

Watermelon general and specific combining ability

Tiago Lima do Nascimento^{1*}, Flávio de França Souza²,
Rita de Cassia Souza Dias², Edson Ferreira da Silva¹

¹Rural Federal University of Pernambuco, Recife, Brazil

²Brazilian Agricultural Research Corporation, Petrolina, Brazil

*Corresponding author, e-mail: tiago_lim.a@hotmail.com

Abstract

The combining ability of six watermelon genotypes was estimated in a diallel cross scheme (6x6), including genotypes JNY (1), 'ORA' (2), 'KOD' (3), 'SOL' (4), 'CHG' (5), 'PEA' (6) and all possible hybrids between them. A randomized complete block design (RCB) was used, with 36 treatments, three blocks, and plots with five plants. The following traits were evaluated: days before female flower anthesis, main branch length, fruit mass, number of fruits per plant, yield, fruit length, fruit width, pulp firmness, soluble solids content, average rind thickness, seed length, seed width, and seed mass. The data obtained were submitted to analysis of variance, and a diallel analysis was performed according to Griffing's experimental method I. According to the general combining ability estimates obtained, genotypes 'KOD' (3) and 'JNY' (1) were the most likely ones to produce hybrids with smaller-sized fruits and smaller seeds. The reciprocal effects confirmed that the results indicate that these genotypes should be used as pollen donors and pollen recipients, respectively. On the other hand, genotypes 'ORA' (2) and 'CHG' (5) can be used for the commercial exploitation of sliced watermelons. According to the specific combining ability estimates obtained, the combinations 'ORA' (2) x 'PEA' (6), 'ORA' (2) x 'JNY' (1), 'CHG' (5) x 'KOD' (3), 'PEA' (6) x 'KOD' (3), and 'CHG' (5) x 'SOL' (4) stood out as being the genotypes most likely to produce the smallest fruits and smallest seeds.

Keywords: Diallel analysis, *Citrullus lanatus*, plant breeding

Introduction

Watermelon [*Citrullus lanatus* (thunb.) Matsum & Nakai] has great social and economic importance (RAMOS et al., 2012) owing to its wide use in the Brazilian diet, its nutritional properties, easy consumption and low caloric content (Gama & VIZA, 2008). The 2015 Brazilian watermelon production was 2,119,599 t, with 97,910 ha of cultivated crops (IBGE, 2016). However, such production can be even higher if new genotypes with different fruit patterns are developed in order to meet the new market requirements (Souza, 2008).

The market demand in Brazil is for smaller fruits for easier transportation, domestic storage,

targeted especially at families with few members. However, the main cultivars commercialized in the country were developed from 'Crimson Sweet', a genotype with fruit mass greater than 10 kg (Nascimento et al., 2018), which provides consumers with fewer options for choice. This demand can be met with the development of new commercial genotypes in breeding programs, using the genetic diversity of local varieties and Germplasm Active Banks (GABs).

Important watermelon diversity sources of local varieties maintained in traditional agriculture were reported by Nantoumé et al. (2012) and Nantoumé et al. (2013). In terms of Germplasm Active Banks (GABs), accessions

Received: 21 June 2017
Accepted: 21 November 2018

with important genetic diversity sources were reported by Adjoumani et al. (2016), Gama et al. (2013) and Gbotto et al. (2016). However, to use such genetic resources, a better understanding of genotypes is necessary as regards their main agronomic traits available for the attainment of greater efficiency in the choice of parents and the use of the most adequate breeding techniques (Souza et al. 2013).

In watermelon crops, the ability to combine potential parents is one of the most important information, which also allows identifying the most suitable parents for the transmission of desirable characters in commercial hybrids.

Studies on the combining ability of different crops have been carried out, such as beans (Rocha et al., 2014), onion (Santos et al., 2015), maize (Barreto et al., 2012), carrot (Carvalho et al., 2014), among others, which have generated important information for the development of commercial hybrids. As regards watermelon crops specifically, studies were conducted by Adjoumani et al. (2016), Singh et al. (2009), Piovesan (2012), Souza et al. (2013)

and Sapovadiya et al. (2014).

In view of the above, this paper aimed to estimate the combining ability of watermelon genotypes in order to identify promising parents for the development of new commercial cultivars with smaller-sized fruits and smaller seeds in breeding programs.

Material and methods

The hybrid seeds of the study were obtained from the experimental field of Embrapa Semiárido, located in the irrigated perimeter of the Bebedouro irrigation project, in the municipality of Petrolina, PE, Brazil (9°7'56" S/40°17'59.57" W), between January and March 2015, using controlled hand pollination (CHP) according to the method used by Gama et al. (2015).

The six parents 'JNY' (1), 'ORA' (2), 'KOD' (3), 'SOL' (4), 'CHG' (5) and 'PEA' (6), the 15 F₁ hybrids, interpopulations and their reciprocals, originated from all possible combinations between parents (Table 1), were evaluated in the same experimental field of Embrapa Semiárido between April and August 2016.

