



Yield potential of super sweet corn genotypes in progressive breeding stages

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ABSTRACT. This study aimed to present the advancements in different breeding stages of super sweet corn (SS), from heterotic field corn populations to the single-cross of SS. Two parental field corn populations, four backcrossed SS populations, four SS intervarietal hybrids (SS-IH), eighteen SS single hybrids (SS-SCH) and two controls were evaluated in two environments over two crop years. The SS-IH and SS-SCH categories presented the highest ear yield, and SS-SCH presented the highest ear yield without husk (11.3 t ha⁻¹). Although SS-SCH was the most productive category, it presented the lowest husk coverage quality. The ear yield and husk cover traits expressed the highest heterosis based on the midparents. The hybrid genotype categories (SS-SCH, SS-IH and controls) had the greatest ear length and diameter, as well as plant and ear height. It was possible to conclude that the techniques used to exploit heterosis are efficient in increasing SS yield but not husk coverage, since this trait requires productive parents. Single-crosses, such as LCSH-116 x LP8HS-129 and LCSH-116 x LP8HS-130, stood out as promising genotypes for registration since they recorded high husk coverage yield and quality.

Keywords: heterosis; partial diallel; plant breeding; intervarietal hybrids; shrunken; single-cross.

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Introduction

Corn (*Zea mays* L.) is one of the most cultivated cereals in the world. Along with wheat and rice, it accounts for approximately 60% of the calories directly and indirectly ingested by humans (Cassman, Dobermann, Walters, & Yang, 2003). In addition, it is one of the most studied species in breeding programs and remains one of the main model species used in genetic studies (Wallace, Larsson, & Buckler, 2014).

Sweet corn is a special corn type that presents mutant recessive alleles from homozygosity. These mutant recessive alleles lead to a failure in the mechanism that converts simple carbohydrates (sucrose) into complex ones (starch) (Tracy, 2001). Low starch amounts make the green corn grain softer and sweeter, in addition to enabling longer green stage-harvest intervals than those recorded for field corn. Phenotypes are classified as sweet (carrying recessive homozygous *sugary*, *amyloidosis extender*, and *dull1* genes) and super sweet (carrying *brittle* and *shrunken* genes). The super sweet type presents higher water-soluble sugar contents and a longer harvesting period; consequently, it is the most commercially used phenotype (Okumura, Mariano, Franco, Zaccheo, & Zorzenoni, 2013).

The most commonly used genotypes to generate superior corn genotypes for commercial use purposes are those derived from the crossbreeding between inbred lines focused on generating single-cross hybrids. In addition to allowing us to extensively explore heterosis, these genotypes stand out in performance and uniformity and allow breeders to keep control over cultivars.

The effect of heterosis on corn was first described by Shull (1909), who claimed that the main goal of corn breeders lies in finding the best hybrid combination rather than obtaining the best line. Heterosis causes traits of the F₁ generation to be greater than the mean of both parents for a given trait. Although the phenomenon is not yet fully elucidated, one of the explanations for the increased vigor lies on the complementarity of favorable alleles between two lines (Giraud et al., 2017; Mezouk & Ross-Ibarra, 2014), as well as on the dominance and pseudo-over-dominance related to unfavorable alleles and to gene blocks in repulsion (Laripe et al., 2012).

Thus, with the goal of generating a super sweet corn genotype with high yield potential, the Darcy Ribeiro State University of Northern Rio de Janeiro (UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro) has been developing genotypes capable of better serving farmers in Northern and Northwestern regions of Rio de Janeiro to compensate for the lack of corn breeding companies in Rio de Janeiro State. The lack of such companies is explained by the fact that the region does not present a consolidated agricultural system for crops other than sugarcane, although it has the potential to do so.

The breeding program developed by UENF aims to achieve this goal by using techniques focused on exploring heterosis, such as reciprocal recurrent selection based on full-sib progenies (Berilli et al., 2011) and partial diallel crosses between *sh2* gene carrier lines derived from heterotic populations (Flint and Dent groups) (Durães et al., 2017).

Therefore, the aim of the current study was to analyze the performance of genotypes developed by UENF in different super sweet corn breeding stages, from reciprocal base populations of field corn and isogenic populations carrying the *sh2* gene to the final generation stage of intervarietal and single hybrids from partial diallel crosses.

