horticultura brasileira

Research

XAVIER, LFS; PESTANA, JK; SEKIYA, A; KRAUSE, MD; MOREIRA, RMP; FERREIRA, JM. 2019. Partial diallel and potential of super sweet corn inbred lines bt_2 to obtain hybrids. *Horticultura Brasileira* 37: 278-284. DOI - http://dx.doi.org/10.1590/S0102-053620190305

Partial diallel and potential of super sweet corn inbred lines bt_2 to obtain hybrids

Larissa Fernanda S Xavier[1]; Jéssica Kelly Pestana[1]; Alline Sekiya[1]; Matheus D Krause[1]; Rosângela Maria P Moreira[1]; Josué M Ferreira[1]

[1]Universidade Estadual de Londrina (UEL), Londrina-PR, Brasil; larissafsx@gmail.com; jessicak.pestana@gmail.com; allinesekiya@gmail.com; krause.d.matheus@gmail.com; rosang.moreira8@gmail.com; josuemf68@gmail.com

ABSTRACT

The aims of this study were to determine the potential of S_4 super sweet corn inbred lines for hybrid synthesis, identify the predominant types of gene action and correlations among different traits, significant for breeding programs. The 81 hybrids obtained from a partial diallel 9x9 and three checks were evaluated. A complete randomized block design, with three replicates, and two sowing seasons was used. We could notice significant hybrid effects, general combining ability (GCA) of GI and GII groups and specific combining ability (SCA) in relation to evaluated traits, highlighting the existence of hybrids with superior performance and the expression of additive and non-additive effects. The inbred lines: L_1, L_3, L_6 and L_9 (GI) and $L_{1'}$, $L_{7'}$ and $L_{9'}$ (GII) showed the best GCA and SCA estimates, being present in the nine selected hybrids with superior and competitive performance in relation to the checks. The estimated correlations indicate that, for a breeding program aiming to increase grain productivity, evaluating, at least, the dehusked ears, prioritizing genotypes with larger ear diameters and longer ear lengths is important.

Keywords: *Zea mays* var. *saccharata*, combining ability, correlations.

RESUMO

Dialelo parcial e o potencial de linhagens de milho superdoce bt_2 para obtenção de híbridos

Os objetivos foram determinar o potencial de linhagens S_4 de milho superdoce para síntese de híbridos, identificar os tipos de ações gênicas predominantes e as correlações para diferentes caracteres importantes para o melhoramento. Os 81 híbridos obtidos em um dialelo parcial 9x9 e três testemunhas foram avaliados em blocos completos casualizados, com três repetições, em duas épocas de semeadura. Houve efeitos significativos de híbridos, de capacidade geral de combinação (CGC) dos grupos GI e GII e de capacidade específica de combinação (CEC) para os caracteres avaliados, evidenciando a existência de híbridos com desempenhos superiores e a expressão de efeitos aditivos e não aditivos. As linhagens L_1, L_3, L_6 e L_9 (GI) e $L_{1'}$, $L_{7'}$ e $L_{9'}$ (GII) apresentaram as melhores estimativas de CGC e CEC, estando presente nos nove híbridos selecionados com desempenhos superiores e competitivos em relação às testemunhas. As correlações estimadas indicam que, para o melhoramento visando o aumento de produtividade de grãos, é importante avaliar ao menos as espigas sem palha, priorizando genótipos com maiores diâmetros e comprimentos de espigas.

Palavras-chave: *Zea mays* var. *saccharata*, capacidade de combinação, correlações.

Received on December 14, 2018; accepted on June 4, 2019

Sweet corn is originated from recessive genetic mutations of common corn, which block starch synthesis, increasing endosperm sugar concentrations. Homozygous genotypes for *shrunken* (sh_1 and sh_2) or *brittle* genes (bt_1 and bt_2) present higher sugar content, being classified as super sweet, whereas other mutant genotypes are classified as sweet corn (Teixeira *et al*., 2013).

Super sweet corn is considered a vegetable and it is dedicated exclusively for human consumption. It has a high nutritional value, being consumed *in natura* or processed by vegetable canning industries in several countries (Kwiatkowski & Clemente, 2007; Teixeira *et al*., 2013; Luz *et al*., 2014). However, in Brazil, super sweet corn is basically consumed industrialized, commonly as canning corn grains, and the consumers themselves have no idea that these grains are a special type of corn.

Hybrids of super sweet corn inbred lines are cultivars which best meet canning industry demands, due to its uniformity and agronomic performance (Kwiatkowski & Clemente, 2007; Luz *et al*., 2014). In Brazil, these days, few cultivars of sweet and super sweet corn seeds are available to farmers, only 65 cultivars are registered by the Ministry of Agriculture, Livestock and Food Supply (Brazil, 2018). Therefore, developing new superior hybrid combinations is essential for expansion of super sweet corn production in Brazil (Santos *et al*., 2014).