Table 1. Origin and main traits of the watermelon genotypes under analysis

Genotypes	Origin	Main traits
'JNY' (1)	Netherlands – NED	Early cycle, prolific, round fruits, striped, red pulp, high soluble solids content, and very small seeds.
'ORA' (2)	United States – EUA	Late cycle, little prolific, round fruits, striped, orange pulp, high soluble solids content, and large seeds.
'KOD' (3)	Japan – JPN	Early cycle, prolific, round fruits, striped, light yellow pulp, high soluble solids content, and small seeds.
'SOL' (4)	Brazil – BRA	Very early cycle, prolific, round fruits, striped, canary-yellow pulp, high soluble solids content, and medium-size seeds.
'CHG' (5)	United States – EUA	Late cycle, little prolific, long fruits, no stripes, rosy pulp, high soluble solids content, and large seeds.
'PEA' (6)	United States – EUA	Late cycle, little prolific, oblong fruits, no stripes, medium red pulp, high soluble solids content, and medium-size seeds.

The seeds were sown in polyethylene trays on May 9, 2016, and the seedlings were transplanted to the field 15 days after sowing. A randomized block design (RBD) with three replications was used. Each plot consisted of a row with five plants, and spaces of 2.5 m between rows and 1.0 m between plants. Drip irrigation was used, and daily water supply was applied according to the crop needs and

climatic conditions, monitored by a weather station located near the experimental area.

Fertilization drew on soil analysis and as recommended by Mendes et al. (2010), with a basal fertilizer containing 30 kg ha⁻¹ of N, 80 kg ha⁻¹ of P₂O₅, and 30 kg ha⁻¹ of K₂O, plus 15 kg ha⁻¹ of zinc sulphate and 10 kg ha⁻¹ of copper sulphate. Top-dressing fertilizer was applied via irrigation water, using 50 kg ha⁻¹ of N of calcium nitrate and

40 kg ha⁻¹ of K₂O (potassium sulphate), applied up to 50 and 60 days after sowing, respectively. Phytosanitary treatments were carried out by applying agrochemicals suitable for the crop and registered by the Brazilian Ministry of Agriculture, Livestock, and Supply, and weed management was performed by hand weeding.

Each genotype was evaluated for the following traits: Days until the first female flower anthesis, main branch length, fruit mass, number of fruits per plant, yield, fruit length, fruit width, pulp firmness, soluble solids content (°Brix), rind thickness, seed length, seed width, and seed mass.

Analyses of variance were performed for the data of each of the evaluated characters, following this model:

$$Y_{ij} = \mu + T_i + B_j + e_{ij}$$

Where: Y_{ij} is the observation of the i-th treatment of the j-th block; μ is the effect of the overall mean; T_i is the effect of the i-th treatment; B_j is the effect of the j-th block; and e_{ij} is the effect of the experimental error.

The effects of the general and specific combining abilities of the parents were estimated

using the method proposed by Griffing (1956) for analysis of diallel with parents, F1 hybrids and F1 reciprocals, (Method I), considering the effect of treatments as fixed. The analysis of variance of the diallel was performed according to the scheme presented by Cruz et al. (2012) using the model:

$$Y_i = \mu + g_i + g_j + s_{ij} + r_{ij} + \varepsilon_{ij}$$

Where: Y_{ij} is the mean of the hybrid (i≠j) or of the parent (i=j); μ is the overall mean of the diallel; g_i and g_j are the effects of the general combining ability of the i-th or the j-th parent; s_{ij} is the effect of the specific combining ability for the cross between the i and j order parents; r_{ij} is the reciprocal effect that measures the differences produced by parent i or j when used as a pollen donor or recipient, and ε_{ij} is the experimental error. The analyses were conducted with the aid of the GENES software (Cruz, 2013).

Results and discussion

Significant differences between the treatments were observed for all the traits evaluated, thus evincing the existence of genetic variability among the treatments (Table 2).

Table 2. Summary of the analysis of variance of the cross between watermelon parents.

Traits ⁽²⁾	Mean squares ⁽¹⁾							
	Average	Maximum	Minimum	CV (%)	FV	Blocks	Treatments	Residues
					DF	2	35	70
FFA (days)	44.19	54.00	33.00	2.3	0.528	27.417**	1.061	
MBL (m)	2.17	2.81	1.58	5.2	0.026	3.648**	0.013	
FM (kg)	5.20	8.22	2.15	14.0	3.484	0.111**	0.532	
NF/P (unit)	2.20	4.00	1.00	19.2	0.210	0.516**	0.178	
YD (t/ha)	45.29	91.61	16.24	21.7	1693.105	273.211**	96.507	
FL (cm)	27.80	39.17	19.17	4.8	11.442	70.009**	1.785	
FW (cm)	20.93	24.87	16.53	5.0	10.864	5.829**	1.098	
PF (%)	453.42	926.30	256.46	12.2	1624.712	45202.108**	3063.016	
SSC (°Brix)	9.97	12.73	7.73	5.5	1.769	1.958**	0.296	
ART (cm)	0.98	1.27	0.58	6.0	0.021	0.047**	0.003	
SL (mm)	8.48	12.40	5.60	2.5	0.107	9.481**	0.046	
SW (mm)	5.31	8.05	3.50	2.8	0.007	4.330**	0.022	
SM (mg)	43.24	100.00	20.00	9.1	28.704	1200.926**	15.370	

⁽¹⁾ ns = Not significant; *, ** Significant, at the 1% and 5% significance level, respectively, by the F test; CV = Coefficient of variation; SV = Sources of variation; DF = Degree of freedom;

⁽²⁾ FFA = Days before female flower anthesis; MBL = Main branch length; FM = Fruit mass; NF/P = Number of fruits per plant; YD = Yield; FL = Fruit length; FW = Fruit width; PF = Pulp firmness; SSC = Soluble solids content; ART = Average rind thickness; SL = Seed length; SW = Seed width; and SM = Seed mass.

