

Heterosis and Heritability Studies for Fruit Characters and Yield in Melon (*Cucumis melo*, L.)

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ABSTRACT

Five parental lines of melon (*Cucumis melo*, L.) named: (line Kooz Assal (P₁), Line Matrouh (P₂), line orange (P₃), line green (P₄) and line Ideal (P₅) obtained from the breeding program of the project of improvement the Cucurbitaceae vegetables, Horticultural Research Institute. The five genotypes were sown and crossed in the green house according to a half diallel mating system to obtain 10 F₁ hybrids combinations, and then a single F₁ plant from this initial mating was selfed to generate F₂ progeny. The hybrid vigour, heritability, inbreeding depression, number of gene pairs were valued in this study. Heterosis values were significant and positive over mid-parent and better parents in most crosses for all characters under studies, and most of dominance degrees had appeared. Most of the crosses showed high broad sense heritability for the traits of plant length, number of branches per plant, flowering date, maturity date, fruit flesh thickness, skin color, T.S.S. moisture content and vitamin C content. On the other hand the traits of plant length and fruit flesh thickness showed high narrow sense heritability. Most of the crosses exhibited inbreeding depression for the characters of plant length, maturity date, T.S.S. moisture content and vitamin C content.

Key words: *Cucumis melo*, heterosis, heritability, inbreeding depression

Introduction

Melon, (*Cucumis melo*, L.) is one of the most important economic species of the family *Cucurbitaceae*. Among the different parts of a melon plant, fruits have the highest diversity in size, form, external ornamentation, internal and external color (Kirkbride, 1993). For instance Kirkbride (1993) and Goldman (2002) reported that fruits as short as 4 cm long (*C. melo*, L. var *agrestis*) and long as 200 cm (*C. melo*, L. var. *flexuosus*) and attaining weights between 50 g and more than 15 kg. Traditional breeding methods in melon have led to a considerable varietal improvement, so melon improvement by traditional hybridization is relatively slow and limited to a restricted gene pool. It is possible to produce viable intraspecific melon hybrids between wild-type genotypes and commercial melon varieties, aiming to the transfer of some particular melon genetic traits, such as resistance to fungi, bacteria, virus, and insects; or tolerance to environmental factors (Dane, 1991). Heterosis for yield or its associated components has been reported in sweet melon and cucumber (Dhaliwal 1996, Abdalla and Aboul-Naser 2002, Christopher and Wehner 1999). The utilization of hybrid vigour in the breeding of various crops has a great practical importance. Accordingly, it is very important to increase melon yield per unit area, as well as improve the fruit traits. Several workers (Abd-El-Salam and Marie 2002, Mohammadi *et al.*, (2014), and Abou Kamer *et al.*, (2011)) had obtained sweet melon F₁ hybrids that performed better in one or more aspects than either parent.

The objectives of this study were to determine the hybrid vigour, heritability, inbreeding depression, number of gene pairs of Melon, (*Cucumis melo*, L.).

Materials and Methods

Experimental materials

The present investigation was carried out during the three successive years of 2012, 2013 and 2014 respectively. The genetic materials in this investigation were five parental lines of melon (*Cucumis melo*, L.) named: (line Kooz Assal (P₁), Line Matrouh (P₂), line orange (P₃), line green (P₄) and line Ideal (P₅) obtained from the breeding program of the project of improvement the *Cucurbitaceae* vegetables, Horticultural Research Institute. The five genotypes were sown at the first of February 2012 and crossed in the green house according to

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a half diallel mating system to obtain 10 F₁ hybrids combinations, and then at the first of august a single F₁ plant from this initial mating was selfed to generate F₂ progeny.

Experimental design and data recorded

These experiments were done at Sabaheya Horticultural Research Station, Alexandria Governorate, and Fowa area, Kafer El- Sheikh Governorate, Egypt. A randomized complete blocks design with three replicated was used in this experiment. Data were recorded on 10 plants basis from all populations for the following traits: Average plant length (cm), average number of branches per plants, flowering date (earliness), fruit maturity date, total fruit yield per plant (kg), number of fruits per plant, average fruit weight per plant (kg), placenta hardness, fruit flesh thickness, fruit shape index, fruit netting degree, skin color, fruit total soluble solids (T.S.S.), fruit moisture content, β - carotene content, Vitamin C content, Total sugars (%).

Statistical analysis

Evaluation of heterosis

The average degree of heterosis (ADH %) was calculated as percentage of increases or decreases of the F₁ performance above / under the mid parent (MP) value and the high parent (HP) value (Sinha and Khanna, 1975). Heritability in the broad sense (bs) was determined using the formula given by Falconer (1989). Narrow sense heritability (ns) was calculated using the following formula as reported by Allard (1960).

Inbreeding depression

Inbreeding depression (ID) was calculated as the difference between the F₁ and F₂ means expressed as a percentage of the F₁ according to Mather and Jinks (1971).

Results and Discussion

Heterosis for vegetative characters, flowering date and maturity date

For plant length the data in Table (1) showed that the significant positive heterosis over mid-parent and high parents for plant length in hybrids P₃×P₄ and for high parents only in hybrids P₂×P₄ and P₃×P₅. The high obtained potence ratio values for most of hybrids were in accordance with the hybrid vigor. Flowering date and maturity date characters explained significant negative heterosis in most crosses. Potence ratio values were in the same direction and negative in most of crosses these results indicate that there were over dominance toward early flowering date and maturity date.

