

Diallel Analysis and Heritability of Fruit Quality Traits in Melon (*Cucumis Melo L.*) Inbred Lines

التهجين الدائري ودرجة توريث صفات الثمار النوعية لسلاسل البطيخ الأصفر المرباة داخلياً

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ABSTRACT

The present study was conducted at Swaida agricultural research center, Syria, during the season 2019, to estimate the genetic components of six melon (*Cucumis melo L.*) inbred line and their 30 F1s hybrids produced by complete diallel mating design, to evaluate some fruit quality traits (dry matter, total soluble content TSS, total sugar, carotene, and vitamin C) using Hyman analysis approach. The results showed that all the studied traits were controlled by overdominant gene effect, and most of the parents carried more dominant genes than recessive, since the variation components due to non-additive effects of genes (H1) was greater than the variation due to additive effects of genes (D) for all studied traits. The low values of narrow-sense heritability indicating the importance of the non-additive gene effect for the studied traits. According to the values of the variance and covariance for parents with their offspring ($W_r + V_r$) showed that P5 (IL-CM116) carried the most dominant genes for most of the studied traits, while P2 (IL-CM106) have the most recessive genes for all studied traits.

Keywords: Cucumis Melo, Melon, Diallel, Hayman Analysis, Narrow sense Heritability.

المخلص

أجريت هذه الدراسة في مركز البحوث العلمية الزراعية بالسويداء سوريا، خلال الموسم (2019)، لتقدير المكونات الوراثية لست سلالات من البطيخ الأصفر (*Cucumis melo L.*) و (30) هجيناً ناتجة عن التهجين التبادلي الكامل، لتقييم بعض صفات الثمار النوعية (المادة الجافة، المواد الصلبة الكلية الذاتية (TSS)، السكريات الكلية، محتوى الثمار من (الكاروتين وفيتامين C)) باستخدام تحليل (هايمان Hyman). أظهرت النتائج أن الصفات المدروسة تخضع لتأثير السيادة الفائقة للجينات، وأن معظم الآباء يحملون جينات سائدة أكثر من المتنحية، حيث كانت مكونات التباين العائدة للتأثير غير المضيف للجينات (H1) أكبر من التباين العائد للتأثير المضيف للجينات (D) للصفات المدروسة. وتشير القيم المنخفضة لدرجة التوريث بالمعنى الضيق إلى أهمية التأثير الجيني غير المضيف في وراثة الصفات المدروسة. أظهرت مجموع قيم التباين والتباين المشترك ما بين الآباء والهجن الناتجة عنها ($W_r + V_r$) أن الأب P5 (IL-CM116) يحمل أكبر عدد من الجينات السائدة لمعظم الصفات المدروسة، بينما يمتلك P2 (IL-CM106) أكثر الجينات المتنحية للصفات المدروسة.

الكلمات المفتاحية: البطيخ الأصفر، التهجين التبادلي، تحليل هايمان، درجة التوريث الضيقة.

INTRODUCTION

Melon (*Cucumis melo L.*, $2n=2x=24$) is one of the most economically important cucurbitaceae family species (Burger *et al.*, 2003; Saha *et al.*, 2018). The origin of melon was firstly considered from Africa. However, recent studies indicated that cucumber and muskmelon are of Asian origin, with a wide diversity of *Cucumis melo* wild species in China and India (Sebastian *et al.* 2010). Melon fruit is one of the most summer fruits because of its high nutritive and medicinal value, musky flavor, sweetness, and aroma (Abo Sedera *et al.*, 2016).

The great diversity of melons around the world and the several botanical types of fruits and chemical content play an important role in marketing good fruit genotype market-standard size, good flesh thickness, small internal cavity, high flesh firmness, and high soluble solids content (Nunes *et al.*, 2005), in addition to the high total sugar content, carotene and the level of vitamin C (Abo Sedera *et al.*, 2016).

The improvement program for fruit quality trait of melon has to focus on more than one melon type since the breeding program of melon is based mainly on exploiting the natural sources of germplasm by means of selection and hybridization followed by selection (Mliki *et al.*, 2001).