The coefficients of variation (CV) for most of the evaluated characters were low, lower than 10.0%, which evidenced high experimental precision and homogeneity within the plots of

parents and hybrids (Table 2). The characters of fruit mass, number of fruits per plant, and pulp firmness exhibited medium coefficient of variation, lower than 20.0%, which demonstrates

good experimental precision. Only the yield character showed a high CV value. Tavares et al. (2018), when evaluating this same character in watermelon genotypes, obtained a CV higher than 20%, and a similar result was obtained by Nascimento et al. (2018). These results show that because it is a polygenic trait and with a strong environmental influence, this value can be considered normal.

Significant differences were observed for the effects of the general combining ability (GCA) as well as the effects of the specific combining ability (SCA), for all the characters, except for the soluble solids content for SCA (Table 3), which showed that the additive and non-additive gene interaction occurred simultaneously in the control

of the traits evaluated. These results are partially in agreement with those reported by Bahari et al. (2012), who worked with four pure lines of watermelon. However, in the present study the analysis of quadratic components (Table 3) showed that the control of the characters 'days before female flower anthesis', number of fruits per plant, yield, and seed mass was due to the prevalence of non-additive effects over additive ones; however, the opposite occurred for fruit mass, length and width, pulp firmness, rind thickness, seed length and seed width. For the main branch length, in turn, the quadratic components for GCA and SCA were the same, which showed simultaneous additive and non-additive action controlling the trait.

Table 3. Mean squares and quadratic components of the general and specific combining ability and reciprocal effects of watermelon characters.

Traits ⁽²⁾	Mean squares ⁽¹⁾					Quadratic components		
	VF	GCA	SCA	RE	Residue	GCA	SCA	RE
	DF	5	15	15	70			
FFA (days)		98.767*	14.817*	16.233*	1.061	2.714	4.585	2.529
MBL (m)		0.160*	0.025**	0.179*	0.013	0.004	0.004	0.028
FM (kg)		19.840*	0.978**	0.919ns	0.532	0.536	0.149	0.065
NF/P (unit)		0.445**	0.944*	0.111ns	0.178	0.007	0.255	-0.011
YD (t/ha)		790.756*	230.644*	143.263ns	96.507	19.285	44.712	7.793
FL (cm)		457.707*	7.709*	3.078ns	1.785	12.665	1.975	0.215
FW (cm)		27.118*	2.613*	1.949*	1.098	0.723	0.505	0.142
PF (%)		211106.588*	11402.250*	23700.473*	3063.016	5778.988	2779.745	3439.576
SSC (°Brix)		9.025*	0.512ns	1.049*	0.296	0.242	0.072	0.126
ART (cm)		0.271*	0.012*	0.006*	0.003	0.007	0.003	0.000
SL (mm)		51.332*	3.965*	1.047*	0.046	1.425	1.306	0.167
SW (mm)		23.391*	1.938*	0.368*	0.022	0.649	0.639	0.058
SM (mg)		6198.519*	597.099*	138.889*	15.370	171.754	193.909	20.586

⁽¹⁾ ns = Not significant; *, ** Significant, at the 1% and 5% significance level, respectively, by the F test; CV = Coefficient of variation; SV = Sources of variation; DF = Degree of freedom; ⁽²⁾ FFA = Days before female flower anthesis; MBL = Main branch length; FM = Fruit mass; NF/P = Number of fruits per plant; YD = Yield; FL = Fruit length; FW = Fruit width; PF = Pulp firmness; SSC = Soluble solids content; ART = Average rind thickness; SL = Seed length; SW = Seed width; and SM = Seed mass.

Regarding the SCA, no significant differences were found for soluble solids content, indicating that the GCA for this character, although negative in some parents, when combined, allelic complementation occurred, which favored the increase of the soluble solids content in the hybrid combinations thus pointing to the action of additive effects controlling the trait. These results differ from those presented by Barros et al. (2011) and Gvozdanovic-Varga et al. (2011), in which the occurrence of non-additive effects controlling the soluble solids content was reported. Such a contrast can be explained by the genetic difference between the genotypes studied or due to the interaction genotype x

environment.

There were significant reciprocal effects (RE) at a 5% significance level among the parents in relation to days before female flower anthesis, main branch length, fruit width, pulp firmness, soluble solids content, rind thickness, seed length, seed width, and seed mass (Table 3), which allowed suggesting that for the genetic control of these traits, extrachromosomal inheritance or maternal effects were involved. Ferreira et al. (2002) corroborate similar results, where significant differences were found for male flower anthesis and soluble solids content, except for the number of fruits per plant, which did not show reciprocal effects. The genetic interaction of RE

is of great importance for breeding programs aimed at the development of hybrids because it allows determining which parents should be used either as pollen donors or pollen recipients.

