

# Genetic Study on Powdery Mildew Resistance and some Economic Traits in Melon (*Cucumis melo* L.)

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**Abstract:** The responses of seventeen melon (*Cucumis melo* L.) genotypes to powdery mildew pathogen (*Erysiphe cichoracearum*) were evaluated. The study was conducted at the experimental station of the Ismailia Research farm during the period from 2019 to 2020 to develop melon inbred lines and their hybrids resistance to powdery mildew to decrease injuries in yield and quality. Seventeen different inbred lines of melon were used to study genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV), heritability and correlation, for twelve traits: number of leaves/plant, number of internodes/plant, number of branches/plant, tenth internodes length/plant, area of tenth plant leaf, fruit weight, fruit length, 1/2the diameter of the fruit, flesh thickness, total soluble solid (%), the average weight of seeds per fruit and 100-seeds weight. Inbred lines L1, L3, L10, L13, and L17 showed tope completely resistance to powdery mildew disease. Analysis of variance revealed high significance ( $P < 0.05$ ) for all characters. The results indicated the presence of substantial variability among the genotypes. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and broad sense heritability ( $h^2$ ) estimates ranged from 11.14-60.69, 20.57-62.90, and 29.32-93.12% respectively. The high estimates of GCV and PCV in this study proved the existence of variability and the selection can be done. Whereas, the variation estimate of  $h^2$  for the tested traits indicated that the selection in these characters were different.

**Keywords:** Correlation, Heritability, Melon, Powdery mildew

## INTRODUCTION

Melon (*Cucumis melo* L.) is one of the most important vegetable crops that belong to Cucurbitaceae family. In Egypt, the cultivated area of melon in 2017 according to the Ministry of Agriculture statistics, reached about 72173 feddan which produce 851194 tons with an average of 11.79 tons/fed. Powdery mildew symptoms first appear as pale, chlorotic spots on leaves that soon turn powdery-white in appearance and spread to petioles and stems. The disease starts on the crown and lower leaves, mainly on the under-leaf shaded surface. Young plants may turn yellow, stunted, and may die. Severely infected leaves become brown, brittle, and expire McCreight (2004), Shashikumar and Pitchaimuthu (2016). Other fruit symptoms include reduced size, malformation, discoloration, unacceptable taste, speckled rind, and shriveled handles. The area cultivated with melon expands every year due to high prices for the product on the external market. High temperatures and other climatic conditions such as levels of high insulation, little rainfall and highly technological melon cropping are the main reasons for the national importance Nunez-Paleniuss *et al.* (2005).

Powdery mildew of cucurbits is caused by two organisms, *Sphaerotheca fuliginea* (syn. *Podosphaera xanthii*) and *Erysiphe cichoracearum* (syn. *Golovinomyces cichoracearum*). *S. fuliginea* is more commonly reported worldwide, and prefers warmer weather, while *E. cichoracearum* prefers cooler weather Kristkova *et al.* (2009). The two organisms have similar conidia, and can only be differentiated by the fibrosin bodies only present in conidia of *S. fuliginea*. Powdery mildew affects all cucurbits, most commonly squash, melon, and pumpkins. Powdery mildew occurs mainly in periods of low relative air humidity and high temperatures Fazza (2006).

Melon powdery mildew could be controlled by applying chemical fungicides which increase the production cost of the crop. In this regard, the importance of alternative control methods has increased significantly due to chemical residues and reduced environmental contamination. One of the alternatives to control powdery mildew is using cultivars with genetic resistance that has the main advantages of easy adoption by the producer. In the case of powdery mildew, control by genetic resistance is complicated because there are races in the pathogen population. Many cultivars have been released by the genetic breeding programs developed in some countries of the world Dogimont (2011).

The Development of resistant varieties is a sustainable approach that can provide the success of melon production. A number of resistant lines and varieties have been developed in the USA, France, and other countries that belong to different variety types (Melon, Charentais type, Galia type, etc.) Pitratand Besombes (2008).

