AUSTRALIAN JOURNAL OF CROP SCIENCE | SUBMITTED: 06-FEB-2017 | REVISED: 21-MAY-2017 | ACCEPTED: 13-JUL-2017

Australian Journal of
Crop Science
AJCS

AJCS 11(09):1188-1194 (2017) ISSN:1835-2707
doi: 10.21475/ajcs.17.11.09.pne538

Combining ability for traits associated with yield and quality in super sweet corn (*Zea mays* L. saccharata)

Nayara Norrene Lacerda Durães, Jocarla Ambrosim Crevelari, Julio Cesar Fiorio Vettorazzi, José Arantes Ferreira Junior, Fernanda de Abreu Santana, and Messias Gonzaga Pereira

Universidade Estadual do Norte Fluminense Darcy Ribeiro, Avenida Alberto Lamego, nº 2000, Parque Califórnia, Cep 28013-602, Campos dos Goytacazes, RJ, Brazil

***Corresponding author: nayaranorrene@hotmail.com**

Abstract

Most commercial super sweet corn lines focus on simple hybrids. Information about the general combining ability (GCA) and about the specific combining ability (SCA) are relevant for hybrid development. The aim of the present study is to estimate the general and specific combining ability effects associated with yield and quality traits of super sweet corn. Nine lines (Flint) and ten lines (Dent) were crossed in a partial diallel fashion to produce 90 F_1 hybrids. The hybrids and ten checks were assessed through the duplicate simple lattice design, with four repetitions, in two environments of Rio de Janeiro State, during the 2015 season. Data of six agronomic traits associated with yield, and five traits associated with quality were recorded. The results showed that GCA and SCA were significant ($P \leq 0.01$) for almost all herein studied traits. The relative magnitude of GCA and SCA mean squares indicated the prevalence of additive effects for the quality traits, as well as non-additive effects for yield traits. The GCA and SCA ($P \leq 0.01$) interactions showed different genotype responses to the different environments. The "Flint" L1 inbred line presented the highest concentration of alleles favoring the increment for most of the traits. This line was the most suitable for the formation of new super-sweet hybrids. Three crosses (L8 x L18, L1 x L13 and L6 x L15) showed desirable SCA effects for almost all traits. These crosses are valuable and could be used in corn breeding programs in order to achieve high yielding and quality combinations.

Keywords: GCA; SCA; Genetic Improvement; Hybrid; Specialty corn.

Abbrevations: GCA_ general combining ability; SCA_ specific combining ability; PH_ plant height; FLOW_ flowering; ST_ stand; NE_ number of ears; UEY_ unhusked ear yield; EY_ husked ear yield; ED_average diameter of 5 ears; CD_ average cob diameter; HEL_ average husked ear length; UEL_ average unhusked ear length; and NGR_ number of grain rows.

Introduction

Super sweet corn (*Zea mays* L. saccharata) is a common corn mutant characterized by high sugar and low starch contents that lead to peculiar flavor, texture and aroma traits. The "sweetness" trait is controlled by simple recessive genes or by genes associated with double or triple combinations. These combinations present different sugar/starch ratio accumulated in the endosperm (Camilo et al., 2015). Among the genes responsible for the super sweet phenotype, shrunken2 (*sh2*) is the most commercially used one because of its high sugar accumulation and longer post-harvest life; therefore, it keeps quality after harvest for longer than standard sweet hybrids (Rodrigues et al., 2009; Solomon et al., 2012). Super sweet corn is quite versatile and adds value to products; it can be used in its fresh form, as well as processed in the canned product industry (Entringer et al., 2016). Since it is a source of tocopherols, carotenoids, vitamin C and phenolic, super sweet corn is considered an important vegetable for cultivation purposes worldwide (Juvik, 2009). The Brazilian super sweet corn cultivation nowadays is limited probably due to lack of knowledge presented by consumers and farmers, to the small number of cultivars, as well as to lack of genetic studies about the traits associated with its yield and quality (Rodrigues et al., 2009). However, market demands have led to the use of high super sweet corn cultivation technologies; that is why super sweet corn is expected to become an important crop, soon (Pereira Filho et al., 2013). Unlike common corn, the super sweet corn has been undergoing intense enhancement of traits associated with quality; however, the high yield remains the primary goal of most plant breeding programs (Ferh, 1987). Accordingly, the research about super sweet corn quality and yield improvement and about its importance to the market stands out. The development of hybrids has been the best strategy towards an immediate effect on the yield and quality of super sweet corn. The successful development of simple hybrids depends on a series of steps, among them one can find the selection of high performance populations in order to extract lines that, once crossbred, allow exploring hybrid vigor or heterosis. It is worth pinpointing that heterosis is a well-known phenomenon that enables hybrids to have a better performance (Cruz et al., 2012).