Table 4 shows the estimates of the general combining ability of the parents. Genotype 'JNY' (1) showed negative values for the character 'days before female flower anthesis', fruit mass, yield, fruit length, soluble solids content, rind thickness, seed length and seed mass, and positive effects for number of fruits per plant, fruit width, and pulp firmness, suggesting that the parent when recombined contributed to the development of early, productive hybrids

and fruits with lower weight and shorter length, and smaller-sized seeds, showing potential for use in genetic breeding programs aimed at the development of genotypes with smaller fruits and with smaller seeds.

Parent 'ORA' (2) showed negative effects for the character 'days before the female flower anthesis', number of fruits per plant, fruit length, pulp firmness, soluble solids content, and positive effects for fruit mass, yield, fruit width, rind thickness, seed length, seed width and seed mass, indicating the parent's contribution to obtain genotypes with heavier productive fruits, with a thicker rind, and larger and heavier seeds.

Table 4. Estimates of the general combining ability effects on watermelon parents

General combining ability ⁽²⁾	Traits ⁽¹⁾												
	FFA (days)	MBL (m)	FM (kg)	NF/P (unit)	YD (t/ha)	FL (cm)	FW (cm)	PF (%)	SSC (°Brix)	ART (cm)	SL (mm)	SW (mm)	SM (mg)
'JNY' (1)	-0.222	-0.049	-0.599	0.097	-0.001	-2.680	0.118	132.051	-0.104	0.001	-1.921	-1.305	-18.796
'ORA' (2)	-0.139	-0.010	0.124	-0.114	2.499	-0.801	0.941	-3.624	-0.255	0.038	1.233	0.799	13.981
'KOD' (3)	0.389	-0.083	-1.014	0.089	-8.037	-3.014	-1.387	-37.760	-0.299	-0.157	-0.855	-0.546	-9.074
'SOL' (4)	-2.861	0.095	-0.069	0.061	-1.083	-1.671	0.857	-91.907	0.254	-0.028	0.305	0.155	1.759
'CHG' (5)	0.611	-0.013	1.038	-0.164	6.130	6.377	-0.449	-30.972	-0.484	0.072	1.023	0.749	14.815
'PEA' (6)	2.222	0.061	0.520	0.031	0.493	1.789	-0.080	32.213	0.888	0.076	0.215	0.147	-2.685
DP ($\hat{\sigma}_j$)	0.157	0.017	0.111	0.064	1.495	0.203	0.159	8.420	0.083	0.009	0.033	0.023	0.596

⁽¹⁾ FFA = Days before female flower anthesis; MBL = Main branch length; FM = Fruit mass; NF/P = Number of fruits per plant; YD = Yield; FL = Fruit length; FW = Fruit width; PF = Pulp firmness; SSC = Soluble solids content; ART = Average rind thickness; SL = Seed length; SW = Seed width; and SM = Seed mass. ⁽²⁾ SD ($\hat{\sigma}_j$) = Standard deviation of the effects of the parents.

Parent 'KOD' (3) showed a positive GCA value for number of fruits per plant, and negative values for fruit mass, fruit length, fruit width, rind thickness, seed length, seed width and seed mass, suggesting that this parent contributes to the development of hybrids with lower fruit mass and smaller size, with thinner rind, smaller seeds and less mass, evidencing their potential for use in breeding programs that aim to obtain cultivars that meet the consumers' demand for smaller fruits.

Parent 'SOL' (4) presented negative GCA effects for 'days before for female flower anthesis', fruit mass, yield, fruit length, pulp firmness and rind thickness, and positive values for number of fruits per plant, fruit width, soluble solids content, seed length, seed width and seed mass, pointing to the contribution of this parent to the development of hybrids with early, prolific, less productive plants with lighter fruits of shorter length, greater width and with soft pulp, thinner rind and larger and heavier seeds.

This parent can be used in breeding programs for the development of intermediate fruit size genotypes.

Parent 'CHG' (5) presented positive GCA effect for 'days before for female flower anthesis', fruit mass, yield, fruit length, rind thickness, seed length, seed width and seed mass, and negative effects for number of fruits per plant, fruit width, pulp firmness and soluble solids content, which indicated the contribution of this parent in the development of late hybrids with greater fruit mass, with a reduced number of fruits per plant, greater yield, longer fruits but with reduced width, soft pulp, less sweet fruits, thicker rind, larger and heavier seeds. Souza et al. (2013), when studying the combining ability of that same genotype, found results partially divergent from those found in the present study, as genotype 'CHG' (5) showed a positive general combining ability for fruit width and soluble solids content. Therefore, the authors suggested the use of this genotype in breeding programs for the development of large

fruits, given the expanded demand for sliced watermelon in supermarkets, open fairs and greengrocers.

Parent PEA (6) showed positive GCA values (Table 4) for days before female flower anthesis, fruit mass, number of fruits per plant, yield, fruit length, pulp firmness, soluble solids content, rind thickness, seed length, seed width and seed mass, and negative values for fruit width, indicating that this genotype, when recombined, contributed to the development of late hybrids, with extensive, prolific, long branch length, with great fruit mass, higher yield, with firm pulp, sweet fruits and larger seeds.

According to Cruz & Vencovsky (1989), the most promising hybrid combinations are those with high SCA effects (positive or negative, depending on the character under study) resulting from crosses between divergent parents, where at least one of them shows a high GCA. However, according to Ferreira et al. (2002), two high GCA parents when crossed will not always originate the best diallel hybrid. Thus,

the opposite can also occur, where two parents with negative GCA values, when combined, may originate hybrids with positive SCA values, as reported in the present study.

