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Research Article

Exploiting combining ability and maternal effects for genotypic selection of best hybrids in sweet corn and normal corn crosses

K. Kavya, R. Ravikesavan*, N. Kumari Vinodhana and A.P. Sivamurugan

Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore,
Tamil Nadu, India.
***E-Mail:** chithuragul@gmail.com

Abstract

Twenty one sweet – normal corn crosses and twenty one normal – sweet corn crosses obtained by [3 × 7] sweet corn × normal corn and [7 × 3] normal corn × sweet corn crosses, respectively were scrutinized for the advantage of reciprocal cross effects in addition to the combining ability studies to screen superior hybrids for yield and quality related traits. Based on the mean reciprocal cross effect of common parental genotypes, NCL_3 and NCT_7 were identified as the best fit for seed and pollen parents for green cob weight, respectively. Potential heterotic combinations were discovered indirect and reciprocal crosses as well. Reciprocal cross effects were significant only for green cob weight, plant height and reducing sugars, however when screened at specific cross combinations levels, many crosses had appreciable hybrid vigour in reciprocal crosses. Thus maternal effect as an added approach for hybrid screening is advisable.

Key words: Maternal effect, specific combining ability, line × tester analysis, field corn, sweet corn

INTRODUCTION

Normal corn also called field corn (*Zea mays*) is well known for its multiple purposes as it serves as, animal feed, industrial corn, besides being consumed by humans directly (Tracy, 1993). Whereas sweet corn (*Zea mays* var. *saccharata*) is well known for its characteristic endosperm sugar concentration associated with genes attributing for sweet kernels (Sturtevant, 1899). Both corn types have different breeding objectives for meeting their respective purposes. There had been many earlier reports on broadening the narrow sweet corn germplasm by introducing field corn heterotic patterns (Cartea *et al.*,1996; Revilla *et al.,* 2000). Establishing new heterotic patterns into sweet corn heterotic groups improve the genetic diversity thereby new heterotic patterns derived could add valuable variation for hybrid development (Cartea *et al.*,1996; Revilla *et al.,* 2000; Kumar *et al.,* 2013).

Immediate exploitation of heterosis is possible through single cross hybrids (Tracy, 1993). Combining ability analysis helps in identifying potential inbreds capable of giving heterotic hybrids on the crossing. Good combiners recognized therefore, will have the inherent potential of yielding outstanding segregants in early generations (Okello *et al.,* 2006). Through general and specific combining ability analysis, the nature of gene action associated with the inheritance of traits could be inferred (Sprague and Tatum, 1942). Both general and specific combining ability could be exploited through the breeding procedure developed by Comstock *et al.* (1949). The inclusion of reciprocal effects add precision in screening potential cross combinations and also widens the opportunities of deriving unexplored genetic variation through various crosses possible (Ordas *et al.,* 2008; Bhandari *et al.,* 2014 and

Dermail *et al.,* 2018). The current trial on deciphering the reciprocal cross effects on combining ability patterns in sweet corn and normal corn crosses was established to identify potential inbreds with mean performance and general combining ability effects associated with favored mean reciprocal cross effects of common parental genotypes and to screen superior hybrids with mean and specific combining ability effects associated with favored reciprocal cross effects of specific cross combinations.

MATERIALS AND METHODS

This experiment was initiated with three sweet corn and seven normal corn inbreds, procured from the Department of Millets, Tamil Nadu Agricultural University. Three sweet corn and seven normal corn inbreds were crossed in line x tester fashion; wherein for L x T block with direct crosses, sweet corn inbreds were used as lines and normal corn inbreds were chosen as testers. For L x T block with reciprocal crosses, normal corn and sweet corn inbred were employed as lines and testers, respectively. The parents and the single cross hybrids thus derived were listed with respective codes (**Table 1**).

The single cross hybrids thus obtained were evaluated through two randomized complete block designs, one accommodating direct crosses and the other accommodating reciprocal crosses with two check hybrids (Misthi as sweet corn check hybrid and CO 6 as normal corn check hybrid). All the proposed packages of practices were followed during the entire cropping period.

The performance of the experimental population had been recorded for early developmental traits like days to 50% tasseling, days to 50% silking and anthesis silking interval and for yield related traits like plant height (cm), cob length (cm), cob girth (cm), kernel rows per cob, kernels per row and green cob weight (g/cob). Kernel quality parameters like total sugars and reducing sugars were estimated in immature kernels of cob.