Studies focused on the combining ability are a crucial step in breeding programs. This ability is one of the key points for the selection of lines for hybrids' synthesis, since it enables combining favorable alleles in the F_1 combination to achieve greater yield and quality (Solomon et al., 2012).

Sprague and Tatum (1942) defined the concepts of general combining ability (GCA) and specific combining ability (SCA). The GCA analysis enables identifying parents with the ability to transmit their desirable characters to the offspring; the additive gene effects prevail in these offspring. The SCA allows identifying promising hybrid combinations; the non-additive gene effects prevail in these combinations (Baldissera et al., 2012; Cruz et al., 2012).

The evaluation of the steps involving the analysis applied to the combining ability of the lines is the most laborious and costly one. The value of a line in hybrids' commercial process depends on its characteristics and on the hybrid combination behavior (Carena et al., 2010 Hallauer, 2010). The GCA and SCA effects can be assessed through different analyses, but the diallel crosses are effective techniques to identify the best hybrid combinations (Silva et al., 2013). Several types of diallels have been proposed and developed, but the most commonly used methods in corn diallel analysis are those described by Griffing (1956).

Among the partial diallel methodologies proposed by Griffing (1956), those based on the combination of parents to form two different groups have allowed maximizing information about the studied groups using less crossings than the number of crossings required by the complete diallels (Bernardo, 2003).

Given the scarcity of information about crossbreeding involving inbred and adapted super sweet corn lines, and given its importance to the hybrids production in the country's commercial sector, the aims of the current study are to estimate the GCA of super sweet corn inbred lines and the SCA of the resulting hybrids, as well as to assess the yield- and quality-related variables of super sweet corn hybrids by performing partial diallel crossings.

Results and Discussion

Analysis of variance and the significance of the diallel analysis

The joint analysis has shown good experimental accuracy. The estimates were above 0.67 in all cases, except for ST, whose estimate value was 0.55 (Table 1).

All the variables assessed ($p \leq 0.01$) through the F test showed significant effects for treatments and for experimental hybrids (Table 1). Such result indicates that the selected genotypes are contrasting and this contrast is a vital factor for breeding programs, because it amplifies the genetic variability and favors the selection.

Almost all variables presented significant differences between environments, thus showing that these environments were sufficiently distinct in the expression of these variables.

The genotypes had different responses to the existing macro-environmental variations, fact that has reflected the significant effect of the 'treatment-environment' interaction on the four variables assessed in the current study. According to Locatelli et al. (2002), such interaction reduces the correlation between phenotype and genotype, and, as a result, restricts the validity of inferences concerning the breeding process and the inheritance of quantitative traits.

The 'hybrid-environment' interaction had significant effects on most of the herein assessed variables (Table 1), and this outcome has indicated hybrids' non-consistent response to different environments. These effects are often observed when these hybrids are compared to double hybrids or to cultivars showing broader genetic base, because the narrow genetic base of simple hybrids leads to different responses to the assessed environments (Troyer, 1996).

The effects of diallel hybrids were expressed through the general (GCA I and II) and specific combination ability (SCA) (Table 1). The GCA showed significant effect on all the variables of the "Flint" heterotic group (GCA I), as well as on the FLOW, ED, CD, NGR and UEL variables of the "Dent" heterotic group (GCA II). This result evidences that the parents had different favorable–alleles frequencies, as well as proved the existence of parents able to form improved populations.

Significant GCA effects were also reported in studies conducted by Oliboni et al. (2013), who assessed variables such as "yield of corn ears with no straw" and "plant height" in a full diallel comprising 66 hybrids assessed in three different environments. Lemos et al. (2002) assessed the variable "yield" in a full diallel comprising ten super sweet corn lines assessed in two different environments and found the same results.

There were significant SCA differences in almost all the variables (Table 1), and it indicates that experimental hybrids had better or worse response than that expected, because of their parents' GCA. This result shows considerable complementation degree in the frequency of alleles presenting dominance or over-dominance (Hallauer et al., 1988; Pfann et al., 2009; Oliboni et al., 2013).

The significant SCA effect observed in the variables associated with corn ear yield indicates that populations generated from these lines may be useful in interpopulation breeding processes focused on generating lines that, once crossbred, could lead to greater-heterosis hybrids (Oliboni et al., 2013). Pfann et al. (2009) and Oliboni et al. (2013) have assessed diallel trials comprising commercial corn hybrids and found significant SCA in the variables associated with grain yield. They also identified promising commercial hybrid combinations.

Although the mean squares do not directly indicate the relative importance of genotypic variance components, the significance of the GCA and SCA effects has varied due to the additive and non-additive gene effects, respectively (Worrajinda et al., 2013).