Breeding programs of super sweet corn, which aim to obtain hybrids, develop many inbred lines, not all these lines will produce hybrids with high agronomic potential, though. Thus, agronomic and genetic evaluations of these inbred lines based on their hybrid combination performance is extremely important (Kashiani *et al*., 2014). Diallel analysis is used as a tool which provides useful estimates to select more promising lines for synthesis of hybrids and to understand the magnitude of the effects which determine genetic traits (Cruz *et al*., 2004; Kwiatkowski *et al*., 2011; Worrajinda *et al*., 2013).

Estimates of combining ability of sweet corn inbred lines obtained using diallel analysis have been studied considering different agronomic traits, allowing selecting superior hybrid combinations and understanding additive and non-additive genetic effects when determining these traits (Kwiatkowski *et al*., 2011; Solomon *et al*., 2012; Rice & Tracy, 2013; Worrajinda *et al*., 2013).

Another important element for breeding is to understand correlation among agronomic traits of interest, since this knowledge can help out select more efficient selection processes, allowing selecting different traits simultaneously, increasing genetic gains in relation to low heritability traits (Entringer *et al*., 2014; Kashiani *et al*., 2014).

Given the above, the aims of this study were to determine potential of super sweet corn inbred lines which carry the gene *brittle-2* for synthesis of hybrids, identify predominant types of gene actions in agronomic traits important for breeding and the association among these traits.

MATERIAL AND METHODS

Eighty one super sweet corn hybrids were produced, using partial dialled crosses of two groups of nine S_4 inbred lines, developed by Universidade Estadual de Londrina (UEL) Corn Breeding Program, homozygous for *brittle-2* gene. These inbred lines were obtained from the backcross among elite common corn inbred lines with two super sweet corn populations, to introduce bt_2 gene, with later self-fertilization. Thus, the inbred lines were separated into two groups, according to a previous knowledge of the performance of the elite crossbred lines and the source population for gene introduction.

The 81 hybrids and three checks (the synthetics ST0509A and ST2109B, developed at Farm School of UEL, and the hybrid Tropical Plus, from Syngenta Seeds), were evaluated at UEL, in the crop season 2013/2014, in two sowing dates (October 28, 2013 and November 28, 2013), both without artificial irrigation.

Climate data were collected at a local weather station. From the first sowing date until havest time, a total rainfall was 305 mm, regular rainfall distribution and maximum temperatures from 30 to 36ºC and minimum temperatures from 13.2 to 20.5ºC. Total rainfall of the second sowing date until harvest was 208 mm, being the last rain observed 6 days before flowering, with a total of only 5 mm, maximum temperatures from 30.8 to 38ºC and minimum temperatures from 17 to 20.5ºC.

The experimental arrangement was in complete randomized blocks, with three replicates and simple row plots, 4.00 m long, spacing 0.80 m between rows and 0.20 between plants, in two sowing dates.

Conventional soil preparation was carried out using plowing and harrowing, and agronomic standard procedures were carried out according to technical recommendations for the crop.

In order to avoid possible contaminations by common corn pollen, the experiments were isolated from other corn plantations. The check Tropical Plus, homozygous for the sh_2 gene, had its tassels removed before flowering, to avoid the conversion of tested hybrids into common corn.

Harvest was done manually as the ears reached kernel milky stage (green corn), when the grains of the ear of each plot presented 70 to 80% water content, considered a suitable content for *in natura* consumption and for canning (Kwiatkowski & Clemente, 2007).

The evaluated traits were a) days to flowering (DF, in days): considering as flowered plot when 50% of plants showed stigma-style measuring at least 1-cm length and one third of tassels releasing pollen; b) plant height (PH, in cm): average height of three plants of each plot, measured from ground level to the flag leaf insertion; c) ear height (EH, in cm): average ear height of three plants of each plot, measured from ground level to the superior ear insertion; d) husked ear yield (HEY, in t ha^{-1}); e) dehusked ear yield (DEY, in t ha^{-1}); f) grain yield at green corn stage (GY, in t ha^{-1}); g) ear length (EL, in cm): average length of five ears of each plot; h) ear diameter (ED, in cm); average diameter of five ears of each plot; i) number of grain rows (NR): grain rows in five ears of each plot were counted; j) total soluble solids (TSS, in %): measured with a digital refractometer, using a sample of 0.3 mL juice extracted from the grain mixture.