Material and methods

The populations and crosses analyzed in this study were as follows: the heterotic field corn parental base populations CIMMYT8 (C8) and Piranão8 (P8) in the eighth cycle of the full-sib reciprocal recurrent selection (C8 belongs to the heterotic group Flint, whereas P8 belongs to the heterotic group Dent); the CIMMYT8 and Piranão8 populations backcrossed with two shrunken (*sh2*) gene donor genotypes, which resulted in four super sweet corn populations: SH2-CIMMYT8 (CSH), SH2-8HS-CIMMYT (C8HS), SH2-Piranão (PSH), and SH2-8HS-Piranão (P8HS), shown in Figure 1; a cross between heterotic groups of super sweet corn populations, which resulted in the intervarietal hybrids CSH x PSH, CSH x P8HS, C8HS x PSH, and C8HS x P8HS; and partial diallel crosses (3 x 6) of inbred lines deriving from the CSH population (LCSH 113, LCSH 116, and LCSH 119) and from the heterotic populations P8HS (P8HS 125, P8HS 129, and P8HS 130) and PSH (PSH 134, PSH 139, and PSH 140). The following controls were used: UENF506 11, an intervarietal hybrid field corn recommended for Northern Rio de Janeiro region and Syngenta's Tropical Plus (*sh2*) super sweet corn single-cross hybrid control totaled 30 treatments.

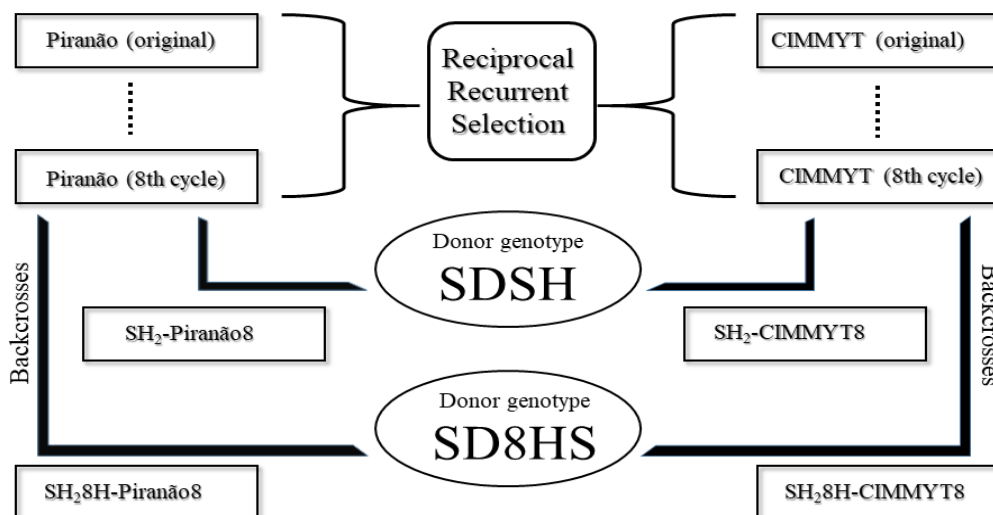


Figure 1. Scheme for obtaining the super sweet corn populations SH2-CIMMYT8, SH2-8HS-CIMMYT8, SH2-Piranão8, and SH2-8HS-Piranão8 from field corn populations Piranão and CIMMYT through eight cycles of reciprocal recurrent selection and backcrossing with the SDSH and SH8HS super sweet corn genotypes. Reproduced with permission from Gonçalves et al. (2018).

Four experiments were carried out in a randomized complete block design with four repetitions. Plots had simple 3.00 m rows, a 0.90 m space between rows and 0.30 m between plants, totaling approximately 37 thousand plants per hectare. The experiments were conducted in Campos dos Goytacazes, Rio de Janeiro State, Brazil (21°24'48" S and 41°44'48" W, altitude 14 m) and Itaocara, Rio de Janeiro State, Brazil (21°40'9" S and 42°04'34" W, altitude 60 m) counties in two different crop years (2016/2017 and 2017/2018). The basal dressing comprised 800 kg ha⁻¹ of the formulated chemical fertilizer N-P-K 04-14-08; the first top dressing

was performed 30 days after sowing using 300 kg ha⁻¹ of formulated fertilizer N-P-K 20-05-20, and the second dressing was performed 45 days after sowing using 200 kg ha⁻¹ of urea (45% N).

Harvesting was performed 22 days after female flowering (stigmas emerging in the ears in more than 50% of the plot) when *sh2* gene genotypes reached the highest fresh weight and volume (Guan et al., 2013), as well as the best flavor and texture (Camilo et al., 2015).

The traits evaluated in the experiments were ear yield with husk; ear yield without husk; prolificacy; husk coverage (scored from 1 to 3: 1 = well-closed husk; 2 = open husk coverage without exposing the tip of the ear; and 3 = the tip of the ear exposed); ear length without husk; ear diameter; ear height; and plant height.