Heterosis for yield and its components

Table (2) showed that, Heterosis values in average fruit number / plant were negative in most of crosses over mid-parent and high parent, and significant in P₁×P₅ over mid-parents and P₃×P₄ over high parent. In average fruit weight the heterosis values were negative in most crosses but not significant. Heterosis values for total yield per plant showed high positive significant values for heterosis in most of the crosses over mid-parents. Potence ratio was in accordance with the hybrid vigor hypothesis. Thingamajig and Pugalendhi (2013) showed that Heterosis breeding is a potential tool to achieve improvement in quantity, quality, and productivity of bitter gourd, which cannot be done through traditional methods. They reported that heterotic vigor over the check was exhibited by the majority of hybrids for node, on which the first female flower appeared, fruit weight, sex ratio, fruit diameter, fruit yield per vine, and number of fruit per vine. Selection based on these previous studied characters would help in identification of high-yielding lines.

Heterosis for fruit characters

Data in Table (3) showed the heterosis values for fruit characters. Heterosis values for placenta hardness were positive in most crosses over mid parents and high parent. Heterosis values in flesh thickness were positive in most crosses over mid-parents and high parent and significant in hybrids P₁×P₄, P₁×P₅ and P₂×P₅ and in P₃×P₅ over mid-parents. Same trend of these results were observed by Hatem *et al.*, (1997) in flesh thickness of melon. Fruit shape index characters explained negative and significant heterosis values in crosses P₁×P₂, P₁×P₃, P₁×P₄, P₁×P₅ and P₂×P₃, over mid-parents and high parent. In netting degree the heterosis values was positive in most hybrids and significant in crosses P₁×P₄ and P₁×P₅ over mid parents. Heterosis values for fruit skin color were

positive in most crosses over mid parents and high parent but not significant with exception of values were in $P_1 \times P_4$, $P_2 \times P_4$, $P_2 \times P_5$, $P_3 \times P_4$ and $P_3 \times P_5$ over mid-parent and in crosses $P_3 \times P_4$, $P_3 \times P_5$ and $P_4 \times P_5$ over high parents. Heterosis values for T.S.S. % were positive in most crosses over the mid parents and high parent. Similar findings were observed by Iria *et al.*, (2008).

Heterosis values for moisture content were negative in most crosses over mid parents and high parent but not significant with exception of values were in $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_2 \times P_3$ and $P_3 \times P_4$ over high parents. Potence ratio values were in the favorable direction and accordance with the hybrid vigor and negative in most crosses. These results may revealed that the hybrid vigor may go towards the direction of low moisture content these results were in accordance with found by Hatem *et al.*, (2009) and Shamel, (2013).

Heterosis for fruit chemical analysis

Heterosis values for fruit chemical analysis are presented in Table (4). for β . Carotene content were positive in most crosses over mid parents and high parent but not significant with exception of values were in $P_2 \times P_3$, $P_3 \times P_5$ and $P_4 \times P_5$ over mid-parent and in crosses $P_2 \times P_3$, $P_3 \times P_4$ and $P_4 \times P_5$ over high parents. Potence ratio values were in the favorable direction and accordance with the hybrid vigor. These results may reveal that the hybrid vigor may go towards the direction of β . Carotene content.

Heterosis values for vitamin c content were positive in some crosses over mid parents and high parent. Heterosis values for total sugars content were positive in most crosses over mid parents and high parent but not significant with exception of values were in $P_1 \times P_3$ and $P_1 \times P_5$ over mid parents and in crosses $P_1 \times P_5$ and $P_2 \times P_5$ over mid parents.

Heritability

Heritability vegetative characters, flowering date and maturity date

Heritability in the broad (bs) and narrow (ns) sense are presented in table (5). It is worth mentioning that heritability values in an important step in conducting breeding programs. For plant length character the broad sense heritability ranged from 42.92% to 93.95% and most of crosses showed high broad sense heritability values. The narrow sense heritability values ranged from 8.40% to 74.04%. Only three crosses showed high value. For number of branches per plant the broad sense heritability ranged from 15.70% to 71.43%, but the narrow sense heritability ranged from 3.39% to 55.80%. For flowering date character, the broad sense heritability ranged from 42.96% to 84.5%, all the crosses gave high and moderate values. The narrow sense heritability ranged from 5.34% to 61.11. For maturity date the broad sense heritability values for all the crosses were highest to moderate where it ranged from 40.37 to 95.75%. The cross $P_1 \times P_5$ recorded the highest narrow sense heritability 53.57% while the lowest was $P_1 \times P_2$ which recorded 3.31%. Similar results and conclusion were reported by (Fatema *et al.*, 2014).