The mean data thus noted was subjected to line x tester analysis to study combining ability as suggested by Kempthorne (1957). The variation contributed by the genotype of maternal parent was estimated by computing reciprocal cross advantage.

$$\text{Reciprocal cross advantage (R\%)} = \frac{\overline{\text{RC}}-\overline{\text{NC}}}{\overline{\text{NC}}} \text{ X } 100$$

Where,

$\overline{\text{NC}}$ - Normal cross mean

$\overline{\text{RC}}$ - Reciprocal cross mean

t- test statistic was adopted to test significance of the reciprocal cross effect (%) as follows.

$$t_{cal} = \frac{|\text{Mean difference}|}{\text{standard error difference}}$$

Where,

$$|\text{Mean difference}| = |\overline{\text{NC}} - \overline{\text{RC}}|$$

Standard error difference (SEd) $= \sqrt{SE_1^2 + SE_2^2}$

Where,

SE_1^2 - Standard error estimate of normal cross trial

SE_2^2 - Standard error estimate of reciprocal cross trial

RESULTS AND DISCUSSION

Variance due to crosses was significant for all the traits studied, with a strikingly higher magnitude of the mean sum of squares in direct cross population over reciprocal cross population, except for days to 50% tasseling, kernel rows per cob, reducing sugars, where it is lower. Variance due to lines was non significant for cob length,

Table 1. Catalogue of lines and testers.

Sweet corn × Normal corn mating			Normal corn × Sweet corn mating		
S.No.	Code	Parents	S.No.	Code	Parents
		Sweet corn lines			**Normal corn lines**
1	SCL_1	SC 11 – 2	1	NCL_1	UMI 1205
2	SCL_2	12039 – 1	2	NCL_2	UMI 1210
3	SCL_3	45684	3	NCL_3	UMI 1220
		Normal corn testers	4	NCL_4	UMI 1223
1	NCT_1	UMI 1205	5	NCL_5	IMR 102
2	NCT_2	UMI 1210	6	NCL_6	IMR 122
3	NCT_3	UMI 1220	7	NCL_7	IMR 142
4	NCT_4	UMI 1223			**Sweet corn testers**
5	NCT_5	IMR 102	1	SCT_1	SC 11 – 2
6	NCT_6	IMR 122	2	SCT_2	12039 – 1
7	NCT_7	IMR 142	3	SCT_3	45684

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kernel rows per cob, reducing sugars in direct crossing population and reciprocal crosses had non significant values for anthesis silking interval and cob girth. Variance due to testers was non significant for cob girth alone in direct crosses and reciprocal crosses had non significant variance due to testers for days to 50% tasseling, anthesis silking interval, cob length, cob girth, kernel rows (**Table 2**). Variance due to interaction between lines and testers was non significant for cob length in direct crosses and for cob girth in reciprocal crosses. These results of varying patterns of variance due to the reciprocal effect were on par with the findings of Dermail *et al.* (2018); Pollmer *et al.* (1979) and Khehra and Bhalla (1976).

Significant variance components reflect the greater divergence, confirming the higher feasibilities of trapping heterotic potential in respective crosses for the target trait development. Also, the differential magnitude of

Table 2. ANOVA for combining ability

Characters	Sources of variation (Sweet corn x Normal corn)					Sources of variation (Normal corn x Sweet corn)				
	Crosses	Lines	Testers	Line x Tester	Error	Crosses	Lines	Testers	Line x Tester	Error
Days to 50% tasseling	4.9643**	4.7857**	6.9921**	3.9802**	0.2452	5.8571**	3.1349*	1.1429	8.0040**	0.1952
Days to 50% silking	7.6238**	8.1667**	10.0238**	6.3333**	0.2952	6.7143**	3.9365**	3.5000*	8.6389**	0.2143
Anthesis silking interval	1.0452**	1.4524**	0.9841**	1.0079**	0.0500	0.481**	0.381	0.4524	0.5357**	0.1238
Plant height	769.7674**	126.8467*	1596.3746**	463.6173**	31.2961	513.1978**	888.6208**	169.9446**	382.6952**	22.9085
Cob length	5.5752**	2.6058	8.3983*	4.6586	2.3728	4.5944**	9.2793**	1.766	2.7234*	0.7674
Cob girth	1.2469**	2.4118*	0.7592	1.2966*	0.4959	0.5637*	0.9092	0.0621	0.4745	0.327
Kernel rows per cob	4.0650**	0.3438	5.7632**	3.8360**	0.9478	4.1500**	5.7222**	0.2143	4.0198**	0.55
Kernels per row	43.8871**	43.6200**	49.7994**	40.9756**	1.2052	19.3786**	28.8175**	17.2143**	15.0198**	0.5643
Total sugars	7.8185**	16.1836**	4.9709**	7.8482**	0.0650	6.6221**	14.4649**	2.9946**	3.3053**	0.0421
Reducing sugars	0.0054**	0.0005	0.0067**	0.0055**	0.0004	0.1947**	0.2850**	0.0673**	0.1707**	0.0008
Green cob weight	4749.0832**	10684.6680**	8029.9607**	2119.3803**	144.3665	3198.3219**	3602.9782**	270.2941**	3483.9983**	53.3132