Genetic control of resistance/tolerance to powdery-mildew has been investigated using progeny resulting from crosses between susceptible and resistant/tolerant genotypes Kenighsbuch and Cohen (1989). Perchepied *et al.* 2005 reported that sources of resistance to powdery mildew in melon have been identified, also the adult plant stage was the important stage for resistance screening, of ten seedlings were assessed for disease reactions under controlled conditions. There is no published study available on heterosis for resistance to powdery mildew in adult melon plants. The genetic relationship between resistance in adult green-house grown plants and adult field-grown plants from the same parents could be used

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to develop elite resistant lines or to identify superior parents or crosses Shashikumar *et al.* (2011).

The objective of the present study was to assess the reaction of melon lines to the *E. cichoracearum* fungus, improvement of some melon inbred lines and studding the genetic behavior of some economic characters.

## MATERIALS AND METHODS

### Plant Materials

The breeding materials used included seventeen different inbred lines of melon (*Cucumis melo*) (illustrated in Table 1). These genotypes were selected from unfamiliar alternative sources to have sufficient genetic diversity in their resistance for diseases, yield, and fruit quality traits. Individual plants from each genotype were selfed - pollination for five successive generations during the summer and fall seasons of

2016 and 2018 to ensure the highest degree of purity and homogeneity

A randomized complete block design with three replicates was used in this study during March 2019 and 2020 at Ismailia Research Station Experimental Farm, Ismailia Governorate, Egypt. The seeds of inbred lines were directly seeded, reserve a minimum space of 75cm apart in rows 3 m long and 1.5 m width. All the recommended package of practices was followed to get a complete expression of traits under study. The examination was detailed on individual plant basis for number of leaves/plant, number of internodes/plant, number of branches/plant, Tenth internodes length/plant (cm), area of tenth plant leaf (cm<sup>2</sup>), fruit weight (g), fruit length (cm), <sup>1/2</sup>the diameter of the fruit (cm), flesh thickness (cm), total soluble solid (%), the average weight of seeds per fruit (g) and 100-seeds weight (g).

**Table (1):** Sources of melon accessions used in the current study

Genotype	code	source
3MMS11	L1	* VBD
3MML9	L2	VBD
Angar	L3	**F.C
86E2143	L4	***IPGR
86E2155	L5	IPGR
3MML2	L6	VBD
3MMS6	L7	VBD
NGB- 12 - 6	L8	****NGB
AYM-1-67-86	L9	VBD
AYM-7-57-32	L10	VBD
CGN-34-87-94-2	L11	*****CGN
AYM-9-60-26	L12	VBD
NGB- 72 – 90-9- 5	L13	NGB
CGN-55-12-94	L14	CGN
CGN 57-66-8-54	L15	CGN
NGB- 154 - 87	L16	NGB
AYM-18-39-29	L17	VBD

\*(VBD) Vegetables Breeding Department \*\*(F.C) Flemran company French

\*\*\*(IPGR) Institute of plant genetic resource sadovo Bulgaria

\*\*\*\*(NGB) Gene bank of Netherland

\*\*\*\*\* (CGN) Gene bank of Sweden

### Disease assessment:

Field assessment was carried out in Ismailia Research Experimental Station. A total of seventeen of melon lines were assessed in a greenhouse under natural infestation of *Erysiphe cichoracearum*.

Disease severity on plants was measured 60 days after sowing. Table (2) indicating average rating of all the leaves used to assess the disease. On the basis of

scoring of 3 individual leaves per plant and 10 plants in each inbred line, Percent Disease Index (PDI) was calculated for each inbred line using the formula proposed by Wheeler (1969):

$$PDI = \frac{\text{Sum of numerical values}}{\text{No of leaves} \times \text{Maximum rating}} \times 100$$

**Table (2):** Powdery mildew disease severity estimating into 5 categories according to James (1971)

Scale	Mildew covering of leaf surface	symptoms	Reaction
0	0%	No symptoms of infection	High resistance (HR)
1	1-12.5%	Very weak infection	Resistance (R)
2	13 - 25%	Weak infection	Tolerance (T)
3	25.5 - 50%	Moderate infection	Susceptible (S)
4	50.5 – 100%	Very severe infection	High susceptible (HS)

Observations were recorded on various characters and subjected to statistical analysis. Collected data were subjected to analysis of variance (ANOVA) using Statistic 8 software version 8.0 (2003) and correlation coefficients were worked out to determine the degree of association among the characters as well as yield. This was done according to the formula given by (Al-Jibouri *et al.*, 1958). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV) were calculated according to Sivasubramanian and Menon (1973) and heritability ( $h^2$ ) was calculated according to Johnson *et al.* (1955).