In the first and second sowing dates, stand averages of 20.55 and 20.16 plants per plot were obtained, respectively, being yields corrected to an optimum stand of 20 plants per plot, using the methodology suggested by Vencovsky & Barriga (1992), and extrapolated to tons per hectare (t ha^{-1}), with a stand of 62500 plants per hectare.

The analyses of variance were performed using program SAS (2002) (Statistical Analysis System) and Scott & Knott clustering test was performed using GENES program (Cruz, 2013).

Individual analyses of variance for each trait were done with the decomposition of treatment effects on effects of checks, hybrids and contrast hybrids vs checks, considering treatment effects as fixed. Degrees of freedom were decomposed through diallel analysis in general combining ability of groups GI and GII (GCA-I and GCA-II), and specific combining ability (SCA).

Griffing method (1956), adapted to partial diallel crosses involving only F1 generations, was used to obtain effect estimates of GCA-I, GCA-II and SCA, using minimum square method (Cruz *et al*., 2004).

Genotype averages for different traits, taken two by two (X and Y), were used to estimate phenotypic correlations and, significance of Pearson correlation estimates were evaluated using t statistics, at 5% significance.

RESULTS AND DISCUSSION

The trials showed adequate

experimental accuracy for most evaluated traits, when compared to other experiments with super sweet corn (Kwiatkowski *et al*., 2011; Santos *et al*., 2014) (Table 1). The average squares for treatments, hybrids and their unfolding in GCA-I, GCA-II and SCA, for the traits evaluated in two sowing dates, were significant, with exception of "days to flowering" in the second sowing date (Table 1). These results show different performances of the evaluated genotypes and that superior hybrid combinations exist, with inbred lines contributing differently for the performance of these hybrids, being possible to observe superior specific combinations of inbred lines, not just explained by their respective general combining abilities (Cruz *et al*., 2004).

Significant effects found in GCA and SCA for all traits, in two sowing dates, show that both additive and non-additive effects were important for genetic control of studied traits (Table 1). Similar results for ear yield, grain yield, plant height and total soluble solids were obtained by Lemos *et al.* (2002); Bordallo *et al.* (2005), Solomon *et al*. (2012), Rice & Tracy (2013) and Suzukawa *et al.* (2018). However, for ear height and ear diameter, Solomon *et al*. (2012) reported that additive gene action had greater importance in relation to non-additive effects, and for TSS, the authors verified no significant difference for GCA and SCA in diallel crosses evaluated, whereas Yuwono *et al.* (2017) verified significant difference of SCA for TSS.

In the first sowing season, significant differences of checks for days to flowering, plant height and ear diameter were observed, but in the second sowing season were significant for dehusked ear yield, total soluble solids, days to flowering, ear height, ear diameter and number of grain rows, indicating that the checks did not show uniform behavior for these traits (Table 1).

Using Scott-Knott clustering average test, we verified that synthetics ST0509A and ST2109B showed potential for genetic breeding and being also competitive in relation to the hybrid Tropical Plus for productivity. This hybrid check exceeded ST0509A for husked ear yield only in the first sowing date and ST2109B for dehusked ear yield in the second sowing date (Table 2).

Contrasts between general averages of hybrids and averages of checks were significant for dehusked ear yield, grain yield, days to flowering, ear height and number of grain rows, in both sowing dates and, for total soluble solids, length and diameter of the ears, only in the second sowing date (Table 1). We could also verify superior average performance of hybrids in relation to the average of checks for these traits, with exception of number of grain rows (Table 2).

The hybrids which more frequently presented better performance for productivity and for other traits, in relation to the hybrid control, were $HS_{37'}$, $HS_{47'}$, $HS_{57'}$, $HS_{64'}$, $HS_{71'}$, $HS_{76'}$, $HS_{77'}$, $HS_{94'}$ and $HS_{95'}$ (Table 2).

Even without artificial irrigation and lack of rain in the second sowing season, which led to a sensitive genotype performance reduction, the averages obtained by the selected hybrids met the requirements presented by Pereira Filho *et al.* (2002) and Souza *et al.* (2013): husked ear yield above 12 t ha^{-1}; minimum of 14 grain rows per

Table 1. Analyses of variance with respective degrees of freedom (DF), average squares, significance F test and coefficient of variation [CV(%)], for different traits evaluated in two sowing seasons. Londrina, UEL, 2013/2014.

