35	18.71**	-5.49**	58.08**	-10.63**
P ₂ × P ₃	-20.00**	-33.33**	6.12	8.70	-0.54	-0.75	-16.18**	-31.43**
P ₂ × P ₄	-11.11**	-33.33**	11.11**	4.00	-24.71**	-24.82**	-53.07**	-70.30**
P ₂ × P ₅	60.00**	33.33**	-2.44	0.00	21.35**	0.25	29.61**	8.56
P ₂ × P ₆	50.00**	20.00**	-16.28**	-20.00**	-6.44**	-6.59**	47.31**	-8.15**
P ₂ × P ₇	-75.00**	-80.00**	0.00	-28.00**	8.09**	-10.30**	-36.35**	-38.24**
P ₂ × P ₈	-71.43**	-75.00**	-13.64**	-20.00**	4.25*	-9.67**	-50.13**	-57.68**
P ₂ × P ₉	-33.33**	-50.00**	13.64**	-24.00**	20.48**	-4.01*	-59.37**	-74.96**
P ₃ × P ₄	-25.00**	-50.00**	0.00	0.00	-0.67	-1.03	-53.08**	-72.57**
P ₃ × P ₅	0.00	0.00	-20.00**	-8.33	20.08**	-0.63	3.79	0.85
P ₃ × P ₆	-71.43**	-80.00**	-19.05**	-33.33**	-0.43	-0.48	-74.90**	-85.48**
P ₃ × P ₇	-42.86**	-60.00**	12.82*	-29.17**	21.83**	1.28	-8.59	-23.39**
P ₃ × P ₈	-33.33**	-50.00**	6.98	-8.33	-36.39**	-44.78**	-33.44**	-51.96**
P ₃ × P ₉	0.00	-33.33**	16.28**	-4.17	26.79**	1.17	-51.85**	-72.36**
P ₄ × P ₅	-75.00**	-83.33**	5.56	4.17	21.24**	0.05	-74.75**	-85.11**
P ₄ × P ₆	-45.45**	-50.00**	15.79**	-5.00	-1.42	-1.72	-73.18**	-74.13**
P ₄ × P ₇	-63.64**	-66.67**	2.86	10.00	11.46**	-7.61**	-68.52**	-80.32**
P ₄ × P ₈	-40.00**	-50.00**	-2.56	-10.00	15.59**	0.04	-63.18**	-74.57**
P ₄ × P ₉	0.00	0.00	2.56	-5.00	24.47**	-0.94	15.69**	8.43**
P ₅ × P ₆	14.29**	-20.00**	29.41**	0.00	12.20**	-7.19**	-48.34**	-69.87**
P ₅ × P ₇	-14.29**	-40.00**	-16.13*	22.22**	55.62**	54.75**	23.78**	6.31
P ₅ × P ₈	-66.67**	-75.00**	-20.00**	-18.75**	-27.84**	-31.81**	-40.46**	-56.22**
P ₅ × P ₉	50.00**	0.00	60.00**	-26.32**	60.26**	53.02**	45.12**	-16.05**
P ₆ × P ₇	-20.00**	-20.00**	-21.21**	47.37**	20.82**	0.39	-47.52**	-67.67**
P ₆ × P ₈	-11.11**	-20.00**	2.70	-27.78**	14.07**	-1.02	-57.86**	-71.46**
P ₆ × P ₉	9.09**	0.00	8.11	0.00	24.08**	-1.02	18.01**	14.56**
P ₇ × P ₈	-33.33**	-40.00**	0.00	5.26	19.05**	13.10**	-15.36**	-29.94**
P ₇ × P ₉	-27.27**	-33.33**	-5.88	-10.53	41.53**	34.42**	-44.12**	-65.95**
P ₈ × P ₉	-20.00**	-33.33**	-5.26	-15.79**	50.91**	36.55**	-41.69**	-61.12**

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

With respect to broad and narrow sense heritability, the results presented in Table 8 show very high broad sense heritability (99%) and intermediate narrow sense heritability (51%) which indicate the large influences of the genetic variance on the expression of this character. Furthermore, the additive gene action variance components are relatively large comparing to the other types of genetic

variance components. These results indicate the relatively high progress which can be achieved by selecting individual plants in segregating generations to improve fruit flesh color in melon.

Table 8: The proportions of the genetic components for some fruit quality characters in 36 melon F₁ hybrids according to Jinks-Hayman analysis.

Trait Genetic component	Flesh color	Total soluble solids content	Total content sugars	Total carotenoids
D	2.86**	1.25**	2.20**	207.44**
F	0.77	0.15	2.77*	78.22
H1	7.82**	4.17**	5.44**	256.79**
H2	6.56**	3.83**	4.24**	218.36**
h ²	2.34**	-0.03	1.47*	79.54*
E	0.01	0.09	0.01	0.12
(H1/D) ^{0.5}	1.65	1.82	1.57	1.11
H2/4H1	0.21	0.23	0.19	0.21
KD/ KR	1.18	1.07	2.34	1.41
R	-0.18	-0.03	-0.66	0.84
r ²	0.03	0.01	0.43	0.70
h ² /H2	0.37	-0.01	0.35	0.36
h ² (n.s)	0.51	0.41	0.22	0.61
h ² (b.s)	0.99	0.95	0.99	0.99

