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3 **Heterosis and combinatorial capacity of melon**

4 **genotypes of *momordica* group.**

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8 **ABSTRACT**

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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, 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.

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

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13 **1. INTRODUCTION**

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

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

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

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

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

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## 44 2. MATERIAL AND METHODS

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

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

Genomes	Provenances
<b>Grupo I</b>	
G-09	Serra Talhada -PE Fazenda Saco/IPA
G-24	Chapadinha-Ma
<b>Grupo II</b>	
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

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55 The seedlings were obtained by indirect sowing in plastic trays containing 128 cells, filled  
56 with coconut shell powder. Plants were individually transplanted 13 days after sowing to  
57 plastic vessels, with a capacity of 5 liters, filled with the coconut shell powder and spaced in  
58 1.2 x 0.5 x 0.6 meters.

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

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

75 The data were submitted to analysis of variance and the means grouped by the Scott-Knott  
76 test ( $p < 0.05$ ). Diallel analysis was performed according to Griffing's Model 1, method 2,  
77 adapted for partial diallels including genitors [11, 12]. Estimates of the heterosis relative to  
78 the genitors' mean ( $H_r$ ) were obtained by the equations  $H = [F1 / (P1 + P2 / 2)]$  and  $H_r = H /$   
79  $P1 + P2 \times 100$  for each F1 hybrid combination. The analyzes were performed using the  
80 GENES program [13].

81

### 82 3. RESULTS AND DISCUSSION

83 The treatments' average squares were significant ( $p < 0.05$ ) for all **evaluated** traits (Table 2),  
84 which was already expected, since the choice of the genitors was based on the genetic  
85 variability presented by them [2]. Thus, the treatments' average squares were differentiated  
86 in general (GCA) and specific (SCA) combining ability effects, according to method 2, model  
87 2 [11].

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

Sources of variation	GL	MFM (kg)	MFL (cm)	MFD (cm)	LDR	MPT (cm)	FIC (cm)
<b>Genotypes</b>	40	0.229**	21.526**	4.928**	0.155**	0.241**	1.231**
<b>Groups</b>	1	1.121**	7.501 <sup>ns</sup>	13.157 <sup>ns</sup>	0.340*	1.151**	1.987**
<b>GCA group I</b>	1	0.010 <sup>ns</sup>	56.688*	1.597*	0.203 <sup>ns</sup>	0.095 <sup>ns</sup>	0.001 <sup>ns</sup>
<b>GCA group II</b>	12	0.359**	27.060**	8.029*	0.196**	0.264**	2.396**
<b>SCA I x II</b>	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

92 <sup>ns</sup> Not significant at 5% level of probability following F test.

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

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

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

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

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

Genotypes	Traits <sup>1</sup>					
	MFM (kg)	MFL (cm)	MFD (cm)	LDR	MPT (cm)	FIC (cm)
<b>General combining ability (group I)</b>						
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
<b>General combining ability (group II)</b>						
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
<b>Specific combining ability</b>						
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

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118 <sup>1</sup>Mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit length/diameter ratio (LDR),  
119 mean pulp thickness (MPT) and fruit internal cavity (FIC).

120

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

128 As for the signs of SCA estimates, both positive and negative values were observed in all  
129 the traits, highlighting the existence of bidirectional dominance deviations regulated by  
130 genes that increase the expression of the trait and by those that reduce it. However, about  
131 30.7% of the hybrid combinations presented good complementation for the traits MFM, MFL,  
132 MFD and MPT, with positive SCA estimates. When the estimated values are high, positive  
133 or negative, there is an indication that the genitor is superior or inferior to the other genitors  
134 of the diallel [17].

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

141 The SCA has an important value, together with the GCA of one of the genitors when the  
142 objective is the exploitation of hybrids, because it is directly related to heterosis, associated  
143 to the non-additive effects of the genes, being a function of the crossing and the trait being  
144 considered [18, 19]. In this sense, heterosis was positive for MFM, MFL, MFD and MPT in  
145 15 hybrid combinations, about 57.7%. And among those hybrid combinations with positive  
146 values of SCA, heterosis was positive in all of them (Table 3).

147 The mean values for MFM were higher in 69.2% of the hybrid combinations, of which 88.8%  
148 presented positive heterosis for this trait. In this group the means varied from 1.5 to 2.1

149 kg.fruit-1 among hybrids and from 1.5 to 1.8 kg.fruit-1 among the genotypes, the means of  
 150 eight of them did not differ from the means of the hybrids. These results were superior to  
 151 those report by reported by other authors [20], which obtained fruits with MFM ranging from  
 152 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  
 153 0.2 and 1.5 kg per plant, both in soil cultivation.

154 For the LDR trait, both positive and negative heterosis values were observed, and in 69% of  
 155 the hybrid combinations heterosis was negative. However, because it is a trait related to the  
 156 shape of the fruit, the results obtained can be considered in two ways, when the objective is  
 157 to obtain fruits of more spherical shape, the genotypes with the means close to the unit  
 158 should be chosen, on the other hand, in order to obtain more elongated fruits, these values  
 159 must exceed the unit.

160 The LDR means of 26.9% of the hybrids were concentrated between 2.6 and 3.0 and did not  
 161 differ from seven of the 15 genitors used. On the other hand, the means of 27 genotypes,  
 162 including around 53% of the genitors whose means were concentrated between 2.42 and  
 163 2.53 and 73% of the hybrids with means between 2.22 and 2.57, did not show statistical  
 164 difference (Table 4).

165 **Table 4.** Mean of the genitors,  $f_1$  hybrids and heterosis relative to genitor means (Hr) for  $f_1$   
 166 hybrids for mean fruit mass (MFM), mean fruit length (MFL), mean fruit diameter (MFD), fruit  
 167 length/diameter ratio (LDR), mean pulp thickness (MPT) and fruit internal cavity (FIC).  
 168 Recife, Brazil, 2015.  
 169

Genotypes	Traits <sup>1</sup>											
	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

170 <sup>1</sup>Means followed by the same letters in the columns do not differ significantly from one another by the Scott-Knott  
171 test at 5% probability.

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

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

185 For MPT the means were superior in 50% of the hybrid combinations and did not differ from  
186 26,6% of the accesses. The means for MPT ranged from 2.62 to 2.98 cm in the hybrids and  
187 from 2.64 to 2.88 cm in the genitors (Table 4). Because it is a raw material for the  
188 preparation of juices, ice creams and even for consumption "*in natura*" the thickness of pulp  
189 must be the largest possible, however, when reaching the point of maturation, the texture of  
190 the pulp gains characteristic farinaceous, brittle and easily melts, and has a low soluble  
191 solids content [3]. However, the protection of fruits with bag in raschel mesh favored the  
192 maintenance of the structure of the fruit, even with the occurrence of burst fruits, maintaining  
193 the quality of the pulp.

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

#### 203 4. CONCLUSION

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

213 **5. REFERENCES**

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