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Diallel analysis of tropical and temperate sweet and supersweet corn inbred lines[1]

Análise dialélica de linhagens tropicais e temperadas de milho doce e super-doce

Andréia Kazumi Suzukawa[2], Carolina Bertuzzi Pereira[2], Mayara Mariana Garcia[2], Rodrigo Iván Contreras-Soto[3], Douglas Mariani Zeffa[2], Marlon Mathias Dacal Coan[2] and Carlos Alberto Scapim[2]*

ABSTRACT - The number of sweet corn cultivars adapted to the climatic conditions and with agronomic traits recommended to the Brazilian market is still limited. Thus, the aim was to investigate the general and specific combining ability (GCA and SCA, respectively) in relation to the grain yield (GY) and total soluble solid (TSS) contents of seven lines of sweet corn (*su*$_1$) and eight lines of supersweet corn (*sh*$_2$) by diallel crosses. For TSS, the inbred lines SC6 and SC7 of sweet corn, and SSC7 and SSC8 of supersweet corn showed higher GCA effect. For GY, the inbred lines SC1 and SC2 of sweet corn and SSC4 and SSC6 of supersweet corn showed higher GCA effect. For TSS in sweet corn, the hybrids '4 × 6' and '1 × 7' showed the superior $\hat{S}_{ij}$ estimates across all evaluated environments. For GY, the hybrid '5 × 7' was the most relevant because it showed higher $\hat{S}_{ij}$ estimates in most of the evaluated environments. Additionally, the hybrids '1 × 4', '3 × 4', and '1 × 7' showed positive $\hat{S}_{ij}$ values across all environments. In supersweet corn, the hybrids '2 × 8', '3 × 6', and '5 × 6' should be selected as the most promising for both traits (TSS and GY), because they presented positive and high $\hat{S}_{ij}$ estimates across the six environments.

Key words: *Zea mays* L. saccharata. General and specific combining ability. Grain yield. Total soluble solids.

RESUMO - O número de cultivares de milho doce adaptada às condições climáticas e com características agronômicas recomendadas para o mercado brasileiro ainda é restrito. Assim, objetivou-se investigar as capacidades de combinações gerais e específicas em relação ao rendimento de grãos (GY) e teor de sólidos solúveis totais (TSS) de sete linhagens de milho doce (*su*$_1$) e oito linhagens de milho super-doce (*sh*$_2$) pela análise de cruzamentos dialélicos. Para TSS, as linhagens SC6 e SC7 de milho doce, e SSC7 e SSC8 de milho super-doce apresentaram valores superiores para capacidade geral de combinação. Para rendimento de grãos, as linhagens SC1 e SC2 de milho doce, e SSC4 e SSC6 apresentaram valores superiores para capacidade geral de combinação. TSS em milho doce, os híbridos 4x6 e 1x7 apresentaram as estimativas $\hat{S}_{ij}$ superiores em todos os ambientes avaliados. Para GY, o híbrido 5x7 foi o mais relevante pois apresentou amais alta estimativa $\hat{S}_{ij}$ na grande maioria dos ambientes. Além disso, os híbridos 1x4, 3x4 e 1x7 destacaram-se com valores positivos em todos os ambientes. Em milho super-doce, os híbridos 2x8, 3x6 e 5x6 devem ser selecionados como os mais promissores para ambos os caracteres (TSS e GY), pois apresentaram estimativas $\hat{S}_{ij}$ positivas e altas nos seis ambientes.

Palavras-chave: *Zea mays* L. saccharata. Capacidades geral e específica de combinação. Rendimento de grãos. Sólidos solúveis totais.

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*Author for correspondence
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[1]Trabalho de Pesquisa ligado ao CNPq
[2]Departamento de Agronomia, Universidade Estadual de Maringá/UEM, MARINGA-PR, Brasil, kazumi.s@gmail.com, carol_bertuzzi@hotmail.com, garcia.mayaram@gmail.com, douglas.mz@hotmail.com, marloncoan@gmail.com, cascapim@uem.br
[3]Instituto de Ciencias Agronómicas y Veterinarias, Universidad de O'Higgins/UOH, Rancagua, Chile, contrerasudec@gmail.com