According to GCA square sums in both groups (GI and GII) and to the SCA square sum in the simple hybrids' group, SCA has mostly contributed to the FLOW, ST, PH, HEL, UEY, EY and NGR variables, and has explained the 52.23% to 84.93% variation between hybrids. These results have shown the prevalence of non-additive effects on corn ear yield (Table 1), as well as have corroborated the studies conducted by Machado et al. (2009) and Santos et al. (2014).

On the other hand, the contribution from the GCA square sums to the ED and CD variables was relatively higher than that from SCA, fact that indicated the greater importance of additive effects and explained the 52.4% to 70.5% variation. The contributions from GCA and SCA to the UEL and NE variables were moderate, and it indicated that both effects (additive and non-additive) were equally relevant (Table 1).

There was significant interaction between the GCA and the environments in the GCA-I and GCA-II groups when variables such as FLOW, NE, UEY, EY and HEL were assessed, as well as in the GCA-I group when the UEL variable was analyzed. This result suggested that the GCA-based parental selection should be applied to each environment; on the other hand, the interaction between SCA

Table 1. Summary of the analysis of variance and the significance of the diallel analysis in both environments (Campos dos Goytacazes and Itaocara) – RJ, in the 2015 agricultural year.

Variation sources	Mean Squares											
	DF	$^{1/}$FLOW	ST	PH	NE	UEY	EY	ED	CD	HEL	UEL	NGR
Treatments	99	31.738**	3.588**	0.101**	49.401**	40.259**	23.068**	0.439**	0.235*	7.583**	14.697**	13.670**
Environment (E)	1	2522.707*	39.293*	2.426^{ns}	85.560*	0.006^{ns}	1.884^{ns}	0.258*	0.039^{ns}	28.131*	569.457*	4.056*
Treatments X E	99	3.327*	1.773 ^{ns}	0.0373 ^{ns}	12.562 ^{ns}	8.672 ^{ns}	4.828 ^{ns}	0.070 ^{ns}	0.002 ^{ns}	1.648*	4.757*	0.928*
Residue	522$^{2/}$							520$^{2/}$	519$^{2/}$		521$^{2/}$	
Selective Accuracy		0.92	0.55	0.67	0.78	0.82	0.86	0.86	0.88	0.85	0.79	0.95
Hybrids (H)	89	35.579*	3.256*	0.083*	52.706*	23.44*	13.62*	0.487*	0.277*	6.257*	17.489*	15.430*
GCA – I	8	60.368*	3.277*	0.272*	281.883*	104.832*	58.83*	3.553*	1.421*	25.900*	62.794*	35.355*
GCA – II	9	18.688*	1.940^{ns}	0.138^{ns}	22.610^{ns}	18.03^{ns}	5.89^{ns}	0.233*	0.179*	8.451*	4.193^{ns}	9.385*
SCA	72	34.936*	3.418*	0.055^{ns}	31.004*	15.32*	9.64*	0.177*	0.162*	3.801*	14.117*	13.971*
Hybrids X E	89	3.322*	1.790*	0.045^{ns}	13.469*	9.418*	5.197*	0.073*	0.032^{ns}	1.913*	5.575*	1.061^{ns}
GCA - Group I X E	8	4.254*	0.899^{ns}	0.041^{ns}	26.845*	20.489*	6.840*	0.060^{ns}	0.026^{ns}	3.761*	4.704*	0.357^{ns}
GCA - Group II X E	9	3.769*	0.925^{ns}	0.074^{ns}	11.459*	6.453*	4.383*	0.041^{ns}	0.037^{ns}	1.009^{ns}	9.564*	0.664^{ns}
SCA X E	72	3.162*	1.997*	0.042^{ns}	12.234*	8.558*	5.116*	0.079*	0.027^{ns}	1.820*	5.174*	1.188^{ns}
Mean		59.17	12.19	2.30	17.60	15.11	10.48	4.62	2.25	20.20	27.69	13.51
%SQGCA$_{-I}$ $^{3/}$		15.3	9.05	29.3	48.1	40.00	38.41	65.6	46.1	37.2	32.3	20.6
%SQGCA$_{-II}$ $^{3/}$		5.3	6.03	16.6	4.3	7.77	4.37	4.9	6.6	13.6	2.4	6.2
%SQSCA $^{3/}$		79.4	84.93	54.1	47.6	52.23	57.22	29.5	47.3	49.1	65.3	73.2

$^{1/}$ FLOW= number of days for flowering, ST = number of plants in the plot, PH= plant height (meters), NE = number of corn ears, UEY= unhusked ears yield (tonnes. ha^{-1}), EY= husked ear yield (tonnes. ha^{-}1), ED= average ear diameter (cm), CD= average cob diameter (cm), HEL= average husked ear length (cm), UEL= average unhusked ear length (cm) and NGR= number of grain rows . * 5% Significance; ** 1% significance; and ^{ns} non-significant according to the F test. $^{2/}$ Degree of freedom of the error. $^{3/}$ Percentage of the squares sum explained through GCA – I and II, and SCA.