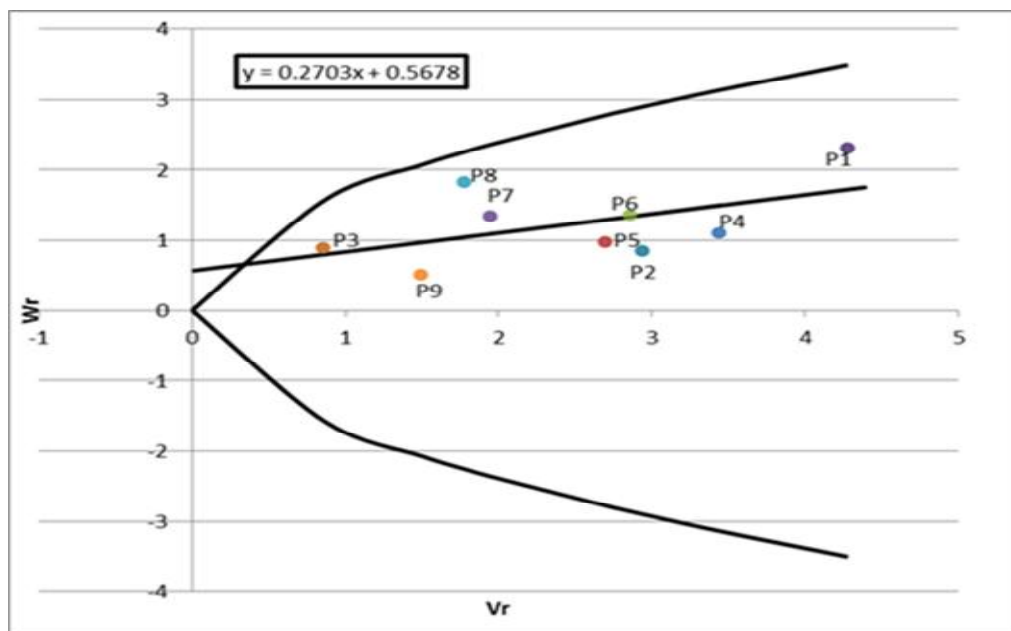


Fig. 3: Variance (V_r) and covariance (W_r) graph of flesh color in F₁ generation of melon genotypes. [P₁: Ananas, P₂: Ananas El Dokki, P₃: Sohag1, P₄: El Behaira 4, P₅: Aswan, P₆: Beni Swif 1, P₇: El Behaire 1, P₈: Ismailawi and P₉: Fayoum].

Fruit total soluble solids content (TSS):

Mean performance, analysis of variance, combining ability and heterosis:

Mean performance of the tested nine melon parental genotypes and their 36 F₁ hybrids are presented in Table 3. The results presented in Tables 3 and 4 indicate highly significant differences among different parental genotypes and their F₁ hybrids concerning fruit TSS content. The cultivars Ananas El Dokki (P₂), Sohag1 (P₃) and Ananas (P₁), respectively, had significantly the highest mean values for TSS content. Meanwhile, the cultivars show the lowest TSS content were El Behaira 1 (P₇) and Aswan (P₅) without significant differences between them. It is worth mentioned that the high fruit TSS content is considered one of the desirable quality characteristics of melon fruits. Similar

conclusion was reported by Molina *et al.* (1989), Monforte *et al.* (2005), Glala *et al.* (2010 and 2012), Reddy *et al.* (2013), Bayoumy *et al.* (2014), Mohammdai *et al.* (2014), Abou kamer *et al.* (2015) and Shashikumar and Pitchaimuthi (2016). The hybrids Aswan (P₅) × Fayoum (P₉), Ananas (P₁) × Sohag1 (P₃) and Ananas El Dokki (P₂) × Sohag1 (P₃) exceeded the cultivar with highest TSS content, i.e., Ananas El Dokki (P₂), while the hybrids Ananas (P₁) × Fayoum (P₉), Ananas El Dokki (P₂) × El Behaira 4 (P₄), Ananas El Dokki (P₂) × Fayoum (P₉) and Sohag1 (P₃) × Fayoum (P₉) were not significantly different from the hybrid with the highest value, whereas, the F₁ hybrids Aswan (P₅) × El Behaira 1 (P₇), Beni Swif 1 (P₆) × El Behaira 1 (P₇), Ananas (P₁) × El Behaira 4 (P₄) and Aswan (P₅) × Ismailawi (P₈) recorded values less than the lowest cultivar, i.e., El Behaira 1 (P₇), (Table 4). High genotypic variation in TSS content among melon genotypes have been reported by Glala *et al.* (2010), Shamloul and Askar (2011), Glala *et al.* (2012), Reddy *et al.* (2013), Bayoumy *et al.* (2014), Mohammdai *et al.* (2014) and Shashikumar and Pitchaimuthi (2016).