Selection and hybridization are the two most methods in plant breeding and crop improvements. The successful selection depends mainly upon the extent of wide genetic background (Singh, 1998). The utilization of divergent genotypes in diallel hybridization design can create a higher genetic base. In addition, the information about gene interaction that covered the main agronomic characters that play an important role in genetic improvement can be established by diallel analysis since the study of the performance of parents and their hybrids gives good information about the inheritance of economic traits (Pandey *et al.*, 2010).

The diallel meeting design gives breeders the ability to study all combinations of the parents' crosses. The analysis of diallel can conduct heterosis, general and specific combining ability

using Griffing approach, and study the genetic control that covered the studied traits by using Hayman approach (Cardoso *et al.*,2015)

The Hayman numerical approach of diallel analysis provides good information about additive and dominance gene effect and the allied statistics. Genetics largely depends upon the relative magnitude of these two components in the prediction of the gene interaction that controls the desirable traits (Walton, 1968). The improvement of the fruit quality traits in melon depends mainly on detecting the genetic interaction that controls them and the suitable breeding program determined by Hayman’s approach (Saha *et al.*, 2018).

The aim of this study was to estimate the genetic parameters that control some fruit quality traits of melon in a set of 6 melon inbred lines as parents and their 30 F₁diallel crosses.

MATERIALS AND METHODS

The present study was carried out in the experimental field at Swaida research center, Syria. During the summer season of 2019 to study the genetic behavior of some quality traits for six inbred melon lines.

▪ Plant Materials

Six inbred melon lines were obtained from the General Commission’s vegetable department for Scientific Agricultural Researches (GCSAR), Syria. The source of these lines was some of the local melon populations. The six inbred lines (Table 1) were crossed in a diallel mating design to obtain 30 F₁ hybrids. During the 2019 season, the 36 muskmelon genotypes (6 parents and 30 F₁) were evaluated for some fruit chemical quality traits.

Table 1 The Six Inbred Melon Lines and Their Parental Number

Genotype name	Parental Number
IL-CM104	P1
IL-CM106	P2
IL-CM108	P3
IL-CM113	P4
IL-CM116	P5
IL-CM118	P6

▪ Experimental Design

The 36 melon (6 parents and 30F₁) genotypes were evaluated in Randomized Complete Blocks Design (RCBD) with four replications. The total number of experimental

plots was 144; each experimental plot was one row of 8 meters in length and 1.5m between lines. The total number of plants in each row was 10 plants, and the distance between plants in each row was 80 cm.

All the cultural practices were done as recommended for melon, and the control of diseases and insects was practiced according to the Ministry of Agriculture’s recommendation.

▪ Measurements

All the measurements were carried out on 5 ripe fruits, which were selected randomly from each experimental plot. These fruits were used to determine the following fruit quality traits.

- Dry Matter

According to Kirk and Sawyer (1989), the dry matter was determined by placing 100g of juice in the oven at 80° until the weight stabilizes.

- Total Soluble Solid (TSS)

It was measured using a refractometer (Matest- 24048 -Italy).

- Total Sugar

The total sugar content in the experimental plot’s fruit is expressed by titration of Fehling’s A and B stock solution and Methylene Blue as an indicator until the blue color disappears (Takahashi, 1959).

- Carotene

The total carotenoids content in the fruit of the experimental plot was determined using the Spectrophotometer (UK-106) according to the method described by Beerh and Siddappa (1959) at wavelengths 470, 645, and 662.

- Vitamin C

The vitamin C contents were determined according to the method described by Ismail *et al.* (2014) by titration using Iodine solution and starch as an indicator.

▪ Statistical Analysis:

Diallel analysis for inbred line parents and their F₁ was carried out according to Hayman’s (1954) approach. Hayman partitioned the total sum of square due to genotypes into four components: The additive component with (P-1) degree of freedom, non-additive effect with p (p-1)/2 degree of freedom, maternal and reciprocal effects with (p-1), and p(p-1)/3 degree of freedom, respectively; where p is the number of parents involved in crosses. The non-additive component

is further partitioned into b1, b2, and b3 with 1, p-1, and p (p-3)/2 degrees of freedom, respectively.

Hayman's method involves the computation of the analysis of variance, variance, and covariance for the parents with their offspring and the establishment of the graph of Vr-Wr.

Depending on data analysis, the following genetic components were estimated: (i) Variation due to additive effects of genes (D); (ii) The covariance of additive and non-additive effects in each array (Fr); (iii) The mean of "Fr" over the arrays (F); (iv) The variation components due to non-additive effects of genes (H1); (v) The predicted ratio of positive and negative genes in the parents (H2); (vi) The dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses).