Table 2. GCA effect estimates in the 19 super sweet corn inbreed lines in both environments (Campos dos Goytacazes and Itaocara) – RJ, in the 2015 agricultural year. For variables, see Table 1. $^{(1)}$Group I: i = 1, 2..., 9; Group II: j = 6, 7... 10.

		Effect											
Groups $^{(1)}$		Lines	FLOW	ST	PH	NE	UEY	EY	ED	CD	HEL	UEL	NGR
Flint	L1:	SH113	-0.486	0.277	0.002	2.179	2.400	1.891	0.182	0.135	0.864	-1.045	0.242
	L2:	SH116	-0.95	-0.063	0.068	-1602	-0.207	0.270	0.340	0.236	-0.29	-1.005	1.166
	L3:	SH111	-0.075	-0.202	0.082	3.277	2.244	1.817	0.072	-0.011	-0.662	0.806	0.199
	L4:	SH120	1.750	0.203	-0.047	1.235	-0.060	-0.298	-0.332	-0.223	0.764	-0.368	-0.227
	L5:	SH119	0.043	-0.154	0.049	-0.093	0.798	0.263	-0.046	0.007	0.473	0.831	-0.611
	L6:	SH 8H S101	-0.262	-0.207	-0.009	-1.370	-0.938	-0.829	0.079	0.056	-0.602	-0.232	-0.126
	L7:	SH 8HS 107	-0.918	-0.129	-0.065	-2158	-1.939	-1.272	-0.003	-0.031	-0.011	0.360	0.173
	L8:	SH 8HS 100	-0.058	0.029	0.005	-1439	-1.398	-0.667	-0.002	-0.066	-0.203	-0.748	0.391
	L9:	SH 8HS 109	0.955	0.245	-0.083	-0.028	-0.902	-1.174	-0.288	-0.101	-0.332	1.399	-1.206
Dent	L10:	SH 140	0.497	0.002	-0.034	0.180	0.167	0.049	0.035	0.068	0.132	-0.016	-0.505
	L11:	SH 134	-0.374	0.409	0.099	0.223	-0.335	0.083	0.044	0.033	0.471	-0.125	0.075
	L12:	SH 137	0.137	-0.034	0.013	-0.205	-0.753	-0.614	-0.047	-0.056	0.201	0.001	-0.45
	L13:	SH 136	-0.420	0.045	-0.066	0.153	0.209	0.201	-0.026	-0.002	0.484	0.219	-0.061
	L14:	SH 139	-0.804	0.036	-0.038	-0.691	0.647	0.162	0.070	-0.002	-0.114	0.184	0.416
	L15:	SH 8HS 128	0.475	-0.049	0.011	0.702	-0.442	-0.220	-0.063	-0.006	-0.501	-0.218	-0.083
	L16:	SH 8HS 125	0.185	-0.024	0.009	-0.048	0.079	0.293	-0.033	0.028	-0.069	-0.301	0.137
	L17:	SH 8HS 177	0.425	-0.056	0.002	0.936	0.073	-0.070	-0.087	-0.108	-0.403	-0.300	-0.235
	L18:	SH 8HS 129	0.515	-0.236	-0.005	-0.468	-0.570	-0.098	0.063	0.029	0.222	0.426	0.148
	L19:	SH 8HS 130	-0.634	-0.095	0.011	-0.782	0.925	0.214	0.043	0.015	-0.424	0.130	0.559

and the environments was significant in most variables assessed in the current study, and it presupposes that the crossbreeding processes did not effectively keep constant response in the herein assessed environments (Table 1).

The super sweet corn breeding process requires special care, since this vegetal intended to human consumption. Thus, it is necessary pursuing good yield, although it often happens in the common corn breeding process (Worrajinda et al., 2013), as well as it is worth pursuing a set of attributes able to generate a final product associated with quality, good appearance and with high aggregated market value (Luz et al., 2014).

Some requisites must be taken into consideration in order to meet green corn market requirements, namely: plant height uniformity; precocity able to allow planting more than one crop per year; smaller cob diameter; yield of corn ears with no straw higher than 12 t ha^{-1}; length of corn ears with no straw longer than 20 cm, upper corn ear diameter 3 cm, and number of grain rows equal to or greater than 14 (Bottini et al., 1995; Pereira Filho et al., 2003). The experimental hybrids have shown satisfactory results in almost all the assessed variables, since they met the agronomic and commercial quality requirements and standards (Table 1). It is worth highlighting that the EY and NGR variables had mean values below the required industrial standard. However, it was possible identifying hybrids presenting EY and NGR values higher than the required ones, as well as great market potential concerning these variables.