The analysis of variance for general and specific combining ability for TSS content are presented in Table 4. The results show highly significant general and specific combining ability effects which indicated the presence of both additive and non-additive types of gene action. Moreover, the calculated ratio of GCA/SCA was 3.64, i.e., more than unity, which indicates that additive type of gene action was more important in the inheritance of TSS content. These results agreed with those of Abadia *et al.* (1985), Kitroongrung *et al.* (1992), Zhihua (1995), Monforte *et al.* (2005), Bayoumy *et al.* (2014) and Shashikumar and Pitchaimuthi (2016). They recorded that TSS is controlled by additive gene effects in melon. Moreover Kalb and Davis (1984), Cuarteiro *et al.* (1985), Singh and Randhawa (1990), Barros *et al.* (2011) and Mohammdai *et al.* (2014) on melon reported additive and non-additive gene actions controlling TSS trait. On the contrary, Monforte *et al.* (2004) found that TSS is controlled by non-additive gene effects.

Estimates of general combining ability effects of the parental genotypes for TSS content are presented in Table 5. The data indicate that the genotypes Sohag1 (P₃), Ananas El Dokki (P₂), Fayoum (P₉) and Ananas, respectively, were the best combiners for development of hybrids with high fruit TSS content, they having highly significant positive values of GCA, while parental genotypes El Behaira 1 (P₇), Aswan (P₅), Beni Swif 1 (P₆) and Ismailawi (P₈) had highly significant negative GCA, the lowest value was associated with the parental cultivar El Behaira 1 (P₇), (Table 5). Barros *et al.* (2011), Bayoumy *et al.* (2014) and Shashikumar and Pitchaimuthi (2016) reported significant differences for GCA effects among melon genotypes.

Estimates of specific combining ability effects of crosses are presented in Table 6. From this data, 7 hybrids had highly significant positive SCA and 5 hybrids recorded significant positive SCA ranged from 0.58 to 2.70, the highest SCA was associated with the hybrid Aswan (P₅) × Fayoum (P₉). On the other hand, 10 hybrids had highly significant negative SCA, the lowest value associated with the hybrid Ananas (P₁) × El Behaira 4 (P₄). This result was confirmed by results and conclusions of Lippert and Legg (1972), Zalapa *et al.* (2006), Paris *et al.* (2008), Barros *et al.* (2011), Glala *et al.*, 2012, Bayoumy *et al.* (2014) and Shashikumar and pitchaimuthu (2016) as they found high SCA effects in melon crosses.

With regard to heterosis, highly significant mean squares for parental genotypes vs. F₁ hybrids were detected for TSS content as an indication of average heterosis (Table 4). Estimates of mid and better parent heterosis of the crosses are presented in Table 7. From this data, 7 hybrids had highly significant positive heterosis over mid-parent and 2 hybrids recorded significant positive values ranged from 10.64 to 60.00 %, the highest mid-parent heterosis were associated with the hybrids Aswan (P₅) × Fayoum (P₉), meanwhile 8 hybrids had highly significant negative mid-parent heterosis, the lowest mid-parent heterosis was associated with the F₁ hybrid Ananas (P₁) × El Behaira 4 (P₄). Moreover, 9 hybrids had highly significant positive heterosis over better-parent, the hybrids Beni Swif 1 (P₆) × El Behaira 1 (P₇) and Aswan (P₅) × El Behaira 1 (P₇) had highly significant positive heterosis over better-parent, while 13 hybrids had highly significant negative better-parent heterosis, the lowest better-parent heterosis was associated with the F₁ hybrid Ananas (P₁) × Aswan (P₅).

Estimation of genetic components:

The estimates of the genetic components of variation in Table 8 showed that the additive component (D) and dominant components (H₁) and (H₂) were highly significant, suggesting the

importance of both additive and non-additive effects in the determination of TSS%. Mohammadai *et al.* (2014) mentioned that both additive and non-additive gene actions were important in controlling TSS%. Meanwhile, Bayoumy *et al.* (2014) indicated that additive gene action played a major role in the inheritance of this character.

The regression line of $V_r - W_r$ intersected the W_r axis above the origin (Fig.4). This indicates the presence of partial dominance in the inheritance of this character. In addition, the sign of h , which measures the direction of dominance, was negative (- 0.03), (Table 8). This result indicates that dominance acted in the direction of plants that give fruits with low TSS content. Moreover, the degree of dominance averaged over all loci, measured by $(H_1 / D)^{1/2}$ was 1.82 (Table 8). This can be considered that the over- dominance was toward the plants that give fruits with high TSS content.

The relative values of the V_r and W_r (Fig. 4) show that the parental cultivars Beni Swif 1 (P_6), Ananas (P_1), El Behaira 4 (P_4) and Aswan (P_5) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivars El Behaira 1 (P_7) and Sohag1 (P_3) had the highest values and hence contained the most recessive genes. Moreover, the values of V_r and W_r associated with the parental cultivars Ananas (P_1), El Behaira 4 (P_4), Aswan (P_5) and Beni Swif 1 (P_6) were close to each other (Fig. 4) which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, the parental cultivars Sohag1 (P_3) and El Behaira 1 (P_7) which had high values of V_r and W_r , had a distinguished genotypes concerning TSS content. Such information is of great value especially in the stage of selecting parental melon cultivars which will inter in a certain breeding program.

