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Research Article

Topcross in supersweet corn doubled haploids for the formation of heterotic groups and hybrid selection[1]

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ABSTRACT

Doubled haploid technology is widely used in conventional corn to accelerate the development of inbred lines. This study aimed to estimate the combining ability of supersweet corn doubled haploid lines, identify new tester lines and establish heterotic groups. Two tester lines (L_A and L_B) were crossed with 28 doubled haploid lines of six supersweet corn populations using the topcross method and evaluated together with five checks for dehusked ear yield, ear diameter, plant height and soluble solids content. The growing seasons and treatments had significant effects on all the investigated traits, as well as season x treatment interaction on ear yield and diameter. The H_{A1}, H_{B1}, H_{B12}, H_{B13}, H_{B14}, H_{B15}, H_{B19}, H_{B20} and H_{B22} hybrids exhibited a superior performance, with average yields ranging from 11.95 to 15.39 t ha^{-1}, and were grouped with the commercial check and Test$_3$. The L_B and L_{19} lines showed the best general combining ability estimates for yield. There were significant specific combining ability effects for most variables. The lines obtained from the PD2005 and PD2006 populations were allocated to the same heterotic group as L_B, and those from the synthetic populations SD3002 and SD3003 to the same group as L_A. The L_{19} line shows potential of use as a tester for SD3005 lines.

KEYWORDS: *Zea mays* L. var. *saccharata* Koern, combining ability, tester lines.

RESUMO

Topcross em duplo-haploides de milho superdoce na formação de grupos heteróticos e na seleção de híbridos

A tecnologia de duplo-haploide é amplamente utilizada em milho comum para acelerar a obtenção de linhagens. Objetivou-se estimar o potencial combinatório de linhagens duplo-haploides de milho superdoce, identificar novas linhagens testadoras e estruturar grupos heteróticos. Duas linhagens testadoras (L_A e L_B) foram cruzadas com 28 linhagens duplo-haploides de seis populações de milho superdoce, segundo um esquema de *topcross*, e avaliadas juntamente com cinco testemunhas para produtividade de espiga sem palha, diâmetro de espiga, altura de planta e teor de sólidos solúveis. Houve efeitos significativos de safras e tratamentos para todas as características e de interação safra x tratamento para produtividade e diâmetro de espigas. Os híbridos H_{A1}, H_{B1}, H_{B12}, H_{B13}, H_{B14}, H_{B15}, H_{B19}, H_{B20} e H_{B22} se destacaram com médias de produtividade entre 11,95 e 15,39 t ha^{-1}, ficando no mesmo grupo da testemunha comercial e Test$_3$. As linhagens L_B e L_{19} apresentaram as melhores estimativas de capacidade geral de combinação para produtividade. Houve efeitos significativos de capacidade específica de combinação para a maioria das variáveis. As linhagens das populações PD2005 e PD2006 foram alocadas no mesmo grupo heterótico de L_B e as das populações sintéticas SD3002 e SD3003 no mesmo grupo de L_A. A linhagem L_{19} tem potencial de uso como testadora para linhagens de SD3005.

PALAVRAS-CHAVE: *Zea mays* L. var. *saccharata* Koern, capacidade combinatória, linhagens testadoras.

INTRODUCTION

Corn (*Zea mays* L.) is one of the most important crops worldwide, with cultivars developed for grain production and specialty applications, distinguished by specific traits and industrial uses, such as supersweet corn (*Zea mays* L. var. *saccharata* Koern) (Swapna et al. 2020).

Supersweet corn is grown globally for fresh consumption or use in canned goods. It originated from naturally occurring, homozygous recessive genetic mutations, primarily in the *brittle-1* (*bt_1*) and *shrunken-2* (*sh_2*) genes, resulting in high kernel sugar concentrations (15-25 %) at the green corn stage (Teixeira et al. 2013, Heryanto et al. 2022). Approximately 75 % of the processing industry

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and almost 100 % of the fresh market use hybrids that include the supersweet sh_2 mutation (Hu et al. 2021). However, according to the Brazilian Ministry of Agriculture, Livestock and Supply, by December 2024, only three supersweet corn cultivars were registered, being two single-cross hybrids (UENF SD 09 and UENF SD 08) and one open-pollinated variety (BRS Deni) (Brasil 2025), whereas 72 cultivars were registered as sweet corn. This suggests that a significant portion of these cultivars may be more accurately classified as supersweet.

Brazil produced approximately 204,063 t of processed or preserved sweet corn in 2022, with a market value of R$ 1.72 billion (IBGE 2022). These figures do not distinguish between sweet and supersweet corn.

Breeding programs for sweet and supersweet corn are largely aimed at developing inbred lines for hybrid production, since hybrids better meet industrial and market demands for higher yields, uniform maturity and desirable ear shape and size (Teixeira et al. 2013).

Supersweet lines are typically obtained by the traditional method of six to eight self-pollination cycles, aimed at achieving high homozygosity. However, as with conventional maize varieties, doubled haploid technology is an effective alternative for obtaining 100 % of homozygous lines within two or three generations, which could significantly accelerate supersweet corn breeding programs (Duarte 2024). Nevertheless, there are few reports on the development of doubled haploid supersweet corn lines and their performance in crosses for hybrid production, making it important to further investigate the use of this technology in supersweet corn (Sekiya et al. 2020).