## RESULTS AND DISCUSSIONS

### Evaluation of melon inbred lines for powdery mildew resistance:

Breeding programs have been focused on the development of resistant varieties to races of powdery mildew that predominantly occur in the region of melon production. Data presented in Table (3) Proved that the tested melon genotypes were reacted differently throughout the natural infestation study. Presented data showed that between seventeen tested inbred lines, five inbred lines *i.e.* L4, L5, L8, L12 and L16 were highly susceptible and susceptible were covered by growth masses of conidia and mycelium of *E. cichoracearum* normally shown at highest level of

their powdery-mildew susceptibility under natural infestation. In contrast, there were no symptoms on the inbred lines L1, L3, L10, L13 and L17 which showed completely resistant to powdery mildew, which could be explained by their high resistance based on the five categories according to James (1971). In the same trend, inbred lines L6, L11 and L16 showed resistant of powdery mildew. Other genotypes such as L2, L7, L9 and L14 revealed to be moderately resistant against powdery mildew under field conditions, and may be classified as tolerant. On the other hand, inbred lines L1 and L3 which showed more resistance to powdery-mildew, recorded the highest value of the fruit yield compared with other tested parents. Stadnik *et al.* (2001) discussed that under ideal development conditions for the fungus, the severely attacked plants lose vigor and there is premature leaf fall and consequently reduced yield. Reduction in total plant leaf area could decrease the efficacy of photosynthesis. In this regard, Viana *et al.* (2001), noted that the damages of the crop yield was due to the decrease in size, number and quality of the fruits produced. In conclusion, the causal agent of powdery mildew is *E. cichoracearum* for the region of Ismailia Governorate. Seventeen different inbred lines of studied melon genotypes responded as immune and resistant to *E. cichoracearum* which can be used as suitable source for breeding program.

**Table (3):** Susceptibility of seventeen melon genotypes to powdery mildew

genotypes	Disease severity %	D. Scale	Susceptibility range
L1	0	0	HR
L2	24.3	2	T
L3	0	0	HR
L4	86.2	4	HS
L5	32.2	3	S
L6	10.3	1	R
L7	24.1	2	T
L8	32.5	3	S
L9	16.2	2	T
L10	0	0	HR
L11	12.3	1	R
L12	34	3	S
L13	0	0	HR
L14	23	2	T
L15	8.1	1	R
L16	30	3	S
L17	0	0	HR

### Mean performance:

Means of 12 horticultural traits for seventeen melon inbred lines during 2019 and 2020 are illustrated in Table (4). Differences among inbred lines for all studied characters were significant, indicating wide diversity among these inbred lines.

#### 1. Number of leaves/plant (NLF)

Data showed that inbred lines L6 and L10 had the highest values of the number of leaves/plant in both seasons (89.4, 90.6, 88.1 and 89.9, respectively), with

significant differences with the other inbred lines in 2019 and 2020. The L3 recorded the lowest number of leaves/plant in the two seasons (38.3 and 39.5) with significant differences compared to the other inbred lines.

#### 2. Number of internodes/plant (NIN)

Data obtained on the trait number of internodes/plant of 17 melon inbred lines are presented in Table (4). Data showed that L2, L10, L12, and L16 gave the highest values of the number of

internodes/plant in both seasons, with significant differences with the other inbred lines in 2019 and 2020. The lowest number of internodes/plant was obtained on L3, L5, and L13 in both seasons, respectively.