Joint variance analyses were carried out by following a fixed model to find the mean-square expected values of $G_i + Y_j + L_k + (B/Y)/L_{ijkm} + GY_{ij} + GL_{ik} + YL_{jk} + GYL_{ijk} + \epsilon_{ijkm}$, wherein G_i is the fixed effect of genotypes; Y_j is the fixed effect of years; L_k is the fixed effect of locations; $(B/Y)/L_{ijkm}$ is the effect of blocks nested in years nested in locations; GY_{ij} is the effect of interaction genotype by year; GL_{ik} is the effect of interaction genotype by location; YL_{jk} is the effect of interaction year by location; GYL_{ijk} is the effect of interaction genotype by year by location; and ϵ_{ijkm} is the aleatory error. Genotype decomposition was performed for the following categories: super sweet single hybrids (SS-SCH); super sweet populations (SS-PB); super sweet intervarietal hybrids (SS-IH); field corn base populations (FC-P); controls; and categories. The least significant difference (LSD) was calculated using Student's t-test at a 5% error probability to allow the comparison between means.

The experimental coefficient of variation (CVe (%)) = $100 \cdot \frac{\sqrt{MSe}}{\mu}$, where: MSe is the error's mean square and μ is the general mean); the genetic coefficient of variation (CVg (%)) = $100 \cdot \frac{\sqrt{MSg - MSe}}{r \cdot l \cdot y} / \mu$, where:

MSg is the genotype's mean square, r is the number of repetitions, l is the number of locations and y is the number of years); variation index (VI = MSg/MSe); and genotypic determination coefficient $H^2 = (MSg - MSe)/MSg$, were estimated from the ANOVA.

To compare the differences among categories, a bar graph with a confidence interval based on the t distribution ($p = 0.05$) was performed using the same model as above, but the genotype effect was replaced by the category effect.

The heterosis of progenies from SS-IH and SS-SCH were calculated based on the midparent genotypes from SS-PB for each population and inbred line crosses. The SS-SCH was divided into two groups belonging to the same midparent (e.g., the midparent of crosses between inbred lines LCSH x LPSH had the same midparent as CSH x PSH, and the midparent of crosses between inbred lines LCSH x LP8HS had the same midparent as CSH x P8HS).

Statistical analyses were performed with the SAS Institute software (SAS Institute Inc., 2018) based on the GLM procedure.

Results and discussion

Differences among genotypes were significant in all evaluated traits. The experimental coefficient of variation was close to 18% for traits such as ear yield with husk, ear yield without husk, prolificacy, husk coverage, and below 7.5% in traits such as ear length, ear diameter, ear height, and plant height (Table 1).

Variation indices were high in all traits, except for prolificacy (0.58), which presented CVg considerably lower than the CVe. Traits such as ear yield with husk and ear length showed a variation index close to one, whereas the others recorded a variation index greater than one; husk coverage recorded a variation index of 1.74. The results indicated great variation between genotypes and the likelihood of selecting superior genotypes. Although most genotypes originated from only two backgrounds (Piranão and CIMMYT), these results were expected due to the different genetic combinations in each single hybrid and the effect of shrunken gene donors on recurrent genotypes (Gonçalves et al., 2018). It is worth highlighting that recurrent genotypes present a broad genetic base that enables generations of recombined inbred lines.

Following the same tendency of the variation index, the genotypic determination coefficients (H^2) in all traits were high, close to one. This heritability calculated with fixed effects of genotypes included additive and nonadditive deviation (broad sense) (Hallauer, Carena, & Miranda Filho, 2010). Although nonadditive deviation cannot be transmitted to progeny, the high H^2 suggests that for all traits, there is a good correlation between genetic value and phenotype.

Genotype x environment interactions (G x E) were not significant in variables such as husk coverage, ear height and plant height. The results of the analyses of classes of genotypes showed G x E interactions in both ear yield variables (with and without husk) in super sweet corn single hybrids (SS-SCH) and super sweet corn backcrossed populations (SS-PB). Ear length and husk coverage also presented significant G x E interactions in SS-PB and super sweet interpopulation hybrids (SS-IH), respectively. The G x E interaction was also observed in variables such as ear yield with husk, ear yield without husk, prolificacy, ear length and ear height, and there was a significant triple interaction (genotype x environment x year) in traits such as ear yield with husk, ear yield without husk and husk coverage.

Table 1. Summary of the joint variance analysis and genetic statistical parameters of eight variables evaluated in super sweet and field corn genotypes in two different environments (Itaocara, Rio de Janeiro State and Campos dos Goytacazes, Rio de Janeiro State, Brazil) in two crop years (2016/2017 and 2017/2018).