Based on the specific combining ability (Table 5), hybrids '1x5, 1x6, 2x3, 2x4, 3x5, 4x6 and 5x6' were noted as the most promising ones in terms of precocity; and the combinations '1x2, 1x6, 2x3, 2x4, 3x4, 3x6, 4x5, 4x6 and 5x6' in terms of fruits with higher mass, whereas '1x3, 1x4, 1x5, 2x5, 2x6 and 3x5' in terms of lower fruit mass; the combinations '1x3, 1x4, 1x6, 2x3, 2x4 and 2x5' were the most promising ones for prolificity; in terms of yield, hybrids '1x2, 1x4, 1x6, 2x3, 2x4, 3x5, 3x6, 4x6 and 5x6' stood out; for smaller fruit size (fruit length and width), the combinations '1x3 and 2x6' were prominent; the combinations '1x2, 1x4, 1x5, 2x3, 4x6 and 5x6' for soft fruit pulp; for the highest concentration of soluble solids, hybrids '1x6, 2x3, 2x4, 2x5, 3x5, 4x5 and 4x6' were noted; as for rind thickness the combinations '1x2, 1x4, 1x6, 2x3, 2x4, 2x5, 3x4, 3x6 and 4x5' were the most promising ones; for seed size (length, width) and

Table 5. Estimates of the specific combining ability effects on watermelon hybrids

Hybrids ⁽¹⁾	Traits analyzed ⁽²⁾												
	FFA (days)	MBL (m)	FM (kg)	NF/P (unit)	YD (t/ha)	FL (cm)	FW (cm)	PF (%)	SSC (°Brix)	ART (cm)	SL (mm)	SW (mm)	SM (mg)
1x1	-0.750	-0.008	0.350	0.003	-7.002	0.396	-0.385	47.677	0.165	0.022	1.248	0.852	14.352
1x2	0.000	0.003	0.080	-0.153	2.008	0.037	0.006	-61.707	-0.242	0.004	-0.768	-0.618	-8.426
1x3	0.972	-0.060	-0.700	0.011	-6.135	-1.242	-1.295	13.976	-0.247	-0.051	0.225	0.183	4.630
1x4	1.556	-0.066	-0.112	0.006	1.587	0.867	0.104	-20.217	-0.006	0.002	0.199	0.206	0.463
1x5	-0.417	0.052	-0.313	-0.186	-1.643	-0.208	0.632	-0.866	-0.005	-0.010	-0.801	-0.543	-10.926
1x6	-1.361	0.079	0.694	0.319	11.186	0.150	0.938	21.136	0.336	0.033	-0.102	-0.081	-0.093
2x2	-0.250	-0.109	-0.320	-0.375	-6.283	-0.323	-0.469	62.018	-0.566	-0.027	0.989	0.796	12.130
2x3	-1.444	0.090	0.566	0.172	6.980	1.232	1.090	-72.350	0.369	0.004	-0.698	-0.419	-4.815
2x4	-0.028	0.000	0.257	0.250	2.873	0.136	-0.112	6.929	0.234	0.022	-0.283	-0.174	-2.315
2x5	0.833	0.060	-0.157	0.292	-2.500	0.346	-0.285	23.919	0.211	0.007	1.275	0.781	11.296
2x6	0.889	-0.044	-0.426	-0.186	-3.077	-1.427	-0.230	41.191	-0.005	-0.010	-0.515	-0.367	-7.870
3x3	-1.639	0.025	-0.124	0.553	-4.518	-1.973	-0.338	15.495	0.274	-0.082	1.032	0.714	8.241
3x4	0.778	-0.031	0.137	-0.586	-0.451	-0.149	0.298	13.529	-0.364	0.038	0.322	0.119	2.407
3x5	-0.694	-0.046	-0.038	-0.061	1.387	1.184	0.044	12.966	0.301	-0.010	-1.576	-1.090	-18.981
3x6	2.028	0.022	0.159	-0.089	2.738	0.949	0.202	16.385	-0.333	0.101	0.695	0.493	8.519
4x4	-4.806	0.096	-0.417	1.008	-7.398	-0.505	-0.896	63.009	-0.225	-0.059	-0.274	0.010	3.241
4x5	2.722	-0.064	0.083	-0.067	-2.265	0.048	-0.080	2.725	0.035	0.011	-0.172	-0.147	-4.815
4x6	-0.222	0.064	0.052	-0.611	5.654	-0.397	0.686	-65.974	0.326	-0.014	0.207	-0.015	1.019
5x5	-1.750	-0.020	0.051	0.325	1.929	-3.129	0.402	26.329	-0.445	0.068	1.479	1.176	27.130
5x6	-0.694	0.017	0.373	-0.303	3.093	1.760	-0.711	-65.073	-0.096	-0.066	-0.205	-0.177	-3.704
6x6	-0.639	-0.138	-0.852	0.869	-19.594	-1.035	-0.885	52.334	-0.227	-0.043	-0.081	0.146	2.130
SD($\hat{s}_{ii}-\hat{s}_{ij}$) ⁽³⁾	0.687	0.076	0.486	0.281	6.549	0.891	0.699	36.896	0.363	0.039	0.143	0.099	2.614
SD($\hat{s}_{ij}-\hat{s}_{ik}$)	0.543	0.066	0.421	0.172	5.672	0.771	0.605	31.953	0.314	0.034	0.124	0.086	2.264
SD($\hat{s}_{ij}-\hat{s}_{kl}$)	0.486	0.060	0.384	0.222	5.178	0.704	0.552	29.169	0.287	0.031	0.113	0.078	2.066

