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Breeding some cantaloupe inbred lines for resistantce to powdery mildew

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In the present study, 10 different inbred lines of melon (*Cucumis melo* L.) were tested for their response to *Erysiphe cichoracearum* the causal agent of Powdery mildew. Plants of the inbred lines No.1,2,3,5,6,7,8,9 and 10 showed clear symptoms of infection and low disease severity powdery mildew when inoculated after artificial inoculation with *Erysiphe cichoracearum*. Plants of line 4 showed high resistance to powdery mildew if compared with the other tested lines. In Contrast, plants of line (4) showed high resistance to powdery Mildew. Two inbred lines chosen P1 (inbred line 2) which was susceptible to powdery mildew while P2 (inbred line4) which was resistance to produce F1, F2, Back cross1 and back cross2 plants (six populations method) were produced to study genetics of powdery mildew resistance and some horticulture characters. The segregation ratios for resistance/susceptibility observed in the different populations, i.e. F1 generation was resistant. However, F2 generation segregated closed to a ratio of 3 resistant: 1 susceptible. Regarding the back crossing F1 plants to the resistant parent gave all progeny resistant. On the other hand back crossing F1 plants to the susceptible parent produced progeny 1 susceptible: 1 resistant. Results showed that main stem length character was found to be controlled by 2 pairs of gens, Estimates of BSH and NSH were 92.7% and 66.2 %, respectively. The positive value of potence ratio indicated over dominance for fruit weight character towards the heavy fruit parent. The estimated of Values of Broad and narrow sense heritability were high 91.6 % and 57.8 %, respectively. Quantitative genetic parameters were obtained for total yield showed positive value of potence ratio (6.23) indicating over dominance for this character towards the high parent. High positive values of heterosis based on mid and high-parent. Were obtained. Estimating number of genes controlling total yield character was found to be 1 pair of genes. Estimates of BSH and NSH for total yield were 88.54 % and 80.3%, respectively. These values indicated that genetics has a major role in the inheritance of this character and most of genetic variance was additive.

Keywords: Melon, Inbred lines, inheritance, powdery mildew, *Erysiphe cichoracearum*. Heterosis, heritability, BSH and NSH.

INTRODUCTION

Cucurbit powdery mildew, is a major problem in melon (*Cucumis melo* L.) production worldwide, is mostly caused by two fungi: *Podosphaera xanthii* and *Golovinomyces cichoracearum* (formerly *Erysiphe cichoracearum*), Jahn et al., (2002). Infection may be by either pathogen alone or it may be a co infection of the two species (Kristkova et al., 2009). The disease is characterized by the appearance of a whitish, talcum-like powder on both surfaces of the leaves, as well as on the petioles and stems. The infected

leaves usually wilt and die, and the plants age prematurely (Zitter et al., 1996). Reductions in fruit quality and crop yield are the most striking aspects of the losses that are caused by the disease. The inheritance of resistance to races 1, 2 and 5 of *Podosphaera xanthii* in the melon was studied. Symptoms of powdery mildew are visible to the naked eye 12 days after artificial inoculation. Plants of the cultivar Bola de Oro showed clear symptoms of infection with powdery Mildew when inoculated with races 1, 2 or 5 2

of *P. xanthii*. In Contrast, plants of the genotype TGR-1551 and the F1 population showed resistance to all three races. The segregation ratios for resistance/susceptibility observed in the different populations and the results of the progeny test indicated that resistance to races 1, 2 and 5 of *P. xanthii* was governed by two independent genes, one dominant and one recessive, which means that the genetic control is a dominant–recessive epistasis. That was the first time a recessive gene confers resistance to more than one race of powdery mildew which had been identified in melon. TGR-1551 could be considered a good genetic source for the development of powdery mildew resistant breeding lines (Yuste-lisbona et al., 2010). Commercial varieties that show resistance to specific races of powdery mildew had been developed. However, these varieties become susceptible to infection shortly after they are exploited commercially, because of frequent changes in pathogen populations (Szunics et al., 1999). James and Michael (2011) studied resistance to race S: A new strain of cucurbit powdery mildew incited by *Podosphaera xanthii* (Castagne) Braun & Shishkoff (formerly *Sphaerotheca fuliginea*) were designated race S was recessive while all F1 and BCTM individuals were susceptible. One recessive gene, designated *pm*-S, conditioned resistance to race S in the F2 and BCPI. Inheritance of resistance of five melon lines to two strains of *Sphaerotheca fuliginea* belonging to races 1 (Sfl) and 2 (Sf2) and to one strain of *Erysiphe cichoracearum* (Ec) have been studied. 'PMR 45' possesses one dominant gene controlling only Sfl. 'WMR 29' has one dominant gene for resistance to Sfl and another for Sf2 and these genes seem to be linked. In line 'PMR 5% one dominant gene (or a group of three closely linked genes) is involved in the control of the three strains with one complementary gene for Sfl and another one for Ec. 'PI 124112' has one dominant gene or two closely linked loci controlling Sfl and Sf2 and two complementary different genes controlling Ec. 'Nantais Oblong' has one dominant gene controlling only Ec. A nomenclature of the genes described is proposed (Epinat *et al*. 1993). Melon growers still rely on the use of protective fungicides to control powdery mildew. However, the use of fungicides over a number of decades has resulted in powdery mildew having become resistant to many chemical compounds (Hollomon and Wheeler 2002). Therefore, there is a pressing need to develop new ways of controlling the disease. Moreover, the increasing concern for public health has motivated breeders to seek different strategies for the control of diseases. The development of new resistant cultivars appears to be the most eco-compatible way to control the disease (De Giovanni et al., 2004). Complete dominance of PM resistance was found in cantaloupe (galia and charentais types), but partial dominance of PM susceptibility was shown in ananas. The negative mid-parents heterosis values of PM resistance were obtained on the first and second crosses. The minimum number of genes controlled in melon PM resistance are 6, 2 and 3 pairs of genes for first, second and third crosses, respectively. High BSH and low to high NSH were found in the three crosses of melon, Selim and Zaid (2015). Consequently, the search for and utilization of new genes that confer resistance to powdery mildew have become primary objectives for melon breeders. So, the aim of this study was using different cantaloupe inbred lines as sources of resistance to powdery mildew to develop new hybrids and to select the top performing cantaloupe hybrids which are powdery mildew resistant with an appropriate yield and good fruit quality.