Heritability for yield and yield components

The broad sense and narrow sense heritability for yield and yield components are presented in Table (6). For the fruit number per plant, the broad sense heritability ranged from 20.30% to 58.55% where the cross $P_1 \times P_2$ gave the highest value, while the narrow sense heritability ranged from 0.58% for the cross $P_3 \times P_5$ to 16.81% for the cross $P_1 \times P_2$. For average fruit weight per plant, all the crosses recorded low broad sense heritability except for the cross $P_1 \times P_2$ which gave high value 80.23%. The same cross gave the highest value for the narrow sense heritability but the others gave low values for the narrow sense heritability. Concerning total fruit yield per plant character, the broad sense heritability ranged from 14.74% to 66.11%, in the narrow sense heritability all the crosses recorded low narrow sense heritability. Abd El- Salam *et al.*, (2010) on snake cucumber found that heritability percentage in the broad sense was found moderate values for number of fruits/plant, yield/Fadden and fruit diameter. Ibrahim (2012) on sweet melon showed that broad sense heritability estimates among all the traits were very high (>90%), and the high heritability estimates indicate the presence of large number of fixable additive factors and hence these traits may be improved by selection. He found that high heritability associated with high genetic advance was found in the characters like fruit weight and yield per plant, and this indicated these two characters were mostly governed by additive gene action. He showed a high heritability accompanied by low genetic advance for gene action predominance which could be exploited through heterosis breeding.

Table 1: Values of heterosis (ADH %) based on the mid parents (MP) and the highest parents (HP) and potence (PR) ratio of 10F₁ crosses of sweet melon for vegetative characters, flowering date and maturity date.

Crosses	Plant length (cm)			No. of branches per plant			Flowering date (day)			Maturity date (day)		
	ADH%		PR	ADH%		PR	ADH%		PR	ADH%		PR
	MP	HP		MP	HP		MP	HP		MP	HP	
P ₁ x P ₂	12.63	12.26	38.11	10.14	0.43	-1.05	-8.28*	-16.28**	0.87	-11.67**	-11.95**	-37
P ₁ x P ₃	14.69	14.27	39.99	4.01	0.43	1.13	-15.34**	-19.77**	-2.78	-10.32**	-12.03**	-5.33
P ₁ x P ₄	10.36	10.20	69.66	-10.91	-13.98	-3.06	-11.80**	-17.44**	-1.73	0.95	-1.26	-3
P ₁ x P ₅	9.40	7.54	5.43	6.26	-6.88	0.44	-10.0**	-16.28**	-1.33	-6.29**	-6.88**	-10
P ₂ x P ₃	1.60	0.88	2.25	2.21	-3.70	0.36	-32.43**	-35.06**	-8	-3.54*	-5.66**	-1.57
P ₂ x P ₄	18.05*	17.51	37.06	-1.96	-7.62	-0.32	9.59**	6.67*	3.50	-1.57	-1.88	-5
P ₂ x P ₅	11.65	9.40	5.65	9.14	4.44	2.03	10.31**	8.11*	5	-3.11*	-3.70**	-5
P ₃ x P ₄	17.40*	17.14*	78.14	0.12	-3.70	0.03	3.95*	2.60	3	13.18**	10.69**	5.86
P ₃ x P ₅	14.88*	16.45	11.01	19.28*	7.85	1.82	-9.93**	-11.69**	-5	-4.94**	6.88**	-1.75
P ₄ x P ₅	11.15	9.43	7.08	6.51	-3.70	0.61	4.70	4.0	7	-5.33**	-5.63**	-17

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 2: Values of heterosis (ADH %) based on the mid parents (MP) and the highest parents (HP) and potence (PR) ratio of 10F₁ crosses of sweet melon for yield and yield components.

Crosses	Fruits No. pre plant			Average fruit weight (kg)			Total fruit yield per plant (kg)		
	ADH%		PR	ADH%		PR	ADH%		PR
	MP	HP		MP	HP		MP	HP	
P ₁ x P ₂	28.76	6.01	1.34	-14.87	0.71	-29.66	14.88	-17	14.88
P ₁ x P ₃	0.23	-13.20	0.01	1.99	-6.53	0.22	-2.02	-6.33	-0.44
P ₁ x P ₄	6.80	-15.77	0.94	-2.03	-20.34	-0.09	17.54	13.52	4.95
P ₁ x P ₅	46.42*	26.80	3	-1.58	-20.93	-0.06	43.33*	32.93*	5.54
P ₂ x P ₃	-12.90	-18.25	1.97	-17.96	-27.06	-1.44	-25.45*	-28.72*	-5.54
P ₂ x P ₄	-0.33	-5.36	-0.06	36.84	34.51	21.31	35.05*	29.46*	9.61
P ₂ x P ₅	5.79	-0.70	0.89	-3.04	-6.14	-0.92	1.66	-5.95	0.20
P ₃ x P ₄	-11.82	-21.14*	-1	8.36	-5.09	0.59	9.20	-1.70	0.32
P ₃ x P ₅	29.39*	26.80	14.40	-8.6	-20.55	-0.51	15.79*	2.80	1.25
P ₄ x P ₅	-0.18	-10.73	-0.01	27.15	25.17	17.17	23.31*	10.49	2.01

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 3: Values of heterosis (ADH %) based on the mid parents (MP) and the highest parents (HP) and potence (PR) ratio of 10F₁ crosses of sweet melon for fruit characteristics.