### 3. Number of branches/plant (NB)

Data obtained on the trait number of branches/plant are illustrated in Table (4) results obtained that L16 only gave the number of branches/plant above 5 branches (5 and 5.2) with significant differences with the other inbred lines in both seasons. On the contrary, L3, L8, and L9 gave the shortest fruit length on both seasons without significant differences with L4 and L14 in 2019 and L10 in 2020.

### 4. Tenth internodes length/plant (SL)

Data obtained on tenth internodes length/plant (cm) are illustrated in the Table (4). L6, L10, and L17 gave tenth internodes length/plant above 7 cm in both seasons, but L12 and L16 gave tenth internodes length/plant above 7 cm in the second season only. The lowest tenth internodes length/plant was observed in inbred lines L9 and L13 in both seasons respectively.

### 5. Area of tenth plant leaf (LR)

The area of the tenth plant leaf (cm<sup>2</sup>) of the studied inbred lines had a wide range from 32.9 to 72.4 cm<sup>2</sup> (Table 4) in both seasons. The inbred lines L5, L16, and L17 had the highest area of the tenth plant leaf with significant differences with the other inbred lines in 2019 and without significant differences with L5, L8, L16, and L17 in 2020. On the other hand, L3, L9, and L11 had the lowest area of the tenth plant leaf with significant differences with the other inbred lines in 2019 and 2020.

### 6. Average fruit weigh (FW)

Data of Table (4) presents the average fruit weight (g), where L15 gave significantly the highest average fruit weight in 2019 and 2020. The least average fruit weight was recorded in L3 with significantly different from other inbred lines in both seasons.

### 7. Fruit length (FL)

Data obtained on the fruit length (cm) are presented in table (4). The results obtained in the two seasons of (2019- 2020) showed that the L2 gave the highest significant fruit length in both seasons (21.8 and 23.0 cm, respectively), with significant differences among the other inbred lines at two seasons. In contrast, L3 and L4 were the shortest in fruit length in both seasons.

### 8. 1/2 Fruit diameter (FD)

The obtained data on average 1/2 fruit diameter (cm) presented in Table (4) revealed that L7, L12, and L13 were the highest on 1/2 fruit diameter and significantly different overall other melon inbred lines in 2019, but L7 and L12 only in 2020. On the other hand, L3, L10, and L11 had the lowest 1/2 fruit diameter compared with the other inbred lines in 2019 and 2020.

### 9. Average flesh thickness (FTH)

In respect to average flesh thickness (cm), L15 and L16 had the greatest flesh thickness with

significant differences over other inbred lines presented in Table (4) in both seasons. In contrast, the narrowest flesh thickness was shown in L2, L3 and L10 with a significant difference from the other inbred lines in both seasons.

### 10. Total soluble solids (T.S.S.)

Results of Table (4) indicated that had total soluble solids (T.S.S. %), had the highest T.S.S. with a significant difference from all inbred lines in 2019, and without significant difference with L11 in 2020. In addition, L2, L6, L7, and L14 ranked lowest in this trait with a significant difference from the other evaluated inbred lines in both seasons.

### 11. Average weight of seeds per fruit (WS/F)

Data were obtained on the average weight of seeds per fruit (g) of 17 melon genotypes are presented in Table (4). Data showed that only L15 in 2019 and L11 in 2020 recorded the greatest value with significant differences from other inbred lines. The lowest weight of seeds per fruit was shown L3 and L4 with a significant difference from over other inbred lines in both seasons.

### 12. 100-seeds weight (W100)

Regarding the weight of 100-seeds (g) of 17 melon inbred Lines, the results indicated that only L16 had the highest 100-seed weight without significant difference with L1, L5, L6, and L11 in 2019 and with a significant difference from other inbred lines in 2020. The lowest 100-seed weight was shown L4, L7, L8, and L17, with significant difference from other inbred lines in both seasons.

### Genetic studies:

Improvement of melon depends on the nature and magnitude of genetic variability in the population. Genetic variability studies provide basic information regarding the genetic properties of the population. The extent of variability presented in melon cultivars was measured in terms of phenotypic variance ( $\sigma^2_{ph}$ ), genotypic variance ( $\sigma^2_g$ ), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and heritability ( $h^2_b$ ) as shown in (Table 5).