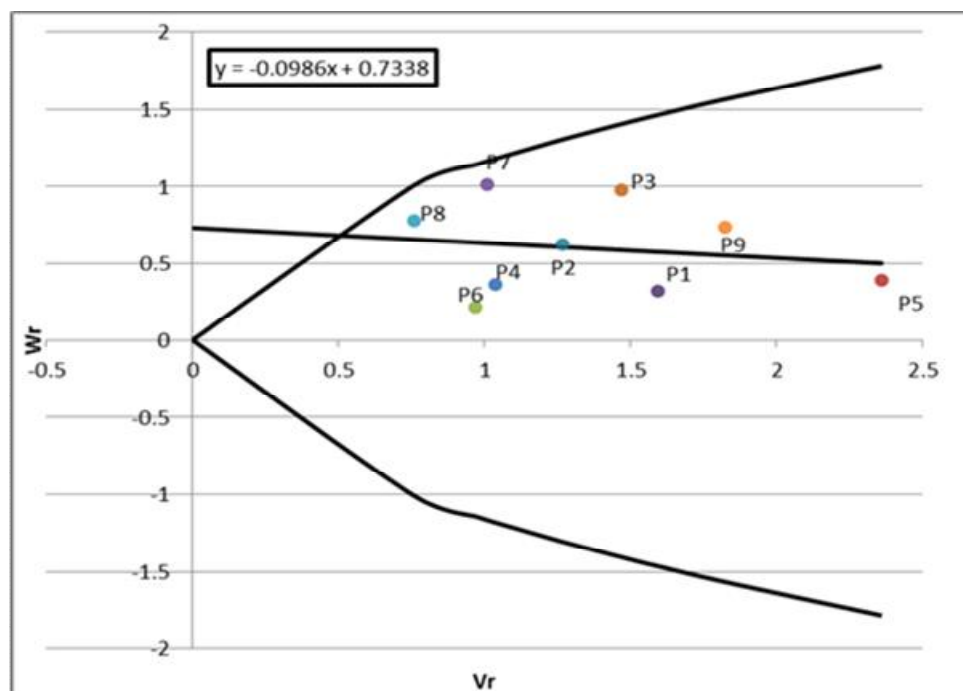


Fig. 4: Variance (V_r) and covariance (W_r) graph fruit TSS content in F_1 generation of melon genotypes.

[P_1 : Ananas, P_2 : Ananas El Dokki, P_3 : Sohag1, P_4 : El Behaira 4, P_5 : Aswan, P_6 : Beni Swif 1, P_7 : El Behaire 1, P_8 : Ismailawi and P_9 : Fayoum]

The ratio, $H_2 / 4H_1$, which is used to estimate the average frequency of negative versus positive alleles in the parents, was 0.23 (Table 8). Since this value was less than 0.25, this result indicates the unequal distribution of alleles which decreased the expression of TSS contents and that which increased it over the related loci. In addition, the ratio KD/KR which measures the total number of dominance to recessive alleles in all parents was > 1 , i.e., 1.07 (Table 8). This result indicates that the nine parents used in the present study carried more dominant than recessive alleles. This conclusion was supported by the positive value of F , i.e., + 0.15 (Table 8) which indicates that there were more dominant than recessive alleles in the parents used in this study. The negative value of (r) (- 0.03) indicates that the parents are containing the most increasing genes. The value of (r^2) (0.01) could

suggest the existence of (yr) and ($wr \pm vr$) and hence, prediction on completely dominant and recessive parents is possible.

With respect to broad and narrow sense heritability, the results presented in Table 8 showed high broad sense heritability (95%) and intermediate narrow sense heritability (41%) which indicated the large influences of the genetic variance on the expression of this character. Furthermore, the non-additive genetic variance components is relatively large comparing to the additive genetic variance. Based on these results, selection in the segregating generations of melon crosses to improve this character should be made on individual plants basis. Relatively high estimates of heritability for TSS in melon fruits have been reported (Abou kamer *et al.*, 2015; Glala *et al.*, 2012; Iban *et al.*, 2007; Mohammdai *et al.*, 2014; Reddy *et al.*, 2013 and Shamloul and Askar, 2011).

Fruit total sugars content:

Mean performance, analysis of variance, combining ability and heterosis:

Mean performance of the tested nine melon parental genotypes and their 36 F₁ hybrids are presented in Table 3. The results presented in Tables 3 and 4 indicate highly significant differences among different parental genotypes and F₁ hybrids concerning fruit total sugars content. The cultivars El Behaira 4 (P₄), Ananas (P₁), Ananas El Dokki (P₂), Beni Swif 1 (P₆) and Sohag1 (P₃), respectively, had significantly the highest mean values for total sugars content. Meanwhile, the cultivar Fayoum (P₉) showed the lowest total sugars content. The high fruit sugars content will improve the taste and the nutritional value of melon fruits. The hybrids Ananas (P₁) × Beni Swif 1 (P₆), Aswan (P₅) × El Behaira 1 (P₇), Sohag1 (P₃) × El Behaira 1 (P₇) and Sohag1 (P₃) × Fayoum (P₉) exceeded the cultivar with highest total sugars content, i.e., El Behaira 4 (P₄). Whereas, the F₁ hybrids Sohag1 (P₃) × Ismailawi (P₈) and Aswan (P₅) × Ismailawi (P₈) recorded mean values less than the lowest cultivar, i.e., Fayoum (P₉), (Table 3). Such differences in fruit total sugars content among different parental genotypes and F₁ hybrids can be used in improving programs of melon in Egypt. High genotypic variation in total sugars content among melon genotypes have been reported by Monforte *et al.* (2005), Glala *et al.* (2010), Shamloul and Askar (2011), Glala *et al.* (2012), Mohammdai *et al.* (2014) and Abou kamer *et al.* (2015).