Crosses	Placenta hardness			Fruit flesh thickness%			Fruit shape index			Fruit netting degree		
	ADH%		PR	ADH%		PR	ADH%		PR	ADH%		PR
	MP	HP		MP	HP		MP	HP		MP	HP	
P ₁ x P ₂	0.05	-3.30	0.01	5.35	0.33	1.64	-22.48**	-35.01**	1.16	11.76	1.82	1.20
P ₁ x P ₃	4.55	2.04	1.85	8.49	4.07	2	-4.15	-17.53**	-0.26	8.68	1.79	0.81
P ₁ x P ₄	0.05	-3.30	0.01	10.59*	6.37	2.67	-15.87**	-31.17**	0.71	11.26*	-1.70	0.85
P ₁ x P ₅	6.21*	5.26	6.88	9.35*	3.63	1.69	-11.74*	-29.22**	-0.48	15.65*	5.36	1.60
P ₂ x P ₃	6.38*	5.26	6	3.36	2.34	3.38	-12.56*	-15.32**	-3.86	-0.90	1.79	1
P ₂ x P ₄	3.63	2.04	2.33	7.08	6.34	10.11	7.46	3.85	2.14	4.55	2.04	1.85
P ₂ x P ₅	3.63	2.04	2.33	6.79*	4.43	3	-4.57	-9.62	-0.82	5.51	3.64	3.06
P ₃ x P ₄	0.82	-1.70	0.32	-0.72	-1.01	-2.46	1.92	-4.50	0.29	3.63	2.04	2.33
P ₃ x P ₅	4.71*	2.04	1.80	8.59*	7.23	6.76	-0.98	-9.01*	-0.11	6.21	5.26	6.88
P ₄ x P ₅	-0.71	-1.70	-0.70	-3.60	-5.09	-2.30	-2.11	-4.12	-1	1.71	-1.70	0.49

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 3 Cont. : Values of heterosis (ADH %) based on the mid parents (MP) and the highest parents (HP) and potence (PR) ratio of 10F₁ crosses of sweet melon for fruit characteristics.

Crosses	Fruit skin color			T.S.S %			Moisture content %		
	ADH%		PR	ADH%		PR	ADH%		PR
	MP	HP		MP	HP		MP	HP	
P ₁ x P ₂	8.20	1.65	-1.27	10.72	2.37	1.31	-1.25	-2.34	1.12
P ₁ x P ₃	-0.05	-1.70	-0.03	12.37	3.09	1.37	-2.18	-2.73*	-3.88
P ₁ x P ₄	12.11*	3.21	1.44	8.97	1.78	1.27	-1.17	-2.89*	-0.66
P ₁ x P ₅	2.30	1.21	2.14	25.71**	15.00**	2.76	-0.52	-2.58*	-0.24
P ₂ x P ₃	6.27	-1.70	0.77	4.32	3.43	5.00	-2.91	-3.43*	-5.25
P ₂ x P ₄	13.98*	11.76	7.06	13.02*	11.79	11.90	-1.23	-1.88	-1.87
P ₂ x P ₅	11.11*	5.26	2	-6.69	-7.71	-5.71	-0.10	-1.09	-0.10
P ₃ x P ₄	16.48**	11.11*	3.41	10.07*	7.96	5.40	-1.20	-2.38*	-0.99
P ₃ x P ₅	12.32*	-16.70*	-2.34	-4.62	-4.91	-15	0.45	-1.09	0.29
P ₄ x P ₅	-6.44	-15.0**	-0.64	8.05*	5.66	3.55	2.29*	1.94	6.68

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 4: Values of heterosis (ADH %) based on the mid parents (MP) and the highest parents (HP) and potence (PR) ratio of 10F1 crosses of sweet melon for fruit chemical analysis.

Crosses	β- carotene mg/100gm(Fw)			Vitamin C mg/100 ml juice			Total sugars mg/100 ml juice		
	ADH%			ADH%			ADH%		
	MP	HP	PR	MP	HP	PR	MP	HP	PR
P ₁ x P ₂	12.35	-26.61	-0.23	-11.89	-15.80	-2.56	6.58	-2.17	0.74
P ₁ x P ₃	14.13	-13.08	0.45	20.41	-8.02	0.66	16.82*	14.12	7.15
P ₁ x P ₄	35.71	-8.06	0.75	-21.87	-33.86*	-1.21	3.06	-4.86	0.37
P ₁ x P ₅	27.47	-6.45	0.76	-4.89	-12.11	-0.60	22.14**	21.69*	60.0
P ₂ x P ₃	-60.73**	-77.22**	0.84	94.17*	43.77	2.69	0.83	-5.42	0.13
P ₂ x P ₄	-24.39	-29.55	-3.33	-7.06	-18.18	-0.52	1.09	0.46	1.75
P ₂ x P ₅	31.25	8.62	1.50	-10.29	-13.39	-2.88	-8.24	-15.48*	-0.96
P ₃ x P ₄	-62.99	-78.06*	-3.14	53.65*	9.93	1.16	1.33	-4.39	0.22
P ₃ x P ₅	38.98*	-13.50	0.64	16.95	-15.35	0.44	7.75	5.65	-3.91
P ₄ x P ₅	143.19**	113.79*	10.43	-0.82	-9.89	-0.08	8.29	0.31	1.04

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Heritability for fruit characteristics

The broad sense and narrow sense heritability for fruit characteristics are presented in Table (7). The broad sense heritability for placenta hardness ranged from 8.42 to 58.25%, the narrow sense heritability all the crosses recorded low values except for the hybrid P₁×P₂ where it showed moderate value for the narrow sense heritability. For fruit flesh thickness most of the crosses showed high broad sense heritability values (71.42 – 94.94%). While the narrow sense heritability ranged from 1.39% to 65.10%. For the fruit shape index all the crosses exhibited low values for the broad sense heritability and for narrow sense heritability.