MATERIALS AND METHODS

In This study melon genotypes (parents), F1, F2, BC1 and BC2 which were produced from the melon genotypes were evaluated for their response to *Erysiphe cichoracearum* and horticulture characters during the period from 2016 -2018 in a screen house under greenhouse conditions at the national research center, plant protection Department and Vegetable Research Departments Horticulture Research Institute, Agricultural Research Center Giza Governorate and 3 Kaha Vegetable Research Farm, Kalubia Governorate, Egypt. The Plants were maintained in the used breeding materials included 10 different genotypes of melon (*Cucumis melo* L.) Table 1.

Source of melon germplasm:

The used breeding materials included 10 different Genotype of melon (*Cucumis melo* L.)Line 1, 2 and 4 were imported from USA Whereas Line 5 and 7, were obtained from Nord Gen Bank. Lines (3-6-8-9 and10) were obtained from Deb. of vegetables breeding (D V B)**.** The susceptible melon cultivar DOKKY 2- (P1) was used as the female parent for crossing with the genotype KAHA 4 (P2) which is resistant to powdery mildew. The F1 generation was self-pollinated, and backcrossed to the susceptible and Resistant parents to give the populations F2, BC1 and BC2, respectively. This population was used to analyze the genetics of resistance to powdery mildew. Seedlings were transplanted on March in a randomized complete block design with 3 replicates. Each replicate contained 10 experimental plots for inbred lines evaluation in 2017 and 2018. Each plot was presented by a single bed, 1.5 m width and 10 m length (EP area = 15 m2) and the plants were spaced at 50 cm. Land preparation, fertilizer application and other field practices were carried out according to recommendations of the Egyptian Ministry of Agriculture. As well as 6 experimental plots (2 parents, F1, F2, BC1 and BC2) of the six population cross experiment, i.e., Six generation P1 (30 plants), P2 (30 plants), F1 (30 plants), F2 (80 plants), BC1 (60 plants) and BC2 (60 plants).

Procurement of culture and seed:

The fungal pathogen inoculums were isolated from naturally infected melon plants, obtained from Department of Vegetable Crop Research, Agricultural Research Centre, Giza, Egypt.

Pathological studies:

Greenhouse experiments:

Melon seeds were sown in plastic pots (25-cm-diam.) containing loamy soil, four seeds/pot. Ten pots were used for each treatment. Irrigation was added as needed under Plant Pathology Department, National Research Centre greenhouse condition.

Preparation of *E. cichoracearum* inoculum

The powdery mildew fungal inoculums were obtained from freshly infected leaves of naturally infected melon plants. Conidia were gently brushed into 100-mL distilled water with 5mL of Tween-20 then counted by haemocytometer to give a mixture of 5 × 105 conidia/ mL. For plant inoculation, the upper surfaces of all the leaves were sprayed with a conidial suspension delivered by a hand sprayer according to Reuveni et al., (2000).

Disease assessment:

Final disease assessment was conducted at 11 days after each spray in each treatment. Conidia production of E. cichoracearum on treated melon leaves was also evaluated. Leaves were detached gently at the early morning and immersed in screw cap jars containing 100 mL of distilled water. Conidia were released from lesions using a brush, and then counted. Fungal conidia/cm2 of leaf area was counted in each treatment.

Table (1): source of melon genotype

Code No. of Genotype	Genotype	Source
Line1	KAHA 1	(Ames26809 US Carolina)
Line2	DOKKY 2-	Deb. Of Vegetables breeding)
Line3	KAHA 77	(Deb. Of Vegetables breeding)
Line4	KAHA 4	(NSL 34600 USA south Carolina)
Line5	KAHA 5	(NGB 9999 Nord Gen Bank)
Line6	KAHA 75	(Deb. Of Vegetables breeding)
Line7	DOKKY 7	(NGB 12020 Nord Gen Bank)
Line8	DOKKY 9	(Deb. Of Vegetables breeding)
Line9	KAHA 2	(Ames26810 USA Carolina)
Line10	DOKKY 53	(Deb. Of Vegetables breeding)

Table 2. Powdery mildew disease severity estimating into 5 categories according to Descalzo et al., 1990.

Scale	Mildew percentage covering leaf surface	Symptom	Reaction
0	0%	No symptoms of infection	High Resistant(HR)
1	1-5 %	Very weak infection	Resistant (R)
2	6-25 %	Weak infection	Tolerant (T)
3	26-50 %	Moderate infection	Susceptible (S)
4	50.5-100 %	Very severe infection	High Susceptible (HS)

Horticulture parameters:

A-Main stem length (cm): main stem length was measured in centimeters from the cotyledon node to the top end.

b- Number of leaves: Counting of leaves begun from the cotyledon node to the top end of the main stem. .

c- Fruit quality: average fruit weight (g), flesh thickness (cm), fruit length (cm), fruit diameter (cm) and Total soluble solids (TSS) was determined in ripe fruits using a hand refractometer .

d- Total yield (gm/plant) was determined by weighing all produced fruits per plant.