The analysis of variance for general and specific combining ability for total sugars content are presented in Table 4. The results show highly significant general and specific combining ability effects which indicated the presence of both additive and non-additive types of gene action. Moreover, the calculated ratio of GCA/SCA was 1.68, i.e. more than unity, which indicates that additive type of gene action was more important in the inheritance of total sugars content of melon fruits. Bayoumy *et al.* (2014) found that the additive genetic variance values were larger in magnitude than the dominance variance for total sugars, this finding could be verified by the A/D ratio which more than one for this character, indicating that additive gene action played a major role in the inheritance of this character.

Estimates of general combining ability effects of the parental genotypes for total sugars content are presented in Table 5. The data indicate that the genotypes Beni Swif 1 (P₆), El Behaira 4 (P₄), Ananas (P₁), Ananas El Dokki (P₂) and Sohag1 (P₃), respectively, were the best combiners for forming melon hybrids with high fruit total sugars content, having highly significant positive values of GCA, while the parental cultivars Ismailawi (P₈), El Behaira 1 (P₇), Aswan (P₅) and Fayoum (P₉) recorded highly significant negative values of GCA (Table 5). These results will be of great value in melon breeding programs. Glala *et al.* (2010) and Bayoumy *et al.* (2014) reported significant differences in GCA effects among melon genotypes.

Estimates of specific combining ability effects for crosses are presented in Table 6. From this data, 18 hybrids had highly significant positive SCA and one hybrid recorded significant positive SCA ranged from 0.20 to 1.69, the highest specific combining ability effects was associated with the hybrid Aswan (P₅) × El Behaira 1 (P₇). On the other hand, 7 hybrids had highly significant negative SCA, the lowest value were associated with the hybrids Sohag1 (P₃) × Ismailawi (P₈) and Aswan (P₅) × Ismailawi (P₈). This result was confirmed by results and conclusions of Glala *et al.* (2010) and Bayoumy *et al.* (2014) who found that the melon crosses having high SCA effects and also involved

at least one good general combiner parent were considered useful because such crosses provide transgressive type of segregants in advanced generations more frequently than crosses with poor general combiner parents.

With regard to heterosis, highly significant mean squares for parental genotypes vs. F₁ hybrids were detected for total sugars content as an indication of average heterosis (Table 4). Estimates of mid and better parent heterosis of crosses are presented in Table 7. From this data, 23 hybrids had highly significant positive heterosis over mid-parent and one hybrid recorded significant positive values ranged from 4.25 to 60.26 %, the highest mid-parent heterosis was associated with the hybrid Aswan (P₅) × Fayoum (P₉), meanwhile 6 hybrids had highly significant negative mid-parent heterosis, the lowest mid-parent heterosis was associated with the F₁ hybrid Sohag1 (P₃) × Ismailawi (P₈). Moreover, 6 hybrids had highly significant positive heterosis over better-parent ranged from 13.10 to 54.75%, the highest better-parent heterosis were associated with the F₁ hybrids Aswan (P₅) × El Behaira 1 (P₇) and Aswan (P₅) × Fayoum (P₉), while 25 hybrids had highly significant negative better-parent heterosis, the lowest better-parent heterosis was associated with the F₁ hybrid Sohag1 (P₃) × Ismailawi (P₈).

Estimation of genetic components:

The estimates of the genetic components of variation in Table 8 showed that the additive component (D) and dominant components (H₁) and (H₂) were highly significant, suggesting the importance of both additive and non-additive effects in the determination of fruit total sugars content. In this regard, Bayoumy *et al.* (2014) found that the additive genetic variance values were larger than the dominance variance for fruit total sugars content.

The regression line of V_r -W_r intersected the W_r axis at the origin point (Fig. 5). This indicates the presence of complete dominance in the inheritance of this character. In addition, the sign of h, which measures the direction of dominance, was positive (+ 1.47), (Table 8). This result indicates that dominance acted in the direction of plants that give fruits with high total sugars content. Moreover, the degree of dominance averaged over all loci, measured by $(H_1 / D)^{1/2}$ was 1.57 (Table 8). This can be considered that the over-dominance was toward the plants that give fruits with high total sugars content.

The relative values of the V_r and W_r (Fig.5) show that the parental cultivars Ananas El Dokki (P₂) and El Behaira 1 (P₇) had the lowest values which indicated that these cultivars contained the most dominant genes. On the other hand, the parental cultivars Ananas (P₁) and Fayoum (P₉) had the highest values and hence contained the most recessive genes. Moreover, the values of V_r and W_r associated with the parental cultivars Ananas El Dokki (P₂) and El Behaira 4 (P₄) were close to each other (Fig. 5) which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, the parental cultivars Ananas (P₁) and Fayoum (P₉) which had high values of V_r and W_r, had a distinguished genotypes concerning total sugar content. Such information is of great value especially in the stage of selecting parental melon cultivars which will inter in a certain breeding program.