The steps for obtaining doubled haploid lines include: a) haploid induction in donor populations through crosses with different inducer genotypes, each with different induction rates, such as CIM2GTAILs (10-14 %) (Chaikam et al. 2018); b) putative haploid seed selection; c) chromosome doubling using different protocols involving the immersion of seeds and newly germinated seedlings (Gayen et al. 1994, Deimling et al. 1997); immersion of seedling roots at the V2 stage (Chaikam et al. 2020) and injection at the base of the apical meristem in V2/V3 seedlings (Eder & Chalyk 2002); d) multiplication of doubled haploid seeds via self-pollination (Khulbe & Pattanayak 2021).

The resulting doubled haploid lines must be assessed for both *per se* performance and performance in hybrid combinations. Evaluating *per se* performance aims to determine the potential of an individual line for seed multiplication and economically viable hybrid development, while assessing combining potential involves using diallel or topcross methods among lines from different heterotic groups, enabling a better exploitation of heterosis effects (Pinto et al. 2001).

Heterotic groups are more closely related genotypes that, when crossed, do not exhibit high heterosis or produce high-performing hybrids. However, crosses between genotypes from different heterotic groups tend to result in greater heterosis and superior hybrids (Hallauer et al. 2010, Akinwale et al. 2014). As such, lines from a heterotic group are evaluated in crosses with a limited number of elite lines from another heterotic group (topcross). This is more efficient than diallel crosses because it reduces the number of hybrid combinations required for assessment, allowing a greater number of lines to be tested (Sawazaki et al. 2000).

Genetic divergence among lines in diallel and topcross designs is assessed based on the concepts of general (GCA) and specific combining ability (SCA) (Sprague & Tatum 1942). GCA is mainly associated with additive gene effects and SCA is primarily determined by non-additive gene effects (dominance and epistasis) (Pinto et al. 2001).

In the development of superior hybrids, line combinations must have high SCA estimates, and at least one of the hybrid parents must have a high GCA estimate (Cruz 2006). Thus, prior identification of heterotic groups can improve yield gains and accelerate hybrid production in supersweet corn breeding programs.

This study aimed to estimate the combining ability of supersweet corn doubled haploid lines for hybrid synthesis through topcrosses with two elite lines, identify new tester lines and allocate doubled haploids from different populations into heterotic groups.

MATERIAL AND METHODS

Two supersweet corn populations (PD2005 and PD2006) and four synthetic varieties (SD3001, SD3002, SD3003 and SD3005), homozygous for the sh_2 gene, were used. These were developed by the Universidade Estadual de Londrina (UEL).

The experiment was conducted at the UEL school farm (23º20'32"S, 51º12'34"W and 550 m of altitude), in Eutroferric Red Oxisol (Rocha et a. 1991), during the second growing season of 2021.

The supersweet populations were pollinated by the inducing hybrid resulting from the cross between the CIM2GTAIL-P1 x CIM2GTAIL-P2 lines, developed by the International Maize and Wheat Improvement Center (CIMMYT). This inducing genotype carries the *R1-nj* marker gene, responsible for anthocyanin expression, which gives the aleurone a purple color. This trait is useful for identifying putative haploid seeds. Thus, the induced F1 seeds were selected based on expression of this gene and classified as diploids (seeds with a purple aleurone and embryo) and haploids (seeds with only a purple aleurone) (Figure 1).

In the 2021/2022 growing season, under greenhouse conditions, the haploid seeds were sown in trays containing peat and grown until V2, when the false haploids were eliminated based on greater seedling vigor and purple coloration of the first leaf sheath, traits absent in the supersweet corn populations used (Sekiya et al. 2020). Next, the haploid seedlings were subjected to chromosomal doubling treatment by injecting 100 µl of a 0.125 % colchicine solution containing 0.5 % DMSO. The solution was injected directly into the basal meristematic tissue at the center of the first leaf sheath of the seedlings, using a syringe and hypodermic needle, aimed at restoring fertility (Eder & Chalyk 2002) (Figure 1). The treated seedlings were transplanted into 12-L pots containing a mixture of soil, sand and organic fertilizer at a 3:1:1 ratio. The plants whose fertility was restored via chromosomal doubling were subjected to self-pollination, making it possible to obtain different numbers of doubled haploid lines from each population (Figure 1).

In the second growing season of 2022, 30 supersweet doubled haploid lines from the UEL breeding program were multiplied. These lines were selected based on *per se* performance for different phenotypic traits and seed yield. In the 2022/2023 growing season, the elite supersweet lines SD3002(D18)5-2 (L_A) and SD3005(D17)10-2 (L_B) were used as testers in a topcross breeding design with the 28 remaining lines (Table 1). Four