The broad sense heritability for the fruit netting ranged from 8.69% to 67.88%. For the narrow sense heritability all the crosses recorded low narrow sense heritability. The broad sense heritability for fruit skin color ranged from 11.56% to 68.41%, Regarding to the narrow sense heritability, the results showed that, most of the crosses showed low narrow sense heritability values. For the total soluble solids content the broad sense heritability value for all the crosses. Iban *et al.*, (2007) on melon found that heritability estimates for fruit : weight , T.S.S , diameter , length and shape index were 19% , 35% , 31% , 29% and 62% respectively . Pornsuriya (2009) on oriental pickling melon showed that the estimates of broad sense heritability for fruit: length, width and shape index were 65%, 55% and 88% respectively.

Heritability for fruit chemical analysis

The broad sense and narrow sense heritability for fruit chemical analysis are presented in Table (8). For β- carotene only two crosses P₁×P₃ and P₁×P₄ showed moderate value (42.66%, 37.21%) respectively for the broad sense heritability. but for the narrow sense heritability all the crosses recorded low values. For vitamin C content trait the result showed that most crosses recorded high values for the broad sense heritability where it ranged from 54.80% to 98.26. In the other hand, for total sugars only one cross exhibited moderate value 50.71% for the broad sense heritability but the other crosses gave low values. For the narrow sense heritability all the crosses showed low values where it ranged from 0.15% to 8.38%. Similar results were reported by Mohammadi *et al.*, (2014).

Inbreeding depression

Inbreeding depression for vegetative characters, flowering date and maturity date.

Inbreeding depression for vegetative characters, flowering date and maturity date are presented in Table (5). For plant length character, all the crosses showed significant and highly significant positive values indicating inbreeding depression. No inbreeding depression was found for the number of branches per plant character, where all the values were insignificant.

For flowering date only three crosses P₁×P₂, P₂×P₃ and P₃×P₄ exhibited significant negative values indicating inbreeding depression, for maturity date the crosses P₂×P₃, P₂×P₄ and P₃×P₄ showed significant and highly significant negative values indicating inbreeding depression for these crosses.

Inbreeding depression for yield and yield components

Inbreeding depression for yield and yield components are presented in Table (6). The results showed that, no inbreeding depression was found for the yield and yield components characters i.e. fruit number per plant,

average fruit weight and total fruit yield per plant for all the evaluated crosses where all the values were insignificant for all the crosses. The same results were found by David and Wehner (1986).

Table 5: Heritability in broad sense (bs) and narrow sense (ns), inbreeding depression and number of gene pairs for the studied vegetative characters; flowering date, and maturity date.

		Plant length (cm)	No. of branches per plant	Flowering date (day)	Maturity date (day)
Cross 1 (P ₁ ×P ₂)					
Heritability%	Bs	68.16	58.26	80.43	68.13
	Ns	19.95	25.23	5.34	3.31
ID%		21.79*	17.98	-16.04*	-8.86
No. of gene		1	1	2	1
Cross 2 (P ₁ ×P ₃)					
Heritability%	Bs	60.12	71.43	64.11	56.84
	Ns	11.06	55.80	14.41	16.43
ID%		15.55**	17.85	-13.66	-15.67
No. of gene		1	1	1	5
Cross 3(P ₁ ×P ₄)					
Heritability%	Bs	69.91	28.57	78.94	67.78
	Ns	50.72	3.64	6.36	15.09
ID%		14.55**	25	-3.25*	2.34
No. of gene		1	1	1	1
Cross 4(P ₁ ×P ₅)					
Heritability%	Bs	93.95	37.67	61.80	95.75
	Ns	69.11	5.45	8.47	53.57
ID%		20.82**	6.66	-6.88	-19.10
No. of gene		1	1	3	1
Cross 5(P ₂ ×P ₃)					
Heritability%	Bs	52.01	19.66	76.50	89.79
	Ns	12.59	3.39	13.57	20.33
ID%		3.42**	7.41	-14.95*	-29.45**
No. of gene		1	1	1	1

Table 5 cont.

		Plant length (cm)	No. of branches per plant	Flowering date (day)	Maturity date (day)
Cross 6 (P ₂ ×P ₄)					
Heritability%	Bs	80.86	50	70.73	68.10
	Ns	74.04	9.09	21.83	31.68
ID%		25.06**	-12.50	-3.02	-3.21*
No. of gene		1	1	1	1
Cross 7 (P ₂ ×P ₅)					
Heritability%	Bs	87.22	22.23	84.5	83.95
	Ns	23.91	4.63	61.11	34.56
ID%		23.15**	8.33	5*	0.0
No. of gene		1	1	1	1
Cross 8(P ₃ ×P ₄)					
Heritability%	Bs	42.92	26.67	82.79	82.11
	Ns	12.23	7.27	31.82	15.23
ID%		21.12**	7.41	-2.95*	-4.41*
No. of gene		1	1	1	1
Cross 9(P ₃ ×P ₅)					
Heritability%	Bs	93.17	27.21	42.96	40.37
	Ns	25.13	7.69	13.56	12.12
ID%		12.61**	21.43	-18.0	-12.44
No. of gene		1	1	1	28
Cross 10 (P ₄ ×P ₅)					
Heritability%	Bs	87.62	15.70	56.91	66.15
	Ns	8.40	3.58	34.75	10.42
ID%		10.55**	15.32	2.12	-5.70
No. of gene		1	1	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Inbreeding depression for fruit characteristics