The ratio, H₂ /4H₁, which is used to estimate the average frequency of negative versus positive alleles in the parents, was 0.19 (Table 8). Since this value was less than 0.25, this result indicates the unequal distribution of alleles which decreased the expression of total sugars content and that which increased it over the related loci. In addition, the ratio KD/KR which measures the total number of dominance to recessive alleles in all parents was > 1, i.e., 2.34 (Table 8). This result indicates that the nine parents used in the present study carried more dominant than recessive alleles. This conclusion was supported by the positive value of F, i.e., +2.77 (Table 8) which indicates that there were more dominant than recessive alleles in the parents used in this study. The negative value of (r) (-0.66) indicates that the parents are containing the most increasing genes. The value of (r²) (0.43) could suggest the existence of (yr) and (wr ± vr) and hence, prediction on completely dominant and recessive parents is possible.

With respect to broad and narrow sense heritability, the results presented in Table 8 showed very high broad sense heritability (99%) and low narrow sense heritability (22%). The low value of the narrow sense heritability estimates indicates the high involvement of the non-additive effects on the expression of this character. Abou kamer *et al.* (2015) found that, for total sugars, only one from 10

crosses exhibited moderate value 50.71% for the broad sense heritability but the other crosses showed low values where it ranged from 15% to 8.38%.

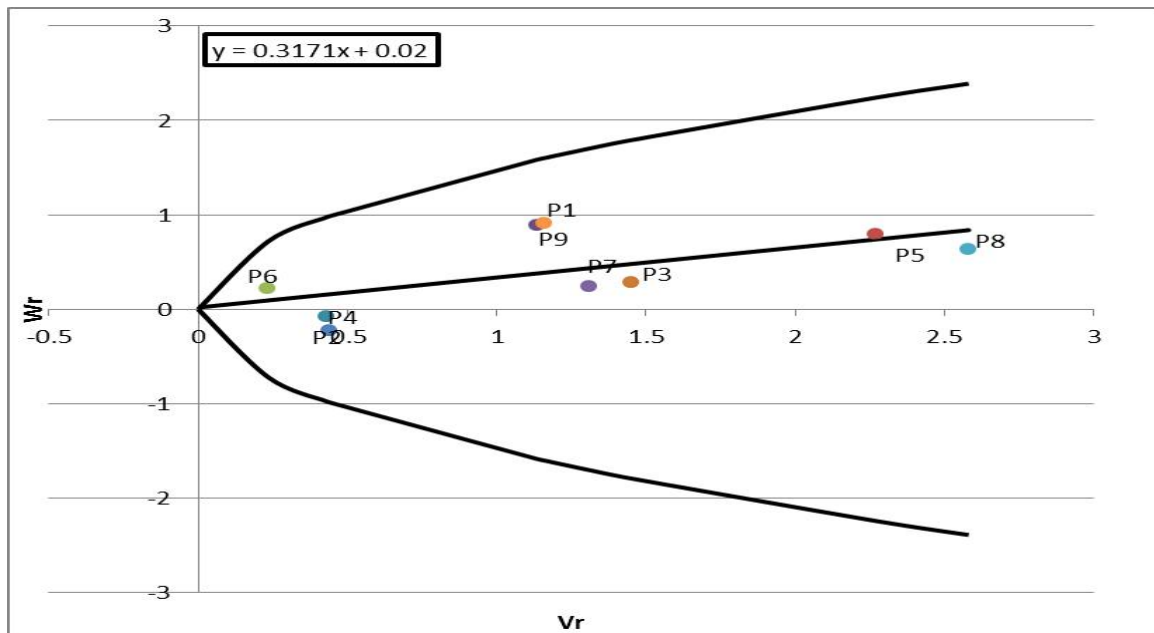


Fig. 5: Variance (V_r) and covariance (W_r) graph total sugars content in F_1 generation of melon genotypes. [P₁: Ananas, P₂: Ananas El Dokki, P₃: Sohag1, P₄: El Behaira 4, P₅: Aswan, P₆: Beni Swif 1, P₇: El Behaira 1, P₈: Ismailawi and P₉: Fayoum]

Fruit total carotenoids content:

Mean performance, analysis of variance, combining ability and heterosis:

Mean performance of the tested nine melon parental genotypes and their 36 F_1 hybrids are presented in Table 3. The results presented in Tables 3 and 4 indicate highly significant differences among different parental genotypes and F_1 hybrids concerning fruit total carotenoids content. The cultivars Fayoum (P₉), Beni Swif 1 (P₆) and El Behaira 4 (P₄), respectively, had significantly the highest mean value for fruit total carotenoids content. Meanwhile, the cultivars showed the lowest fruit total carotenoids content were Ananas (P₁), Sohag1 (P₃) and Aswan (P₅). It is worth mentioning here that the high fruit total carotenoids content, in general, may be considered as desirable fruit quality characteristic, the high fruit total carotenoids content will improve the taste and nutritional value of melon fruits. The hybrids Beni Swif 1 (P₆) × Fayoum (P₉) and Behaira 4 (P₄) × Fayoum (P₉) exceeded the cultivar with the highest total carotenoids content. Whereas, the F_1 hybrids Ananas (P₁) × Ananas El Dokki (P₂), Ananas (P₁) × Ismailawi (P₈), Ananas (P₁) × El Behaira 1 (P₇), Ananas (P₁) × Sohag1 (P₃) and El Behaira 4 (P₄) × Aswan (P₅) recorded values less than the lowest cultivar Ananas (P₁), (Table 3). Such differences in fruit total carotenoids content among different parental genotypes and F_1 hybrids can be used in improving programs of melon in Egypt. High genotypic variation in fruits total carotenoids content among melon genotypes have been reported by Cuevas *et al.* (2008 and 2010), Bayoumy *et al.* (2014) and Abou kamer *et al.* (2015).