SOV	DF	MS							
		EY	EYu	PRL	HSK	EL	ED	EH	PH
Block (Location x Year)	12	4.31	2.24	0.05**	0.14	0.83	6.59	0.011	0.033**
Location (L)	1	0.12	0.29	0.75**	1.38**	14.14**	133.7**	3.75**	5.327**
Year (Y)	1	662.33**	221.64**	1.18**	3.97**	418.4**	90.83**	2.41**	4.848**
L x Y	1	183.53**	99.38**	0.03	0.82**	4.16*	64.21**	0.05*	0.49
Genotypes (G)	29	122.47**	88.68**	0.31**	4.88**	16.15**	148.9**	0.26**	0.336**
SS-SCH	17	55.36**	46.09**	0.36**	3.81**	4.59**	84.59**	0.14**	0.068**
SS-PB	3	59.26**	20.79**	0.02	0.32*	6.52**	29.39**	0.13**	0.109**
SS-IH	3	17.47	10.81*	0.06	0.58**	2.65*	33.83**	0.03*	0.050*
FC-P	1	9.39	5.20	0.10	0.45*	17.85**	4.01	0.11**	0.056
Control	1	4.96	28.66**	0.17	0.01	2.21	859.4**	1.08**	0.778**
Categories	4	590.28**	412.87**	0.60**	18.50**	84.81**	456.8**	0.87**	1.823**
G x L	29	20.18**	9.65**	0.10**	0.14	2.24**	9.59*	0.013	0.016
SS-SCH x L	17	18.62**	9.87**	0.05	0.15	1.48	7.24	0.011	0.016
SS-PB x L	3	12.90*	5.77*	0.02	0.06	2.77*	2.27	0.011	0.031*
SS-IH x L	3	13.98	3.11	0.05	0.30*	0.51	15.86	0.009	0.011
FC-P x L	1	0.135	0.47	0.01	0.10	0.69	5.16	0.006	0.012
Control x L	1	3.37	1.61	0.02	0.21	0.02	40.50*	0.010	0.001
Categories x L	4	46.88**	21.32**	0.28**	0.05	6.56**	13.05	0.023*	0.015
G x Y	29	12.89*	6.06*	0.09*	0.35**	2.70**	7.42	0.013	0.029*
SS-SCH x Y	17	10.11	6.81**	0.13**	0.39**	1.06	5.25	0.012	0.019
SS-PB x Y	3	8.13	4.18	0.04	0.06	0.18	4.39	0.014	0.024
SS-IH x Y	3	19.95*	4.79	0.01	0.29*	2.50*	11.76	0.005	0.014
FC-P x Y	1	0.924	0.50	0.02	0.06	0.003	17.36	0.0004	0.001
Control x Y	1	22.68	6.01	0.03	0.03	4.06*	32.32*	0.012	0.0002
Categories x Y	4	21.91*	6.22	0.03	0.62**	11.47**	7.06	0.023	0.098**
G x L x Y	29	10.73*	5.18*	0.03	0.18*	1.22	6.18	0.012	0.015
SS-SCH x L x Y	17	9.63	5.51	0.05	0.22**	0.75	3.98	0.014	0.016
SS-PB x L x Y	3	12.32*	4.01	0.01	0.04	1.99*	0.13	0.024*	0.028*
SS-IH x L x Y	3	3.74	1.11*	0.01	0.05	0.28	1.68	0.005	0.010
FC-P x L x Y	1	10.92	3.15	<0.01	0.21	3.57	14.72	0.001	0.002
Control x L x Y	1	22.77	11.03	<0.01	0.45*	0.66	60.72**	0.0002	0.003
Categories x L x Y	4	17.45*	7.49	0.06	0.16	2.82*	7.96	0.006	0.0067
Error	348	7.29	3.23	0.049	0.099	0.951	6.541	0.0098	0.015
Total	479								
CVe (%)		17.78	17.83	18.58	18.28	5.80	5.36	7.34	5.37
CVg (%)		17.67	22.93	10.73	31.78	5.80	6.26	9.33	6.21
VI		0.99	1.29	0.58	1.74	1.00	1.17	1.27	1.16
H ²		0.940	0.963	0.842	0.979	0.941	0.956	0.962	0.955

SOV – Source of variation; MS – Mean square; Loc – Locations; DF – Degrees of freedom; EY – Ear yield with husk (ton.ha⁻¹); EYu – Unhusked ear yield (ton.ha⁻¹); PRL – Prolificacy; HSK – Husk coverage; EL – Ear length (cm); ED – Ear diameter (mm); EH – Ear height; PH – Plant height; CVe – Experimental coefficient of variation; CVg – Genetic coefficient of variation; VI – Variation index; H² – Genotypic determination coefficient.