Variation source	DF	First sowing season									
		HEY	DEY	GY	TSS	DF	PH	EH	EL	ED	NR
Checks (C)	2	ns	ns	ns	ns	*	*	ns	ns	*	ns
H vs C	1	ns	*	*	ns	*	ns	*	ns	ns	*
Hybrids (H)	80	*	*	*	*	*	*	*	*	*	*
GCA (GI)	8	36.92*	31.55*	12.430*	10.740*	9.877*	628.4*	471.1*	4.580*	0.414*	6.439*
GCA (GII)	8	39.97*	28.72*	6.049*	5.017*	16.760*	3586.2*	1691.6*	8.846*	0.153*	8.429*
SCA	64	14.19*	6.85*	2.207*	2.026*	2.923*	211.8*	137.7*	1.583*	0.065*	1.454*
Error	158	5.324	3.113	0.884	1.064	2.034	84.43	68.66	0.677	0.027	0.595
CV (%)		11.4	12.4	20.9	6.0	2.6	4.2	7.6	4.3	3.4	5.5
		Second sowing season									
Checks (C)	2	ns	*	ns	*	*	ns	*	ns	*	*
H vs C	1	ns	*	*	*	*	ns	*	*	*	*
Hybrids (H)	61	*	*	*	*	ns	*	*	*	*	*
GCA (GI)	8	16.170*	10.270*	2.820*	5.643*	0.0	785.0*	605.1*	8.071*	0.220*	4.834*
GCA (GII)	8	6.555*	4.027*	2.018*	9.891*	0.0	2417.4*	1879.8*	6.331*	0.129*	8.348*
SCA	45	4.902*	2.518*	1.011*	1.733*	0.0	237.9*	159.4*	1.204*	0.044*	0.954*
Error	128	2.480	1.041	0.433	1.019	0.036	96.50	65.76	0.702	0.022	0.541
CV (%)		11.8	11.2	14.3	5.7	0.4	4.7	7.7	5.0	3.6	5.5

*and ns= significant and non-significant at 0.05 probability using F test, respectively; HEY= husked ear yield (t ha^{-1}); DEY= dehusked ear yield (t ha^{-1}); GY= green corn grain yield (t ha^{-1}); TSS= total soluble solids (%); DF= days to flowering; PH= plant height (cm); EH= ear height (cm); EL= ear length (cm); ED= ear diameter (cm); NR= number of grain rows.

ear; length and diameter of ears above 15 and 3 cm, respectively.

Husked ear yield, dehusked ear yield and grain yield at green corn stage presented a strong positive association among them. These yield traits also presented positive correlations with ear diameter, ear length and number of grain rows (Table 2). Kashiani &

Table 2. Averages of selected hybrids (HS_{ij}), check averages, general average of diallel hybrid, general averages of checks and coefficient of phenotypic correlation, in two sowing seasons (S1 and S2). Londrina, UEL, 2013/2014.

Treatments	HEY (t ha^{-1})		DEY (t ha^{-1})		GY (t ha^{-1})		TSS (%)		DF (days)	
	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2
$HS_{37'}$	23.40a	15.57a	16.24a	10.53a	5.45b	5.57a	19.3a	17.9a	55c	52b
$HS_{47'}$	20.99a	14.73a	14.70a	10.53a	5.01b	4.69a	16.6b	17.0b	56b	52b
$HS_{57'}$	25.72a	14.32a	16.89a	9.33a	6.56a	4.87a	16.7b	17.3b	55c	52b
$HS_{64'}$	21.82a	14.42a	14.62a	9.94a	4.80b	5.42a	15.3c	16.2b	54c	52b
$HS_{71'}$	23.16a	15.50a	18.33a	11.86a	6.53a	6.35a	17.8a	18.9a	56b	52b
$HS_{76'}$	20.83a	14.04a	16.20a	10.25a	4.92b	5.84a	17.7a	18.3a	55c	52b
$HS_{77'}$	21.58a	13.95a	15.65a	10.35a	5.30b	5.14a	16.8a	17.4b	55c	52b
$HS_{94'}$	23.89a	15.87a	16.75a	11.00a	6.72a	5.57a	16.2b	15.9b	54c	52b
$HS_{95'}$	24.01a	15.64a	17.39a	10.73a	7.40a	5.58a	17.0a	17.2b	55c	52b
ST0509A	20.03b	12.47b	11.49b	7.10c	3.38c	3.32c	16.8a	18.3a	58a	52b
ST2109B	20.59a	11.01b	12.12b	5.65d	3.63c	2.19c	17.6a	17.6b	59a	52b
Tropical Plus	20.78a	13.39b	12.72b	7.77c	3.60c	3.02c	16.5b	14.3b	62a	59a
Dialled average (m)	20.19	13.35	14.21	9.19	4.54	4.69	17.1	17.9	55.7	52.0
Check averages	20.47	12.29	12.11	6.84	3.54	2.84	17.0	16.7	59.4	54.4
Traits	**Correlations between yield and other traits**									
HEY	1.00	1.00	0.90*	0.87*	0.76*	0.77*	-0.16	-0.05	-0.28*	0.01
DEY	0.90*	0.87*	1.00	1.00	0.83*	0.90*	-0.14	-0.01	-0.40*	-0.14
GY	0.76*	0.77*	0.83*	0.90*	1.00	1.00	-0.26*	0.11	-0.28*	-0.26*