Some researchers have prioritized the study about variables associated with corn ears with no straw; however, the variables associated with corn ears with straw are undoubtedly the most important ones to the industry, since corn ears are traded per unit with straw due to the transportation and conservation of sugars (Lemos et al., 2002). The indices of these straw-related variables should show 50% increase when they are compared to the variables found in corn ears with no straw. The present study has also shown satisfactory results concerning these variables (Table 1).

General combining ability (GCA) effects

According to Sprague and Tatum (1942), low GCA estimates indicate that the line value or the value of its combination with other lines do not differ from the average of all diallel crossings, whereas the high and positive GCA estimates are of interest when the aim is to increase the value of the variable of interest.

With respect to the GCA effects on the yield of corn ears with no straw, 10 out of the 19 lines presented positive estimates, mainly the "Flint" lines L1 and L3, and the "Dent" line L16. This outcome highlighted that these lines are superior to other diallel lines when it comes to the mean performance of their hybrids (Table 2).

Since the best hybrids result from the crossing between lines presenting the highest GCA estimates, the L1 x L16 and L3 x L16 hybrids should show strong SCA effect, as well as the best mean performance. However, it just happened with the L3 x L16 hybrid, which recorded positive SCA result, and whose average was included in the most productive group, according to the clustering test. With respect to the L1 xL16 hybrid, it was possible inferring that these lines had high degree of kinship and that it resulted in low heterosis after crossing and in negative SCA value.

As for the other variables, the GCA highlights were: L1, L2, L3, L6, L7, L8, L11, L13, L14 and L19 in FLOW; L1, L4, L8, L9, L10, L11, L13 and L14 in ST; L1, L2, L3, L5, L8, L11, L12, L15, L16 and L17 in PH; L1, L3, L4, L11, L13, L15 and L16 in NE; L1, L3, L5, L10, L13, L14, L16, L17 and L19 in UEY; L1, L 2, L3, L6, L10, L11, L14, L18 and L19 in ED; L1, L2, L5, L6, L10, L11, L16, L18 and L19 in CD; L1, L4, L5, L10, L11, L12, L13, and L18 in UEL; L3, L5, L7, L9 , L12, L13, L14, L18 and L19 in HEL; and L1, L2, L3, L7, L8, L11, L14, L16, L18 and L19 in NGR (Table 2).

The Scott Knott test allowed forming four groups based on the hybrids' mean EY. It was possible seeing that the lines included in the most productive no-straw group clearly showed the benefits from the GCA-positive estimate lines. It is worth emphasizing that the lines showing unfavorable GCA values do not imply their discharge from the breeding programs. These lines may show favorable estimates when they are crossbred with other heterotic groups (Oliboni et al., 2013).

Specific combining ability (SCA) effects

General and specific combination ability estimates are complementary information that should be interpreted together, at the time to assess the lines. It is ideal associating high GCA and SCA values, since it would allow associating the two fundamental criteria used to select populations, namely: high mean and the greatest genetic variance possible (Ferreira et al., 2004, Cruz et al., 2012).

The results showed favorable hybrid combinations for most traits related to the herein assessed yield and quality (Supplementary table 1 and 2). It is possible seeing the five most favorable hybrid combinations in Table 3.

The hybrid combinations simultaneously coinciding with the highest SCA estimates were L8 x L18 for NE, UEY, EY and NGR; L1 x L13 for NE, UEY and EY; and L6 x L15 for UEY, EY, ED and NGR. These results comply with the Scott Knott's test results, since these hybrids were included in the highest-mean groups to measure most of the herein described variables (Supplementary table 1 and 2).

By considering the five highest SCA estimates for EY, it was possible seeing that L1 x L13 and L4 x L14 involved 2 and 1 of the parents presenting positive GCA estimates, respectively. However, by considering the five highest means (L1 x L13, L1 x L10, L3 x L10, L3 x L14 and L3 x L13) grouped according to the Scott Knott's test, it was possible concluding that all of these means combine the benefits from the two parents presenting positive GCA and high SCA estimates. With respect to NGR, the five best combinations based on SCA did not show the highest means, except for L2 x L13. As for GCA, most combinations presented at least one positive parent, except for L6 x L15.

With regard to the other variables, mainly to ST, UEL, HEL and NGR, high SCA estimates involved at least one parent presenting high GCA, in general. However, there were also cases wherein the two parenting partners presented negative GCA estimates and even high SCA; thus suggesting that these lines showed high complementation degree and, consequently, strong SCA effect.

It is worth emphasizing that the recommendations concerning the selection of super sweet corn genotypes based on GCA and SCA should take into consideration and meet a planned system involving the real needs of commercial plantations. This selection should start in the cultivation system and go all the way up to the integration of activities developed by producers, and the schedule set by the industry. Thus, the selection of parents and hybrids of higher GCA and SCA estimates, respectively, would be ideal for most variables. However, the selection should not always be performed as a way to increase the expression of variables such as FLOW, PH and CD. It is necessary taking into consideration the entire previously described system, so that the selection may happen in the opposite direction, depending on the interest, or may even keep the expression observed in the variable.