Estimation of total phenolic content.

Total phenolic content in melon leaves of each treatment was determined according the methods described by Descalzo et al., (1990). as follows: melon leaves was immersed in liquid nitrogen, homogenized in 80% methanol (1 g plant material in10 mL) and stored at −20oC. Later, the homogenate was centrifuged at 15,000 ×g for 30 min at 4oC. The pellet was discarded. After addition of ascorbic acid (0.1 g/5 mL), the homogenate was evaporated in rotary evaporator at 65oC 3 times for 5 min. The residues were dissolved in 5 mL of 80% methanol. For the determination, 0.02 mL methanol extract was incubated for 1 hr with 0.5 mL Folin-Ciocalteu reagent, 0.75 mL of Na2CO3 solution (20%) and 8-mL water. Total phenolic content was assayed spectrophotometrically at 767 nm.

Statistical analysis:

All obtained data from the two seasons were subjected to the statistical analysis according to Steel and Torrie (1984). The means were compared by Duncan's Multiple Range Test (DMRT) at 5%. Genetic analysis for this study were: The relative potency of gene set (P) was used to determine the direction of dominance according to Smith1952, Heterosis based on the mid and high parent value was estimated according to Sinha and Khanna1975, The minimum number of genes controlling the character in each cross was calculated using

Castle 5 and Wright, 1921. Broad (BSH) and narrow (NSH) sense heritabilities were calculated according to Allard 1960, A chi-square test was performed to check the segregation of resistance to powdery mildew in the different populations.

RESULTS

Evaluation of parental genotypes to powdery mildew infection:

Obtained Data on ten inbred lines evaluated after the infection with powdery mildew, Symptoms of powdery mildew were visible to the naked eye 9-12 days after artificial inoculation. Plants of the inbred lines (1-2-3-5-6-7-8-9-10) showed clear symptoms of infection with powdery Mildew when inoculated with *Erysiphe cichoracearum*. In Contrast, plants of line (4) showed high resistance to powdery Mildew Which was clearly shown in the following pictures and according to data in Fig (1), (2) and (3) According to the previous data which are shown in fig (1) two inbred lines were chosen P1 (inbred line 2) which was susceptible to powdery mildew and P2 (inbred line4) which was resistance to produce F1, F2, Back cross1 and back cross2 plants (six populations) to study genetics of powdery mildew resistance and some horticulture characters.

Evaluation of some horticulture characters of the inbred lines:

Vegetative growth:

Data obtained on ten inbred lines evaluated during 2016 and 2017 summer seasons are presented in Table (4). There were significant differences for this trait among the evaluated genotypes. Main stem length of the cultivated genotypes ranged from (424.5 to 188.0).

Table 4. Plant length, Number of leaves, of some melon Inbred lines evaluated during 2016-2017.

Inbred lines	Plant length		No. of leaves	
	First season	second season	First season	second season
1	280.3D	34.66C	280.3D	34.33D
2	188.0G	24.33E	190.3H	24.0000H
3	322.6C	325.0C	34.66C	34.33D
4	197.0G	199.3G	23.00E	22.667H
5	211.3F	213.6F	26.66D	26.33G
6	262.0E	264.3E	28.66D	28.33F
7	207.3F	209.6F	32.66C	32.33E
8	424.5A	426.8A	43.16A	42.66A
9	424.5A	359.0B	40.66B	40.33B
10	356.6B	324.3C	38.66B	38.33C