⁽¹⁾ 1=JNY; 2=ORA; 3=KOD; 4=SOL; 5=CHG; 6=PEA; ⁽²⁾ FFA = Days before female flower anthesis; MBL = Main branch length; FM = Fruit mass; NF/P = Number of fruits per plant; YD = Yield; FL = Fruit length; FW = Fruit width; PF = Pulp firmness; SSC = Soluble solids content; ART = Average rind thickness; SL = Seed length; SW = Seed width; and SM = Seed mass; ⁽³⁾ SD ($\hat{s}_{ii} - \hat{s}_{ij}$) = Standard deviation of the effects with a parent and hybrid; SD ($\hat{s}_{ij} - \hat{s}_{ik}$) = Standard deviation between an F1' and a common parent; SD ($\hat{s}_{ij} - \hat{s}_{kl}$) = Standard deviation between two random F1' s.

seed mass the combinations '1x2, 1x5, 1x6, 2x3, 2x4, 2x6, 3x5, 4x5 and 5x6' stood out in terms of smaller sized seeds and seed mass because the effect of the SCA was in agreement with the GCA of their parents, for most of the characters evaluated.

In relation to all the characters studied, some hybrid combinations, as well as their reciprocal ones, showed negative and positive values or vice versa, which indicates the action of reciprocal effects (Ferreira et al., 2002). Based on the reciprocal effects of the characters 'days before female flower anthesis', fruit mass, number of fruits per plant, yield, pulp firmness, soluble solids content, rind thickness, seed length, seed width and seed mass (Table 6), it was found that 'JNY' (1), when crossed with parents 'ORA' (2), 'KOD' (3), 'SOL' (4), 'CHG' (5) and 'PEA' (6), should be used as a pollen recipient, because in this case greater increases were observed in terms

of precocity, prolificacy, yield and reduction of seed size; genotype 'ORA' (2), when crossed with 'KOD' (3), 'SOL' (4), 'CHG' (5) and 'PEA' (6), should be used as a pollen recipient owing to its increased fruit mass, prolificacy, yield, firmer pulp, sweeter fruits, with thicker rind and small seeds; the genotypes 'SOL' (4), 'CHG' (5) and 'PEA' (6) when crossed with 'KOD' (3), should be used as a pollen donor due to higher reduction of fruit mass, increased prolificacy, sweet fruits with firmer pulp and smaller seeds; genotype 'SOL' (4), when crossed with 'CHG' (5) and 'PEA' (6), should be used as a pollen recipient for its contribution to precocity, prolificacy, sweet fruits with firmer pulp and smaller seeds; in the cross between genotypes 'PEA' (6) and 'CHG' (5), the latter should be used as a pollen recipient, since the reciprocal effects demonstrate the superiority of the hybrids obtained.

Table 6. Estimates of the reciprocal effects on watermelon hybrids

Hybrids ⁽¹⁾	Traits analyzed ⁽²⁾												
	FFA (days)	MBL (m)	FM (kg)	NF/P (unit)	YD (t/ha)	FL (cm)	FW (cm)	PF (%)	SSC (°Brix)	ART (cm)	SL (mm)	SW (mm)	SM (mg)
2x1	0.833	-0.327	-0.639	0.100	-8.317	-1.247	-0.828	55.470	-0.185	0.027	-0.102	-0.035	0.000
3x1	1.333	-0.272	0.338	-0.133	3.198	0.665	1.132	-148.225	-0.523	-0.050	0.117	-0.063	0.000
4x1	0.667	-0.230	-0.639	-0.033	-6.453	0.360	-0.162	-74.017	0.307	-0.012	0.060	0.155	3.333
5x1	1.167	-0.243	0.178	0.250	2.497	0.573	1.260	120.884	-1.120	0.083	-0.092	-0.160	-1.667
6x1	0.167	0.023	-0.088	0.050	-8.588	0.217	0.262	67.005	0.193	0.010	-0.083	-0.080	-1.667
3x2	-0.667	0.083	0.268	0.183	1.273	0.535	-0.003	-7.354	-0.135	-0.050	1.398	0.843	13.333
4x2	-1.167	0.012	-0.115	0.000	-2.240	-0.015	-0.128	-28.766	-0.007	0.000	0.167	0.080	-3.333
5x2	1.167	-0.043	-0.197	-0.117	-1.520	0.900	0.193	8.054	0.402	0.015	-0.223	-0.115	-6.667
6x2	1.500	0.090	0.143	-0.200	-2.640	-0.305	0.007	-9.752	0.365	-0.005	0.112	-0.078	3.333
4x3	0.500	-0.015	-0.450	-0.167	-2.353	-0.067	0.273	12.689	0.322	0.015	-0.717	-0.337	-8.333
5x3	3.500	-0.272	-0.425	0.067	-5.725	-0.838	-0.517	22.370	0.468	0.000	-0.027	-0.025	0.000
6x3	3.167	-0.090	-0.639	-0.033	-8.258	-1.408	-0.490	49.253	-0.287	-0.025	-0.043	-0.073	0.000
5x4	2.333	-0.095	-0.214	0.033	-2.653	-0.485	-0.323	64.715	-0.245	-0.013	-0.023	-0.010	1.667
6x4	1.667	0.217	0.571	0.183	3.092	-0.632	0.695	5.206	-0.075	0.005	0.105	0.040	3.333
6x5	0.333	-0.015	-0.148	0.167	4.253	0.823	-0.018	-35.758	0.382	0.033	-0.035	0.015	-1.667
SD(r_{ij}^{\wedge}) ⁽³⁾	0.421	0.054	0.344	0.199	4.631	0.630	0.494	26.090	0.257	0.027	0.101	0.070	1.848
SD($r_{ij}^{\wedge}-r_{kl}^{\wedge}$)	0.595	0.066	0.421	0.244	5.672	0.771	0.605	31.953	0.314	0.034	0.124	0.086	2.264