Table 2 presents the genotype means of eight traits. The mean ear yield with husk was 15.18 t ha⁻¹, and the genotype classes presenting the highest mean were SS-SCH (16.6 t ha⁻¹) and SS-HI (15.5 t ha⁻¹). In the SS-SCH group, the highest means were LCSH 113 x LP8HS 129, LCSH 113 x LPSH 139, and LCSH 116 x LP8HS 130; two of them shared the same parent, LCSH 113.

SS-SCH genotypes presented the lowest mean husk coverage, which varied from 1.14 to 2.71. On the other hand, they presented the highest ear yield without husk. This result may indicate a negative correlation between these two variables in this genotype group, i.e., larger ears may not be supported by the husk, as seen in the inverse relation between mean ear length and husk coverage quality. Although the genotypes are very productive, husk coverage is a fundamental trait in regard to ear protection against pests and diseases (McMillian, Widstrom, & Wilson, 1987; Tembo, Asea, Gibson, & Okori, 2016), as good husk coverage means husks are longer than ears, which helps to avoid the inflow of water and the attack by insects.

Genotypes presented a mean ear length of 16.81 cm, with an emphasis on the SS-SCH (17.3 cm), SS-IH (17.1 cm) and control (16.7 cm) groups. Seven genotypes in the SS-SCH group and one in the SS-IH group presented the highest ear length means (18.1 to 17.6 cm) and did not differentiate from one other.

Table 2. Means of eight variables evaluated in super sweet and field corn genotypes from two different locations (Itaocara, Rio de Janeiro State and Campos dos Goytacazes, Rio de Janeiro State, Brazil) in two crop years (2016/2017 and 2017/2018).

Genotype	EY	EYu	PRL	HSK	EL	ED	EH	PH
Super sweet corn single hybrids								
LCSH 113 x LP8HS 125	16.9	11.2	1.6	2.71	16.5	45.9	1.36	2.28
LCSH 113 x LP8HS 129	18.6	12.6	1.3	2.31	18.1	49.0	1.38	2.23
LCSH 113 x LP8HS 130	17.0	10.5	1.2	1.95	17.6	48.3	1.48	2.34
LCSH 113 x LPSH 134	17.7	13.1	1.4	2.36	17.2	49.5	1.46	2.48
LCSH 113 x LPSH 139	20.1	14.2	1.4	2.71	17.2	50.0	1.38	2.40
LCSH 113 x LPSH 140	18.2	12.7	1.3	2.59	17.9	51.2	1.44	2.38
LCSH 116 x LP8HS 125	16.7	12.5	1.3	2.39	16.9	50.2	1.46	2.38
LCSH 116 x LP8HS 129	16.9	12.5	1.1	1.66	18.0	51.6	1.49	2.38
LCSH 116 x LP8HS 130	19.0	12.5	1.1	1.63	18.0	52.8	1.62	2.52
LCSH 116 x LPSH 134	14.6	11.3	1.1	2.19	16.7	49.1	1.33	2.39
LCSH 116 x LPSH 139	16.7	11.9	1.1	2.21	16.8	51.7	1.27	2.38
LCSH 116 x LPSH 140	16.5	11.9	1.0	1.93	17.1	51.9	1.37	2.37
LCSH 119 x LP8HS 125	16.4	10.7	1.3	2.63	17.7	46.1	1.46	2.40
LCSH 119 x LP8HS 129	12.8	8.2	1.3	1.14	17.4	46.9	1.42	2.37
LCSH 119 x LP8HS 130	13.2	7.3	1.1	1.23	16.6	46.5	1.56	2.42
LCSH 119 x LPSH 134	14.3	9.9	1.2	1.90	17.0	46.1	1.36	2.44
LCSH 119 x LPSH 139	16.0	10.3	1.1	1.60	16.8	47.1	1.23	2.36
LCSH 119 x LPSH 140	16.5	10.8	1.2	1.59	17.8	46.8	1.34	2.37
Super sweet corn parental populations								
PSH	7.7	4.9	1.0	1.21	15.0	45.4	1.09	2.04
P8HS	10.5	6.5	1.1	1.06	14.8	43.8	1.27	2.16
CSH	12.3	7.6	1.1	1.39	16.0	45.8	1.26	2.10
C8HS	10.1	6.0	1.0	1.34	14.7	42.9	1.13	1.98
Super sweet corn interpopulation hybrids								
CSH x PSH	16.5	10.6	1.2	1.54	17.6	48.3	1.30	2.25
C8HS x PSH	14.0	8.8	1.2	1.31	17.0	46.8	1.29	2.15
CSH x P8HS	15.9	10.3	1.2	1.15	16.7	47.8	1.38	2.27
C8HS x P8HS	15.7	9.6	1.1	1.15	17.3	45.0	1.37	2.26
Field corn parental populations								
PIRANÃO8	13.0	7.5	1.2	1.00	14.4	42.6	1.28	2.12
CIMMYT8	11.9	6.7	1.1	1.24	15.9	43.3	1.15	2.03
Controls								
UENF506 - 11	15.1	8.8	1.2	1.24	16.5	43.0	1.43	2.36
Tropical Plus	14.3	10.8	1.0	1.20	17.0	53.4	1.06	2.05
Mean	14.7	9.8	1.1	1.22	16.7	48.2	1.24	2.20
General mean	15.18	10.08	1.19	1.72	16.81	47.65	1.34	2.29
LSD (T test at 5%)	1.89	1.26	0.15	0.22	0.68	1.79	0.07	0.09