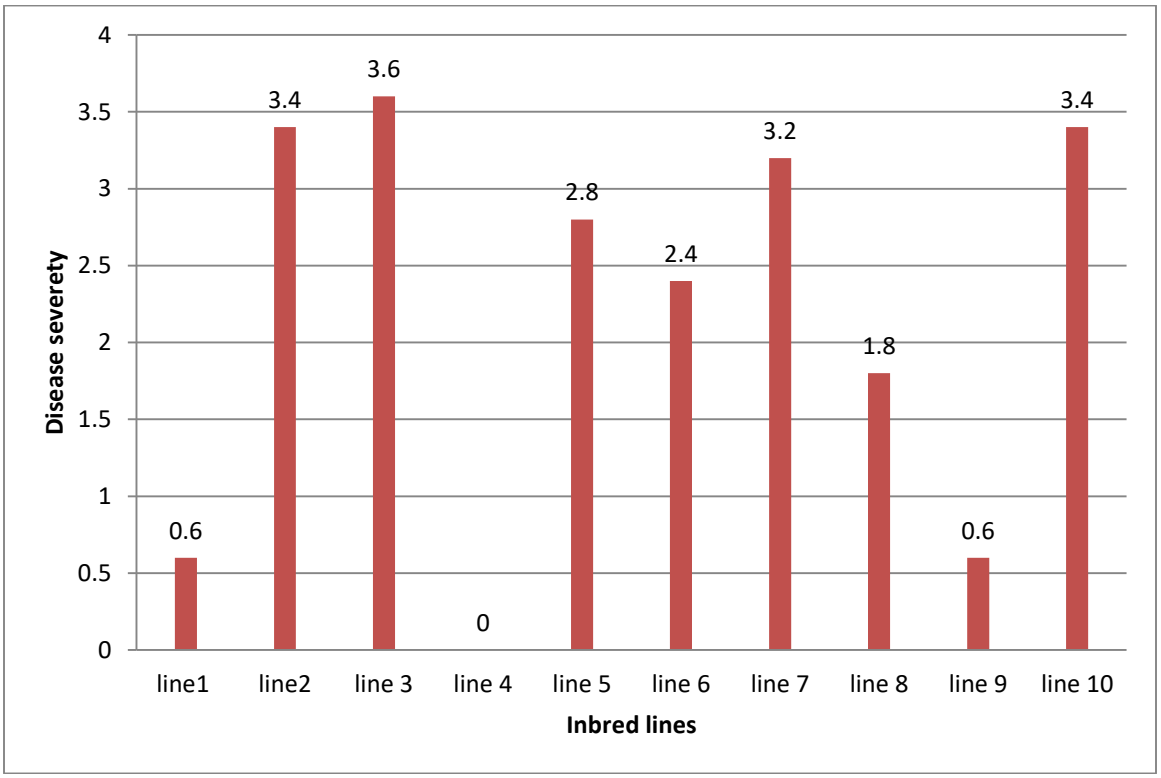

Figure 1. Disease severity and phenotypic classes, based on the response to powdery mildew in the inbred lines of powdery mildew in melon leaves

Fig.2: Phenotypic Segregation of resistance to *Erysiphe cichoracearum* in parents and progeny of the cross between line 2 and line 4

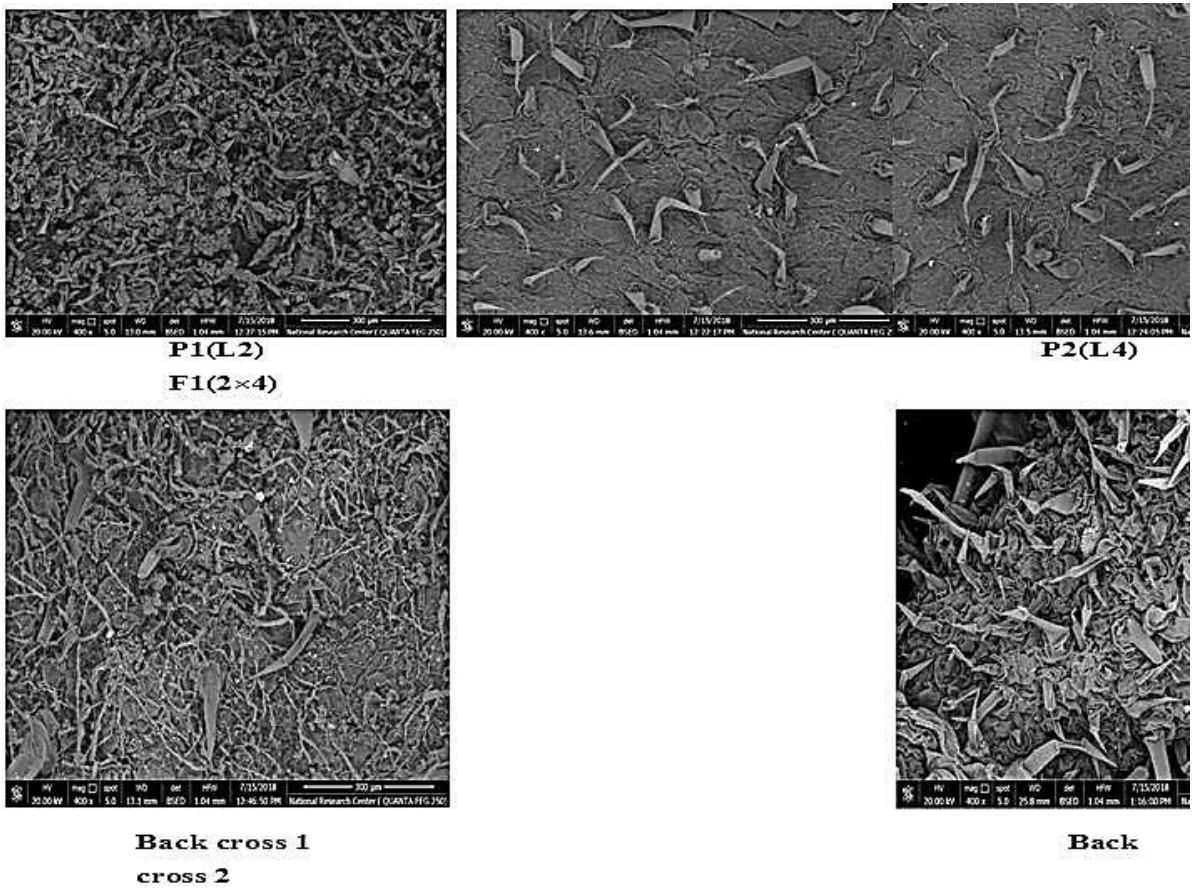

Fig. 3: electronic microscope photos and Segregation of resistance to *Erysiphe cichoracearum* in progeny of the cross between line 2 and line 4

Table 5.Fruit weight, Fruit length, Fruit diameter, Flesh thickness, TSS and Total yield of some melon Inbred lines evaluated during 2016-2017.