Photos: Josué Maldonado Ferreira

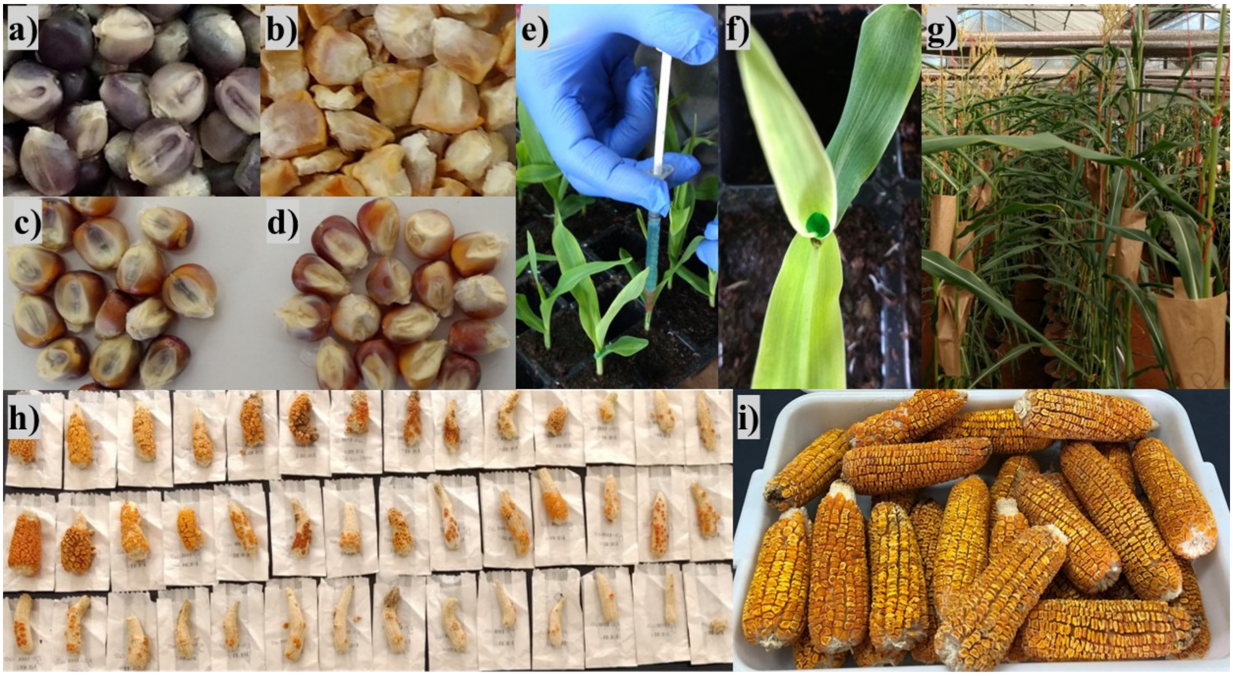

Figure 1. Obtaining supersweet corn doubled haploid lines: a) seeds of the haploid inducer hybrid (CIM2GTAIL-P1 x CIM2GTAIL-P2); b) seeds from the supersweet corn donor population; c) selection of diploid seeds from the F1 ear; d) selection of haploid seeds from the F1 ear; e) injection of colchicine solution into the basal meristem; f) droplet of colchicine solution that emerged during injection, indicating correct application; g) self-pollination of doubled haploid plants whose fertility was restored by chromosomal doubling; h) ears from the doubled haploid lines; i) ears from a multiplied doubled haploid line used in topcross breeding.

experimental hybrids and the Bayer supersweet hybrid SV9298SN were used as checks (Test5).

The experiment was conducted in a randomized complete block design, with two replicates, each consisting of 4-m-long single-row plots spaced at 0.80 x 0.20 m. Evaluations were carried out in the 2023/2024 (first) and 2024 (second) growing seasons, with sowing on October 19, 2023, and March 1, 2024, respectively. Crop management followed technical recommendations for maize. Harvesting was performed at the green corn stage (90 to 100 days after sowing).

The following traits were assessed in both seasons: a) dehusked ear yield (t ha^{-1}); b) ear diameter (cm): average of 5 ears plot^{-1}; c) plant height (cm): average of 3 plants plot^{-1}; d) total soluble solids (ºBrix). The dehusked ear yield data were adjusted to the ideal stand of 20 plants plot^{-1} (Vencosky & Barriga 1992) and then extrapolated to t ha^{-1}.

Table 1. Topcross breeding design between supersweet doubled haploid lines, involving two testers (L_A and L_B) and 28 tested lines (L_1 to L_{28}), along with hybrid checks (Test).