INTRODUCTION

Sweet corn (*Zea mays* L. saccharata) is considered one of the most popular vegetables in the US and Canada (TRACY, 2001) because of its improved shelf life and taste (DODSON-SWENSON; TRACY, 2015). In Brazil, the cultivation area of sweet corn is 36,000 ha (SANTOS *et al*., 2014), which represents only 14.4% of the area occupied by US sweet corn (UNITED STATES DEPARTMENT OF AGRICULTURE, 2014). The destination of sweet corn, mainly used as green maize, is exclusively for human consumption, due to the fact that it has sweet taste, fine pericarp and endosperm, and delicate texture (SA *et al.*, 2010; TEIXEIRA *et al*., 2001; TEIXEIRA *et al*., 2014; TRACY, 2001).

The sweetness of sweet corn is a recessive trait controlled by the mutant genes sugary 1 (su_1), shrunken 2 (sh_2), brittle 1 (bt_1), sugary enhancer (*se*) and brittle 2 (bt_2). These genes may act in a single, double or triple combination (SINGH; LANGYAN; YADAVA, 2014). All of them promote changes in carbohydrate composition in the endosperm and differ in the starch and sugar proportions in the kernel and in relation to chromosome position (TRACY, 2001). Supersweet corn is a variety of corn in which the homozygous hybrid has the shrunken-2 (sh_2) gene (TRACY, 2001; YOUSEF; JUVIK, 2002) with about a 9 to 14% sugar content, and present about 15 to 25% of accumulated sugar in the endosperm. This higher accumulation results in a longer harvesting period, which implies a slower conversion of sugar to starch (MARSHALL; TRACY, 2003).

Sweet corn breeding programs target quality characteristics such as flavor, sweetness, creamy texture, appearance, aroma and low starch content. Specifically, high productivity stands out as the main objective of sweet corn breeding programs (LERTRAT; PULAM, 2007). In Brazil, some government and private companies are working to develop commercial cultivars adapted to tropical conditions. However, the number of cultivars recommended for the Brazilian market is still small in relation to the growing demand. Currently, 58 cultivars are registered in Brazil, although there is still the possibility for research and development of new cultivars (BRASIL, 2016). In order to be successful in breeding programs, it is essential to know *a priori* the available lines of behavior, their performance *per se* and their hybrid combinations. In this context, the diallel crosses system is an efficient genetic design to obtain information on the genetic control of quantitative traits (JINKS; HAYMAN, 1953). The most common methodologies of diallel analysis used are those proposed by Griffing (1956), which estimates the general and specific combining ability and provides information on the predominance of genetic action; the method proposed by Gardner and Eberhart (1966), which evaluates the effects of varieties and varietal heterosis; and the method proposed by Hayman (1954), which provides information on the basic inheritance mechanisms, genetic values and selection limits.

Thus, the aim was to investigate the general and specific combining abilities based on diallel crosses of sweet and supersweet corn and their F1's in different environments and evaluate the quality and yield traits.

MATERIAL AND METHODS

Six inbred lines of sweet (su_1) and eight of supersweet corn (sh_2) in S6 were obtained from successive self-crosses. The descriptions of the inbred lines are shown in Table 1.

The joint analyses of variance for each trait were performed according to the randomized complete block design with three replications. For the sweet group (su_1), 21 F_1 hybrids were evaluated in five environments: E1-Maringá, E2-Iguatemi, E3-Cidade Gaúcha, E4-Sabáudia, and E5-Umuarama. The variety Doce Cristal was used as check, and for the supersweet group (sh_2), 28 F_1 hybrids were evaluated in six environments: E1-Maringá, E2-Iguatemi, E3-Cidade Gaúcha, E4-Sabáudia, E5-Umuarama and E6-Cascavel (Table 2). The hybrid Tropical Plus® (Syngenta) was used as check, because it is the most planted sweet corn cultivar in the country, and is considered a standard for the crop by breeders. For sweet and supersweet corn, the hybrids were arranged in randomized complete block design with three replications and were evaluated in the 2013–2014 crop season at each of the five and six environments, respectively. The plot size consisted of double rows with 5 m long, and 0.9 m spacing between rows, totaling a useful area of 9 m^2. Fertilizer and field management practices recommended for optimum maize production were used in each environment.