Inbred lines	Fruit weight		Fruit length		Fruit diameter		Flesh thickness		TSS		Total yield(kg/fed)	
	First season	Second season	First season	Second season	First season	Second season	First season	Second season	First season	Second season	First season	Second season
1	1023.3D	1016.7D	16.00B	15.96B	10.53E	10.56E	3.10D	3.06D	6.40E	6.36E	11500ab	8586.8cd
2	589.7G	583.0G	11.16E	11.13E	9.76F	9.80F	3.10D	3.06D	8.16C	8.13C	6625.2b	6970.8d
3	741.7F	735.0F	14.10C	14.06C	11.06E	11.10E	3.23D	3.20D	6.46E	6.43E	8286.8b	8786.8cd
4	2225.3A	2215.3A	19.10A	19.06A	16.06A	16.10A	5.10A	5.06A	6.76E	6.80E	17234.8a	19056a
5	775.3F	768.7F	12.10D	12.06D	11.06E	11.10E	3.40D	3.36D	6.40E	6.36E	8768b	8298.8cd
6	1250.7C	1244.0C	16.10B	16.06B	12.26D	12.30D	3.80C	3.76C	7.40D	7.36D	12936ab	14218.8cd
7	892.0E	885.3E	12.10D	12.06D	12.06D	12.10D	4.40B	4.36B	9.16B	9.13B	10101.2ab	10416cd
8	579.0G	572.3G	10.10F	10.06F	11.06E	11.10E	3.20D	3.16D	10.76A	11.7A	6649.2b	6845.2d
9	1248.3C	1241.7C	19.00A	18.96A	14.83B	14.86B	3.40D	3.36D	9.26B	9.23B	13553.2ab	14733.2bc
10	1494.7B	1488.0B	16.10B	16.06B	14.06C	14.10C	4.46B	4.43B	9.13B	9.10B	16512a	17837.2ab

The inbred (8) gave the highest value of plant length. On the other hand inbred (2) gave the lowest value of main stem length and there were no significant between it and inbred (4). Concerning, number of leaves were ranged from (43.16 to 24.0) data showed that, inbred (8) gave the highest number of leaves but inbred (2) gave the lowest number of leaves and there were not significant between it and inbred (4).

Fruit quality:

Table (5) show significant differences between the inbred lines for fruit characters, which are very important for breeders to produce hybrids with high quality. Fruit weight was ranged from (2225.3 to 572.3) data showed that, inbred (4) gave the highest value of fruit weight on the other hand inbred (8) gave the lowest value. Concerning fruit length there was significant difference between inbred lines where inbred (4) gave the highest value with not significant differances between it and inbred (9). on the other hand, inbred (8) gave the lowest value. Fruit diameter, data in Table (5) showed that, there were significant differences among inbred . inbred (4) gave the highest value of fruit diameter but inbred line (2) gave the lowest value.

Regarding flesh thickness, it was found that inbred (4) gave the highest value of Flesh thickness while inbred (1) gave the lowest value .TSS was ranged from (11.7% to 6.36%) showing significant differences among inbred lines were inbred (8) gave the highest value of total soluble solids (TSS) but inbred line (1) gave the lowest value with no significant differences between it and inbreeds (3-4-5). Concerning total yield (kg/fed) was ranged from (4764.0 to 1656.3), inbred (4) gave the highest value of total yield and there were not significant between it and inbreed (10) during the two seasons. on the contrary, inbred (2) gave the lowest value with no significant between it and inbreeds (1-3-5-6-7-8) during the two seasons.

Genetic studies

Inheritance of powdery mildew resistance:

The results in Table (6) cleared that the plants of P1 (line 2) were susceptible while P2 (line 4) plants as resistant to powdery mildew infection. F1 generation was resistant, while F2 generation segregated to a ratio of 3 resistant: 1 susceptible. Regarding the back crossing F1 plants to the resistant parent gave all progeny resistant on the other hand back crossing F1 plants to the susceptible parent produced progeny 1 susceptible: 1 resistant. These results are Partial agree with Yuste-Lisbona *et al.*, (2010) who found that Plants of the cultivar Bola de Oro showed clear symptoms of infection with powdery mildew when inoculated with races 1, 2 or 5 of *P. xanthii*. In contrast, plants of the genotype TGR-1551 and the F1 population showed resistance to all three races. In the F2 population, each plant showed the same response to the three races, which suggested the existence of a unique genetic control for resistance to races 1, 2 and 5 of powdery mildew in TGR-1551. Generally, 248 plants showed resistance and 47 were susceptible to the three races. This segregation fitted a ratio of 13 resistant plants: three susceptible plants (x^2 = 1.54, P = 0.21), and it did not fit to a 3: 1 segregation ratio, which would correspond to the closest genetic model of one dominant gene. In the BC1 population, 33 plants were resistant and 37 were susceptible to race 5 of *P. xanthii*,. These results showed that the genetic control of the resistance to powdery mildew in TGR-1551 is a dominant–recessive epistasis.

Inheritance of plant length:

Obtained data on main stem length (MSL) of parental, F_1, F_2, and backcross populations of the cross (2× 4) and are presented in Table 7.

Parents were highly significantly different in (MSL). F_1's and F_2's means were intermediate between their respective parents with tendency towards the higher parent. F_2 plants were widely distributed between its two parents. Backcross plants in the two crosses were widely distributed between their two parents with high tendency towards their parents. Quantitative genetic parameters obtained for HFC are presented in Table 16.

Negative P values were estimated for MSL, indicating partial dominance to the lower parent. Positive mid-parent heterosis for MSL was estimated as 14.6 % Also, positive heterosis based on high parent (43.8) Table 8. These results are in agreement with Hussein and Hamed (2015) found tow out of 10 evaluated hybrids exhibited were significant positive heterosis over taller parent (39.50%).

Results in Table (8) showed that MSL character was found to be controlled by 2 pairs of genes. Estimates of BSH for MSL was 92.7% and NSH was 66.2 %.