Inbreeding depression for fruit characteristics is presented in Table (7). For placenta hardness there was no inbreeding depression for this character. The crosses P₁×P₄, P₁×P₅, P₂×P₄, P₂×P₅ and P₃×P₅ showed highly significant positive values for fruit flesh thickness indicating inbreeding depression, No inbreeding depression was detected for the fruit shape index character where all the crosses showed insignificant values. For netting degree, only the cross P₁×P₂ showed significant positive value indicating inbreeding depression in this hybrid.

No inbreeding depression was detected for the skin color character where all the crosses exhibited insignificant values. Regarding results are in agreement with those found by Abd-El-Hadi *et al.*,(2005).

For total soluble solids only one cross P₂xP₅ showed highly significant value indicating inbreeding depression. For moisture content only the two crosses P₁xP₃ and P₂xP₄ recorded highly significant negative values but the crosses P₁xP₂, P₁xP₄, P₁xP₅, and P₃xP₅ showed significant positive values indicating inbreeding depression.

Table 6: Heritability in broad sense (bs) and narrow sense (ns), inbreeding depression and number of gene pairs for yield and yield components

		Fruits No. per Plant	Average fruit weight (kg)	Total fruit yield per plant (kg)
Cross 1 (P ₁ xP ₂)				
Heritability%	Bs	58.55	80.23	66.11
	Ns	16.81	65.41	18.88
ID%		27.77	9.0	34.89
No. of gene		2	4	1
Cross 2 (P ₁ xP ₃)				
Heritability%	Bs	37.59	10.63	18.51
	Ns	0.91	0.47	2.54
ID%		0.0	18.50	19.47
No. of gene		1	1	1
Cross 3 (P ₁ xP ₄)				
Heritability%	Bs	31.17	21.51	23.86
	Ns	10.38	6.26	7.24
ID%		12.5	15.56	37.86
No. of gene		1	1	1
Cross 4 (P ₁ xP ₅)				
Heritability%	Bs	31.71	8.38	20.90
	Ns	3.45	0.27	1.25
ID%		31.58	7.86	34.99
No. of gene		1	6	1
Cross 5 (P ₂ xP ₃)				
Heritability%	Bs	41.57	22.53	22.71
	Ns	4.55	2.36	6.76
ID%		6.67	-10.28	3.30
No. of gene		1	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 6. Cont.

		Fruits No. per Plant	Average fruit weight (kg)	Total fruit yield per plant (kg)
Cross 6 (P ₂ xP ₄)				
Heritability%	Bs	42.71	29.17	24.6
	Ns	0.89	0.36	2.23
ID%		40	-8	38.92
No. of gene		1	1	1
Cross 7 (P ₂ xP ₅)				
Heritability%	Bs	24.02	17.84	44.95
	Ns	5.77	0.47	4.52
ID%		17.65	-41.35	-12.75
No. of gene		1	1	1
Cross 8 (P ₃ xP ₄)				
Heritability%	Bs	20.30	13.94	55.75
	Ns	3.77	1.44	34.15
ID%		12.50	15.81	37.76
No. of gene		1	1	1
Cross 9 (P ₃ xP ₅)				
Heritability%	Bs	38.78	6.56	14.74
	Ns	0.58	0.09	0.91
ID%		15.79	11.01	27.24
No. of gene		1	3	1
Cross 10 (P ₄ xP ₅)				
Heritability%	Bs	34.13	13.46	18.43
	Ns	12.50	1.90	2.58
ID%		17.65	-15.53	4.38
No. of gene		1	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 7: Heritability in broad sense (bs) and narrow sense (ns) , inbreeding depression and number of gene pairs for fruit characteristics.

		Placenta hardness	Fruit flesh thickness %	Fruit shape index	Fruit netting degree	Fruit skin color	T.S.S %	Moisture content %
Cross 1 (P ₁ xP ₂)								
Heritability%	Bs	58.25	73.64	94.95	67.88	68.41	35.45	82.63
	Ns	41.74	53.81	16.50	19.44	22.11	2.94	5.52
ID%		0.0	-4.38**	-22.40	10.71	-1.69	4.09	0.17*
No. of gene		1	1	11	1	2	20	1
Cross 2(P ₁ xP ₃)								
Heritability%	Bs	36.0	90.23	8.36	57.67	53.13	35.91	66.11
	Ns	16.67	53.29	0.07	5.71	35.58	8.19	28.19
ID%		0.0	2.94	2.09	7.14*	-1.69	2.88	-0.64**
No. of gene		1	1	1	2	1	1	1
Cross 3 (P ₁ xP ₄)								
Heritability%	Bs	11.02	86.97	6.34	8.67	55.43	65.08	77.31
	Ns	1.92	36.99	0.02	0.96	2.59	15.10	58.70
ID%		-3.44	1.34**	4.38	1.69	13.33	-3.73	3.18*
No. of gene		1	1	12	8	1	1	1
Cross 4 (P ₁ xP ₅)								
Heritability%	Bs	14.55	91.31	6.50	44.21	60.83	56.29	61.13
	Ns	0.98	65.10	0.13	21.70	7.84	13.36	14.70
ID%		3.33	5.08**	3.50	3.39	6.67	6.82	2.04*
No. of gene		1	1	39	2	1	1	2
Cross 5 (P ₂ xP ₃)								
Heritability%	Bs	8.42	41.86	6.93	44.54	53.48	72.38	85.31
	Ns	0.98	1.39	0.17	7.41	3.85	19.84	19.03
ID%		0.0	-2.27**	-8.90	6.67	8.47	-6.74	-0.43
No. of gene		1	1	1	1	1	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 7. Cont.