Origin		SD3002(D18)-5-2	SD3005(D17)-10-2
		L_A	L_B
PD2005(D21)-001	L_1	H_{A1}	H_{B1}
PD2005(D21)-002	L_2	H_{A2}	H_{B2}
PD2006(D21)-001	L_3	H_{A3}	H_{B3}
PD2006(D21)-002	L_4	H_{A4}	H_{B4}
SD3001(D21)-001	L_5	H_{A5}	H_{B5}
SD3001(D21)-002	L_6	H_{A6}	H_{B6}
SD3001(D21)-003	L_7	H_{A7}	H_{B7}
SD3001(D21)-004	L_8	H_{A8}	H_{B8}
SD3001(D21)-005	L_9	H_{A9}	H_{B9}
SD3002(D21)-001	L_{10}	H_{A10}	H_{B10}
SD3002(D21)-002	L_{11}	H_{A11}	H_{B11}
SD3002(D21)-003	L_{12}	H_{A12}	H_{B12}
SD3002(D21)-004	L_{13}	H_{A13}	H_{B13}
SD3003(D21)-001	L_{14}	H_{A14}	H_{B14}
SD3003(D21)-002	L_{15}	H_{A15}	H_{B15}
SD3003(D21)-003	L_{16}	H_{A16}	H_{B16}
SD3003(D21)-004	L_{17}	H_{A17}	H_{B17}
SD3003(D21)-005	L_{18}	H_{A18}	H_{B18}
SD3003(D21)-006	L_{19}	H_{A19}	H_{B19}
SD3003(D21)-007	L_{20}	H_{A20}	H_{B20}
SD3003(D21)-008	L_{21}	H_{A21}	H_{B21}
SD3003(D21)-009	L_{22}	H_{A22}	H_{B22}
SD3003(D21)-010	L_{23}	H_{A23}	H_{B23}
SD3005(D21)-001	L_{24}	H_{A24}	H_{B24}
SD3005(D21)-002	L_{25}	H_{A25}	H_{B25}
SD3005(D21)-003	L_{26}	H_{A26}	H_{B26}
SD3005(D21)-004	L_{27}	H_{A27}	H_{B27}
SD3005(D21)-005	L_{28}	H_{A28}	H_{B28}
Checks			
SD3002(D18)5-2 x SD3005(D17)10-2			$Test_1$
SD3005(D17)10-2 x SD3002(D18)5-2			$Test_2$
SD3005(D17)10-2 x PD3001(D17)-001			$Test_3$
SD3002(D18)5-2 x SD3003(D18)-001			$Test_4$
SV9298SN			$Test_5$

Individual and combined analyses of variance were performed in the SAS statistical software and the treatment means grouped by the Scott-Knott test at 5 % of probability, using the Genes software.

The statistical model used for individual analysis was: $Y_{ij} = m + t_i + b_j + e_{ij}$, where Y_{ij} is the observed value for the *i*-th treatment in the *j*-th block; m the overall mean; t_i the fixed effect of the *i*-th treatment; b_j the random effect of the *j*-th block; and e_{ij} the random error associated with the *i*-th treatment in the *j*-th block.

The treatment effects from the individual analyses were partitioned into effects of the checks and topcross hybrids, and the comparison between checks and topcross hybrids. The degrees of freedom for the topcross hybrids were further partitioned into GCA of the tester (GCA-I) and tested lines (GCA-II), and SCA, using a statistical model adapted from Griffing (1956): $Y_{ij} = m + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + e_{ij}$, where: Y_{ij} is the mean value of the hybrid combination between the *i*-th tester line and *j*-th tested line; m the overall mean of the topcross hybrids; $\hat{g}_i$ the GCA effect of the *i*-th tester line; $\hat{g}_j$ the GCA effect of the *j*-th tested line; $\hat{s}_{ij}$ the SCA effect between the *i*-th and *j*-th parents; e_{ij} the experimental error associated with the mean. Model estimates and the corresponding sums of squares were obtained using the least squares method $X'X\beta = X'Y$, where Y is the vector of observed hybrid means (topcross); X the design matrix containing the constants (0 and 1) associated with the parameters m, $\hat{g}_i$, $\hat{g}_j$ and $\hat{s}_{ij}$; β the vector of these parameters; and ε the vector of the residual errors (e_{ij}) (Cruz 2006).

The Hartley's test was used to assess the homogeneity of variances across the experiments for each growing season, and combined analysis was performed in the SAS software. The mathematical model used for combined analysis was $Y_{ijk} = m + b/a_{jk} + t_i + a_k + (ta)_{ik} + e_{ijk}$, where Y_{ijk} is the observed value of the *i*-th treatment in the *j*-th block of the *k*-th season; m the overall mean; b/a_{jk} the random effect of the *j*-th block within the *k*-th season; t_i the fixed effect of the *i*-th treatment; a_k the fixed effect of the *k*-th season; $(ta)_{ik}$ the fixed effect of the interaction between the *i*-th treatment and *k*-th season; and e_{ijk}

the random error associated with the *i*-th treatment in the *j*-th block of the *k*-th season. The treatment and treatment-season interaction effects were further decomposed according to Miranda Filho & Venconvsky (1995).

RESULTS AND DISCUSSION

The experiments showed homogeneity of residual variances and adequate experimental precision, with coefficients of variation ranging 3.2-14.2 % (Table 2), which are comparable to those reported in the literature for the same traits evaluated in supersweet corn (Gava et al. 2021, Souza et al. 2021).

There were significant differences between the two growing seasons for all the assessed traits, with lower mean values in the second season, when compared to the first one, decreasing by 29.9, 10.2, 12.7 and 9.5 % for dehusked ear yield, ear diameter, plant height and total soluble solids, respectively (Table 2). These results indicate that the sowing date directly influenced the average genotype performance. Shorter photoperiod, reduced water availability and temperature fluctuations are factors that typically compromise the corn performance in the second growing season (Borghi et al. 2023).

Table 2. Mean squares from the analysis of variance based on means and significance levels, seasonal means and coefficient of variation (CV) for dehusked ear yield (DEY), ear diameter (ED), plant height (PH) and total soluble solids (TSS).