	PH (cm)		EH (cm)		EL (cm)		ED (cm)		NR	
	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2
$HS_{37'}$	227b	222b	115a	111b	18.2c	16.5b	4.5b	4.2a	15.7a	16.2a
$HS_{47'}$	233a	227a	115a	110b	19.9a	17.8a	4.7b	4.3a	13.7c	14.4a
$HS_{57'}$	219b	207b	109b	103b	19.5a	16.1b	4.9a	4.1b	14.9b	13.8a
$HS_{64'}$	225b	217b	116a	111b	18.5b	15.9b	4.9a	4.4a	15.1b	13.8a
$HS_{71'}$	233a	233a	124a	127a	20.1a	16.7a	5.1a	4.3a	15.7a	14.9a
$HS_{76'}$	202c	198c	116a	103b	20.3a	17.3a	4.7b	4.1b	14.1b	13.3b
$HS_{77'}$	215b	204c	108b	99c	18.7b	16.3b	4.8a	4.1b	16.0a	13.8a
$HS_{94'}$	228b	218b	123a	214a	20.1a	17.5a	5.0a	4.3a	12.7c	13.1b
$HS_{95'}$	222b	212b	123a	104b	20.3a	17.5a	5.1a	4.3a	14.4b	13.1b
ST0509A	232a	209b	127a	121a	18.7b	16.4b	4.6b	4.1b	14.6b	14.4a
ST2109B	223b	218b	118a	112b	18.5b	16.3b	4.8a	3.8b	14.3b	12.9b
Tropical Plus	209c	198c	122a	129a	20.0a	15.3b	4.5b	4.0b	15.6a	14.9a
Dialled average (m)	216	209	108	105	19.1	16.7	4.7	4.1	14.0	13.4
Check averages	221	208	122	121	19.1	16.0	4.6	4.0	14.8	14.1
Traits	**Correlations between yield and other traits**									
HEY	0.23*	0.07	0.26*	-0.09	0.33*	0.43*	0.43*	0.56*	0.31*	0.32*
DEY	0.18	0.12	0.25*	-0.06	0.46*	0.52*	0.50*	0.67*	0.32*	0.31*
GY	0.10	0.08	0.13	-0.08	0.39*	0.42*	0.66*	0.57*	0.36*	0.19

*significant at 0.05 probability by t test. Averages followed by same lowercase letters in the column belong to the same group by Scott-Knott test, at 0.05 probability. HEY= husked ear yield (t ha^{-1}); DEY= dehusked ear yield (t ha^{-1}); GY= green corn grain yield (t ha^{-1}); TSS= total soluble solids (%); DF= days to flowering; PH= plant height (cm); EH= ear height (cm); EL= ear length (cm); ED= ear diameter (cm); NR= number of grain rows.

Table 3. Estimates of general combining ability of inbred lines of groups GI ($\hat{g}_i$) and GII ($\hat{g}_j$) for different traits, evaluated in two sowing seasons (S1 and S2). Londrina, UEL, 2013/2014.