The analysis of variance for general and specific combining ability for fruits total carotenoids content are presented in Table 4. The results show highly significant general and specific combining ability effects which indicated the presence of both additive and non-additive types of gene action. Moreover, the calculated ratio of GCA/SCA was 7.70, i.e., more than unity, which indicates that additive type of gene action was more important in the inheritance of fruit total carotenoids content. This result was confirmed with that reported by Cuevas *et al.* (2010) and Bayoumy *et al.* (2014) as they found that the additive genetic variance for quantity b-carotene was generally greater than the dominance.

Estimates of general combining ability effects of the parental genotypes for fruits total carotenoids content are presented in Table 5. The data indicated that the genotypes Fayoum (P₉), Beni Swif 1 (P₆) and Behaira 4 (P₄), respectively, were the best combiners for forming hybrids with high fruit total carotenoids content, having highly significant positive values of GCA, while the 6 other

cultivars recorded highly significant negative GCA, the lowest value was associated with the parental cultivar Sohag1 (P₃), (Table 5). These results will be of great value in melon breeding programs. In this respect, Bayoumy *et al.* (2014) mentioned that GCA were highly significant for β carotene content.

Estimates of specific combining ability effects of crosses are presented in Table 6. From this data, 14 hybrids had highly significant positive SCA and one hybrid recorded significant positive SCA ranged from 0.77 to 16.14, the highest SCA was associated with the hybrid Ananas El Dokki (P₂) \times Beni Swif 1 (P₆). On the other hand, 19 hybrids had highly significant negative SCA the lowest specific value was associated with the hybrid El Behaira 4 (P₄) \times Beni Swif 1 (P₆). Bayoumy *et al.* (2014) showed that SCA were significant or highly significant for β carotenoid content.

With regard to heterosis, highly significant mean squares for parental genotypes vs. F₁ hybrids were detected for fruit total carotenoids content as an indication of average heterosis (Table 4). Estimates of mid and better parent heterosis for the crosses are presented in Table 7. From this data, 6 hybrids had highly significant positive heterosis over mid-parent ranged from 23.78 to 58.08 %, the highest mid-parent heterosis value was associated with the hybrid Ananas (P₁) \times Fayoum (P₉), meanwhile 25 hybrids had highly significant negative mid-parent heterosis, the lowest mid-parent heterosis values were associated with the F₁ hybrids Sohag1 (P₃) \times Beni Swif 1 (P₆) and El Behaira 4 (P₄) \times Aswan (P₅). Moreover, 3 hybrids had highly significant positive heterosis over better-parent ranged from 8.43 to 34.16 %, the highest better-parent heterosis value was associated with the F₁ hybrids Ananas (P₁) \times Aswan (P₅), while 30 hybrids recorded highly significant negative better-parent heterosis, the lowest values were associated with the F₁ hybrids Sohag1 (P₃) \times Beni Swif 1 (P₆) and El Behaira 4 (P₄) \times Aswan (P₅).

Estimation of genetic components:

The estimates of the genetic components of variation in Table 8 show that the additive component (D) and dominant components (H₁) and (H₂) were highly significant, suggesting the importance of both additive and non-additive effects in the determination of fruit total carotenoids content. Bayoumy *et al.* (2014) found that the additive genetic variance value was larger in magnitude than dominance variance for β carotene, this finding could be verified by the A/D ratio which was more than one for this character, indicating that additive gene action played a major role in the inheritance of this character.

The regression line of Vr -Wr intersected the Wr axis above the origin (Fig.6). This indicates the presence of partial dominance in the inheritance of this character. In addition, the sign of h, which measures the direction of dominance, was positive (+79.54), (Table 8). This result indicates that dominance acted in the direction of plants that give fruits with high total carotenoids content. Moreover, the degree of dominance averaged over all loci, measured by (H₁ / D)^{1/2} was 1.11 (Table 8). This can be considered that the over- dominance was toward the plants that give fruits with high total carotenoids content.