Source of variation	DF	DEY	ED	PH	TSS
		t ha^{-1}	——— cm	———	ºBrix
Season (S)	1	420.8400*	6.7516*	22,296.6*	74.131*
Treatment	60	8.3462*	0.1283*	281.64*	0.9244*
Checks (C)	4	7.6644*	0.1873*	9.4813^{ns}	0.5727^{ns}
C x T	1	5.9486*	0.1014*	7.4287^{ns}	1.2689^{ns}
Topcross (T)	55	8.4394*	0.1245*	306.42*	0.9437*
GCA-I	1	76.9890*	1.8902*	2,959.7*	5.1001*
GCA-II	27	6.0595*	0.1271*	307.00*	1.2946*
SCA	27	8.2804*	0.0566*	207.58*	0.4389^{ns}
S x Treatment	60	2.1168*	0.0316*	22.197^{ns}	0.6365^{ns}
S x C	4	0.8692^{ns}	0.0152^{ns}	11.459^{ns}	0.0910^{ns}
S x (C x T)	1	1.3040^{ns}	0.0176^{ns}	67.746^{ns}	1.4873^{ns}
S x topcross	55	2.2223*	0.0331*	22.150^{ns}	0.6607^{ns}
S x GCA-I	1	31.1470*	0.0831*	14.899^{ns}	0.9108^{ns}
S x GCA-II	27	1.6761^{ns}	0.0461*	19.136^{ns}	0.7445^{ns}
S x SCA	27	1.6971^{ns}	0.0182^{ns}	25.432^{ns}	0.5676^{ns}
Error	120	1.1330*	0.0151*	20.268^{ns}	0.4814^{ns}
Mean 1st season	-	12.42	4.6	213	16.4
Mean 2nd season	-	8.71	4.1	186	14.8
Mean	-	10.567	4.4	200	15.6
CV (%)	-	14.2	4.0	3.2	6.3

^{ns} and *: not significant and significant according to the F test at 5 % of probability, respectively. DF: degrees of freedom. SCA: specific combining ability; GCA: general combining ability.

Combined analysis of variance revealed significant treatment effects for all the traits, indicating differences in treatment performance. However, a significant season x treatment interaction was only observed for dehusked ear yield and ear diameter, demonstrating that treatments responded differently across the two seasons (Table 2). Similar results were reported by Gava et al. (2021) and Zaluski et al. (2021) for dehusked ear yield and ear diameter with different sowing dates. This indicates that the interaction between genotypes and sowing dates altered the relative performance of genotypes across the growing seasons.

In the first season, the Scott-Knott clustering test identified 15 topcross hybrids and one experimental check (Test$_3$) in the same group as the commercial check (Test$_5$) for dehusked ear yield, with performance exceeding the means reported by Albuquerque et al. (2008) and Lima et al. (2020), in different environments during the first growing season. However, only five experimental hybrids were grouped with the commercial check for ear diameter in the first season (Table 3). In the second season, 33 topcross hybrids and the experimental hybrids Test$_2$ and Test$_3$ were grouped with the commercial hybrid, highlighting the adaptive potential of the UEL genotypes under the climate conditions of the second growing season and surpassing the performance reported by Moraes et al. (2010) for conventional green maize during this period. For ear diameter in the second season, more than 50 % of the topcross hybrids were grouped with the commercial check (Table 3).

The partitioning of season x treatment interaction revealed no significant season x check or season x (check x treatment) interactions. This indicates that neither the checks nor the check x topcross comparison exhibited differential performance across seasons, showing a uniform reduction in performance in the second season. However, a significant season x topcross interaction was observed only for dehusked ear yield and ear diameter, indicating that the topcross hybrid performance varied between seasons for these traits (Table 2).

Significant treatment effects were recorded for plant height, attributed to the topcross hybrids (Table 2). Nevertheless, the mean plant height

Table 3. Mean dehusked ear yield (DEY), ear diameter (ED), plant height (PH) and total soluble solids (TSS) values for the treatments and estimates of specific combining ability (s_{ij}) and standard deviation of s_{ij} [SD(s_{ij})] for DEY and ED.