The genetic components of variation were used to estimate the following statistics:

- $(H1/D)^{1/2}$: The mean degree of dominance over all loci, If $(H1/D)^{1/2}$ in the range between 0-1 indicating partial dominance effect, greater than 1 denotes over dominance effect.
- $H2/4H1$: The proportion of genes with positive and negative effects in the parents. The value should have a maximum of 0.25 when the positive and negative alleles in a symmetrical distribution. Asymmetrical distribution in a value less than 0.25.
- $(Kd/Kr) = ((4DH1)^{1/2} + F) / ((4DH1)^{1/2} - F)$: The proportion of dominant to recessive genes.
- $(h^2/H2)$: Number of groups of genes that control the trait.
- Coefficient of correlation (r) between Wr + Vr and Yr: If the correlation is negative, it tends to increase the trait.
- $(1/4 D / (1/4(D+H1-F)+E)) * 100$: Narrow sense heritability

The Wr/Vr graph is the other powerful tool in Hayman's analysis. Parents who possess smaller values of (Wr+Vr) have more of the dominant genes and lie near the origin point, and those with higher values of (Wr+Vr) possess the most recessive genes and lie furthest from the origin point. The degree of dominance is determined by the intercept of Wr/Vr regression line.

Hayman diallel analysis was carried out using AGD_R software, a free software developed

by International Maize and Wheat Improvement Center (CIMMYT).

RESULTS

According to the Hayman diallel approach, the analysis of variance showed highly significant differences among the 36 genotypes (6 parents and 30 F1 crosses) for all studied fruit quality traits (Table 2). These results indicated that the genetic parameter estimates could be performed on all the observed characters. Significant mean squares were observed for additive and non-additive components for all studied characters indicating the importance of both gene actions in the inheritance of these traits. The non-additive components were further partitioned into b1 with 1 degree of freedom, b1 was highly significant in total sugar and carotene traits implying the presence of directional dominance, b2 with p-1 degree of freedom, were highly significant in all studied trait except vitamin C indicating gene asymmetry among parents. In other words, some parents have more dominant genes than others, b3 with $p*(p-2)/2$ degree of freedom, b3 were highly significant for all studied traits showing that dominance effect is specific to some individual crosses.

Table 2 Mean Square for Hyman Diallel Analysis for Fruit Quality Traits

Source of variance	df	Dry mater	TSS	Total Sugar	Caroten	Vitamine C
Replication	3	0.28	0.970	0.520	56.67	489.748
Genotype	35	4.79**	1.984**	2.305**	184.734**	847.645**
Additive	5	4.59*	4.080**	2.598**	776.388**	1081.272*
Non-Additive	15	5.16**	2.283**	3.507**	127.703**	867.023**
b ₁	1	0.003	1.176	20.053**	461.781**	629.068
b ₂	5	6.72***	3.985**	2.601**	139.458**	455.019
b ₃	9	4.87**	1.460**	2.172**	84.053*	1122.353**
Maternal	5	6.65**	0.525	1.150	61.549	308.442
Reciprocal	10	3.40*	1.218*	0.934	36.047	971.367**
Error	105	1.46	0.545	0.781	33.092	377.200

*and **, significant and highly significant at 5 and 1% respectively.

■ Gene Interaction:

The regression coefficient test b (Wr, Vr) was not significant for all studied traits (Table 3). That means no interaction among genes controlling these traits. These results indicated that one of Hayman's diallel assumptions could be met.

▪ **Estimation of Genetic Components:**

- **The Effect of Additive and Dominant Gene Action:**

The estimation of additive genetic components D and dominance components H1 and H2 showed highly significant differences for dry matter, TSS, and carotene, indicating the importance of additive and non-additive effects in the inheritance of these traits. On the other hand, only the dominance components H1 and H2 were highly significant for total sugar and vitamin C, suggesting that the non-additive effect plays an important role in the inheritance of these two traits.

- **The Mean Degree of Dominance:**

The degree of dominance $((H1/D)^{1/2})$ was 1.51, 2.03, 3.8, 1.32, and 2.5. Since these values were >1, the overdominance effect directs the inheritance towards plants that contains a high level of dry matter, TSS, total sugar, carotene, and vitamin C, respectively.