EY – Ear yield with husk ($t\ ha^{-1}$); EYu – Unhusked ear yield ($t\ ha^{-1}$); PRL – Prolificacy; HSK – Husk coverage; EL – Ear length (cm); ED – Ear diameter (mm); EH – Ear height; PH – Plant height; LSD – Least significant difference.

Genotypes presented a mean ear yield without husk of $9.8\ t\ ha^{-1}$; SS-SCH genotypes presented a significantly higher mean ear yield without husk ($11.3\ t\ ha^{-1}$) than the other groups. Two genotypes, LCSH 113 x LPSH 134 ($13.1\ t\ ha^{-1}$) and LCSH 113 x LPSH 139 ($14.2\ t\ ha^{-1}$), presented the highest means, in addition to sharing the same parental lines belonging to the CIMMYT heterotic group (LCSH 113). It is worth emphasizing that the genotypes presenting the highest ear yield with and without husk may not be the same, and the husk weight/ear weight ratio may vary between genotypes. In addition, Ilker (2011) and

Williams (2014) conducted studies with sweet corn and found that the ear yield without husk was more efficient in predicting the yield of sweet corn fresh grains than the ear yield with husk. Therefore, although corn is overall commercialized with husk, the processing industry should select genotypes based on ear yield without husk.

The genotypes presented a mean prolificacy of 1.19 ears per plant; all groups presented values close to the mean. The SS-SCH genotype LCSH 113 x LP8HS 139 had the highest mean with 1.6 ears per plant. Although prolificacy is a yield increase predictor, it has been avoided by breeders focused on high-density crops (Williams, 2014). According to Williams (2014), high prolificacy indicates low efficiency, which must be corrected by increasing plant density.

The mean ear diameter of treatments was 47.85 mm; it was higher in the SS-SCH (48.9 mm) and control (48.2 mm) groups, mainly in Syngenta's Tropical Plus control (53.4 mm), which increased the mean of controls. The importance of this trait can be seen in a correlation study conducted with the same single hybrids. Such a study compared yield traits and found a stronger positive direct effect of ear diameter on the base variable "ear yield without husk" than on other variables (Gonçalves et al., 2018).

Traits such as plant and ear height and ear yield were considerably affected by heterosis resulting from the crossing of heterotic groups. The genotypic group SS-SCH had the highest means when compared to other genotypes, presenting a 2.38 m plant height mean, varying from 2.23 to 2.52 m, and a 1.41 m ear height mean, varying from 1.23 to 1.62 m between genotypes (Table 2 and Figure 2). Although the correlation between plant yield and height is often positive (Olivoto et al., 2017; Pavlov et al., 2015), it is desirable to have plants presenting smaller stature in both plant height and ear height to enable greater densification and to reduce the risk of lodging under strong wind conditions (Duvick, 2005).

The heterosis among progenies generated from all the crosses was highly significant for all traits using the base populations (SS-PB) as midparents. The CVe exceeded 40% in all traits and reached 128.5% for PRL.

Among all the traits measured, EY and EYu had the highest heterosis for all the crosses (Table 3), with greater variation among the SS-SCH progenies, ranging from 14.1 to 101.2%.

Table 3. Percentage of heterosis in genotypes of super sweet corn from the SS-IH and SS-SCH groups, calculated using the mean of parental genotypes from SS-PB for each population combination.