Treatment	DEY (t ha^{-1})				ED (cm)				PH (cm)	TSS
	1st season	2nd season	Mean	SCA	1st season	2nd season	Mean	SCA	Mean	Mean
H_{A1}	15.16 a	9.93 a	12.55 a	0.416	5.2 a	4.7 a	4.9 a	-0.14	211 a	15.6 a
H_{B1}	15.86 a	10.89 a	13.37 a	-0.416	5.3 a	4.6 a	5.0 a	0.14	208 b	15.0 a
H_{A2}	10.03 c	9.58 a	9.80 b	0.394	4.9 b	4.6 a	4.7 a	0.05	202 b	16.1 a
H_{B2}	13.13 b	8.21 b	10.67 a	-0.394	4.6 c	4.2 a	4.4 b	-0.05	203 b	16.4 a
H_{A3}	12.46 b	9.50 a	10.98 a	0.813	4.5 c	4.3 a	4.4 b	0.06	204 b	16.2 a
H_{B3}	12.51 b	9.52 a	11.01 a	-0.813	4.2 d	3.9 b	4.0 b	-0.06	192 c	15.6 a
H_{A4}	11.19 c	9.27 a	10.23 a	0.041	4.8 b	4.4 a	4.6 a	0.12	193 c	15.2 a
H_{B4}	15.37 a	8.25 b	11.81 a	-0.041	4.5 c	3.8 b	4.1 b	-0.12	186 d	16.6 a
H_{A5}	13.46 b	10.51 a	11.99 a	0.789	4.7 b	4.5 a	4.6 a	0.03	180 d	15.7 a
H_{B5}	13.62 b	10.52 a	12.07 a	-0.789	4.3 d	4.2 a	4.3 b	-0.03	203 b	15.3 a
H_{A6}	12.15 c	6.71 b	9.43 b	-0.679	4.6 c	4.0 b	4.3 b	-0.14	190 c	14.7 a
H_{B6}	15.21 a	9.69 a	12.45 a	0.679	4.6 c	4.0 b	4.3 b	0.14	190 c	14.9 a
H_{A7}	6.39 d	6.72 b	6.55 b	-0.998	4.4 d	4.0 b	4.2 b	-0.09	184 d	14.2 a
H_{B7}	11.71 c	8.71 a	10.21 a	0.998	4.4 d	3.8 b	4.1 b	0.09	192 c	15.4 a
H_{A8}	13.12 b	10.86 a	11.99 a	1.756	4.8 b	4.6 a	4.7 a	0.08	188 c	15.3 a
H_{B8}	11.72 c	8.55 b	10.14 a	-1.756	4.5 c	4.1 b	4.3 b	-0.08	190 c	14.5 a
H_{A9}	11.27 c	9.96 a	10.61 a	0.148	4.7 b	4.3 a	4.5 a	-0.02	188 c	15.8 a
H_{B9}	15.64 a	8.31 b	11.98 a	-0.148	4.6 c	3.9 b	4.3 b	0.02	196 c	16.5 a
H_{A10}	10.94 c	5.52 b	8.23 b	-0.534	4.8 b	3.8 b	4.3 b	-0.11	191 c	15.9 a
H_{B10}	14.60 a	7.31 b	10.95 a	0.534	4.7 b	3.8 b	4.3 b	0.10	198 c	15.2 a
H_{A11}	6.12 d	6.84 b	6.48 b	-1.710	4.4 d	4.3 a	4.4 b	-0.08	185 d	15.1 a
H_{B11}	14.90 a	8.22 b	11.56 a	1.710	4.4 d	4.1 b	4.3 b	0.08	197 c	14.9 a
H_{A12}	7.76 d	5.11 b	6.44 b	-2.560	4.7 b	3.9 b	4.3 b	-0.24	195 c	14.8 a
H_{B12}	16.58 a	9.85 a	13.22 a	2.560	4.8 b	4.3 a	4.5 a	0.24	193 c	15.9 a
H_{A13}	5.11 d	7.24 b	6.18 b	-2.637	4.2 d	4.4 a	4.3 b	-0.19	205 b	15.4 a
H_{B13}	15.74 a	10.47 a	13.11 a	2.637	4.6 c	4.2 a	4.4 b	0.19	193 c	15.5 a
H_{A14}	9.62 c	7.99 b	8.80 b	-0.914	4.5 c	4.0 b	4.3 b	0.01	197 c	15.5 a
H_{B14}	15.58 a	9.00 a	12.29 a	0.914	4.3 d	3.7 b	4.0 b	-0.01	198 c	15.5 a
H_{A15}	10.91 c	8.37 b	9.64 b	-1.041	4.7 b	4.6 a	4. 6a	-0.07	228 a	16.8 a
H_{B15}	15.96 a	10.79 a	13.38 a	1.041	4.6 c	4.4 a	4.5 a	0.07	219 a	15.0 a
H_{A16}	9.16 c	7.37 b	8.26 b	0.013	4.4 d	4.0 b	4.2 b	0.02	220 a	15.9 a
H_{B16}	11.07 c	8.72 a	9.89 b	-0.013	4.0 d	3.8 b	3.9 b	-0.02	219 a	15.3 a
H_{A17}	10.35 c	7.13 b	8.74 b	-0.540	4.5 c	4.2 a	4.4 b	-0.03	212 a	17.0 a
H_{B17}	14.25 b	8.71 a	11.48 a	0.540	4.6 c	3.7 b	4.2 b	0.03	212 a	16.4 a
H_{A18}	7.55 d	8.19 b	7.87 b	-0.682	4.5 c	4.4 a	4.4 a	-0.03	214 a	15.6 a
H_{B18}	12.14 c	9.63 a	10.89 a	0.682	4.3 d	4.2 a	4.2 b	0.03	194 c	17.1 a
H_{A19}	12.99 b	9.16 a	11.08 a	-1.329	4.8 b	4.3 a	4.5 a	-0.03	192 c	16.4 a
H_{B19}	17.32 a	13.47 a	15.39 a	1.329	4.6 c	4.1 b	4.3 b	0.03	215 a	15.9 a
H_{A20}	11.33 c	10.22 a	10.77 a	-0.468	4.9 b	4.5 a	4.7 a	0.18	214 a	16.5 a
H_{B20}	15.61 a	11.13 a	13.37 a	0.468	4.4 d	3.8 b	4.1 b	-0.18	216 a	16.1 a
H_{A21}	12.13 c	9.11 a	10.62 a	0.013	5.1 a	4.4 a	4.8 a	0.07	211 a	15.1 a
H_{B21}	13.99 b	10.52 a	12.25 a	-0.013	4.6 c	4.1 b	4.4 b	-0.07	207 b	14.9 a
H_{A22}	12.39 b	6.42 b	9.40 b	-1.111	5.0 a	4.2 a	4.6 a	-0.09	208 b	14.3 a
H_{B22}	14.92 a	11.64 a	13.28 a	1.111	4.6 c	4.5 a	4.5 a	0.09	203 b	15.0 a
H_{A23}	11.11 c	7.69 b	9.40 b	-0.580	4.9 b	4.2 a	4.5 a	-0.12	205 b	16.0 a
H_{B23}	13.31 b	11.10 a	12.21 a	0.576	4.9 b	4.1 b	4.5 a	0.12	213 a	16.8 a
H_{A24}	12.83 b	8.21 b	10.52 a	1.632	4.9 b	4.5 a	4.7 a	0.22	213 a	16.1 a
H_{B24}	12.00 c	5.84 b	8.92 b	-1.632	4.5 c	3.5 b	4.0 b	-0.22	210 a	15.6 a
H_{A25}	13.15 b	9.56 a	11.36 a	2.682	4.9 b	4.6 a	4.7 a	0.11	196 c	15.4 a
H_{B25}	9.59 c	5.71 b	7.65 b	-2.682	4.4 d	4.1 b	4.2 b	-0.11	210 b	15.6 a
H_{A26}	11.71 c	8.07 b	9.89 b	2.067	4.7 b	4.2 a	4.5 a	0.13	200 c	15.5 a
H_{B26}	9.65 c	5.18 b	7.42 b	-2.067	4.3 d	3.6 b	3.9 b	-0.13	189 c	16.2 a
H_{A27}	12.94 b	10.09 a	11.52 a	2.312	5.0 a	4.5 a	4.8 a	0.16	172 e	16.4 a
H_{B27}	11.62 c	5.49 b	8.55 b	-2.312	4.5 c	3.9 b	4.2 b	-0.16	192 c	15.1 a
H_{A28}	13.86 b	9.10 a	11.48 a	2.702	4.9 b	4.6 a	4.7 a	0.15	185 d	16.7 a
H_{B28}	9.55 c	5.92 b	7.74 b	-2.702	4.4 d	3.9 b	4.2 b	-0.15	170 e	16.1 a
SD (s_{ij})				0.739				0.09		
$Test_1$	12.69 b	7.90 b	10.30 a	-	4.7 b	4.1 b	4.4 b	-	204 b	15.1 a
$Test_2$	13.20 b	9.20 a	11.20 a	-	4.6 c	4.3 a	4.5 a	-	200 c	15.4 a
$Test_3$	14.45 a	9.45 a	11.95 a	-	4.3 d	3.9 b	4.1 b	-	200 c	16.0 a
$Test_4$	10.10 c	7.73 b	8.92 b	-	4.6 c	4.5 a	4.5 a	-	198 c	15.4 a
$Test_5$	17.10 a	11.23 a	14.17 a	-	5.2 a	4.7 a	5.0 a	-	201 b	14.5 a