Traits	HEY ($t\ ha^{-1}$)		DEY ($t\ ha^{-1}$)		GY ($t\ ha^{-1}$)		TSS (%)		DF (days)
	S1	S2	S1	S2	S1	S2	S1	S2	S1
General combining ability of inbred lines of group I ($\hat{g}_i$)									
$\hat{g}_{L1}$	1.84	0.30	1.34	0.45	0.82	0.17	-1.0	-0.6	-0.1
$\hat{g}_{L2}$	0.10	-0.10	-0.35	-0.53	0.03	-0.29	0.4	0.7	0.6
$\hat{g}_{L3}$	0.69	0.81	0.27	0.31	-0.75	0.20	0.9	0.6	-0.3
$\hat{g}_{L4}$	-1.85	-0.67	-1.83	-0.53	-0.82	-0.66	-0.4	0.0	1.0
$\hat{g}_{L5}$	-0.94	-1.29	-0.93	-1.18	-0.31	-0.42	0.3	0.1	0.4
$\hat{g}_{L6}$	0.21	0.03	0.45	0.30	0.39	0.19	-0.9	-0.8	-1.0
$\hat{g}_{L7}$	-0.04	-0.36	0.97	0.45	0.23	0.09	0.5	0.5	0.2
$\hat{g}_{L8}$	-1.17	-0.52	-0.96	-0.51	-0.63	-0.03	0.2	-0.4	-0.4
$\hat{g}_{L9}$	1.16	1.80	1.05	1.24	1.04	0.75	-0.0	-0.1	-0.4
General combining ability of inbred lines of group II ($\hat{g}_j$)									
$\hat{g}_{L1'}$	2.09	0.51	1.88	0.69	0.61	0.36	-0.3	-0.5	0.2
$\hat{g}_{L2'}$	-0.98	-0.80	-0.35	-0.46	0.09	-0.42	0.3	0.6	1.8
$\hat{g}_{L3'}$	0.03	-0.52	-0.07	-0.59	0.16	-0.52	0.2	-0.4	0.7
$\hat{g}_{L4'}$	-1.62	-0.72	-1.45	-0.58	-0.47	-0.25	-0.5	-0.7	-0.2
$\hat{g}_{L5'}$	-0.67	-0.06	-0.80	-0.07	-0.23	-0.17	-0.5	0.1	-0.8
$\hat{g}_{L6'}$	0.00	0.11	0.31	0.20	-0.38	0.40	0.2	0.4	-0.3
$\hat{g}_{L7'}$	1.45	1.03	0.87	0.59	0.80	0.30	-0.4	-0.1	-0.4
$\hat{g}_{L8'}$	-0.97	0.05	-0.96	-0.04	-0.58	0.20	0.8	1.3	-0.2
$\hat{g}_{L9'}$	0.67	0.42	0.58	0.25	0.00	0.10	0.2	-0.6	-0.7

	PH (cm)		EH (cm)		EL (cm)		ED (cm)		NR	
	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2
General combining ability of inbred lines of group I (gi)										
$\hat{g}_{L1}$	-1.8	-6.9	1.9	-4.4	-0.4	-0.1	0.2	0.1	0.7	0.8
$\hat{g}_{L2}$	2.9	-3.5	-6.3	-11.3	0.3	-0.1	-0.1	-0.1	-0.7	-0.3
$\hat{g}_{L3}$	1.7	3.5	2.0	2.3	-0.4	-0.3	-0.1	0.0	0.1	0.5
$\hat{g}_{L4}$	11.2	18.8	1.2	9.9	-0.2	0.4	-0.1	-0.0	-0.1	-0.3
$\hat{g}_{L5}$	-2.5	-4.6	-2.7	-3.4	-0.2	-0.8	-0.2	-0.2	-0.4	-0.8
$\hat{g}_{L6}$	-3.3	-0.1	-6.4	-2.4	-0.2	-0.8	0.0	0.1	0.5	0.5
$\hat{g}_{L7}$	-2.2	-0.8	3.2	3.9	0.7	0.5	0.1	0.0	0.5	0.0
$\hat{g}_{L8}$	-1.1	-2.4	5.3	3.9	-0.2	-0.2	-0.1	-0.1	-0.3	-0.2
$\hat{g}_{L9}$	-4.7	-4.0	1.9	1.5	0.6	1.3	0.2	0.2	-0.4	-0.3
General combining ability of inbred lines of group II ($\hat{g}_j$)										
$\hat{g}_{L1'}$	22.0	21.9	15.0	18.0	0.4	0.5	0.1	0.0	0.1	0.3
$\hat{g}_{L2'}$	2.0	3.7	0.8	3.8	0.3	0.2	0.1	0.1	0.3	0.4
$\hat{g}_{L3'}$	-19.8	-21.0	-8.4	-10.6	0.5	-0.0	0.0	-0.1	-0.6	-1.0
$\hat{g}_{L4'}$	9.6	6.1	9.5	8.1	-0.7	-0.7	-0.1	-0.1	-0.6	-0.6
$\hat{g}_{L5'}$	1.1	7.5	-1.1	1.2	-0.8	-0.8	0.0	0.1	0.2	0.5
$\hat{g}_{L6'}$	-1.0	0.0	1.3	2.9	0.6	0.5	-0.1	-0.1	-0.3	-0.4
$\hat{g}_{L7'}$	-1.6	-0.6	-3.0	-4.0	-0.3	-0.3	0.0	0.1	1.2	1.2
$\hat{g}_{L8'}$	-8.6	-10.4	-5.6	-2.2	-0.4	-0.1	-0.0	0.1	0.0	0.0
$\hat{g}_{L9'}$	-3.6	-7.1	-8.5	-17.0	0.5	0.8	-0.1	-0.1	-0.2	-0.5

HEY= husked ear yield (t/ha); DEY= dehusked ear yield (t/ha); GY= green corn grain yield (t/ha); TSS= total soluble solids (%); DF= days to flowering; PH= plant height (cm); EH= ear height (cm); EL= ear length (cm); ED= ear diameter (cm); NR= number of grain rows.

