Original Research Article

Heterosis and combining ability of melon genotypes of *momordica* group.

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ABSTRACT

The objective of this study was to estimate, through partial diallel cross, the combinatorial capacity of melon genotypes of the *momordica* group and the expression of heterosis in the hybrids obtained for the characters: mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR), fruit internal cavity (FIC) and mean pulp thickness (MPT). Forty-one treatments (26 Hybrids and 15 parents) were evaluated in a randomized complete block design with four replications, conducted in a greenhouse at the Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil, between February and June 2015. The results showed the importance of the additive and non-additive genes effects, with a greater participation of additive gene action in the control of most characters. In accordance with estimation of the general combining ability – GCA, the genitors G-03, G-11, G-14, G-16 and G-18 were the ones that presented the best results for MFM, MFL, MFD and MPT. The effect of the specific combining ability – SCA was important in controlling the majority of the characters, in 30.7% of the hybrid combinations and in 15 of them the heterosis was positive for MFM, MFL, MFD and MPT. The genotypes presented good productivity, thick pulp and satisfactory fruit size and can be used in breeding programs to obtain superior genotypes.

Key words: Cucumis melo L., partial diallel, hydroponics, productivity.

1. INTRODUCTION

The melon (*Cucumis melo* L.) has different botanical groups (*inodorus, cantalupensis, conomom, dudaim, flexuosus* and *momordica*) [1]. Among these, melons of the *momordica* group, in Brazil known by several common names (melon papoco, snow melon, caxi, melon vitamin and etc). It is native to India, where it is widely cultivated and commonly called "phut", which means 'to divide', because the cracks on the ripe fruit, they still present a low percentage of soluble solids, which cause their fruits to be consumed "*in natura*" accompanied by sugar, honey or other sweeteners, besides being used in the preparation of juices, salads and pickles when ripe or cooked when immature, as well as sources of vitamin C, iron and calcium [2, 3, 4, 5].

In addition to the culinary attributes, melons from *momordica* group have been used as a source for resistance to fungal and viral diseases, nematodes and insects, among them *Fusarium oxysporium*, *Podosphaera xanthii*, *Meloidogyne incognita*, PRSV (Papaya Ring Spot Vírus) [5], *Liriomyza trifolii* Burgess and *Aphis gossypii* [6] and *Myrothecium roridum* [7] and also tolerant to drought, soil salinity and high temperature [8].

The choice of good genitors is of fundamental importance for the success of an improvement program. Among the most efficient and commonly used methodologies for this purpose are diallel crossing, which provides estimates of genetic parameters, useful for the selection of genitors to be used in hybridization and in the understanding of the gene action involved in determining the characters and existence of heterosis [9].

Griffing [11] is one of the main methods used, this method provides information on the general combining ability (GCA), associated with concentration of predominantly additive genes, and the specific combining ability (SCA) associated with gene concentration with non-additive effect (dominance and epistasis) [10]. The difficulty of evaluating a large number of genitors in complete diallels stimulated adaptations to be suggested, among them that of partial diallels. These adaptations involve the evaluation of genitors arranged in two groups, belonging or not to a common set, and the inferences made for each group [9].

In view of the above, the present work had the objective of estimating the combinatorial and heterosis capacity manifested in experimental hybrids of melon genotypes of the *momordica* group obtained from partial diallel cross, in order to identify promising hybrid combinations.

2. MATERIAL AND METHODS

The experiment was conducted between February and June of 2015 in the Department of Agronomy of the Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil. Previously, crossbreed between 15 melon genotypes of the *momordica* group were performed according to the partial diallel scheme 2x13. The genotypes were selected according to the genetic variability presented for the traits considered and were derived from data collected in different places in Brazil (Table 1) [2, 3].

Table 1. Genomes of *C. melo* (*momordica* group) with their respective identifications and provenances. Recife, Brazil, 2015.