In each plot, ears had the husks removed and those more than 15 cm in length, greater than 3 cm in diameter and free of pests and diseases were weighed in order to determine the marketable grain yield (GY) without the husk. Grain yield (GY) adjusted to 70% moisture was computed from grain weight in kg ha^{-1}. Total soluble solid (TSS, °Brix) contents were determined using a digital refractometer (PAL -1, Atago Co., Ltd., Tokyo, Japan).

Bartlett's test with χ^2 distribution (p<0.05) was applied to verify the homogeneity of residual variances and thus performed the joint analysis of environments.

The model of the joint analysis studied was as follows:

$$Y_{ijk} = \mu + B_{(j)k} + G_i + E_j + GE_{ij} + \varepsilon_{ijk} \quad (1)$$

where: Y_{ijk} is the observation of the k^{th} block, evaluated in the i^{th} genotype and in the j^{th} environment; μ is the overall mean; $B_{(j)k}$ is the effect of the block *k* within environment *j*; G_i is the effect of the genotype *i*; E_j effect of the environment *j*; GE_{ij} is the effect of interaction between genotype *i* and the environment *j*; ε_{ijk} is the experimental error associated to the *ijk* observation.

The joint diallel analysis for Griffing's method 4 (GRIFFING, 1956) is illustrated in Table 3 and represented by the following model:

$$Y_{ijk} = \mu + g_i + g_j + e_K + S_{ij} + (eg)_{ik} + (eg)_{jk} + (es)_{ijk} + \bar{E}_{ijk} \quad (2)$$

where: Y_{ijk} is the overall mean observed between the hybrid combination of the i^{th} inbred line and the j^{th} inbred line (i ≠ j) into the k^{th} environment; μ is the overall mean; *e* is the environment effect; g_i is the general combining ability effect associated to the i^{th} inbred line; g_j is the general combining ability effect associated to the j^{th} inbred line; S_{ij} is the specific combining ability effect between the inbred lines *i* and *j*; $(eg)_{ik}$ e $(eg)_{jk}$ is the general combining ability effect of the inbred lines with environments; $(es)_{ijk}$ is the specific combining ability effect between the i^{th} and j^{th} inbred lines with environments, and $\bar{E}_{ijk}$ is the mean experimental error. The degrees of freedom of the genotype × environment interaction (G × E) were partitioned into the effects of GCA × E and SCA × E, according to Vencovsky and Barriga (1992) (Table 3).

Table 1 - Description of the seven inbred lines of sweet corn (su_1) and eight inbred lines of supersweet corn (sh_2) used at the diallel crosses

Inbred line	Origin and description
SC1	Sweet corn (su_1), Doce Cristal
SC2	Sweet corn (su_1), Doce Cubano
SC3	Sweet corn (su_1), Doce Cubano
SC4	Sweet corn (su_1), Doce 43 In (Viçosa)
SC5	Sweet corn (su_1), Doce Cristal
SC6	Sweet corn (su_1), Doce 13 In (Viçosa)
SC7	Sweet corn (su_1), Doce I (EMBRAPA)
SSC1	Supersweet corn (sh_2), Inbred line extracted of Tropical Plus®
SSC2	Supersweet corn (sh_2), Inbred line extracted of Tropical Plus®
SSC3	Supersweet corn (sh_2), Inbred line extracted of American commercial hybrid (Doce Garden)
SSC4	Supersweet corn (sh_2), Inbred line extracted of the commercial hybrid Splendor (Syngenta)
SSC5	Supersweet corn (sh_2), Inbred line extracted of RB6324
SSC6	Supersweet corn (sh_2), Inbred line extracted of RB6324
SSC7	Supersweet corn (sh_2), Inbred line of Bônus (Syngenta)
SSC8	Supersweet corn (sh_2), Inbred line extracted of Penta (common maize) with the gene $sh_2 sh_2$

Table 2 - Geographic location, altitude and climate classification of the environments

Environments	Geographic location	Altitude (m)	Climate classification[a]
E1 - Maringá	23º25' S; 51º57' W	596	Cfa
E2 - Iguatemi	23º25' S; 51º57' W	550	Cfa
E3 - Cidade Gaúcha	23º21' S; 52º55' W	350	Cfa
E4 - Sabáudia	23º19' S; 51º33' W	690	Cfa
E5 - Umuarama	23º45' S; 53º19' W	447	Cfa
E6 - Cascavel	24º57' S; 53º27' W	782	Cfa