Saleh (2010), Entringer *et al.* (2014) and Nardino *et al.* (2016) also observed positive correlations between husked and dehusked ear yield and ear length, ear diameter and number of grain rows per ear. Kashiani & Saleh (2010) reported similar results: yield traits were negatively associated with days to flowering, showing that higher yield of super sweet corn was associated with greater values of earliness of these genotypes.

Grain yield is more strongly related to dehusked ear yield, with coefficients of determination of 69% and 81%, comparing with husked ear yield, 58% and 59%, in the first and second sowing dates, respectively (Table 2). Therefore, as the Brazilian market of super sweet corn intended mainly for the industrialization and production of canned green corn grains, the evaluations of yields should be done, at least, with dehusked ears since they present more coefficients of correlation, favoring the indirect selection for grain yield. However, in order to produce sweet corn aiming *in natura* market, evaluation of husked ear yield would be already sufficient.

The inbred lines with better estimates of general combining ability ($\hat{g}_i$ and $\hat{g}_j$) for yields were: L_1, L_3, L_6 and L_9 (GI) and $L_{1'}$, $L_{7'}$ and $L_{9'}$ (GII) (Table 3). Among these inbred lines, favorable estimates of GCA were observed in L_3 for TSS; L_1, L_6, L_9, $L_{7'}$ and $L_{9'}$ for flowering and height of plants; L_1, L_6, $L_{7'}$ and $L_{9'}$ for ear height; L_9, $L_{1'}$ and L_9 for ear length; L_1, L_3, L_6, $L_{1'}$ and $L_{7'}$ for number of grain rows (Table 3). These favorable estimates of GCA highlighted higher accumulation of favorable alleles for these traits (Cruz *et al*., 2004; Kwiatkowski *et al*., 2011). In their study on diallels of super sweet corn inbred lines, Elayaraja *et al.* (2014) and Suzukawa *et al.* (2018) highlighted that it is difficult to obtain inbred lines with good general combining ability for productivity and total soluble solids, this trend being observed in this study, with an only exception of L_3 inbred line.

SCA (s_{ij}) can be estimated for a given trait through the model $s_{ij} = HS_{ij} - (m+g_i+g_j)$ using estimates of general average of diallel hybrids (m), average individual hybrid performance (HS_{ij}) (Table 2) and GCA estimations of each inbred line (Table 3). The best estimates of SCA, in two sowing seasons, for yield were observed in eight selected hybrids, with an exception of $HS_{77'}$ which presented negative values of SCA for yield in the first sowing season. Besides favorable estimates of SCA, for hybrid seed yield, it is important that at least one hybrid of inbred lines presents high estimates of favorable GCA for yield. Among selected hybrids, only $HS_{76'}$ did not show any inbred lines containing favorable estimates of GCA for yield.

ACKNOWLEDGEMENTS

To The National Council for Scientific and Technological Development (CNPq) Brazil, for the financial support for this project; Araucaria Foundation for Social Inclusion scholarship granted and to Universidade Estadual de Londrina (UEL) for supporting the realization of this work.

REFERENCES

BORDALLO, PN; PEREIRA, MG; AMARAL JÚNIOR, AT; GABRIEL, APC. 2005. Análise dialélica de genótipos de milho doce e comum para caracteres agronômicos e proteína total. *Horticultura Brasileira* 23: 123-127.

BRASIL - Ministério da Agricultura, Pecuária e Abastecimento. 2018. *Registro Nacional de Cultivares – RNC*. Available at: http://www.agricultura.gov.br. Accessed February 06, 2018.

CRUZ, CD. 2013. Genes: a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum. Agronomy* 35: 271-276.

CRUZ, CD; REGAZZI, AJ; CARNEIRO, PCS. 2004. *Modelos biométricos aplicados ao melhoramento genético*. Viçosa: UFV. 315p.

ELAYARAJA, K; GADAG, RN; KUMARI, J; SINGODE, A; PAUL, D. 2014. Analysis of combining ability in experimental hybrids of sweet corn (*Zea mays* var. *saccharata*). *Indian Journal of Genetics and Plant Breeding* 74: 387-391.

ENTRINGER, GC; SANTOS, PHAD; VETTORAZZI, JCF; CUNHA, KS; PEREIRA, MG. 2014. Correlação e análise de trilha para componentes de produção de milho superdoce. *Revista Ceres* 6: 356-361.