- **The Proportion of Genes with Positive and Negative Effects:**

The proportion of genes with positive and negative effects $(H_2/4H_1)$ was less than 0.25 (Table 3), indicating gene asymmetry and unequal distribution for alleles that increased and decreased all studied traits except vitamin C. These results were in the same trend with significant and non-significant values of b2 which indicates asymmetrical and symmetrical gene distribution, respectively.

- **The Proportion of Dominant to Recessive Genes:**

The proportion of Dominant to Recessive Genes (KD/KR) was >1 for all studied traits (Table 3), showing that the six parents used in this study carry more dominant genes than recessive genes for all traits. This was supported by F's positive values, which indicates that there were more dominant alleles than recessive alleles in the parents used in this study. On the one hand, the correlation coefficient r between parental mean Yr and the value of $(Vr+Wr)$ was negative for all studied traits except dry matter. The negative values of r indicating that dominance tends to increase traits. On the other hand, the positive value of r for the dry matter trait indicates that dominance tends to decrease the dry matter contents.

Table 3 Estimation of Genetic Parameter for Melon Fruit Quality Traits Using the Diallel Analysis of Hayman Method

Genetic parameters	Dry mater	TSS	Total Sugar	Caroten	Vitamin C
Covariance-variance regression (b(Wr, Vr))	0.93 _{NS}	0.47 _{NS}	0.307 _{NS}	0.866 _{NS}	0.37 _{NS}
Additive effect (D)	1.76**	0.449**	0.119 _{NS}	71.19**	144.16 _{NS}
Dominance effect (H ₁)	3.99 _{NS}	1.85**	1.72**	124.41**	902.1**
Proportion of dominance due to positive and negative effect of genes (H ₂)	3.44**	1.76**	1.69**	112.36**	903.22**
F _r mean (F)	1.99 _{NS}	0.88 _{NS}	0.311 _{NS}	59.44**	195.95 _{NS}
F ₁ deviation from the average parent (h ²)	-0.19 _{NS}	0.08 _{NS}	2.68**	60.05**	34.54 _{NS}
Environment (E)	0.365 _{NS}	0.14 _{NS}	1.93 _{NS}	8.43**	95.08**
Mean degree of dominance $((H1/D)^{1/2})$	1.51	2.03	3.80	1.32	2.50
Proportion of positive genes to negative genes $(H_2/4H_1)$	0.215	0.23	0.245	0.225	0.25
The proportion of dominant to recessive genes (K_d/K_r)	2.21	2.87	2.044	1.93	1.74
Number of groups of genes (h^2/H_2)	-0.05	0.04	1.58	0.53	0.038
Coefficient of correlation (r) between Wr + Vr and Yr	0.69	-0.82	-0.87	-0.77	-0.69
Narrow-sense heritability $(h^2_{NS})\%$	33.71	14.42	1.55	41.90	11.70

NS: not significant, *and **, significant and highly significant at 5 and 1% respectively.

- **Number of Groups of Genes Controlling the Studied Traits.**

The number of gene groups controlling the fruit quality traits was estimated from h^2/H_2 values. These values were less than 1 for all studied traits except total sugar. Indicating that these traits are covered by one group of genes, while the total sugar trait ($h^2/H_2=1.58$) is controlled by two main groups of genes (Table3).

- **Direction and Order of Dominance**

The order of dominance of the 6 parents to dry matter was IL-CM104, IL-CM118, IL-CM113, IL-CM116, IL-CM108 and IL-CM106 (Table 4). The parent IL-CM106 possesses the most recessive gene because it is the most distance from the point of origin. In the meantime, IL-CM104 contained the most dominant genes since it is the closest to the point of origin. The regression line of Wr-Vr graph intercepts the Wr axis under the origin 0, indicating the overdominance effect on dry matter inheritance (Figure1).

The order of dominance of parents for total soluble contents (TSS) was IL-CM113, IL-CM116, IL-CM104, IL-CM108, IL-CM118 and

IL-CM106 (Table4). IL-CM106 carried the most recessive genes, while IL-CM113 carried the most dominant genes. The regression line of $W_r - V_r$ cut W_r axis under the origin (0), indicating overdominant gene action (Figure 2).