#### - PCV and GCV.

Estimates of phenotypic variance Table (5) were larger than the corresponding genotypic variance for all examined traits. Moreover, close estimates of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were noted in all characters, which imply the contribution to the phenotypic expression of these characters were mostly due to genetic factors, while the environmental ones were not of great importance. Characters having a high genotypic coefficient of variation indicate a high potential for effective selection. These findings are in agreement with those reported by Rakhi and Rajamony (2006), Mehta *et al.* (2009), Potekar *et al.* (2014), Choudhary *et al.* (2011) and Janghel *et al.* (2018).

Greater variability ensures better chances of producing new desirable forms. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was computed for twelve studied characters on seventeen melon inbred lines Table (5).

**Table (4):** Growth and fruit yield performance of seventeen melon genotypes

Inbred lines	NLF		NIN		NB		SL		LR		FW		FL		FD		FTH		T.S.S		WS/F		W100	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
<b>L1</b>	68.8	70.0	20.9	21.1	3.7	3.9	5.2	5.4	42.9	46.1	519.2	528.4	13.2	13.4	5.6	5.8	2.8	3.0	9.9	10.8	8.9	9.1	3.4	3.6
<b>L2</b>	60.8	62.0	24.5	25.7	3.3	3.5	5.5	5.7	53.9	57.1	626.1	614.9	21.8	23.0	4.6	4.5	2.0	2.2	6.5	6.6	11.3	12.5	2.5	2.4
<b>L3</b>	38.3	39.5	14.6	15.5	2.9	3.1	5.0	5.2	32.9	33.1	223.3	229.2	7.1	8.0	4.2	4.4	2.0	2.2	11.7	11.9	3.3	3.8	2.6	2.4
<b>L4</b>	58.8	57.1	18.1	16.4	3.2	3.6	5.6	6.0	50.5	52.9	271.7	265.8	7.2	6.0	4.9	5.3	2.6	3.0	9.0	10.4	4.2	3.5	1.7	2.1
<b>L5</b>	55.7	57.3	17.8	19.4	3.9	3.7	5.8	5.6	63.6	63.4	642.6	651.8	10.9	12.5	5.1	4.9	3.1	2.9	9.2	8.4	12.3	13.9	3.4	3.2
<b>L6</b>	89.4	90.6	21.9	23.1	4.0	3.8	7.2	7.0	57.8	57.6	464.4	473.6	10.7	11.9	5.1	4.9	2.6	2.4	6.9	7.1	10.6	11.8	3.2	3.0
<b>L7</b>	52.7	53.9	20.6	21.8	3.6	3.8	6.0	6.2	56.8	57.0	455.3	464.5	14.4	15.6	6.5	6.7	2.7	2.9	6.6	6.8	7.5	8.7	1.9	2.1
<b>L8</b>	52.7	51.5	19.2	18.0	2.9	3.1	5.5	5.7	63.1	63.3	496.9	502.8	10.7	9.5	5.2	5.4	2.9	3.1	7.3	7.5	10.1	8.9	2.2	2.0
<b>L9</b>	47.5	48.7	19.4	20.6	3.3	3.1	4.1	3.9	37.9	34.7	298.8	287.6	9.5	9.4	5.0	4.8	3.4	3.2	7.9	7.7	6.4	7.6	2.3	2.1
<b>L10</b>	88.1	89.9	25.3	27.1	3.7	3.5	7.9	7.7	49.0	48.8	605.6	594.4	12.6	14.0	4.1	3.9	2.1	1.9	9.6	8.4	11.7	13.5	2.5	2.3
<b>L11</b>	71.3	72.5	19.2	20.4	3.8	3.6	5.2	5.0	40.4	35.2	562.1	568.0	13.6	14.8	4.4	4.2	2.3	2.1	13.2	13.0	14.2	15.4	3.3	3.1
<b>L12</b>	77.2	78.4	23.6	26.8	3.7	4.3	6.6	7.2	59.9	60.5	517.9	523.8	15.7	16.9	6.4	7.0	3.1	3.7	11.6	12.7	9.9	11.1	2.5	2.7
<b>L13</b>	59.5	58.3	15.5	14.3	3.7	3.9	4.7	4.9	61.6	61.8	715.8	725.0	15.3	14.1	6.1	6.3	2.9	3.1	8.7	8.9	14.4	13.2	2.5	2.7
<b>L14</b>	64.4	65.6	19.9	21.1	3.1	3.6	5.7	6.2	53.2	56.7	622.0	631.2	18.6	19.8	4.6	5.1	2.4	2.9	6.8	7.3	10.8	12.0	2.6	2.9
<b>L15</b>	80.1	78.9	21.3	20.1	4.0	4.2	5.6	5.8	54.7	54.9	761.8	750.6	15.3	14.1	5.6	5.8	3.7	3.9	9.2	10.4	15.3	14.1	2.5	2.7
<b>L16</b>	79.8	78.6	25.9	24.7	5.0	5.2	6.9	7.6	65.7	72.4	707.6	696.4	14.7	13.5	4.7	5.4	3.4	3.8	11.1	11.8	12.5	11.3	3.6	4.3
<b>L17</b>	68.8	67.6	20.5	19.3	3.9	3.7	7.5	7.3	63.9	68.1	523.0	532.2	11.2	10.0	5.0	4.8	2.9	2.7	7.8	9.0	6.3	5.1	1.7	1.5
<b>LSD</b>	4.2	4.4	3.3	3.5	0.5	0.4	0.9	1.1	8.4	9.0	30.6	31.5	2.2	2.4	0.4	0.5	0.3	0.4	0.7	0.8	0.6	0.6	0.7	0.6