Genomes	Provenances	
Grupo I		
G-09	Serra Talhada -PE	Fazenda Saco/IPA
G-24	Chapadinha-Ma	
Grupo II		
G-01	São José do Egito-PE	
G-03	Triunfo – PE	
G-04	Petrolina - PE	
G-07	Lagoa de Itaenga - PE	
G-08	Serra Talhada - PE	Açude Cachoeira
G-11	Floresta – PE	Riacho do Navio
G-12	Arcoverde - PE	
G-13	Buíque – PE	
G-14	Belo Jardim - PE	
G-15	Mocambinho - MG	
G-16	Juazeiro - BA	
G-17	Jeremoabo - BA	
G-18	Santa Tereza do Oeste - PR	

The seedlings were obtained by indirect sowing in plastic trays containing 128 cells, filled with coconut shell powder. Plants were individually transplanted 13 days after sowing to plastic vessels, with a capacity of 5 liters, filled with the coconut shell powder and spaced in 1.2 x 0.5 x 0.6 meters.

The plants were cultivated in hydroponics, in a greenhouse, adopting cultural treatments such as pruning, fruit thinning and staking. The pruning was performed after the appearance of the fifth leaf, and nipping on the third, elimination of the tertiary buds until the eighth leaf and conduction with only two secondary stems. The tertiary branches that appeared after the eighth leaf were pruned after the second. During fruiting, fruit thinning was performed, leaving only two fruits per plant and in different tertiary branches in order to reduce the competition between them, favoring their development and higher quality for harvesting. The plants were vertically staked with twisted nylon thread and the fruits protected with mesh bags or raschel bags (nets).

Mineral nutrition and water requirement of the plants were supplied through a balanced nutrient solution at each stage of plant development, through a drip irrigation system controlled automatically by a digital timer. A total of 41 treatments (Hybrids and genitors) were used in the randomized block design with four replications and four plants per plot, where the following characteristics were evaluated: mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR), internal fruit cavity (FIC) and mean pulp thickness (MPT).

The data were submitted to analysis of variance and the means grouped by the Scott-Knott test (p<0.05). Diallel analysis was performed according to Griffing's Model 1, method 2, adapted for partial diallels including genitors [11, 12]. Estimates of the heterosis relative to the genitors' mean (Hr) were obtained by the equations H = [F1 / (P1 + P2 / 2)] and Hr = H / P1 + P2 x100 for each F1 hybrid combination. The analyzes were performed using the GENES program [13].

3. RESULTS AND DISCUSSION

The treatments' average squares were significant (p <0.05) for all evaluated traits (Table 2), which was already expected, since the choice of the genitors was based on the genetic variability presented by them [2]. Thus, the treatments' average squares were differentiated in general (GCA) and specific (SCA) combining ability effects, according to method 2, model 2 [11].

Table 2. Average squares of the partial diallel analysis for mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR), mean pulp thickness (MPT) and fruit internal cavity (FIC) in melon genotypes of the *momordica* group. Recife, Brazil, 2015.

Sources of variation	GL	MFM (kg)	MFL (cm)	MFD (cm)	LDR	MPT (cm)	FIC (cm)
Genotypes	40	0.229**	21.526**	4.928**	0.155**	0.241**	1.231**
Groups	1	1.121**	7.501^{ns}	13.157^{ns}	0.340*	1.151**	1.987**
GCA group I	1	0.010ns	56.688*	1.597*	0.203ns	0.095^{ns}	0.001^{ns}
GCA group II	12	0.359**	27.060**	8.029*	0.196**	0.264**	2.396**
SCA I x II	26	0.144*	18.159**	3.308**	0.123**	0.201**	0.712**
Residue	120	0.085	8.959	1.754	0.067	0.197	0.286

^{ns} Not significant at 5% level of probability following F test.

* Significant at 5% level of probability following F test.

The effects of SCA and GCA of groups I and II were significant (p <0.05) for the characters mean fruit length (MFL) and mean fruit diameter (MFD) (Table 2). This significance for both combining abilities shows the importance of additive and non-additive gene effects as causes of the genetic variation observed for MFL and MFD [14]. However, the averages squares of group II's GCA were significant and magnitudes higher than the SCA for all the traits, which indicates a greater participation of the additive gene action in their control. On the other hand, for the genitors of group I, only the traits MFL and MFD presented significant values, which indicates that the genitors of groups I and II are quite divergent and that the action of the additive gene effects are able to influence the expression of these characters (Table 2).

In regards of SCA, there were significant differences for all the studied traits, which show that the existence of genetic differences in these characters is due to the non-additive gene effects (Table 2). Non-additive gene effects can be exploited to obtain promising hybrid combinations, since dominance interaction favors the generation of superior hybrids, especially those from genitors with favorable GCA effects [15].