Table 6: Segregation of resistance to *Erysiphe cichoracearum* in Progeny of the cross (2× 4)

population	observed segregation		expected		total	X^2	Probability(P)
	Resistant	susceptible	Resistant	susceptible			
P1	0	30	0	30	30		
P2	30	0	30	0	30		
F1	32	0	32	0	32		
F2	71	13	62	22	84	1.29	3:1
BC1 BC2	38 60	22 0	30 60	60 0	0 60	2.10 0.0	1:1 1: 0

Table (7) Frequency distribution of main stem length of P1, P2 F1, F2, BC1 and BC2 of cross (2× 4**)**

Frequency of main stem length				Generation					
				P1	P2	F1	F2	BC1	BC2
205				15					
220				10			7	2	
235							15	15	
250							12	10	2
265							12	11	18
280							15	12	10
295						13	10	5	5
310					11	17	5		*11*
325					15		2		*10*
Total				25	26	30	78	55	56
Mean				211.0	318.6	303.5	264.0	258.4	289.3
Sx$^-$				1.5	1.4	1.3	3.2	2.9	3.2
C.V %				0.711	0.465	0.455	1.19	1.115	1.117
Mid-parent= 264.8									

Table (8) quantitative genetic parameters (main stem length) in the cross (2× 4**)**

Parameter	Estimated value
Potence ratio(P)	-0.71
Mid- parent heterosis %	14.6 %
high parent heterosis %	43.8 %
Minimum number of genes (N)	2.00
Broad sense heritability (BSH)	92.7
Narrow sense heritability (NSH)	66.2

Inheritance of fruit weight (AFW):

The frequency distribution of fruit weight for P1, P2, F1, F2, BC1 and BC2 populations are presented in Table (9). Parents were significantly different in AFW, On the other hand, the observed mean of the F1 population was not significant with the higher parent and. The means of F2, BC1 and BC2 were higher than the means of mid- parent. From another point of view, The F2 plants were widely distributed between the two parents with a high tendency towards the high parent. Concerning the plants of the backcross to P1 was widely distributed with a high tendency towards this parent; the same trend was noticed in the plants of the backcross to P2.

Quantitative genetic parameters obtained of fruit weight are presented in Table (10). The positive value of potence ratio (p) (1.52) indicated that, over dominance for fruit weight character towards the heavy fruit parent. MP and HP for AFW varied from 8.62 – 2.81 these results are disagreement with Hussein and Selim (2014) stated that All hybrids were highly significant positive over MP and BP, AFW varied from -60.2% to 32.51% when both types of heterosis were considered. The estimates of Values of Broad and narrow sense heritability were in high values 91.6 % 57.8 % respectively. The value of BSH estimates was high indicated that the minor role of environment and major role of genetics of this character. These results were in agreement with Hussein and Selim (2015) stated that Broad sense heritability was high (78.85 for AFW**)** in all studied traits which indicates the presence of large number of fixable additive genes regulating the inheritance of traits and the environmental effects had a minor role.

Table (9) Frequency distribution of fruit weight of P1, P2 F1, F2, BC1 and BC2 of cross (2× 4)

Frequency of Fruit weight				Generation					
				P1	P2	F1	F2	BC1	BC2
750					15				
850				15	9	13	18		5
950				7		17	15		15
1050							12	10	2
1150							12	11	18
1250							15	12	10
1350							10	5	
1450								15	
1550								2	
Total				22	24	30	82	55	50
Mean				881.8	787.5	906.7	1075.6	1268.2	1076.0
Sx^{-}				10.1	10.0	9.2	19.2	21.0	19.1
C.V %				1.15	1.28	1.01	1.78	1.66	1.77
Mid-parent= 834.65									

Table (10) quantitative genetic parameters (fruit weight) in the cross (2× 4**)**

Parameter	Estimated value
Potence ratio(P)	1.52
Mid- parent heterosis %	8.62 %
high parent heterosis %	2.81 %
Minimum number of genes (N)	0.040
Broad sense heritability (BSH)	91.6
Narrow sense heritability (NSH)	57.8

Inheritance of flesh thickness (FTH):

Data obtained on (FTH) of parental, F_1, F_{1r}, F_2, and backcross populations are presented in Table 11**.** Narrow range was observed among Parents in this trait. F_1 and F_2 means were lower than the high parent. F_2 plants were widely distributed between their two parents with a highly tendency towards the low parent in addition to some transgressive segregations under the low parent. Plants of the backcrosses had means lower than that of the high parent. Negative P values -0.71 estimated for FTH, indicating partial dominance of the lower parent. Positive mid-parent heterosis for FTH was estimated as 11.58 % Also, positive heterosis based on high parent 23.94 in (Table 12). These results are in partial agreement with Hussein and Selim (2015) found that Flesh thickness MP and BP ranged from -32.99% to 18.92%, The hybrid P3 **×** P5 exhibited significantly the highest desirable heterosis over MP.

Percentage of FTH was found to be controlled by three pairs of genes. Concerning Heritability, Table 12 showed that estimates of BSH for FTH were 88.24 % and 84.98 %.these results are in agreement with Hussein and Selim (2015) reported that broad sense heritability for FTH was 84.80.