GRIFFING, BA. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal Biology Science* 9: 463-493.

KASHIANI P; SALEH G. 2010. Estimation of genetic correlations on sweet corn inbred lines using SAS Mixed Model. *American Journal of Agricultural and Biological Sciences* 5: 309-314.

KASHIANI, P; SALEH, G; ABDULLA, NAP; SIN, MA. 2014. Evaluation of genetic variation and relationships among tropical sweet corn inbred lines using agronomic traits. *Maydica* 59: 275-282.

KWIATKOWSKI, A; CLEMENTE, E. 2007. Características do milho doce (*Zea mays* L.) para industrialização. *Revista Brasileira de Tecnologia Agroindustrial* 1: 93-103.

KWIATKOWSKI, A; CLEMENTE, E; SCAPIM, CA. 2011. Agronomic traits and chemical composition of single hybrids of sweet corn. *Horticultura Brasileira* 29: 531-536.

LEMOS, MA; GAMA, EEG; MENEZES, D; SANTOS, VF; TABOSA, JN. 2002. Avaliação de dez linhagens e seus híbridos de milho superdoce em um dialelo completo. *Horticultura Brasileira* 20: 167-170.

LUZ, JMQ; CAMILO, JS; BARBIERI, VHB; RANGEL, RM; OLIVEIRA, RC. 2014. Produtividade de genótipos de milho doce e milho verde em função de intervalos de colheita. *Horticultura Brasileira* 32: 163-167.

NARDINO, M; BARETTA, D; CARVALHO, IR; FOLLMANN, DN; KONFLANZ, VA; SOUZA, VQ; OLIVEIRA, AC; MAIA, LC. 2016. Correlações fenotípica, genética e de ambiente entre caracteres de milho híbrido da Região Sul do Brasil. *Revista Brasileira de Biometria* 34: 379-394.

PEREIRA FILHO, IA; CRUZ, JC; GAMA, EEG. 2002. Cultivares de milho para o consumo verde. In: PEREIRA FILHO, IA. (ed). *O cultivo do milho verde*. Brasília: Embrapa. p.17-27.

RICE, RR; TRACY, WF. 2013. Combining ability and acceptability of temperate sweet corn inbreds derived from exotic germplasm. *Journal of the American Society for Horticultural Science* 138: 461-469.

SANTOS, PHAD; PEREIRA, MG; TRINDADE, RS; CUNHA, KS; ENTRINGER, GC; VETTORAZZI, JCF. 2014. Agronomic performance of super-sweet corn genotypes in the north of Rio de Janeiro. *Crop Breeding and Applied Biotechnology* 14: 8-14.

SAS INSTITUTE. 2002. Getting started with the SAS learning edition. Cary: SAS Institute. 200p.

SOLOMON, KF; ZEPPA, A; MULUGETA, SD. 2012. Combining ability, genetic diversity and heterosis in relation to F_1 performance of tropically adapted shrunken (*sh2*) sweet corn lines. *Plant Breeding* 131: 430-436.

SOUZA, RS; VIDIGAL FILHO, PS; SCAPIM, CA; MARQUES, OJ; QUEIROZ, DC; OKUMURA, RS; RECHE, DL; CORTINOVE, VB. 2013. Produtividade e qualidade do milho doce em diferentes populações de plantas. *Semina: Ciências Agrárias* 34: 995-1010.

SUZUKAWA, AK; PEREIRA, CB; GARCIA, MM; CONTRERAS-SOTO, RI; ZEFFA, DM; COAN, AMD; SCAPIM, CB. 2018. Diallel analysis of tropical and temperate sweet and supersweet corn inbred lines. *Revista Ciência Agronômica* 49: 607-615.

TEIXEIRA, FF; MIRANDA, RA; PAES, MCD; SOUZA, SM; GAMA, EEG. 2013. Melhoramento do milho-doce. *Documentos/ Embrapa Milho e Sorgo* 154: 12-15.

VENCOVSKY, R; BARRIGA, P. 1992. Genética biométrica no fitomelhoramento. *Revista Brasileira de Genética* 365p.

WORRAJINDA, J; LERTRAT, K; SURIHARN, B. 2013. Combining ability of super sweet corn inbred lines with different ear sizes for ear number and whole ear weight. *SABRAO Journal of Breeding and Genetics* 45: 468-477.

YUWONO, PD; MURTI, RH; BASUNANDA, P. 2017. Heterosis and specific combining ability in sweet corn and its correlation with genetic similarity of inbred lines. *Journal of Agricultural Science* 9: 246-253.