Genotype	EY	EYu	PRL	HSK	EL	ED	EH	PH
LCSH 113 x LP8HS 125	48.3	58.6	49.7	121.9	6.9	2.5	7.8	6.9
LCSH 113 x LP8HS 129	63.1	79.7	22.3	87.7	17.7	9.5	8.7	4.5
LCSH 113 x LP8HS 130	49.2	47.9	11.8	57.5	14.1	7.7	17.2	9.9
LCSH 116 x LP8HS 125	46.1	77.2	22.0	95.3	9.9	12.0	15.5	11.7
LCSH 116 x LP8HS 129	50.4	80.4	5.1	36.0	16.5	15.3	17.2	11.9
LCSH 116 x LP8HS 130	67.2	77.5	-2.2	32.9	16.5	17.9	27.8	18.4
LCSH 119 x LP8HS 125	43.6	51.6	22.8	114.8	15.1	2.8	15.6	12.5
LCSH 119 x LP8HS 129	14.1	17.1	21.4	-7.7	13.6	4.4	12.1	11.1
LCSH 119 x LP8HS 130	15.9	3.7	4.0	0.2	7.4	3.9	22.9	13.4
LCSH 113 x LPHS 134	77.7	109.2	36.6	81.7	10.6	8.6	24.3	20.0
LCSH 113 x LPHS 139	101.2	126.1	33.3	108.6	10.8	9.8	17.5	15.8
LCSH 113 x LPHS 140	82.1	103.3	23.5	99.0	15.1	12.2	22.1	14.8
LCSH 116 x LPHS 134	45.8	79.8	2.9	68.2	7.6	7.8	12.7	15.3
LCSH 116 x LPHS 139	65.5	87.9	6.8	69.2	8.1	13.3	7.9	15.0
LCSH 116 x LPHS 140	65.1	90.1	-1.7	48.0	10.0	13.8	16.3	14.5
LCSH 119 x LPHS 134	43.4	58.2	13.5	46.1	9.2	1.2	15.1	17.9
LCSH 119 x LPHS 139	59.8	64.5	10.3	23.0	8.2	3.4	4.8	14.2
LCSH 119 x LPHS 140	65.1	72.6	18.2	22.1	14.9	2.7	13.9	14.7
CSH x PSH	65.2	69.9	16.8	18.2	13.3	5.9	10.9	8.7
C8HS x PSH	58.5	61.6	15.3	2.9	14.2	6.1	16.2	7.0
CSH x P8HS	40.9	47.6	15.3	-6.3	8.3	6.9	10.0	7.1
C8HS x P8HS	51.8	52.3	4.5	-4.1	17.2	3.6	13.7	8.8
F - Test	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
LSD (T)	18.23	20.10	14.22	17.85	4.31	3.77	5.39	3.96
CVe(%)	47.5	42.2	128.5	50.7	51.9	69.9	51.9	45.9

EY – Ear yield with husk ($t\ ha^{-1}$); EYu – Unhusked ear yield ($t\ ha^{-1}$); PRL – Prolificacy; HSK – Husk coverage; EL – Ear length (cm); ED – Ear diameter (mm); EH – Ear height; PH – Plant height.

Prolificacy had the highest CVe (128.5%); thus, this cannot be reliably used to find the genetic differences among progenies. However, the LCSH 113 x LP8HS 125 hybrid had high heterosis (49.7%) for this trait, and despite the high CVe, it showed significant differences. It was not significantly superior only compared with LCSH 113 x LPHS 134.

On average, in SS-SCH crosses, HSK had the highest heterosis, as shown in Table 3. However, SS-IH crosses such as C8HS x PSH, CSH x P8HS, and C8HS x P8HS showed heterosis close to zero for HSK. In general, heterosis did not negatively impact this trait in SS-IH crosses.

The heterosis of EL was similar between the SS-SCH and SS-IH groups. Although some of the hybrids in the SS-SCH group had a low mean for ED compared to hybrids from SS-IH, the average heterosis was higher in SS-CH. EH ranged from 4.8% in LCSH 119 x LPHS 139 cross to 27.8% in LCSH 116 x LP8HS 130 (Table 3). Additionally, on average, PH showed higher heterosis in the LCSH x LPSH group compared to the other groups (LCSH x LP8HS, SS-IH).

Figure 2 clearly shows the effect of heterosis on most traits and the higher means of all traits in SS-SCH and SS-IH than those in SS-PB and FC-P, with emphasis on SS-SCH. However, SS-PB and FC-P presented similar performance, which indicated an overall low effect of the *shrunk* gene introduction in the populations. This reinforces the role of heterosis on all agronomic traits evaluated in our study.