The contract between producers working in irrigated areas and the industries often follows a tight schedule, fact that requires producers to exert a great control over raw-material shipments. Thus, using earlier genotypes that present less losses caused by bedding and breaking would be the ideal procedure (Bordallo et al., 2005); based on these interests, the selection should prioritize earlier and smaller genotypes. Therefore, with respect to FLOW and PH, taking into consideration the lowest GCA and SCA estimates would be the best scenario. It is worth keeping in mind that the genotypes assessed in the current study presented the brachytic gene (*br2*); accordingly, keeping the variable expression within estimates close to zero would be the best choice. As for the CD variable, preference should be given to phenotypes presenting the smaller diameters and the selection should prioritize the low GCA and SCA estimates.

The prevalence of non-additive effects (SCA) over the additive effects (GCA) has been reported in the literature, mainly when it comes to yield-related variables (Pfann et al., 2009; Worrajinda et al., 2013).

The results in the current study showed the importance of non-additive effects for the yield-related variables. However, it was also possible showing the importance of the additive effects for the quality-related variables. Therefore, the information herein gathered can effectively and scientifically guide breeding methods that comprise variables related to super sweet corn yield and quality.

Materials and Methods

Nineteen (19) super sweet corn S_7 inbred lines (*sh2*) obtained from the breeding program of Darcy Ribeiro Northern Fluminense State University were used in the current study. These inbred lines' pedigree is presented in the supporting information (Supplementary Table 3).

The lines were divided in two groups according to grain type in order to set distinct heterotic groups: I- "Flint" lines; and II - "Dent" lines. These lines were extracted from brachytic corn populations belonging to the Cimmyt and Piranão groups. These groups had their *Sh2* gene previously introgressed through successive backcross cycles (Entringer et al., 2014). The two groups of lines were combined in compliance with the partial diallel method, according to the methodology adapted by Griffing (1956).

Field experiments

The 90 simple hybrids resulting from the 10x9 partial diallel were assessed in two different environments - Campos dos Goytacazes and Itaocara counties (Rio de Janeiro) – located at the geographic coordinates: latitude 21°24'48" S, longitude 41°44'48" W, and altitude 14 m; and latitude 21°40'09" S, longitude 42°04'34" W, and altitude 60 m, respectively, during the 2015 crop season. The plantings were carried out in isolation from other corn fields, and followed the 10 x 10 duplicate simple lattice design, with 4 repetitions and 10 controls (parental populations of the lines and their interpopulational hybrids). The experimental units in both experiments consisted of 3m-long rows, with 1.0 m spacing between rows, and 0.30 m spacing between plants in the row, thus totaling 11 plants.

According to the soil analysis, the fertilization was carried out using 400 kg ha^{-1} of the 8-28-16 formulation. In addition, two cover fertilizations were carried out at the 30th day after planting, by using 300 kg ha^{-1} of the 20-00-20 formulation, as well as at the 45th day, by using 200 Kg ha^{-1} of urea. Thinning was carried out after the 15th emergence day in order to keep 33.333 plants/ha^{-1} in the stand density. The other managements, as well as the control of undesirable plants and pests, were conducted according to the technical recommendations and the minimum culture indications.

Assessing the agronomic and quality traits

The green ears were harvested approximately 20 to 23 days after silking, when the corn ears reached the harvest point adopted by the industry. The following yield-related variables were assessed: plant height (PH) – average height (in meters) of six competitive plants measured from soil level up to the insertion of the node of the flag leaf; female flowering (FLOW) – number of days from sowing to flowering in 50% of the plants in the plot; stand (ST) - total number of plants in each plot at harvest time; number of ears (NE) – number of ears per plot; unhusked ear yield (UEY) - total weight (in tonnes per hectare) of the unhusked ears in the plot; husked ear yield (EY) - total weight (in tonnes per hectare) of the husked ears in the plot.

Five (5) marketable corn ears were sampled in each plot for quality-related variable for average ears diameter (ED) assessment: average diameter (in centimeters) of the 5 husked ears; average cob diameter (CD), average cob diameter (in centimeters) of the 5 ears; average husked ear length (HEL), average length (in centimeters) of the 5 husked ears; average unhusked ear length (UEL) – average length (in centimeters) of the of 5 unhusked ears; and number of grain rows (NGR). The quality-related variables were assessed in a digital scanner model BENQ 5000.The images were processed and analyzed in the Image J software (version 1.50c).