The relative values of the Vr and Wr (Fig. 6) show that the parental cultivars Sohag1 (P₃), El Behaira 1(P₇) and Ismailawi (P₈) had the lowest values which indicate that these cultivars contained the most dominant genes. On the other hand, the parental cultivars Beni Swif 1 (P₆), Behaira 4 (P₄) and Fayoum (P₉) had the highest values and hence contained the most recessive genes. Moreover, the values of Vr and Wr associated with the parental cultivars Sohag1 (P₃), El Behaira 1(P₇) and Ismailawi (P₈) were close to each other (Fig. 6) which indicate that these cultivars have similar genotypes concerning the studied character. On the other hand, the parental cultivars Behaira 4 (P₄), Beni Swif 1(P₆) and Fayoum (P₉) which had high values of Vr and Wr, had a distinguished genotypes concerning fruit total carotenoids content. Such information is of great value especially in the stage of selecting parental melon cultivars which will inter in a certain breeding program.

The ratio, H₂ /4H₁, which is used to estimate the average frequency of negative versus positive alleles in the parents, was 0.21 (Table 8). Since this value was less than 0.25, this result indicated the unequal

distribution of alleles which decreased the expression of fruit total carotenoids content and that which increased it over the related loci. In addition, the ratio KD/KR which measures the total number of dominance to recessive alleles in all parents was > 1 , i.e., 1.41 (Table 8). This result indicates that the nine parents used in the present study carried more dominant than recessive alleles. This conclusion was supported by the positive value of F, i.e., + 78.22 (Table 8) which indicates that there were more dominant than recessive alleles in the parents used in this study. The positive value of (r) (+ 0.84) indicates that the parents are containing the most decreasing genes. The value of (r^2) (0.70) could suggest the existence of (yr) and ($wr \pm vr$) and hence, prediction on completely dominant and recessive parents is possible.

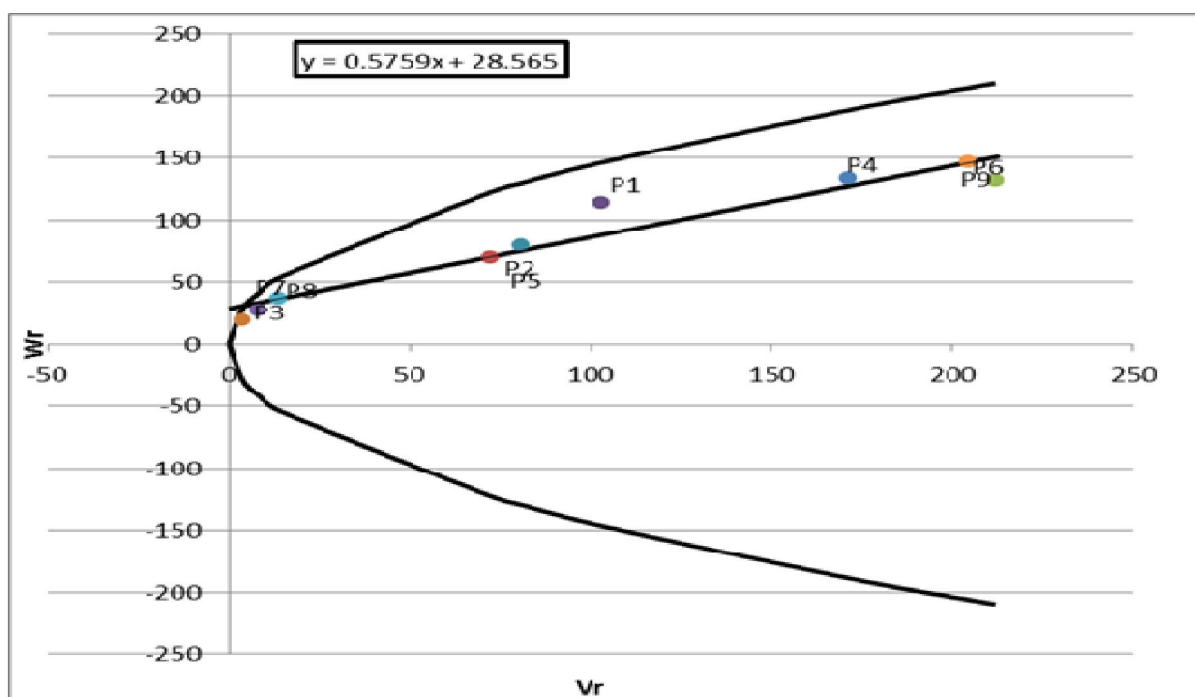


Fig. 6: Variance (V_r) and covariance (W_r) graph of fruit total carotenoids content in F_1 generation of melon genotypes.

[P₁: Ananas, P₂: Ananas El Dokki, P₃: Sohag1, P₄: El Behaira 4, P₅: Aswan, P₆: Beni Swif 1, P₇: El Behaire 1, P₈: Ismailawi and P₉: Fayoum]

With respect to broad and narrow sense heritability, the results presented in Table 8 show very high broad sense heritability (99%) and high narrow sense heritability (61%) which indicate the large influence of the genetic variance on the expression of this character. Furthermore, the additive genetic variance components is relatively large comparing to the non-additive genetic variance. These results indicate that selection in segregating generations on individual plant basis will be effective in melon breeding programs to reach the desired expression of this character. These results agreed with that of Cuevas *et al.* (2010) who reported that broad sense heritability estimates were high (0.74–0.99). Narrow-sense heritability was 0.55. Also, Abou kamer *et al.* (2015) found that only two from 10 crosses showed moderate BSH values (37.21% and 42.66%). But for the narrow sense heritability all the crosses recorded low values.

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