⁽¹⁾ 1=JNY; 2=ORA; 3=KOD; 4=SOL; 5=CHG; 6=PEA; ⁽²⁾ FFA = Days before female flower anthesis; MBL = Main branch length; FM = Fruit mass; NF/P = Number of fruits per plant; YD = Yield; FL = Fruit length; FW = Fruit width; PF = Pulp firmness; SSC = Soluble solids content; ART = Average rind thickness; SL = Seed length; SW = Seed width; and SM = Seed mass. ⁽³⁾ SD (r_{ij}^{\wedge}) = Standard deviation between two random parents; SD ($r_{ij}^{\wedge}-r_{kl}^{\wedge}$) = Standard deviation between the effects of two random reciprocal F1's.

Conclusions

1 – In terms of general combining ability, genotypes 'JNY' (1) and 'KOD' (3) are evidenced as being the most promising ones to obtain hybrids with smaller fruit size and smaller seeds.

2 - Genotypes 'ORA' (2) and 'CGH' (5) can be used to produce hybrids with greater fruit mass.

3 – The reciprocal effects indicated that

genotypes 'KOD' (3) and 'JNY' (1) should be used as a pollen recipient and a pollen donor, respectively, for the development of genotypes with smaller fruit size and smaller seeds.

4- In terms of specific combining ability, combinations 'ORA' (2) x 'PEA' (6); 'ORA' (2) x 'JNY' (1); 'CHG' (5) x 'KOD' (3); 'PEA' (6) x 'KOD' (3) and 'CHG' (5) x 'SOL' (4) stand out for their potential for the development of genotypes with

the smallest fruit size and smallest seeds.

Acknowledgements

We thank the Brazilian National Council for Scientific and Technological Development (CNPq) for granting a scholarship to the postgraduate student. We also thank colleagues Taise Oliveira Passos and Ronny Elisson Ribeiro Cavalcante for their friendship, care and help with the evaluations.