Means followed by the same letter in the column belong to the same group according to the Scott-Knott test at 5 % of probability. SCA: estimates of specific combining ability.

values of the topcross hybrids ranged from 170 to 228 cm, similarly to those reported in the literature (Kwiatkowski et al. 2011, Gonçalves et al. 2024). Likewise, the hybrid topcrosses contributed most to the significant treatment effect for total soluble solids, but all means fell within a single group according to the Scott-Knott test, along with the commercial check, ranging from 14.2 to 17.1 ºBrix (Table 3).

The H_{A1}, H_{B1}, H_{B12}, H_{B13}, H_{B14}, H_{B15}, H_{B19}, H_{B20} and H_{B22} hybrids showed a superior performance for dehusked ear yield, since they were grouped among the best-performing genotypes in both growing seasons, along with the commercial check, with mean values of 12.55 to 15.39 t ha^{-1} (Table 3). These mean dehusked ear yield values were higher than those recorded by Souza et al. (2021) for sweet corn varieties (12.1 t ha^{-1}), and comparable to those obtained by Chiquito et al. (2021) for supersweet hybrids.

The partitioning of the significant season x topcross interaction revealed significant effects on the season x GCA-I interaction for dehusked ear yield and ear diameter, indicating that the GCA estimates of the testers differed between seasons (Table 2). The L_B tester line showed a positive GCA in the first and second seasons for dehusked ear yield, increasing yield by 1.356 and 0.302 t ha^{-1}, respectively, in the hybrids resulting from its crosses. This suggests that L_B has a superior GCA, which may indicate a higher concentration of favorable alleles. Of the ten most productive topcross hybrids, nine were combinations involving the L_B tester line, highlighting the influence of high GCA on these crosses. For all the investigated traits, the mean squares for GCA-I were higher than those obtained for SCA, indicating the predominance of additive gene effects for these variables, what is useful for selecting testers (Paiva et al. 2021). However, the L_A line has the added benefit of increasing ear diameter and reducing plant height (Table 4).