[a]Köppen climate classification (MCKNIGHT; HESS, 2000)

Table 3 - Summary of analysis of variance for total soluble solids (TSS) and grain yield (GY), conducted at different environments in 2013/2014 crop season for sweet and supersweet corn

Sources of variation	DF	Sweet corn Mean squares		DF	Supersweet corn Mean squares	
		TSS	GY		TSS	GY
Genotypes (G)	20	303.5*	132,993,227.7*	27	128.2*	125,561,540.4*
GCA	6	281.6*	140,698,466.6*	7	59.3*	484,615,82.5*
SCA	14	312.9*	129,690,982.4*	20	152.3*	152,546,525.6*
Environments (E)	4	17.6*	1,399,882.7*	5	5.3*	6,558,525.5*
G x E	80	46.2*	17,107,874.6*	135	4.1*	1,647,710.8^{ns}
GCA x E	24	29.8*	14,023,044.9*	35	3.6*	1,562,902.0^{ns}
SCA x E	56	53.3*	18,429,944.5*	100	4.2*	1,677,393.9^{ns}
Residual mean	300	2.2	1,731,602.2	486	2.1	1,409,854.9
Mean		18.5	16,785.99		18.1	15,160.0
CV (%)		8.0	8.72		8.1	7.1

* and ^{ns} = significant and non-significant at 5% probability according to F-test; DF = degrees of freedom; CV (%) = mean coefficient of environmental variation

Phenotypic, genotypic and environmental correlation between total soluble solids and grain yield for sweet and supersweet corn was implemented into the software GENES (CRUZ, 2013).

RESULTS AND DISCUSSION

In sweet and supersweet corn, for TSS and GY, Bartlett's test showed homogeneity of residual mean squares among the individual analyses (data not shown). Thereby, joint analysis of variance was conducted for sweet and supersweet corn across the five environments and six environments, respectively.

In sweet and supersweet corn, the average environmental coefficient of variation showed values of 8.00 and 8.10% for TSS, and 8.70 and 7.10% for GY, respectively (Table 3). These mean values were considered low when compared with Assunção *et al.* (2010) and Kwiatkowski, Clemente and Scapim (2011), suggesting the reliability of our results.

For GY and TSS, statistical differences (p<0.05) were observed among the sweet and supersweet inbreds and hybrids. Furthermore, for TSS and GY, significant (p<0.05) effects were observed for the G × E mean squares, except for the GY of supersweet corn (Table 3). The significant differences detected for both sweet and supersweet corn among the inbreds and hybrids for TSS and GY indicated that there was adequate genetic variability among the inbreds and hybrids to allow satisfactory progress from selection for the improvement of traits. These results were consistent with the findings of Allam *et al.* (2016), Djemel *et al.* (2015), Ordás *et al.* (2010), and Revilla *et al.* (2010), and represent a relevant report, since there is a need for lines to be adapted to different environments to obtain superior hybrids.

In sweet corn, both GCA and SCA effects for TSS and GY were estimated by environment because their interaction was significant (p<0.05) (Tables 4 and 5). The lines SC6 and SC7 showed the higher and more positive estimates of GCA ($\hat{g}_i$) across the five evaluated environments for TSS, suggesting that both inbred lines could generate promising hybrid combinations. For GY, the lines SC1 and SC2 showed higher and more positive estimates of GCA ($\hat{g}_i$) across the five evaluated environments. Hence, these inbred lines could contribute positively to their crossing, suggesting that higher and positive estimates of GCA could represent favorable allele frequencies when compared to contrasting lines in the diallel result.

In supersweet corn, for GY, GCA and SCA effects were estimated based on environment general mean, on the other hand, for TSS, GCA and SCA effects were estimated by environment, since GCA and SCA by environments were significant (p<0.05) (Tables 6 and 7). For GY, the lines SSC4 and SSC6 showed the higher and positive estimates of GCA ($\hat{g}_i$) across the mean of the six evaluated environments. For TSS, the lines SSC7 and SSC8 showed the best performance at the six evaluated environments revealing positive estimates of $\hat{g}_i$. Consequently, these inbreds contribute with additive genetic effect and could increase the contents of TSS. In supersweet corn, the inbred line SSC4 showed positive estimates of $\hat{g}_i$ for TSS in five of the six evaluated environments and positive average $\hat{g}_i$ across environments for GY. However, the GY estimate showed low values compared to the other inbred lines (Table 6).