References

- Adjoumani, K., Kouonon, L.C., Koffi, G.K., Bony, B.S., Brou, K.F., Akaffou, D. S.; Sie, R. S. 2016. Analysis on genetic variability and heritability of fruit characters in *Citrullus lanatus* (Thunb.) Matsumura and Nakai (Cucurbitaceae) cultivars. *Journal of Animal & Plant Sciences* 28: 4340-4355.
- Bahari, M., Rafii, M.Y., Saleh, G.B., Latif, M.A. 2012. Combining Ability Analysis in Complete Diallel Cross of Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai). *The Scientific World Journal* 2012: 1-6.
- Barreto, R.R., Scapim, C.A., Amaral Júnior, A.T., Rodvalho, M.A., Vieira, R.A., Schuelter, A.R. 2012. Avaliação da capacidade de combinação de famílias S2 de milho pipoca por meio de diferentes testadores. *Ciências Agrárias* 33: 873-890.
- Barros, A.K.A., Nunes, G.H.S., Queiróz, M.A.Q., Pereira, E.W.L., Costa Filho, J.H. 2011. Diallel analysis of yield and quality traits of melon fruits. *Crop Breeding and Applied Biotechnology* 11: 313-319.
- Carvalho, A.D.F., Silva, G.O., Pereira, R.B., Pinheiro, J.B., Vieira, J.V. 2014. Capacidade combinatória em cenoura para componentes de produção e tolerância à queima-das-folhas. *Horticultura Brasileira* 32: 190-193.
- Cruz, C.D. 2013. GENES: a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum* 35: 271-276.
- Cruz, C.D., Regazzi, A.J., Carneiro, P.C.S. 2012. *Modelos biométricos aplicados ao melhoramento genético*. UFV: Imprensa Universitária, Viçosa, Brasil 514 p.
- Ferreira, M.A.J.F., Braz, L.T., Queiroz, M.A., Crurata-Masca, M.G.C. 2002. Capacidade de combinação em sete populações de melancia. *Pesquisa Agropecuária Brasileira* 37: 963-970.
- Gama, F.C., Viza, R. 2008. Uso culinário. In: Neto, C.R., Teixeira, C.A.D., Fernandes, C.F., Gama, F.C., Souza, F.F., Franderson, J.E., Costa, J.N.M., Queiróz, M.A., Dias, R.C., Viza, R., Holanda Filho, Z.F. *Cultivo da melancia em Rondônia*. Embrapa Informação Tecnológica, Brasília, Brasil, p. 96-103.
- Gama, R.N.C, Santos, C.A.F., Dias, R.C.S. Genetic variability of watermelon accessions based on microsatellite marker. *Genetics and Molecular Research* 12: 747-754
- Gama, R.N.C.S., Santos, C.A.F., Dias, R.C.S., Alves, J.C.S.F., Nogueira, T.O. 2015. Microsatellite markers linked to the locus of the watermelon fruit stripe pattern. *Genetics and Molecular Research* 14: 269-276.
- Gbatto, A.A., Koff, K.K., Fouha Bi, N.D., Doubi Bi, S.T., Tro, H.H., Baudoi, J.P., Zoro Bi, I.A. Morphological diversity in oleaginous watermelon (*Citrullus mucosospermus*) from the Nangui Abrogoua University germplasm collection. *African Journal of Biotechnology* 15: 917-929
- Griffing, B.A. 1956. Concepto of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences* 9: 463-493.
- Gvozdanovic-Varga, J.; Vasic, M.; Milic, D.; Cervenski, J. 2011. Diallel cross analysis for fruit traits in watermelon. *Genetika* 43: 163-174.
- IBGE. Instituto Brasileiro de geografia e Estatística. Produção agrícola municipal: culturas temporárias e permanentes/SIDRA. 2016. <http://biblioteca.ibge.gov.br/index.php/atálogo?view=detalhes&id=766> <Acess on 02 jun. 2017>
- Mendes, A.M.S. Faria, C.M.B. Silva, D.J. In: Dias, R. de C. S. et al. (Eds.). Sistema de produção de melancia. Petrolina: Embrapa Semiárido, 2010. Available at: <<https://sistemasdeproducao.cnptia.embrapa.br/FontesHTML/Melancia/SistemaProducaoMelancia/adubacao.htm>>. Acesso em: 20 maio. 2017.
- Nantoumé, A.D., Traoré, S., Christiansen, J.L., Andersen, S.B., Ensen, B.D. 2012. Traditional uses and cultivation of indigenous watermelons (*Citrullus lanatus*) in Mali. *International Journal of Biodiversity and Conservation* 4: 461-471.
- Nantoumé, A.D., Andersen, S.B., Jensen, B.D. 2013. Genetic differentiation of watermelon landrace types in Mali revealed by microsatellite (SSR) markers. *African Journal of Biotechnology* 12: 5513-5521
- Nascimento, T.L. do, Souza, F.F., Dias, R.C.S, Silva, E.F. 2018. Agronomic characterization and heterosis in watermelon genotypes. *Pesquisa Agropecuária Tropical* 48: 170-177.
- Oliveira, R.A., Nunes, G.H.S., Oliveira, D.A., Guimarães, I.P. 2008. Divergência genética entre

acessos de melancia coletados no Estado do Rio Grande do Norte. *Revista Brasileira de Ciências Agrárias* 3: 213-217.

Piovesan, J.I. 2012. *Capacidade combinatória e ação gênica em genótipos de melancia*. 52 f. (Dissertação de Mestrado) Universidade Federal do Tocantins, Tocantins, Brasil.

Ramos, A.R.P., Dias, R.C.S., Aragão, C.A., Batista, P.F., Pires, M.M.L. 2012. Desempenho de genótipos de melancia de frutos pequenos em diversas densidades de plantio. *Horticultura Brasileira* 30: 333-338.

Rocha, F., Stinghen, J.C., Gemeli, M.S., Coimbra, J.L.M., Guidolin, A.F. 2014. Análise dialélica como ferramenta na seleção de genitores em feijão. *Revista Ciência Agronômica* 45: 78-81

Santos, R.L., Pavan, M.A., Silva, N., Gioria, R., Souza Neto, I.L. Estimativas de capacidades de combinação em cebola para resistência a raiz rosada e caracteres agronômicos. *Summa Phytopathol* 41: 133-137.

Sapovadiya, M.H., Mehta, D.R., Dhaduk, H.L., Babariya, C.A. 2014. Combining ability in watermelon (*Citrullus lanatus* (Thumb.) Mansf.). *Electrocnic Journal of Plant Breeding* 5: 327-330.

Singh, N.P., Dadwadia, G., Annapurna, G. 2009. Analysis of heterosis and combining ability status among diallel set of hybrids for yield and quality traits in watermelon (*Citrullus lanatus* Thunb). *Vegetation Science* 36: 323-326.

Souza, F.F. 2008. Cultivares. In: Neto, C.R., Teixeira, C.A.D., Fernandes, C.F., Gama, F.C., Souza, F.F., Franderson, J.E., Costa, J.N.M., Queiróz, M.A., Dias, R.C., Viza, R., Holanda Filho, Z.F. *Cultivo da melancia em Rondônia*. Embrapa Informação Tecnológica, Brasília, Brasil, p. 34-44.

Souza, F.F., Dias, R.C.S., Queiróz, M.A. 2013. Capacidade de combinação de linhagens avançadas e cultivares comerciais de melancia. *Horticultura Brasileira* 31: 595-601.

Tavares, A.T., Vaz, J.C., Coelho, R.S., Lopes, D.A. da S., Alves, F.Q.G., Nascimento, I.R. 2018. Aptidão agronômica de genótipos de melancia no sul do estado do Tocantins. *Agropecuária Científica no Semiárido* 14: 59-64.