Concerning the GCA effects of the 15 genotypes, group I and II, for MFM, MFL, MFD and MPT, positive values were observed in five of them (G-03, G-11, G-14, G-16 and G-18), indicating that these genotypes are superior to the others with respect to the average performance of crosses for the most important traits, unlike others that presented negative values of GCA for most of the investigated traits (Table 3).

Table 3. Estimates of the general combining ability of groups I and II and specific combining ability of 26 hybrid combinations resulting from partial diallel cross between melon genotypes of the *momordica* group. Recife, Brazil, 2015.

Genotypes	Traits[1]					
	MFM (kg)	MFL (cm)	MFD (cm)	LDR	MPT (cm)	FIC (cm)
General combining ability (group I)						
G-09	0.009	0.646	0.108	0.039	-0.026	-0.003
G-24	-0.009	-0.646	-0.108	-0.039	0.026	0.003
General combining ability (group II)						
G-01	-0.012	-0.501	-0.1932	-0.015	0.002	-0.088
G-03	0.087	0.459	0.9079	-0.126	0.091	0.111
G-04	-0.033	-0.290	-0.1040	-0.003	-0.046	-0.293
G-07	-0.271	-1.683	-1.4070	0.202	-0.257	-0.824
G-08	0.069	-0.060	0.1019	-0.041	0.042	0.125
G-11	0.035	0.073	0.1202	-0.027	0.141	0.058
G-12	-0.090	-0.232	-0.3713	0.057	-0.088	-0.145
G-13	-0.102	-1.903	-0.2512	-0.117	-0.062	-0.061
G-14	0.105	1.572	0.1444	0.101	0.093	0.193
G-15	-0.076	-0.476	-0.1260	-0.019	-0.029	0.068
G-16	0.065	1.174	0.0565	0.080	0.037	0.081
G-17	-0.008	0.363	0.1949	-0.021	-0.028	0.287
G-18	0.228	1.504	0.9269	-0.069	0.104	0.489
Specific combining ability						
H-09x01	0.209	0.828	0.380	-0.025	0.063	0.179
H-09x03	-0.004	-0.022	1.936	-0.204	0.036	-0.095
H-09x04	0.273	4.395	1.390	0.101	0.245	0.637
H-09x07	0.119	1.945	0.470	0.013	0.138	0.423
H-09x08	-0.028	0.040	0.087	-0.029	0.092	-0.069
H-09x11	-0.313	-2.833	-1.487	0.077	-0.320	-0.627
H-09x12	0.009	-1.711	-0.135	-0.132	0.064	0.056
H-09x13	-0.105	-0.542	-0.560	0.065	-0.149	-0.049
H-09x14	-0.347	-1.290	-1.056	0.109	-0.282	-0.232
H-09x15	-0.087	-0.547	-0.268	-0.008	-0.032	-0.082
H-09x16	-0.144	-1.074	0.030	-0.117	-0.057	-0.400
H-09x17	0.207	2.680	0.472	0.099	0.268	0.250
H-09x18	0.178	-1.487	0.237	-0.186	-0.160	0.027
H-24x01	-0.241	-2.416	-0.777	-0.040	0.300	-0.563
H-24x03	0.027	-0.378	-0.063	-0.049	-0.097	0.608
H-24x04	-0.171	-1.209	-0.861	0.080	-0.213	0.192
H-24x07	-0.189	-2.864	-0.733	-0.132	-0.150	-0.522

H-24x08	0.036	0.299	0.146	-0.004	0.021	-0.251
H-24x11	0.104	0.053	0.743	-0.141	-0.022	0.457
H-24x12	0.024	1.323	-0.149	0.149	0.009	0.146
H-24x13	0.222	1.126	1.491	-0.196	0.431	0.764
H-24x14	0.401	1.949	1.579	-0.174	0.484	0.566
H-24x15	0.080	1.468	-0.001	0.121	-0.100	-0.129
H-24x16	0.130	0.397	0.462	-0.073	0.165	0.105
H-24x17	0.085	4.621	-0.637	0.553	-0.015	-0.606
H-24x18	-0.077	-0.423	0.666	-0.131	-0.068	0.075

[1]Mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR), mean pulp thickness (MPT) and fruit internal cavity (FIC).