In relation to the GCA-II effects of the tested lines, no interaction with seasons was observed for dehusked ear yield, plant height and total soluble solids (Table 3). Among the tested lines, L_{19}, L_1, L_{20}, L_5 and L_{15} exhibited the highest GCA effects, contributing with 2.734, 2.459, 1.569, 1.527 and 1.008 t ha^{-1}, respectively, to the dehusked ear yield of the hybrids they were involved in. These five lines were present in four of the five highest-yielding hybrids (Table 4). High GCA estimates indicate a high concentration of favorable alleles, demonstrating the strong *per se* genetic potential of the tested lines, which could contribute to the development of high-performing hybrids (Cruz 2006).

There were significant differences in SCA for most traits, except total soluble solids (Table 1). The hybrids with the highest SCA for dehusked ear yield were H_{A28}, H_{A25}, H_{B13}, H_{B12} and H_{A27}, and for ear diameter H_{B12}, H_{A24}, H_{B13}, H_{A20} and H_{A27} (Table 3).

The L_A tester line, obtained from the SD3002 donor population crossed with lines from SD3005, resulted in hybrids with high SCA. Similarly, the L_B tester line, derived from SD3005 crossed with lines

Table 4. Estimates of mean (m) and general combining ability (g) for dehusked ear yield (DEY), ear diameter (ED), plant height (PH) and total soluble solids (TSS).

Estimates		DEY	ED	PH	TSS
		t ha^{-1}	——— cm	———	ºBrix
	m	10.501	4.4	200	15.7
g_A	Season I	-1.356	0.1	-5	-0.3
	Season II	-0.302	0.2	-6	-0.1
g_B	Season I	1.356	-0.1	5	0.3
	Season II	0.302	-0.2	6	0.1
	g_1	2.459	0.6	19	0.5
	g_2	-0.262	0.2	13	-0.6
	g_3	0.497	-0.2	12	0.3
	g_4	0.517	0.0	12	0.2
	g_5	1.527	0.0	8	0.9
	g_6	0.440	-0.1	2	0.3
	g_7	-2.119	-0.2	4	-0.3
	g_8	0.561	0.1	-10	1.2
	g_9	0.795	0.0	-14	0.3
	g_{10}	-0.910	-0.1	9	-0.1
	g_{11}	-1.482	-0.1	2	-0.1
	g_{12}	-0.674	0.0	3	-0.2
	g_{13}	-0.859	0.0	-2	-1.0
	g_{14}	0.045	-0.3	0	-0.5
	g_{15}	1.008	0.2	-2	-0.9
	g_{16}	-1.422	-0.4	-3	-0.9
	g_{17}	-0.391	-0.1	-3	0.2
	g_{18}	-1.123	-0.1	5	1.0
	g_{19}	2.734	0.0	2	0.3
	g_{20}	1.569	0.0	4	-0.3
	g_{21}	0.935	0.2	-10	-0.4
	g_{22}	0.840	0.2	4	-0.4
	g_{23}	0.301	0.1	-2	-0.5
	g_{24}	-0.782	-0.1	-9	0.3
	g_{25}	-0.997	0.1	-11	0.2
	g_{26}	-1.848	-0.2	-8	-0.4
	g_{27}	-0.466	0.1	-9	0.4
	g_{28}	-0.892	0.0	-16	0.1
	SD(g_i)	0.142	0.02	1	0.09
	SD(g_j)	0.739	0.09	3	0.48

g_A and g_B: estimated general combining ability (GCA) effects of the tester lines (g_i); g_1 to g_{28}: estimated GCA effects of the tested lines (g_j); SD: standard deviation of the GCA estimates.

from the SD3002 population, produced hybrids with positive SCA values (Table 3). This suggests that the selected testers have contrasting genetic backgrounds and belong to different heterotic groups, making them efficient for differentiating lines into distinct heterotic groups. According to Li et al. (2022), a successful simple hybrid maize breeding depends on determining the heterotic groups of elite and tester lines to maximize heterosis in the crosses.

Considering the SCA standard deviation, the tested lines from the PD2005 and PD2006 populations exhibited positive SCA only when crossed with L_A, while those from SD3002 and SD3003 only showed positive SCA exclusively in crosses with L_B. This pattern suggests that these populations belong to different heterotic groups and can help to guide future crosses in breeding programs. The lines obtained from the donor population SD3001 displayed a range of positive and negative SCA estimates for both testers, making it difficult to assign them to any particular heterotic group (Table 3).

CONCLUSIONS

1. The doubled haploid lines L_A and L_B belong to different heterotic groups and are suitable testers for identifying lines with potential in the synthesis of supersweet corn hybrids;
2. The L_1, L_{15}, L_{19} and L_{20} tested lines have the highest general combining ability and are present in the best-performing hybrids, namely H_{A1}, H_{B1}, H_{B15}, H_{B19} and H_{B20};
3. The lines obtained from the donor populations PD2005 and PD2006 belong to the heterotic group of L_B tester line;
4. The lines obtained from the donor populations SD3002 and SD3003 belong to the heterotic group of L_A;
5. The L_{19} line shows potential for testing the lines from the SD3005 population.

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