Statistical analysis

The collected data were subjected to individual preliminary analysis of variance to check the homogeneity of residual variances through the Bartlett test, at 5% probability (Bartlett, 1937). Subsequently, a joint analysis was performed according to the genetic statistical model by Cochran and Cox (1957):

$$Y_{il(j)(p)} = \mu + A_{(p)} + R_{(j)} + B/R/A_{(l)(j)(p)} + G_{(i)} + GA_{(i)(p)} + eil_{(j)(p)}$$

Wherein: μ = general constant; $A_{(p)}$ = fixed effect of the p environment; $R_{(j)}$ = effect of the j repetition ~NID $(0,\sigma^2_r)$; $B/R/A_{(l)(j)(p)}$ = effect of the l block within the j repetition within the p environment ~NID $(0,\sigma^2_b)$; $G_{(i)}$ = effect of the i genotype ~NID $(0, \sigma^2_g)$; $GA_{(i)(p)}$ = effect of the interaction between the i genotype and the I environment ~NID (0, σ^2_{ga}); $eil_{(j)(P)}$ = experimental error ~NID (0,σ^2).

The mean values of the treatments in relation to the assessed variables were grouped through the Scott Knott test (1974), at 5% probability level. The diallel analysis was based on the means of the 90 simple hybrids, according to the methodology by Griffing (1956) adapted to partial diallels, in compliance with the following statistical genetic model:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \bar{e}_{ij}$$

Wherein: Y_{ij} is the mean value of the hybrid combination between the G_1 and G_2 lines; μ is the general mean of the hybrid combinations; g_i is the effect of the general combining ability of group i; g_j is the effect of the general combining ability of group j; s_{ij} is the effect of the specific combining ability (SCA) in crossbreeding processes involving parents belonging to orders i and j; $\bar{e}_{ij}$ is the associated mean experimental error.

All analyses of variance were performed in compliance with the *Proc* GLM procedure of the SAS software (Littel et al., 2006). The diallel analysis and the Scott Knott test were performed in the Genes software (Cruz, 2013).

Conclusion

The partial diallel analysis was efficient to estimate the GCA effects of super sweet corn inbred lines, as well as the effects of the SCA on the hybrids generated by crossings between lines belonging to different heterotic groups. The “Flint” heterotic group showed genetic variability higher than that of the “Dent” group. The additive and non-additive effects were equally important for the herein assessed variables. The additive effects stood out especially for quality-related traits, whereas the non-additive effects stood out specially for yield-related traits. The significance of the interaction between GCA/SCA and the environments showed distinct genotype responses to the environments, thus indicating the need of different selections and recommendations depending on the environment. The “Flint” L1 line presented the highest concentration of favorable alleles to the FLOW, PH, NE, UEY, EY, ED, CD, UEL and NGR variables. Thus, it is the most suitable line for the formation of new super sweet hybrids. The L8 x L18, L1 x L13 and L6 x L15 combinations have simultaneously enabled greater combinatorial effects on the UEY and EY variables. Thus, they are promising super sweet corn hybrids.

Acknowledgments

The authors are grateful to the Graduate Program in Genetics and Plant Breeding and to the Coordination of Higher Education Personnel Improvement (CAPES), as well as to the Research Support Foundation of Rio de Janeiro State (FAPERJ) and to National Council for Scientific and Technological Development (CNPq).

References

Baldissera JNC, Valentini, G, Coan, MMD, Almeida, CB, Guidalin, AF, Coimbra, JLM (2012) Capacidade combinatória e efeito recíproco em características agronômicas do feijão. Semina: Cienc Agra. 33: 471-480.

Bartlett MS (1937) Properties of sufficiency and statistical test. Proc Royal Soc A. 160: 318-335.

Bernardo R (2003) Parental selection, number of breeding populations, and size of each population in inbred development. Theor and Appl Genet. 107: 1252-1256.

Bordallo PN, Pereira, MG, Amaral Junior, AT, Gabriel, APC (2005) Análise dialélica de genótipos de milho doce e comum para caracteres agronômicos e proteína total. Hortic Bras. 23: 123-127.

Bottini PR, Tsunechiro, A, Costa, FAG da (1995). Viabilidade da produção de milho verde na "safrinha”. Inform Econ. 25: 49-53.

Camilo JS, Barbieri VHB, Rangel RM, Bonnas DS, Luz JMQ, Oliveira RC (2015) Aceitação sensorial de híbridos de milho doce e híbridos de milho verde em intervalos de colheita. Rev. Ceres. 62: 001-008.

Carena MJ, Wanner DW, Yang J (2010) Linking pre-breeding for local germplasm improvement with cultivar development in maize breeding for short-season (85-95RM) hybrids. J Plant Registration. 4: 86-92.

Cochran WG, Cox CM (1957) Experimental designs. In: John Wiley & Sons (ed), 2ª edn. New York.

Cruz CD (2013) Programa Genes: a software package for analysis in experimental statistics and quantitative genetics. Acta Scienti Agro. 35:271-276.

Cruz CD, Regazzi AJ, Carneiro PCS (2012) Modelos biométricos aplicados ao melhoramento genético, 4st edn. UFV, Viçosa.