Table (11) Frequency distribution of flesh thickness of P1, P2 F1, F2, BC1 and BC2 of cross (2× 4**)**

Frequency of flesh thickness				Generation					
				P1	P2	F1	F2	BC1	BC2
2.8									
3.0					**10**		**18**		**5**
3.2					**15**	**17**	**15**		**15**
3.4						**15**	**12**		**12**
3.6							**22**	**11**	**18**
3.8							**16**	**12**	
4.0								**16**	
4.2				**8**				**15**	
4.4				**15**				**2**	
Total				**23**	**25**	**32**	**83**	**56**	**50**
Mean				**4.33**	**3.12**	**3.29**	**3.40**	**3.94**	**3.37**
Sx$^-$				**0.020**	**0.020**	**0.018**	**0.032**	**0.031**	**0.029**
C.V %				**0.469**	**0.641**	**0.544**	**0.936**	**0.791**	**0.864**
Mid-parent= 3.725									

Table (12) quantitative genetic parameters (flesh thickness) in the cross (2× 4**)**

Parameter	Estimated value
Potence ratio(P)	-0.71
Mid- parent heterosis %	11.58 %
high parent heterosis %	23.94 %
Minimum number of genes (N)	2.47
Broad sense heritability (BSH)	88.24
Narrow sense heritability (NSH)	84.98

Inheritance of Total soluble solids (TSS):

The frequency distribution of TSS for P1, P2, F1, F2, BC1 and BC2 populations are presented in Table (13). Parents were significantly different in TSS. From another point of view, The F2 plants were widely distributed between the two parents with a high tendency towards the high parent. Concerning the plants of the backcross to P1 was widely distributed with a high tendency towards this parent; the same trend was noticed in the plants of the backcross to P2.

Quantitative genetic parameters obtained of TSS are presented in Table (14). The positive value of potence ratio (p) (1.40) indicated that, over dominance for TSS character towards the high parent. Positive mid-parent heterosis for TSS was estimated as 27.27 % Also, positive heterosis based on high parent 6.53 in (Table 14). These results were in partial agreement with Hussein and Selim (2014) studied The heterotic expression for TSS % the significant and highly significant values of MP heterosis ranged from 10.29 to 40.09 % and for BP heterosis ranged from 12.88 to 30.25 %. The two crosses P3 **×** P5 and P2 **×** P4 exhibited highly significant values of MP and BP heterosis (40.09 %, 30.25 % and 19.41 %, 17.37 %, respectively). Also, the cross P1 **×** P2 showed highly significant value of MP heterosis (20.38 %) and significant value of BP heterosis (12.88 %). These indicate to over-dominance of high TSS trait. While, both crosses P3 **×** P4 and P1 **×** P4 gave significantly values of MP heterosis (12.28% and 10.29%, respectively), but they had insignificantly values of BP heterosis (9.68% and 1.75%, respectively). This indicates to complete dominance towards the high TSS. It is evident from Table 14 that Percentage of TSS was found to be controlled by three pairs of genes. The estimates of Values of Broad and narrow sense heritability were in high values 88.79 % and 85.8 % respectively. The value of BSH estimates was high indicated that the minor role of environment and major role of genetics of this character; these results. These results were in agreement with Hussein and Selim (2015) found that Broad sense heritability was high (80.59 for TSS**)** according to the presence of large number of fixable additive genes regulating the inheritance of traits and the environmental effects had a minor role.

Inheritance of Total yield (TY):

Data obtained on TY trait of parental, F_1, F_{1r}, F_2, and backcross populations of the cross 2×4 are presented in Table 15**.**

It is clear from results in Table 15 that the two parents in each cross were significantly different in this trait. However, F_1 mean was higher than the highest parent and the F_2 plants were widely distributed between its two parents with transgressive segregations over the highest parent. Backcrosses plants in the two crosses were widely distributed between their two parents and the backcross to line 4(Bc2) tended to its parent, except the backcross to line 2(Bc1) which had a mean higher than its parent.

Quantitative genetic parameters obtained for TY character are presented in Table 16. The positive value of potence ratio (p) 6.23 indicated that, over dominance for TY character towards the high parent. High positive values of heterosis based on mid and-parent. These results were in agreement with Hussein and Selim (2014) found that MP hetrosis of EY ranged from -48.92 % to 35.43 %. Two out 10 hybrids P3×P4 and P3 × P5 showed highly significant of positive MP and BP heterosis. For TY, data illustrated that all crosses (10 F1s), significantly exceeded their respective MP values, suggesting the presence of dominance towards high total yield. Relative to the better parent, also, all crosses showed heterobeltiosis with average degree of heterosis values ranging from 38.40% (in cross P2×P5) to 73.42% (in hybrid P2×P3), suggesting hybrid vigor (over-dominance) for high total yield. Estimating number of genes controlling TY character was found to be 1 pair of genes. Concerning heritability, Table 16 shown that estimates of BSH and NSH for TY were 88.54 % and 80.3, respectively. These values indicated that genetics has a major role in the inheritance of this character and most of genetic variance was additive. These results were in agreement with Hussein and Selim (2015) found that Broad sense heritability was high (93.64 for TY**)** which reflected the presence of large number of fixable additive genes regulating the inheritance of traits and the environmental effects had a minor role.

Effect of the infestation with powdery mildew on the total phenols contents and total flavonoides in leaves of the melon genotypes:

Data in fig (4) showed the difference between inbred lines in total phenols and total flavonoides in leaves where, phenols is one of the main methods used by the plant to resist powdery mildew infection. It was found that, inbred (5) gave the highest value of total phenols content and there were not significant between it and inbreeds (4-6) on the other hand inbred (1) gave the lowest value of total phenols content. The same trend

was found for total flavonoides.