Regarding the total sugar trait, the parent 5 (IL-CM116) carried the most dominant genes since it was the closest to the origin point, while parent P2 (IL-CM106) has the most recessive genes. The regression line of $W_r - V_r$ intercepted W_r axis under the origin, indicating over dominance gene action covering total sugar inheritance (Figure3).

The order of dominance of parents for Carotene was IL-CM116, IL-CM113, IL-CM108, IL-CM118, IL-CM104, and IL-CM106. The parents IL-CM116 and IL-CM106 carried the most dominant and recessive genes since they were the closest and furthest to the point of origin, respectively. The $W_r - V_r$ regression line cut the W_r axis over the point of origin indication partial dominant gene effect (Figure4).

According to the $W_r + V_r$ values for Vitamin C content, the order of dominant parent was IL-CM116, IL-CM108, IL-CM118, IL-CM113, IL-CM104, and IL-CM106. Parent 5 (IL-CM116) possesses the most dominant genes, and parent 2(IL-CM106) has the most recessive gene of this trait. The partial dominant effect was controlling the inheritance of Vitamin C fruit contents since the $W_r - V_r$ regression line cutting the W_r axis over the point of origin (Figure 5).

- Heritability

The narrow-sense heritability was less than 50% for all studied traits (Table 3), indicating the predominant non-additive gene action for all studied traits. These results were supported by the positive values of “F” suggested that the heterosis breeding might be the good manner to get higher quality trait of melon.

DISCUSSION

Diallel analysis is the most balanced and systemic experimental design to examine continuous variation. The genetic knowledge about the parental population becomes available in the early generation, which plays an important role

in defining the breeding strategy without losing much time (Debnath, 1988).

The estimation of the genetic parameter using diallel crosses analysis can be carried out if there is a significant difference among genotypes using the variance of the observed variable (Singh & Chaudhary 1979).

In the present study, the fruit quality traits showed highly significant differences among the studied genotypes (6 parents and 30F₁s), leading to the further analysis of the Hyman approach that can be done. These results were in agreement with Mohammadai et al. (2014) and Abo Sedera et al. (2016).

Table 4 $W_r + V_r$ Values of the Six Parents for Melon Fruit Quality Traits.

Genotype	Dry mater	TSS	Total Sugar	Carotene	Vitamin C
IL-CM104(p1)	-0.01	0.32	0.53	85.18	298.28
IL-CM106(P2)	3.57	1.22	1.81	129.08	427.53
IL-CM108(p3)	1.82	0.38	0.23	56.37	37.01
IL-CM113(p4)	0.31	0.13	0.22	36.65	208.86
IL-CM116(p5)	0.62	0.15	0.07	7.73	35.74
IL-CM118(p6)	0.20	0.41	0.23	59.37	158.28

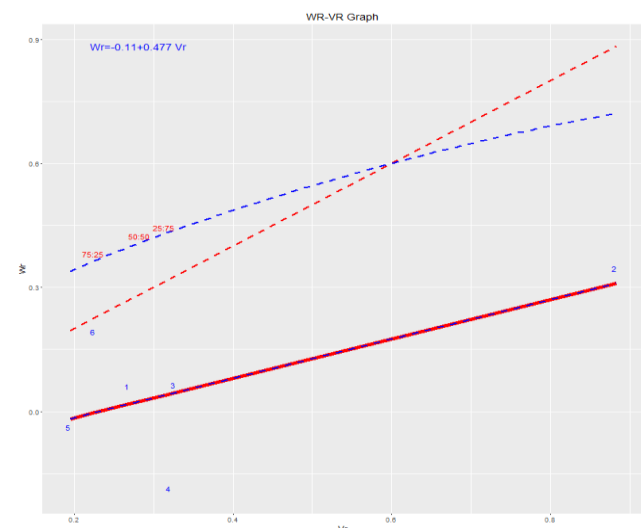


Figure 1: The graph of variance (V_r) and covariance (W_r) for dry mater of fruit in the F₁ generation of melon genotypes. [1: parent IL-CM104, 2: parent IL-CM106, 3: parent IL-CM108, 4: parent IL-CM113, 5: parent IL-CM116, 6: parent IL-CM118].