Table 4 - Estimates of general combining ability for total soluble solids (TSS) and grain yield (GY) in seven inbred lines of sweet corn evaluated in five environments (E1: Maringá, E2: Iguatemi, E3: Cidade Gaúcha, E4: Sabáudia and E5: Umuarama)

Inbred lines	TSS (°Brix)					GY (kg ha^{-1})				
	E1	E2	E3	E4	E5	E1	E2	E3	E4	E5
SC1	-0.2	-0.5	-0.8	-2.9	-1.5	73	147	377	193	193
SC2	0.3	0.7	-0.9	-1.2	0.4	1160	894	612	1360	1087
SC3	-4.1	-1.2	-4.1	-1.8	-4.5	-669	-1464	-826	-1298	-929
SC4	0.3	-0.6	-0.2	2.6	1.0	1535	2214	2159	-229	2772
SC5	1.7	1.2	2.3	-1.1	1.0	-236	298	-43	390	-1010
SC6	0.7	0.0	1.3	1.6	2.0	536	-469	707	-841	529
SC7	1.5	0.3	2.3	2.8	1.6	-2400	-1620	-2986	425	-2642

Table 5 - Estimates of specific combining ability for total soluble solids (TSS) and grain yield (GY) in 21 hybrids of sweet corn evaluated in five environments (E1: Maringá, E2: Iguatemi, E3: Cidade Gaúcha, E4: Sabáudia and E5: Umuarama)

Hybrids	TSS (°Brix)					GY (kg ha^{-1})				
	E1	E2	E3	E4	E5	E1	E2	E3	E4	E5
1x2	0.9	-2.5	-0.3	-0.3	-2.5	-2804	-4945	-1461	-1901	-4155
1x3	-0.5	1.6	-0.6	3.5	-0.9	-746	512	-2545	-895	-1046
1x4	-1.9	-1.4	-1.7	-3.9	-1.8	1525	3722	2712	202	2462
1x5	-5.8	-5.8	-7.4	1.5	-6.6	-2039	-2655	-2461	704	-1976
1x6	1.7	3.7	0.6	-1.9	1.4	3274	97	3698	-162	4092
1x7	5.6	4.4	9.3	1.1	10.5	790	3269	57	2051	623
2x3	0.3	3.5	4.5	6.1	0.0	1823	2254	1923	-1067	2159
2x4	-0.9	-0.3	-5.2	-8.1	0.5	2724	2883	-14	2059	1507
2x5	0.4	0.8	1.7	5.6	1.5	-2725	-4076	-3329	1865	-2652
2x6	-2.5	-2.7	-1.9	0.6	-2.0	1636	5174	2181	-1145	2629
2x7	1.9	1.3	1.1	-3.8	2.6	-655	-1290	699	190	512
3x4	-1.2	-3.5	-2.2	-2.0	-0.8	1802	810	4379	698	1936
3x5	1.1	0.9	0.6	-2.8	1.9	-1510	-2157	-2626	2006	-3293
3x6	-3.1	-5.6	-4.2	2.2	-4.4	-590	-1426	-515	199	758
3x7	3.5	3.1	1.8	-7.0	4.3	-780	8	-616	-942	-515
4x5	1.9	1.6	5.0	2.0	1.4	1052	3823	3441	-2352	4442
4x6	8.0	9.8	10.5	4.3	9.7	-3969	-6539	-6481	2168	-6294
4x7	-5.9	-6.2	-6.4	7.6	-8.9	-3134	-4700	-4038	-2775	-4053
5x6	1.8	0.0	0.5	-6.8	2.9	546	2523	1097	-2379	-570
5x7	0.7	2.5	-0.3	0.5	-1.0	4676	2541	3878	156	4048
6x7	-5.8	-5.1	-5.6	1.6	-7.5	-898	171	19	1319	-615

Table 6 - Estimates of general combining ability for total soluble solid (TSS) and grain yield (GY) in eight inbred lines of supersweet corn evaluated in six environments (E1: Maringá, E2: Iguatemi, E3: Cidade Gaúcha, E4: Sabáudia, E5: Umuarama and E6: Cascavel)