		Placenta hardness	Fruit flesh thickness %	Fruit shape index	Fruit netting degree	Fruit skin color	T.S.S %	Moisture content %
Cross 6 (P ₂ xP ₄)								
Heritability%	Bs	16.65	71.42	8.04	22.95	43.19	32.79	20.22
	Ns	1.96	62.08	0.11	7.84	3.28	12.35	0.09
ID%		3.33	0.89**	4.32	3.33	5.26	4.58	-21.63**
No. of gene		1	1	1	1	1	1	1
Cross 7 (P ₂ xP ₅)								
Heritability%	Bs	28.86	94.94	6.24	29.34	37.95	81.39	81.47
	Ns	0.98	25.47	0.09	8.93	7.84	14.85	61.38
ID%		3.33	0.29**	-9.19	-1.72	3.33	0.25**	-1.03
No. of gene		1	1	2	1	1	1	1
Cross 8 (P ₃ xP ₄)								
Heritability%	Bs	39.84	88.80	6.62	30.32	53.46	55.45	92.95
	Ns	1.92	23.39	0.20	9.80	29.31	1.14	7
ID%		5.08	-5.13**	9.40	1.67	5	11.45	-0.02
No. of gene		1	1	1	16	2	1	1
Cross 9 (P ₃ xP ₅)								
Heritability%	Bs	16.65	90.85	6.02	24.36	11.56	49.49	56.45
	Ns	1.96	11.53	2.5	0.96	1.84	29.63	8.68
ID%		3.33	12.53**	-4.62	10	8	-11.15	1.73*
No. of gene		1	1	13	1	1	1	12
Cross 10 (P ₄ xP ₅)								
Heritability%	Bs	44.05	62.05	6.07	41.44	50.81	57.20	63.93
	Ns	0.96	19.97	0.06	18.87	8.82	36.94	23.26
ID%		3.39	0.37	-23.57	3.39	15	5.91	0.85
No. of gene		1	1	1	1	1	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Inbreeding depression for fruit chemical analysis.

Inbreeding depression for fruit chemical analysis is presented in Table (8). For β- carotene, the results showed that all the crosses exhibited insignificant values indicating no inbreeding depression for this trait. For vitamin C content the crosses P₁xP₃, P₁xP₅, P₂xP₄, P₂xP₅, P₃xP₄, and P₄xP₅ showed significant and highly significant with positive values indicating inbreeding depression, on the other hand, the crosses P₁xP₂, P₁xP₄, P₂xP₃, and P₃xP₅ exhibited highly significant negative values indicating no inbreeding depression. For total

sugars content all the crosses showed insignificant values indicating that no inbreeding depression was observed for this character.

Table 8: Heritability in broad sense (bs) and narrow sense (ns), inbreeding depression and number of gene pairs for fruit chemical analysis.

		β - carotene mg/100gm (Fw)	Vitamin C mg/100 ml juice	Total sugars mg/100 ml juice
Cross 1 (P ₁ xP ₂)				
Heritability%	Bs	13.16	89.74	21.22
	Ns	1.53	14.42	2.48
ID%		-24.31	-21.63**	-4.01
No. of gene		3	1	1
Cross 2 (P ₁ xP ₃)				
Heritability%	Bs	42.66	90.62	21.94
	Ns	0.47	41.01	3.83
ID%		-51.85	16.29*	8.51
No. of gene		1	1	1
Cross 3 (P ₁ xP ₄)				
Heritability%	Bs	37.21	54.80	6.92
	Ns	0.16	8.85	0.15
ID%		-0.29	-34.65**	-9.76
No. of gene		1	1	1
Cross 4 (P ₁ xP ₅)				
Heritability%	Bs	15.73	91.77	24.33
	Ns	3.75	10.19	5.24
ID%		29.60	25.24**	-10.12
No. of gene		1	1	1
Cross 5 (P ₂ xP ₃)				
Heritability%	Bs	8.63	98.26	23.94
	Ns	0.90	28.74	8.10
ID%		34.88	-8.16**	-7.10
No. of gene		4	1	1

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Table 8. Cont.