Entringer GC, Santos PHAD, Vettorazzi JC, Cunha KS, Pereira MG (2014) Correlação e análise de trilha para componentes de produção de milho super doce. Rev Ceres, 61:356-361.

Entringer GC, Vettorazzi JC, Santos EA, Pereira MG, Vianna AP (2016) Genetic gain estimates and selection of S1 progenies based on selection indices and REML/ BLUP in super sweet corn. Aust J crop Sci. 10: 411-417.

Ferh WR (1987) Principles of cultivar development. MacMillian, 1st edn.New York.

Ferreira FM, Ribeiro Junior JI, Pacheco CAP, Silva CHO, Cruz CD (2004) Efficiency of circulant diallels as compared to complete diallels for the estimation of general and specific combining ability. Crop Breed Appl Biot. 4:145-151.

Griffing AR (1956) Concept of general and specific combining ability in relation to diallel crossing systems. Aust J Biol Sci. 9: 463-493.

Hallauer AR, Carena MJ, Miranda Filho JB (2010) Quantitative Genetics in Maize Breeding. New York, Springer, 459.

Hallauer AR, Miranda Filho JB de (1988) Quantitative genetics in maize breeding. Ames, Iowa State University, 468.

ImageJ, Internet site address: http://rsb.info.nih.gov/ij/ acessado em 12/12/2016.

Juvik JA (2009). Feasibility for improving phytonutrient content in vegetable crops using conventional breeding strategies: case study with carotenoids and tocopherols in sweet corn and broccoli. J. Agric. Food Chem. 57: 4636-4644.

Lemos MA, Gama EEG, Menezes D, Santos VF dos, Tabosa JN (2002) Avaliação de dez linhagens e seus híbridos de milho superdoce em um dialelo completo. Hortic Bras. 20: 167-170.

Littel RC (2006).SAS for mixed models. 2nd ed.Cary: SAS Institute.

Locatelli AB, Federizzi LC, Naspolini VFo (2002) Capacidade combinatória de nove linhagens endogâmicas de milho (Zea mays L.) em dois ambientes. Cienc Rural. 32: 365-370.

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. Hortic Bras. 32: 163-167.

Machado JC, Souza JC de, Ramalho, MAP, Lima JL (2009) Stability of combining ability effects in maize hybrids. Sci Agric. 66: 494-498.

Oliboni R, Faria MV, Neumann M, Resende JTV, Battistelli GM, Tegoni RG, Oliboni DF (2013) Análise dialélica na avaliação do potencial de híbridos de milho para a geração de populações-base para obtenção de linhagens. Semina: Cienc Agrar. 34: 7-18.

Pereira Filho IA, Cruz JC, Costa RV da (2013) Milho doce. In: Cruz J C (Ed.). Milho. Brasília. DF: EMBRAPA informação tecnológica.

Pereira Filho IA, Cruz JC, Gama EE G (2003) Cultivares para o consumo verde. In: Pereira Filho IA. O cultivo do milho verde. Brasília. DF: EMBRAPA informação tecnológica. 204p.

Pfann AZ, Faria MV, Andrade, AA, Nascimento IR, Faria CMDR, Bringhentti RM (2009) Capacidade combinatória entre híbridos simples de milho em dialelo circulante. Cienc Rural, 39: 128-134.

Rodrigues F, Pinho RGV, Albuquerque CJB, Faria Filho EM, Goulart J de C (2009) Capacidade de combinação entre linhagens de milho visando à produção de milho verde. Bragantia. 68: 75-84.

Santos PHA, Pereira MG, Trindade R dos S, Cunha KS, Entringer GC, Vettorazzi JCF (2014) Agronomic performance of super sweet corn genotypes in the north of Rio de Janeiro. Crop Breed Appl Biotechnol. 14: 8-14.

Scott A, Knott M (1974) Cluster-analysis method for grouping means in analysis of variance. Biometrics. 30: 507-512.

Silva VMP, Carneiro PCS, Menezes Júnior JAN de, Carneiro VQ, Carneiro JE de S, Cruz CD, Borém A (2013) Genetic potential of common bean parents for plant architecture improvement. Sci Agric. 70:167-175.

Solomon KF, Martin I, Zeppa A (2012) Genetic effects and genetic relationships among shrunken (*sh2*) sweet corn lines and F1 hybrids. Euphytica. 185: 385-394.

Sprague GF, Tatum LA (1942) General vs. specific combining ability in single crosses of corn. J Am Soc Agron. 34: 923-932.

Troyer AF (1996) Breeding widely adapted, popular maize hybrids. Euphytica. 92:163-174.

Worrajinda J, Lertrat K, Suriharn B (2013) Combinig ability of super sweet corn inbred lines with diferente ear sizes for ear number and whole ear weight. J Breed Genet. 45: 468-477.