High values, positive or negative for a given genitor indicate a higher concentration of favorable alleles to increase or reduce the mean, when compared to the other genitors [9], that means that when the objective is to increase the mean of a trait it is used a genitor with a high and positive GCA, on the other hand, when the lowest mean of the trait is the objective, genitors with high and negative GCA are used. Thus, in the selection of populations, it is sought those crosses that present a high average and that at least one of the genitors have a high absolute value of GCA [16].

As for the signs of SCA estimates, both positive and negative values were observed in all the traits, highlighting the existence of bidirectional dominance deviations regulated by genes that increase the expression of the trait and by those that reduce it. However, about 30.7% of the hybrid combinations presented good complementation for the traits MFM, MFL, MFD and MPT, with positive SCA estimates. When the estimated values are high, positive or negative, there is an indication that the genitor is superior or inferior to the other genitors of the diallel [9].

In relation to the SCA, from the 30.7% of combinations with positive values, only 37.5% presented at least one genitor with high GCA (Table 3). This result can be explained by the fact that GCA does not depend only on the loci in heterozygosis, but also on the number of loci fixed with favorable alleles. Therefore, the ratio of loci in favorable homozygosis in relation to loci with unfavorable homozygosis is important in the estimation of SCA, since it represents a deviation from the mean [17].

The SCA has an important value, together with the GCA of one of the genitors when the objective is the exploitation of hybrids, because it is directly related to heterosis, associated to the non-additive effects of the genes, being a function of the crossing and the trait being considered [18, 19]. In this sense, heterosis was positive for MFM, MFL, MFD and MPT in 15 hybrid combinations, about 57.7%. And among those hybrid combinations with positive values of SCA, heterosis was positive in all of them (Table 3).

The mean values for MFM were higher in 69.2% of the hybrid combinations, of which 88.8% presented positive heterosis for this trait. In this group the means varied from 1.5 to 2.1 kg.fruit-1 among hybrids and from 1.5 to 1.8 kg.fruit-1 among the genotypes, the means of eight of them did not differ from the means of the hybrids. These results were superior to those report by reported by other authors [20], which obtained fruits with MFM ranging from 0.5 to 1.9 kg [5], between 0.18 and 1.4 kg [21], between 0.7 and 1.2 kg, and [22], between 0.2 and 1.5 kg per plant, both in soil cultivation.

For the LDR trait, both positive and negative heterosis values were observed, and in 69% of the hybrid combinations heterosis was negative. However, because it is a trait related to the shape of the fruit, the results obtained can be considered in two ways, when the objective is to obtain fruits of more spherical shape, the genotypes with the means close to the unit should be chosen, on the other hand, in order to obtain more elongated fruits, these values must exceed the unit. Fruits with ratio ≤ 1.0 are classified as spherical and those with ratio between 1.0 - 1.5 are rather oval shaped. Fruits with ratio > 1.5 are classified as long [23].

The LDR means of 26.9% of the hybrids were concentrated between 2.6 and 3.0 and did not differ from seven of the 15 genitors used. On the other hand, the means of 27 genotypes, including around 53% of the genitors whose means were concentrated between 2.42 and 2.53 and 73% of the hybrids with means between 2.22 and 2.57, did not show statistical difference (Table 4). Variation for this trait were reported by other authors [2, 3, 24].

Table 4. Mean of the genitors, f_1 hybrids and heterosis relative to genitor means (Hr) for f_1 hybrids for mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR), mean pulp thickness (MPT) and fruit internal cavity (FIC). Recife, Brazil, 2015.