Inbred lines	TSS (°Brix)						GY (kg ha^{-1}) Mean
	E1	E2	E3	E4	E5	E6	
SSC1	-0.93	-1.16	-1.15	-1.26	-0.93	-1.26	-567
SSC2	0.57	1.26	-0.27	0.41	0.32	0.45	-186
SSC3	-0.59	-0.70	-1.15	-0.22	-0.72	-1.39	-936
SSC4	0.74	0.26	0.69	0.20	0.57	-0.14	765
SSC5	0.03	-0.41	0.35	-0.30	-0.26	0.41	216
SSC6	-0.22	-0.37	-0.52	0.03	0.37	0.45	659
SSC7	0.03	0.55	1.23	0.41	0.07	0.70	190
SSC8	0.37	0.55	0.81	0.74	0.57	0.78	-142

Table 7- Estimates of specific combining ability for total soluble solid (TSS) and grain yield (GY) in 28 hybrids of supersweet corn evaluated in six environments (E1: Maringá, E2: Iguatemi, E3: Cidade Gaúcha, E4: Sabáudia, E5: Umuarama and E6: Cascavel)

Hybrids	TSS (°Brix)						GY (kg ha^{-1}) Mean
	E1	E2	E3	E4	E5	E6	
1x2	3.70	2.48	1.94	2.60	2.52	3.02	-5
1x3	-2.88	-2.82	-1.19	-0.03	-2.19	-2.40	-808
1x4	2.79	2.23	1.98	2.80	3.52	2.60	66
1x5	0.49	-0.36	0.06	0.30	0.86	0.31	-2316
1x6	-2.76	-2.90	-2.32	-4.28	-3.52	-3.73	2934
1x7	1.99	2.94	2.94	0.60	2.52	3.02	-2706
1x8	-3.34	-1.57	-3.40	-1.99	-3.73	-2.82	2834
2x3	-1.38	-0.23	0.19	-1.45	-0.69	-0.61	-1450
2x4	1.54	1.06	2.85	1.89	1.52	2.39	2687
2x5	-4.51	-4.27	-5.82	-3.61	-4.89	-3.65	-3954
2x6	-1.26	-2.07	-0.94	0.30	-0.77	-2.19	-1904
2x7	-0.76	1.27	-0.94	-1.07	0.52	-0.19	1294
2x8	2.66	1.77	2.73	1.35	1.77	1.23	3332
3x4	-2.55	-1.48	-1.77	-2.74	-1.69	-5.27	-1113
3x5	1.16	0.94	-0.69	1.76	2.40	1.69	3421
3x6	2.91	3.39	2.44	2.93	1.52	4.14	1252
3x7	-1.09	-3.52	-1.32	-1.95	-2.94	-1.86	-1166
3x8	3.83	3.73	2.35	1.47	3.57	4.31	-135
4x5	2.58	2.73	1.48	0.35	-0.14	2.69	146
4x6	-0.67	-0.57	-1.40	-1.99	0.23	-0.11	-1389
4x7	-0.42	-0.48	0.10	2.64	-0.23	-0.61	2947
4x8	-3.26	-3.48	-3.23	-2.95	-3.23	-1.69	-3343
5x6	1.29	2.10	3.94	2.01	1.82	0.85	2982
5x7	-2.21	-1.82	-1.07	-2.61	-1.89	-2.15	417
5x8	1.20	0.69	2.10	1.80	1.86	0.27	-696
6x7	2.04	1.39	-0.44	1.55	1.48	2.06	-1334
6x8	-1.55	-1.36	-1.27	-0.53	-0.77	-1.02	-2540
7x8	0.45	0.23	0.73	0.85	0.52	-0.27	548

In sweet and supersweet corn breeding programs, the identification of inbred lines with high favorable genes for GY and grain quality traits such as TSS is highly desirable. However, in the present study, no inbred lines showed this condition. Similar results were showed by Ha (1999) and Kumari, Gadag and Jha (2007) who mentioned the difficulty in finding hybrids showing high GY and TSS.