NLF= number of leaves /plant, NIN= number of internodes/plant, NB= number of branches/plant, SL= tenth internodes length/plant (cm) , LR= area of tenth plant leaf (cm<sup>2</sup>), FW= fruit weight (g), FL= fruit length (cm), FD= 1/2the diameter of the fruit (cm), FTH= flesh thickness (cm), T.S.S.=total soluble solid %, WS/F= average weight of seeds per fruit (g), and W100= 100-seeds weight (g).

The GCV ranged from 11.14% (number of branches/plant) to 60.69% (T.S.S.). The PCV for different characters ranged from 20.57% (number of branches/plant) to 62.90% (T.S.S.). A high amount of fixable variation in snake cucumber characters has been reported by Abed (2018). In the present study, high estimates of both GCV and PCV were registered for the studied traits, viz., fruit weight (60.69 and 62.90% respectively) and the average weight of seeds per fruit (55.07 and 61.76% respectively) which suggest greater phenotypic and genotypic variability among the accession and responsiveness of the attributes for making further improvement by selection.

Moderate estimates of GCV and PCV were registered for the traits fruit weight (38.7 and 50.30% respectively), fruit length (44.29 and 51.63% respectively), and 100-seeds weight (33.50 and 42.3% respectively).

Low estimates of GCV and PCV were registered for the traits viz., number of leaves/plant (27.12 and 37.40% respectively), number of internodes/plant (19.35 and 26.03% respectively), number of branches/plant (11.14 and 20.57% respectively), tenth internodes length/plant (23.61 and 30.17% respectively), area of tenth plant leaf (26.77 and 33.88% respectively), 1/2 the diameter of the fruit (25.92 and 31.71 % respectively) and flesh thickness (30.5 and 31.7% respectively) which indicated that these traits were less affected by the environment. Indires (1982) reported similar results in bitter melon. This suggests that these characters may be less influenced by the environment which is in agreement with the findings of Tomar *et al.* (2008) in muskmelon.