	Traits[1]											
Genotypes	MFM (kg)	Hr	MFL (cm)	Hr	MFD (cm)	Hr	LDR	Hr	MPT (cm)	Hr	FIC (cm)	Hr
G-01	1.45 b		29.43 b		11.08 b		2.65 a		2.26 b		6.07 b	
G-03	1.62 a		30.75 a		12.15 a		2.55 b		2.65 a		6.02 b	
G-04	1.34 b		27.46 b		10.80 b		2.53 b		2.33 b		5.05 d	
G-07	0.95 b		26.73 b		8.59 b		3.11 a		1.93 b		4.46 d	
G-08	1.59 a		29.34 b		11.36 b		2.59 b		2.46 b		6.46 b	
G-11	1.63 a		31.17 a		11.88 a		2.63 b		2.89 a		6.26 b	
G-12	1,26 b		29,36 b		10,67 b		2,76 a		2,22 b		5,66 c	
G-13	1,19 b		25,54 b		10,30 b		2,48 b		2,17 b		5,58 c	
G-14	1,64 a		32,45 a		11,30 b		2,89 a		2,52 b		6,27 b	
G-15	1,31 b		28,22 b		11,15 b		2,56 b		2,44 b		6,30 b	
G-16	1,59 a		32,32 a		11,14 b		2,91 a		2,46 b		6,36 b	
G-17	1,30 b		26,71 b		11,74 a		2,28 b		2,25 b		6,81 a	
G-18	1,86 a		33,60 a		12,67 a		2,67 a		2,76 a		6,98 a	
G-09	1,79 a		31,52 a		11,79 a		2,68 a		2,74 a		6,45 b	
G-24	1,53 a		27,16 b		11,17 b		2,42 b		2,43 b		6,05 b	
H-09x01	1,81 a	11,92	31,00 a	1,73	12,09 a	5,72	2,57 b	-3,77	2,63 a	5,20	6,35 b	1,40
H-09x03	1,70 a	-0,35	31,11 a	-0,09	14,75 a	23,21	2,28 b	-12,55	2,69 a	-0,11	6,27 b	0,62
H-09x04	1,86 a	18,59	34,78 a	17,93	13,19 a	16,80	2,70 a	3,35	2,76 a	9,08	6,60 a	14,77
H-09x07	1,47 b	6,86	30,94 a	6,21	10,97 b	7,64	2,82 a	-2,61	2,45 b	4,80	5,85 c	7,39
H-09x08	1,66 a	-1,98	30,65 a	0,72	12,09 a	4,48	2,54 b	-3,67	2,70 a	3,75	6,31 b	-2,23
H-09x11	1,34 b	-21,78	27,91 b	-10,95	10,54 b	-10,98	2,66 a	0,08	2,39 b	-15,22	5,69 c	-10,47
H-09x12	1,54 a	0,62	28,73 b	-5,63	11,40 b	1.49	2.53 b	-6.87	2.54 b	2.40	6.17 b	1.83
H-09x13	1.41 b	-5.56	28.23 b	-1.06	11.09 b	0.42	2.55 b	-1.07	2.35 b	-4.12	6.15 b	2.25
H-09x14	1.37 b	-19.88	30.96 a	-3.22	10.99 b	-4.78	2.82 a	1.20	2.38 b	-9.66	6.22 b	-2.27
H-09x15	1.45 b	-6.23	29.65 b	-0.74	11.51 b	0.34	2.58 b	-1.47	2.50 b	-3.38	6.24 b	-2.04
H-09x16	1.54 a	-9.13	30.77 a	-3.60	11.99 a	4.59	2.57 b	-8.01	2.54 b	-2.06	5.94 b	-7.32
H-09x17	1.82 a	17.67	33.72 a	15.80	12.57 a	6.83	2.68 a	8.16	2.80 a	12.32	6.79 a	2.49
H-09x18	2.02 a	10.73	30.69 a	-5.74	13.07 a	6.84	2.35 b	-12.12	2.51 b	-8.73	6.77 a	0.86
H-24x01	1.35 b	-9.52	26.47 b	-6.46	10.72 b	-3.68	2.47 b	-2.56	2.92 a	24.62	5.61 c	-7.42
H-24x03	1.71 a	8.94	29.46 b	1.76	12.53 a	7.48	2.35 b	-4.89	2.61 a	2.90	6.98 a	15.69
H-24x04	1.40 b	-2.62	27.88 b	2.10	10.72 b	-2.38	2.61 b	4.70	2.36 b	-0.78	6.16 b	10.98
H-24x07	1.14 b	-7.96	24.84 b	-7.82	9.55 b	-3.36	2.60 b	-6.14	2.21 b	1.54	4.91 d	-6.42
H-24x08	1.71 a	9.31	29.62 b	4.85	11.93 a	5.96	2.48 b	-0.84	2.68 a	9.66	6.13 b	-1.94
H-24x11	1.74 a	10.08	29.51 b	1.18	12.55 a	8.89	2.36 b	-6.55	2.74 a	2.96	6.78 a	10.16
H-24x12	1.54 a	9.98	30.47 a	7.83	11.17 b	2.27	2.73 a	5.56	2.54 b	9.21	6.26 b	6.94
H-24x13	1.72 a	26.37	28.61 b	8.57	12.93 a	20.41	2.22 b	-9.70	2.99 a	29.92	6.96 a	19.85
H-24x14	2.11 a	32.95	32.90 a	10.40	13.41 a	19.38	2.46 b	-7.50	3.19 a	29.14	7.02 a	13.95
H-24x15	1.60 a	13.06	30.37 a	9.69	11.56 b	3.58	2.63 b	5.67	2.49 b	2.22	6.20 b	0.45
H-24x16	1.80 a	15.01	30.95 a	4.08	12.20 a	9.43	2.54 b	-4.84	2.82 a	15.49	6.45 b	3.89
H-24x17	1.68 a	18.79	34.37 a	27.59	11.24 b	-1.84	3.06 a	30.05	2.57 b	10.00	5.94 b	-7.55
H-24x18	1.75 a	3.28	30.46 a	0.29	13.28 a	11.40	2.33 b	-8.58	2.65 a	2.37	6.82 a	4.77