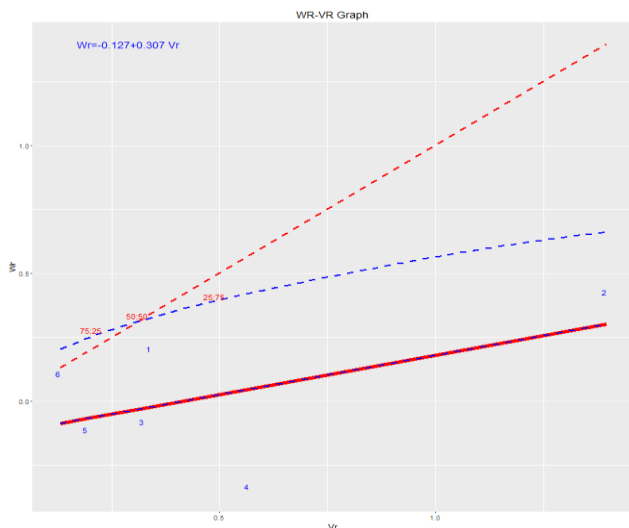


Figure 2: The graph of variance (V_r) and covariance (W_r) for TSS of fruit in the F_1 generation of melon genotypes. [1:parent IL-CM104, 2: parent IL-CM106, 3: parent IL-CM108, 4: parent IL-CM113, 5: parent IL-CM116, 6: parent IL-CM118].

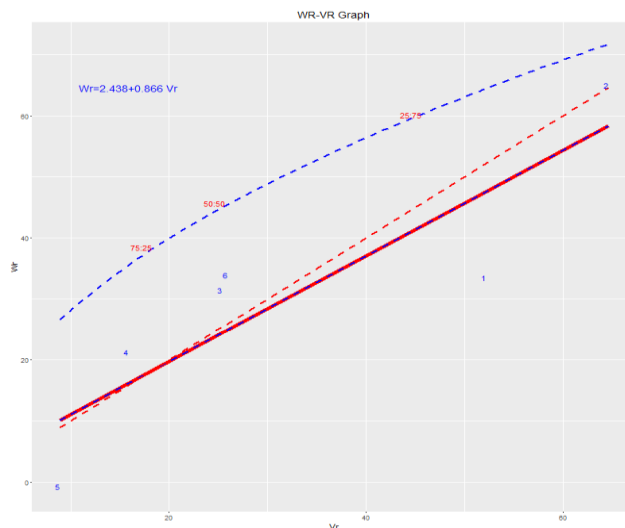


Figure 4: The graph of variance (V_r) and covariance (W_r) for Carotene of fruit in the F_1 generation of melon genotypes. [1:parent IL-CM104, 2: parent IL-CM106, 3: parent IL-CM108, 4: parent IL-CM113, 5: parent IL-CM116, 6: parent IL-CM118]

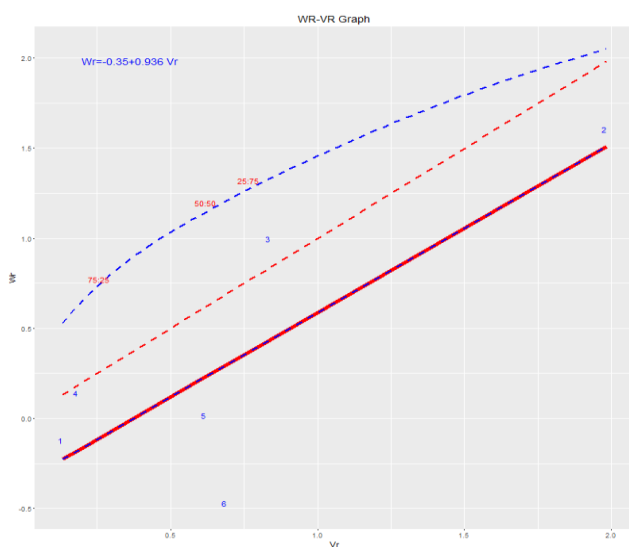


Figure 3: The graph of variance (V_r) and covariance (W_r) for total sugar of fruit in the F_1 generation of melon genotypes. [1:parent IL-CM104, 2: parent IL-CM106, 3: parent IL-CM108, 4: parent IL-CM113, 5: parent IL-CM116, 6: parent IL-CM118].