In sweet corn, as mentioned, the GCA and SCA effects were estimated by environment. Consequently, our results indicated that hybrid vigor or positive heterosis is a major factor in the superior performance of F_1s in terms of TSS. This confirms similar findings in sweet corn (ASSUNÇÃO *et al*., 2010; KHANDURI *et al*., 2010; SOLOMON; MARTIN; ZEPPA, 2012). Thus, for TSS, the hybrids '4 × 6' and '1 × 7' showed the superior $\hat{S}_{ij}$ estimates across all the evaluated environments. For GY, the hybrid '5 × 7' was the most relevant because it showed the best $\hat{S}_{ij}$ estimates (across environment means). Additionally, the hybrids '1 × 4', '3 × 4', and '1 × 7' showed positive $\hat{S}_{ij}$ values across all environments. In fact, the simultaneous selection of hybrids based on both traits indicated that the hybrid '1 × 7' was the most promising.

In supersweet corn, the hybrids '2 × 8', '3 × 6', and '5 × 6' should be selected as the most promising for both traits, because they presented positive and high $\hat{S}_{ij}$ estimates across the six environments. These hybrids have at least one of the parents with high GCA (inbred line SSC8 for TSS and SSC6 for GY).

In sweet corn, the hybrids '1 × 7' and '4 × 6' showed the highest percentages of TSS, surpassing the Doce Cristal check. Specifically, the hybrid '4 × 6' demonstrated the best performance for TSS across all evaluated environments, with values ranging from 27 (Environment E4) to 32 °Brix (Environment E5). These TSS values were higher than those reported by Pinho *et al*. (2010). For GY, the hybrids did not show a similar pattern of behavior. Consequently, none of the sweet corn hybrids could be considered as superior for TSS and GY, simultaneously. For supersweet corn, the hybrids '2 × 4', '2 × 8', and '3 × 8' showed the best performances for TSS across all the evaluated environments, with similar or superior behavior than that of the Tropical Plus® check.

The genotypic, phenotypic and environmental correlation for TSS and GY, in both sweet and supersweet corn, was not significant in most of the evaluated environments. Only, in supersweet corn in environments E1, E2, E3 and E4, positive and significant phenotypic correlation was observed for TSS and GY (Table 8). On the other hand, in supersweet corn, non-significant genotypic and environmental correlations were observed between these traits in the same environments. There are very few studies correlating GY with TSS in sweet and supersweet corn, but our results may indicate that there is no possibility for indirect selection in sweet and supersweet corn breeding programs, because genetic gain in TSS through indirect selection of GY will not be possible.

Table 8 - Genotypic, phenotypic and environmental correlation for total soluble solids and grain yield in sweet and supersweet corn by environments

Correlation	Supersweet corn					
	E1	E2	E3	E4	E5	E6
Genotypic	0.40^{ns}	0.44^{ns}	0.44*	0.41^{ns}	0.35^{ns}	0.20^{ns}
Phenotypic	0.37*	0.40*	0.42*	0.37*	0.32^{ns}	0.18^{ns}
Environmental	0.02^{ns}	-0.15^{ns}	0.16^{ns}	0.02^{ns}	-0.02^{ns}	0.02^{ns}
Correlation	Sweet corn					
	E1	E2	E3	E4	E5	
Genotypic	0.10^{ns}	0.02^{ns}	-0.11^{ns}	-0.27^{ns}	-0.01^{ns}	
Phenotypic	-0.03^{ns}	0.03^{ns}	-0.10^{ns}	-0.04^{ns}	-0.01^{ns}	
Environmental	-0.02^{ns}	0.02^{ns}	0.02^{ns}	0.06^{ns}	-0.1^{ns}	

* = significant at 5% of probability by t-test; ns = not significant by t-test

CONCLUSIONS

1. For TSS, the inbred lines SC6 and SC7 of sweet corn, and SSC7 and SSC8 of supersweet corn, showed superior GCA effects. For GY, the inbred lines SC1 and SC2 of sweet corn, and SSC4 and SSC6 of supersweet corn, showed higher GCA effects;
2. For TSS in sweet corn, the hybrids ‘4 × 6’ and ‘1 × 7’ showed the most favorable $\hat{S}_{ij}$ estimates across all the evaluated environments, and for GY, the hybrid ‘5 × 7’ was the most relevant because it showed the most favorable $\hat{S}_{ij}$ estimates. In supersweet corn, the hybrids ‘2 × 8’, ‘3 × 6’, and ‘5 × 6’ should be selected as the most promising for both traits (TSS and GY), because they showed positive and high $\hat{S}_{ij}$ estimates across the six environments.

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