		β - carotene mg/100gm (Fw)	Vitamin C mg/100 ml juice	Total sugars mg/100 ml juice
Cross 6 (P ₂ xP ₄)				
Heritability%	Bs	8.90	66.88	17.47
	Ns	0.79	5.23	4.86
ID%		-61.24	10.65**	0.31
No. of gene		1	1	1
Cross 7 (P ₂ xP ₅)				
Heritability%	Bs	13.18	83.78	50.71
	Ns	1.28	28.31	8.38
ID%		-95.14	6.94**	-2.07
No. of gene		1	1	1
Cross 8 (P ₃ xP ₄)				
Heritability%	Bs	7.42	91.74	16.99
	Ns	0.11	27.53	0.45
ID%		11.09	17.64**	10.22
No. of gene		10	1	1
Cross 9 (P ₃ xP ₅)				
Heritability%	Bs	14.04	88.87	22.21
	Ns	1.70	20.02	7.26
ID%		19.94	-18.09**	-5.18
No. of gene		5	1	1
Cross 10 (P ₄ xP ₅)				
Heritability%	Bs	10.80	73.89	19.66
	Ns	1.04	47.90	4.80
ID%		48.52	31.58**	3.32
No. of gene		1	1	3

** Significant and highly significant at the 0.05 and 0.01 level of probability, respectively

Number of gene pairs

For vegetative characters, flowering date and maturity date.

Number of gene pairs for vegetative characters, flowering date and maturity date are presented in Table (5). Vegetative characters i.e., plant length and number of branches per plant were controlled by one pair of

gene, indicating that the environmental effects on these traits was low and the improvement by selection through the early generation would be effective. Concerning flowering date it was found to be controlled by one to three groups of dominant gene pairs. For maturity date the results showed that one to five groups of dominant gene pairs were controlled this trait.

Number of gene pairs for yield and yield components

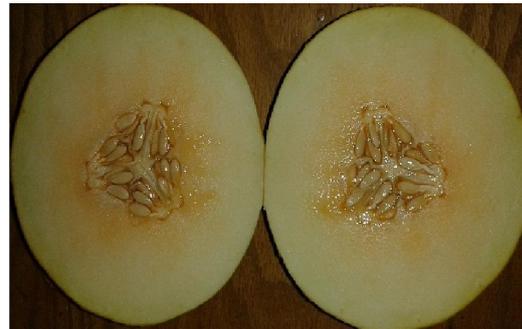
Number of gene pairs for yield and yield components date are presented in Table (6). For fruit number per plant and total fruit yield, the results showed that these traits were controlled by one gene pair, while the average fruit weight character controlled by one to four groups of dominant gene pairs.

Number of gene pairs for fruit characteristics

Number of gene pairs for fruit characteristics are presented in Table (7). Concerning placenta hardness and fruit flesh thickness, few groups of dominant genes were found to be controlled these traits. Concerning fruit shape index and fruit netting degree it was clear that the environmental influence were high where they found to be controlled by one to thirteen groups of dominant gene pairs and one to sixteen groups of dominant gene pairs, respectively. These results indicated that the improvement by selection through the early generation would be not effective. The skin color was found to be controlled by one to fifteen groups of dominant gene pairs. On the other hand, the total soluble solids were found to be controlled by one to twenty groups of gene pairs. Concerning the moisture content character it was found to be controlled by one to twelve groups of gene pairs. These results are in harmony with those obtained by Monforte *et al.*, (2005).

Number of gene pairs for fruit chemical analysis

Number of gene pairs for fruit chemical analysis is presented in Table (8). β - Carotene content found to be controlled by one to ten groups of dominant gene pairs. The vitamin C content was found to be controlled by one pair of gene. On the other hand, the total sugars were found to be controlled by one to three groups of gene pairs. Similar findings were observed by Ibrahim (2007).



F1 (P1xP2): fruit weight (0.850) kg, T.S.S. (14.6) %, days to maturity (68), orange flesh, total yield/plant (2.473) kg.



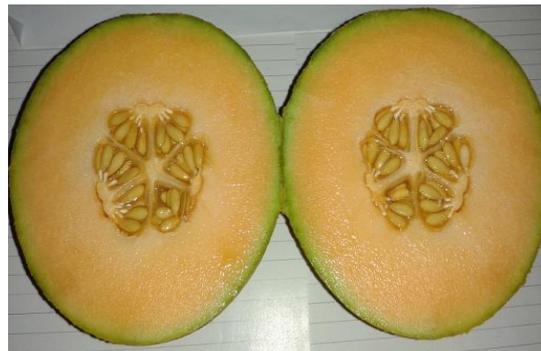
F1 (P1xP5): fruit weight (0.930) kg, T.S.S. (16.8) %, days to maturity (74), orange flesh, total yield/plant (2.900) kg.



F1 (P2xP4): fruit weight (1.029) kg, T.S.S. (16.0) %, days to maturity (78), green flesh, total yield/plant (3.000) kg.



F1 (P3xP4): fruit weight (0.970) kg, T.S.S. (15.7) %, days to maturity (87), green flesh, total yield/plant (2.600) kg.



F1 (P4xP5): fruit weight (0.925) kg, T.S.S. (15.5) %, days to maturity (76), orange flesh, total yield/plant (2.550) kg.

Conclusion

In conclusion, the high heritability indicated that the characters were less influenced by environment demonstrating either this were simply inherited characters governed by a few major genes or additive gene effect therefore, selection of these characters would be more effective. On the other hand, the lower heritability indicated low influence of the additive genetic variance and a large influence of the environmental effect, suggesting that selection based on early selective generation would be not relatively effective for these studied traits. This work confirmed that it is possible to produce new melon hybrids under the Egyptian conditions which can competitive with the foreign hybrids, meet the needs of farmers and reduce a lot of money annually spend to buy the foreign hybrids.

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