Table (13) Frequency distribution of Total soluble solids (TSS) of P1, P2 F1, F2, BC1 and BC2 of cross (2× 4**)**

Frequency of **(TSS)**				Generation					
				P1	P2	F1	F2	BC1	BC2
6.0					18		17		19
6.5					10		18		17
7.0							18		16
7.5							12		8
8.0							22	10	1
8.5								15	
9.0				16				17	
9.5				8.0		15		15	
10.0						17		2	
Total				24	28	32	87	59	61
Mean				9.16	6.17	9.76	7.02	8.86	6.63
Sx^-				0.049	0.046	0.045	0.079	0.073	0.070
C.V %				0.536	0.746	0.459	1.122	0.828	1.056
Mid-parent= 7.67									

Table (14) quantitative genetic parameters (TSS) in the cross (2× 4**)**

Parameter	Estimated value
Potence ratio(P)	1.40
Mid- parent heterosis %	27.27 %
high parent heterosis %	6.53%
Minimum number of genes (N)	2.34
Broad sense heritability (BSH)	88.79
Narrow sense heritability (NSH)	85.8

Table (15) Frequency distribution of Total yield of P1, P2 F1, F2, BC1 and BC2 of cross (2× 4**)**

Frequency of Total yield				**Generation**					
				P1	**P2**	**F1**	**F2**	**BC1**	**BC2**
9000					20		10		16
9600					9		19		19
10200				18			18		18
10800				9			12		8
11400							22	2	1
12000							1	15	
12600								17	
13200						11		15	
13800						19		11	
Total				27	29	30	82	60	62
Mean				2600	2296	3395	2586	3195	2450
Sx^-				13.86	13.11	13.42	23.50	22.06	20.09
C.V %				0.533	0.571	0.395	0.909	0.691	0.820
Mid-parent= 2448.3									

Table (16) quantitative genetic parameters (Total yield) in the cross (2× 4)

Parameter	Estimated value
Potence ratio(P)	6.23
Mid- parent heterosis %	38.66 %
high parent heterosis %	30.57%
Minimum number of genes (N)	0.288
Broad sense heritability (BSH)	88.54
Narrow sense heritability (NSH)	80.3

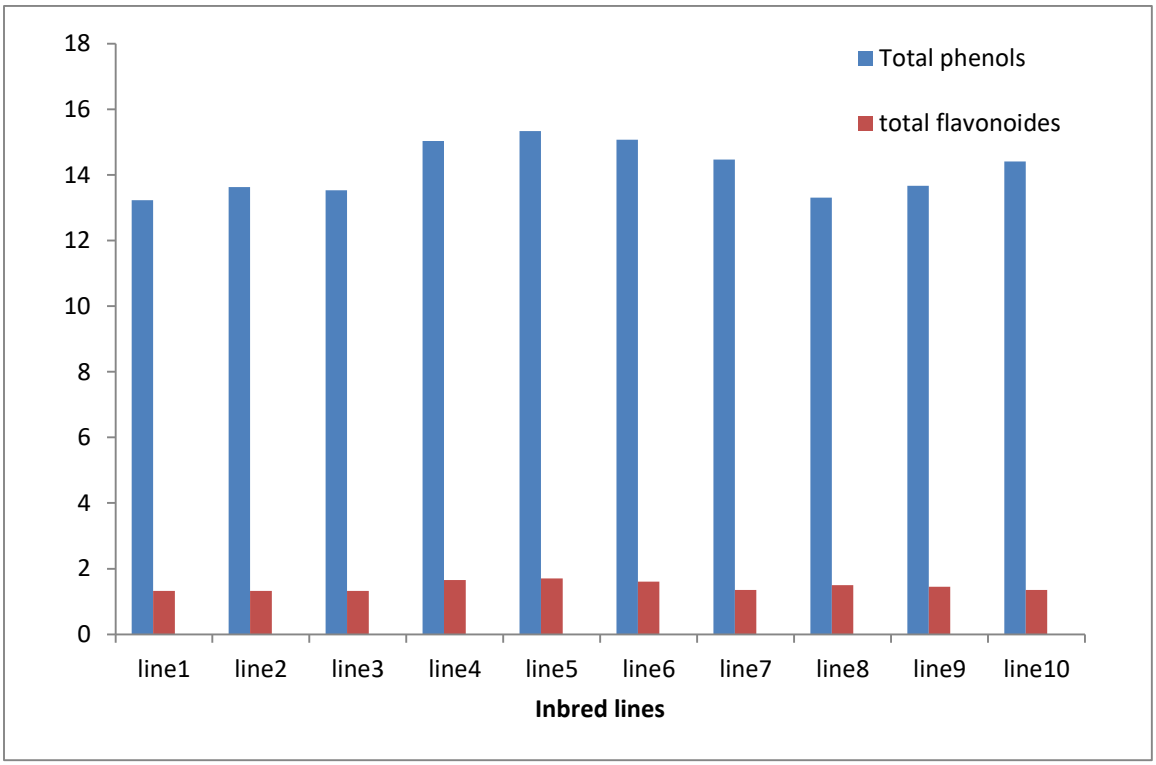

Figure (4) Total phenols contents and total flavonoids in inbred lines leaves.

CONCLUSION

It is concluded from the present study that cultivation of resistant and moderately resistant genotypes in fields highly infested with *Erysiphe cichoracearum* would help reduce powdery mildew reproduction enough to affect the residual powdery mildew population density as uninterrupted cultivation of susceptible cultivars is exacerbating the powdery mildew problem in Egypt. Furthermore, The existence of the genetic system described, which controls resistance to *(Erysiphe cichoracearum* means that inbred line (4) is a good genetic source for the development of breeding lines with resistance to powdery mildew and could be used in breeding programs to develop new hybrids resistant to the powdery mildew by transfer the resistance status of inbred liens that are resistant to the economic cultivars but require some time and effort.

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CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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