#### - Heritability:

In the present study, different heritability values were exhibited in all the characters and ranged from 29.32 to 93.12% (Table 5). High heritability values were obtained for 7 traits: tenth internodes length/plant (61.22%), fruit length (79.40%), 1/2 the diameter of the fruit (66.80%), flesh thickness (66.80%), T.S.S. (93.12%), the average weight of seeds per fruit (79.49%), and 100-seeds weight (62.5%). These values suggest that these traits may generally be governed by additive gene action and hence the phenotype would provide a fairly reliable measure of the inbred line which provides scope for selection based on the phenotypic performance. According to El-Mighawry and EL-Raheem (1991) Sarutayopha and Nualsri (2010), the efficiency of selection depends not only on the selection method but also on the heritability of

different traits in different species. Also, Mohsin *et al.* (2009), suggested that heritability provides an idea of the extent of genetic control for the expression of a particular trait and the reliability of phenotype in predicting its breeding value. Songsri *et al.* (2008) reported that high heritability indicates less environmental influence on observed variation. Whereas the low and moderate heritability estimate obtained for number of leaves/plant, number of internodes/plant, number of branches/plant, area of tenth plant leaf and fruit weight indicated that, little progress could be achieved if selection is based on these characters.

In general, we can notice that the differences between phenotypic and genotypic variance for all studied traits were low. In other words, the large portion of phenotypic variance (PV) was due to the genetic variance (GV). Consequently, estimated broad-sense heritability showed high values for most traits, indicating that the observed significant phenotypic differences among the studied inbred lines are genetic and there are small environmental effects on the phenotypic variation. Therefore, these characters can be improved through selection based on phenotypic observations in early segregating generations in melon germplasm.

#### - Correlation

A simple correlation coefficient among seventeen melon inbred lines is presented in (Table 6). The indicated results a highly significant positive correlation for the number of internodes/plant with the number of branches/plant (0.02), tenth internodes length/plant (0.27), and area of tenth plant leaf (0.05). Whereas, negative correlation was recorded with fruit weight (-0.23), fruit length, and 1/2 fruit diameter (-0.15). Significant and highly positive correlation was observed for the number of branches/plant with flesh thickness (0.26) and T.S.S. (0.23). Significant and highly positive correlation for fruit weight was detected with other traits studied, in addition to significant and highly positive correlation for fruit length with flesh thickness (0.73), the average weight of seeds per fruit (0.49), and 100-seeds weight (0.81). On the other hand, negative correlation was recorded with 1/2 fruit diameter (-0.4). A significant and positive correlation was recorded for T.S.S. with all traits studied. A significant and highly positive correlation was recorded for the average weight of seeds per fruit with 100-seeds weight -0.27 similar results were reported by Lee *et al.* (1996).

**Table (5):** Estimation of PCV, GCV, heritability, and genetic advance as percent of mean for various characters in melon

No.	Traits	V <sub>E</sub>	V <sub>G</sub>	V <sub>P</sub>	GCV%	PCV%	h <sup>2</sup> (%)
1	NLF	283.76	312.37	596.13	27.12	37.46	52.40
2	NIN	12.37	15.27	27.65	19.35	26.03	55.25
3	NB	0.39	0.16	0.55	11.14	20.57	29.32
4	SL	1.18	1.87	3.05	23.61	30.17	61.22
5	LR	118.33	196.76	315.09	26.77	33.88	59.20
6	FW	29312.0	42531.2	71843.2	38.7	50.30	59.20
7	FL	9.12	35.17	44.29	46.01	51.63	79.40
8	FD	0.25	0.51	0.76	25.92	31.71	66.80
9	FTH	0.3	0.5	0.8	30.5	31.7	66.8
10	T.S.S.	1.09	14.69	15.78	60.69	62.90	93.12
11	WS/F	8.176	31.697	39.87	55.07	61.76	79.49
12	W100	0.5	0.8	1.2	33.5	42.3	62.5

NLF= number of leaves/plant, NIN= number of internodes/plant, NB= number of branches/plant, SL=tenth internodes length/plant (cm) , LR= area of tenth plant leaf(cm<sup>2</sup>),FW= fruit weight (g), FL=fruit length (cm), FD=<sup>1/2</sup>the diameter of the fruit (cm), FTH= flesh thickness (cm), T.S.S.=total soluble solid %, WS/F= average weight of seeds per fruit (g), and W100= 100-seeds weight (g)