[1]Means followed by the same letters in the columns do not differ significantly from one another by the Scott-Knott test at 5% probability.

The LDR evaluation alone is not interesting, because genotypes that produce small fruits may have an LDR considered to be ideal, which may result in erroneous classification of fruit size. Thus, the measures of length and average diameter of the fruit as well as LDR are essential for this distinction and the means and values of heterosis can be analyzed from two perspectives, since it is possible to select genotypes of different shapes and sizes.

For the MFD trait the means were about 53.8% higher of the hybrid combinations, whose values were between 11.93 and 14.74 cm, however, they would not differ from the means of accesses G-03, G-09, G- 11, G-17, G-18 and G-19 with values between 11.74 and 12.67 cm. Similar performance was observed for the MFL trait, where 57.69% of the hybrid combinations showed means between 30.37 and 34.78 cm and did not differ from the accesses G-03, G-09, G-11, G-14, G-17 and G-18 with means ranging from 30.37 to 34.78 cm (Table 4). Fruits with lengths between 12.1 and 40.7 cm for genotypes collected in India were reported [21] and of 12.9 to 25.4 cm for accesses collected in northeastern Brazil [20].

For MPT the means were superior in 50% of the hybrid combinations and did not differ from 26,6% of the accesses. The means for MPT ranged from 2.62 to 2.98 cm in the hybrids and from 2.64 to 2.88 cm in the genitors (Table 4). Because it is a raw material for the preparation of juices, ice creams and even for consumption "*in natura*" the thickness of pulp must be the largest possible, however, when reaching the point of maturation, the texture of the pulp gains characteristic farinaceous, brittle and easily melts, and has a low soluble solids content [3]. However, the protection of fruits with bag in raschel mesh favored the maintenance of the structure of the fruit, even with the occurrence of burst fruits, maintaining the quality of the pulp [24].

For FIC, the variation in the formation of the groups was greater in relation to the other traits, where only three hybrid combinations presented the lowest means, between 5.60 and 5.68 cm, not differing from the G-12 and G-13 accesses with means of 5.66 and 5.57 cm respectively (Table 2). Heterosis was positive in 61.5% of the hybrid combinations, however heterosis negative for this trait is interesting, since the internal cavity of the fruit should be the smallest possible, to give the fruit resistance to handling and transportation, preventing the displacement of the placenta, a fact that anticipates the degradation of the fruit and also prolonging the post-harvest life, small internal cavity and greater pulp thickness are characteristics of the melon fruit that make it more valued and accepted by the market [23].

4. CONCLUSION

The results showed the importance of the additive and non-additive genes effects, with a greater participation of additive gene action in the control of most characters. In accordance with estimation of the general combining ability – GCA, the genitors G-03, G-11, G-14, G-16 and G-18 were the ones that presented the best results for MFM, MFL, MFD and MPT. The effect of the specific combining ability – SCA was important in controlling the majority of the characters, in 30.7% of the hybrid combinations and in 15 of them the heterosis was positive for MFM, MFL, MFD and MPT. The genotypes presented good productivity, thick pulp and satisfactory fruit size and can be used in breeding programs to obtain superior genotypes.

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