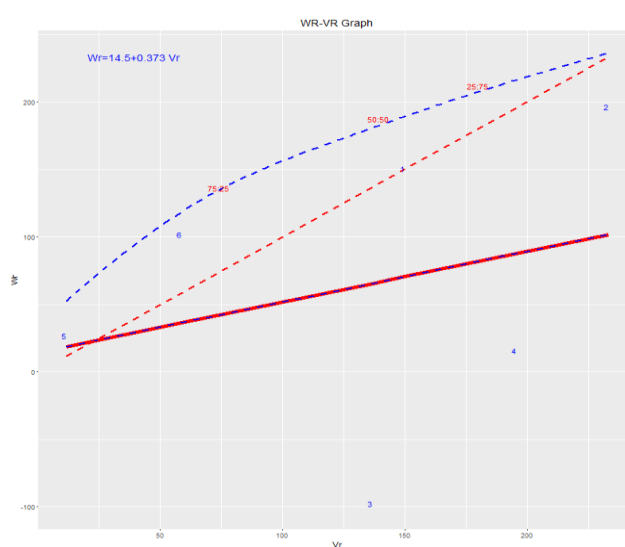


Figure 5: The graph of variance (V_r) and covariance (W_r) for Vitamin C of fruit in the F_1 generation of melon genotypes. [1:parent IL-CM104, 2: parent IL-CM106, 3: parent IL-CM108, 4: parent IL-CM113, 5: parent IL-CM116, 6: parent IL-CM118].

The genetic interaction among the genes that controlled the studied traits can be seen from the value of the regression coefficient b (W_r, V_r). If the value is not significantly different from one, indicating no interaction among the genes (Sousa and Maluf 2003). In the study, the b values were not significant for all studied traits. Regarding these results, one of the Hayman diallel assumptions can be met.

The mean degree of dominance $(H_1/D)^{1/2}$, which was over than 1 for all fruit quality traits, confirmed the overdominance action. These

results were supported by the dominant component of variance H1, which was higher than the additive component D for all studied traits. In addition, the existence of overdominant gene action and the low values of the narrow sense heritability suggested that selection in the segregation generation to improve fruit quality traits depends mainly on heterotic individual plants. These results were in accordance with (Abou kamer et al., 2015; Glala et al., 2012; Iban et al., 2007; Mohammadi et al., 2014; Reddy et al., 2013; and Shamloul & Askar, 2011).

The proportion of dominant to recessive genes in the 6 inbred line parents was estimated by the value of Kd/Kr . This value was > 1 for all studied traits, indicating that there were more dominant than recessive genes in the parents used in this study. On the other hand, the proportion $h^2/H1$ was less than 0.25 for all studied traits except Vitamin C. The values of $h^2/H1$ less than 0.25 showed the unequal distribution of dominant genes among parents. In the same trend, the number of dominant genes among parents is determined by the value of $Wr+Vr$. Parents who showed the lowest value of $Wr+Vr$ carried the most dominant genes that controlled the studied trait. According to that, parent P2 (IL-CM106) carried the most recessive genes for all studied traits. On the other hand, parent P5 (IL-CM116) was the most dominant parent for all studied traits except TSS. In contrast, parent P4 (IL-CM113) carried the most dominant genes for the TSS trait. These results were in the same trend as Bayoumy et al. (2014) and Abo Sedera et al. (2016).

The correlation coefficient r between parental mean Yr and the value of $(Vr+Wr)$ was negative for all studied traits except dry matter. The negative values of r indicating that the dominant alleles work to increase the mean value of TSS, Total sugar, carotene, and vitamin C. The parent P5 (IL-CM116) showed the most dominant genes for Total sugar, carotene, and Vitamin C, indicating the possibility of obtaining a line with greater magnitude of these traits by selecting P5 segregation populations. In the same trend, the r between parental mean Yr and the value of $(Vr+Wr)$ was negative for the TSS trait. The parent P4 and P5 showed very close values of $(Vr+Wr)$, thus indicating that these two parents play an important role in improving the TSS trait since they carried the most dominant alleles. On the

other hand, the positive value of r between parental mean Yr and the value of $Vr+Wr$ for dry matter trait indicates that the recessive alleles tend to increase the mean value of these traits. The highest value of dry matter can be obtained from the high concentration of recessive alleles contained in P2 (IL-CM106). These results were in the same trend as Cardoso et al. (2015).

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