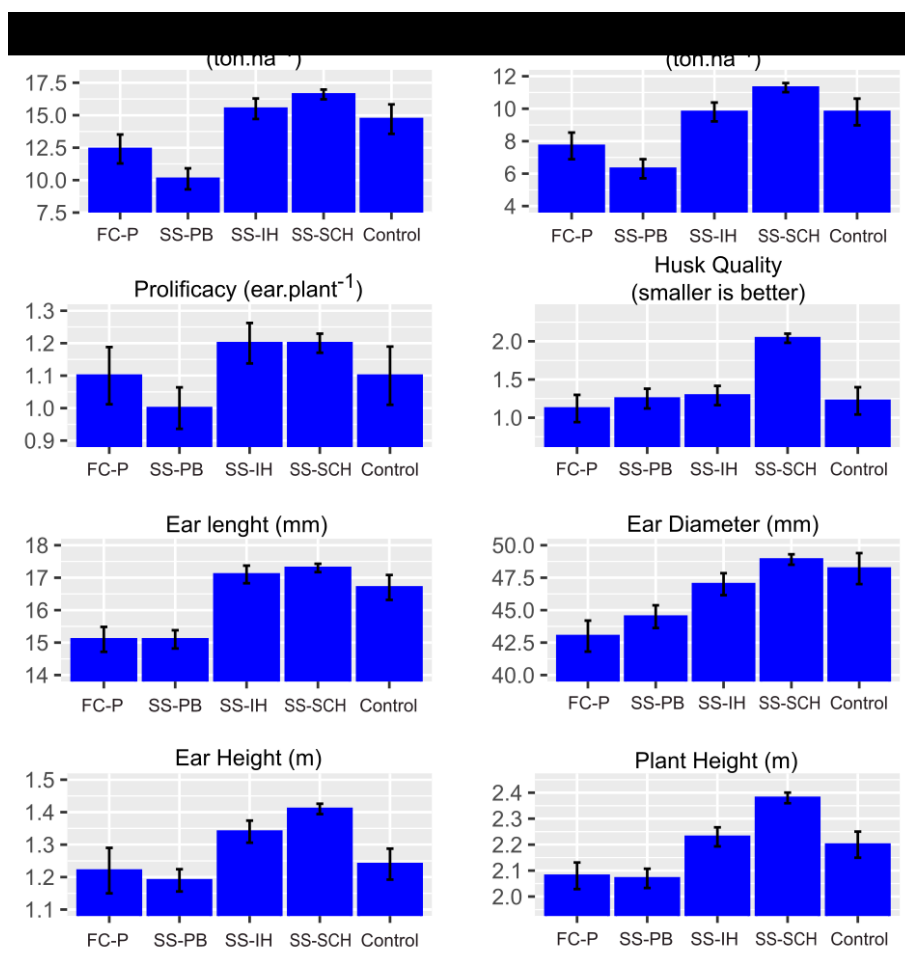


Figure 2. Mean of genotypes grouped in the following categories: super sweet single hybrids (SS-SCH), super sweet backcrossed populations (SS-PB), super sweet intervarietal hybrids (SS-IH), field corn parental populations (FC-P) and commercial hybrids (Control), for eight traits evaluated in two different environments (Itaocara, Rio de Janeiro State and Campos dos Goytacazes, Rio de Janeiro State, Brazil) in two different crop years (2016/2017 and 2017/2018).

We expected high heterosis in traits related to yield since the heterotic groups were improved towards that goal (Berilli et al., 2011). The use of genotypes belonging to different heterotic pools can increase the variances and improve the selection for specific combining ability (Hallauer et al., 2010), and for this reason, genotypes belonging to heterotic pools are widely used in heterosis studies (Larièpe et al., 2012; Li et al., 2018). The results of heterosis of single hybrids were high for traits such as EY and EYu compared with other studies (Shama, Dhakal, Kharel, & Shrestha, 2016; Dhoot et al., 2017). However, this is expected when using parental inbred lines as the midparent to calculate heterosis as opposed to using parental populations as the midparent to calculate heterosis, which was the case in our study, since the inbred lines inherently have low yield compared to parental populations.

Controls formed by the field corn interpopulation hybrid “UENF506 11” and by the Tropical Plus single-cross hybrid presented a similar performance to SS-SCH and SS-IH for most traits, on average, depicting overlapping of confidence intervals (Figure 2). The SS-SCH also stood out, but with lower husk coverage quality, as well as with higher ear and plant heights. If one considers husk coverage as the most critical trait for selection, due to the supposed inverse relation between husk coverage quality and ear yield, it is possible to see that the SS-SCH genotype group presents crosses, such as LCSH 116 x LP8HS 129 and LCSH 116 x LP8HS 130, which are capable of presenting two positive traits since both present good yield and husk coverage quality. Therefore, they are good options to be recommended for Northern and Northwestern Rio de Janeiro State.

Conclusion

Although the phenomenon known as heterosis is not yet fully understood, techniques based on heterosis have been shown to be effective in increasing the super sweet corn yield.

Hybrids did not show increased husk coverage quality. In fact, there was a decrease in husk coverage quality due to ear increase. Therefore, it is suggested to use good parents capable of meeting the husk coverage trait.

Genotypes LCSH 116 x LP8HS 129 and LCSH 116 x LP8HS 130, which belonged to the single hybrid category, stood out as promising genotypes to be registered and recommended to farmers since both presented high yield and husk coverage quality.

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