**Table (6):** Simple correlations coefficient among 17 melon inbred lines:

	number of internodes/ plant	number of braches/ plant	Tenth internodes length/plant	area of tenth plant leaf	fruit weight	fruit length	<sup>1/2</sup> diameter of fruit	flesh thickness	T.s.s.	average weight of seeds per fruit
number of branches / plant	0.20									
Tenth internodes length / plant	0.27	0.07								
area of tenth plant leaf	0.05	0.11	0.42							
fruit weight	-0.23	0.19	-0.04	0.25						
fruit length	-0.37	0.07	-0.08	0.11	0.58					
<sup>1/2</sup> diameter of fruit	-0.15	-0.08	-0.11	0.02	0.04	-0.03				
flesh thickness	-0.06	0.23	-0.10	0.22	0.37	0.07	0.26			
T.s.s.	0.09	0.26	0.09	0.09	0.14	0.03	0.27	0.31		
average weight of seeds per fruit	-0.12	0.16	-0.15	0.15	0.49	0.42	0.09	0.24	0.02	
w100	-0.04	0.26	-0.03	0.16	0.18	0.09	-0.22	0.23	-0.24	0.27

## CONCLUSION

Evaluation of 17 melon inbred lines indicated that, the inbred lines L1, L10, L13, and L17, are highly resistant to powdery mildew, but they are moderate to horticultural characteristics. Therefore, it might be recommended to be evaluated on a large scale and continue the breeding program to produce a commercial variety. With better growth and yield characteristics combined with high resistance to powdery-mildew.

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## دراسة وراثية لصفة المقاومة للبياض الدقيقي وبعض الصفات الاقتصادية في الشمام

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أجريت هذه الدراسة بهدف دراسة صفة المقاومة للبياض الدقيقي بالإضافة إلى بعض الصفات الاقتصادية الهامة للحد من الخسائر في الجودة والإنتاج لمحصول الشمام وذلك بمحطة الإسماعيلية - مركز البحوث الزراعية بالتعاون مع قسم النبات الزراعي جامعه قناة السويس في الفترة من ٢٠١٩ إلى ٢٠٢٠. استخدمت في الدراسة ١٧ سلالة مرباة داخليا عن طريق معهد بحوث البساتين. هذه السلالات تم التلقيح الذاتي فيها لعدد ٦ أجيال لضمان الحصول علي اعلي درجة من النقاوة و التجانس لدراسة معامل التباين الوراثي (GCV) ومعامل التباين المظهري (PCV) ومعامل التباين البيئي (ECV) ودرجه التوريث والارتباط لعدد ١٢ صفة هي عدد الأوراق/النبات، عدد السلاميات/نبات، عدد الأفرع/نبات، طول السلامية العاشرة/نبات، مساحه الورقة العاشرة/نبات، وزن الثمرة، طول الثمرة، نصف قطر الثمرة، سمك اللحم، نسبة السكريات الذاتية الكلية(%)، متوسط وزن بذور/ثمره، متوسط وزن الـ ١٠٠ بذره. أظهرت السلالات (L1, L3, L10, L13, L17) مقاومة عالية للبياض الدقيقي، بينما أظهرت باقي السلالات درجات مختلفة من الحساسية للإصابة بالبياض. كما أظهر تحليل التباين معنوية عالية لجميع الصفات مما يشير إلى وجود تباين كبير بين الطرز الوراثية. وكانت قيم معامل التباين الوراثي (GCV) ، ومعامل التباين المظهري (PCV) ودرجة التوريث ( $h^2$ ) متباينة حيث كانت القيم لها (١١.١٤-٦٠.٦٩، ٢٠.٥٧-٦٢.٩٠، ٢٩.٣٢-٩٣.١٢٪) على التوالي. وتشير التقديرات العالية لـ GCV و PCV في هذه الدراسة إلى وجود تباين يمكن الاختيار بين السلالات بسهولة. في حين اظهر أن الصفات قابلة للتوريث بدرجة عالية وانه يمكن الاختيار فيما بينها أيضا.