* = Significant at 0.05 probability level; ** = Significant at 0.01 probability level

Table 3. Variance due to *gca* and *sca* effects

Characters	Sweet corn x Normal corn			Normal corn x Sweet corn		
	gca variance	sca variance	gca variance/ sca variance	gca variance	sca variance	gca variance/ sca variance
Days to 50% tasseling	0.0384	1.8675	0.0206	-0.0839	3.9044	-0.0215
Days to 50% silking	0.0504	3.019	0.0167	-0.0752	4.2123	-0.0179
Anthesis silking interval	0.0015	0.479	0.0031	-0.0021	0.206	-0.0102
Plant height	11.959	216.1606	0.0553	5.0978	179.8934	0.0283
Cob length	0.0358	1.1429	0.0313	0.0731	0.978	0.0747
Cob girth	-0.0019	0.4003	-0.0047	0.0035	0.0738	0.0474
Kernel rows per cob	0.0089	1.4441	0.0062	0.0051	1.7349	0.0029
Kernels per row	0.1137	19.8852	0.0057	0.1703	7.2278	0.0236
Total sugars	-0.0012	3.8916	-0.0003	0.1296	1.6316	0.0794
Reducing sugars	0	0.0026	0	0.0009	0.085	0.0106
Green cob weight	102.7228	987.5069	0.104	-11.1592	1715.343	-0.0065

gca = general combining ability; sca = specific combining ability variance components was evidenced in the two crossing populations for different traits. These wide disparities between the two crossing populations highlight the advantage of exploiting the genetic variation in the reciprocal crosses that could not be explored in direct crosses.

Variance due to *gca* was lower than that of *sca*, for all the traits in both direct and reciprocal crosses, indicating the predominance of non additive gene action (**Table 3**). Therefore, heterosis breeding and recurrent selection for *sca* as the potential breeding strategies is advisable. These results were in parallel with the studies of Ravikesavan *et al.* (2020), Chinthiya *et al.* (2019) and Kumara *et al.* (2013). Variance due to *gca* in reciprocal crosses was higher than direct crosses, except for plant height, kernel rows per cob and green cob weight. Also, variance due to *sca* in reciprocal crosses was higher except for anthesis silking interval, plant height, cob length, cob girth, kernels per row and total sugars (**Table 3**). Thus the potential heterotic combinations existing in the reciprocal crosses is indispensable. This proportionate difference in magnitudes of genetic variance due to *gca* and *sca* between direct and reciprocal crosses had been supported by the findings of Kalapakdee *et al.* (2020).

Table 4. Comparison of mean; *gca* (line) and mean reciprocal cross effect (%) of common maternal parent genotypes for flowering traits

Traits		SCL$_1$	SCL$_2$	SCL$_3$	NCL$_1$	NCL$_2$	NCL$_3$	NCL$_4$	NCL$_5$	NCL$_6$	NCL$_7$
Days to 50% tasseling	Mean	52.50	49.50**	50.50	57.00	58.50	58.00	60.50	50.50**	50.00**	51.50**
	gca (line)	0.14 ns	-0.64 **	0.50 **	-0.69 **	-0.69 **	1.31 **	-0.52 **	0.31 ns	-0.02 ns	0.31 ns
	Mean R%	0.66	1.73	0.49	0.33	3.55	-3.36*	2.51	-2.81	-3.84	-3.09
Days to 50% silking	Mean	56.50	53.50**	54.50	60.50	62.50	62.00	64.50	54.50**	54.00**	54.50**
	gca (line)	-0.17 ns	-0.67 **	0.83 **	-0.74 **	-0.74 **	1.26 **	-0.57 **	0.43 *	-0.40 *	0.76 **
	Mean R%	0.92	0.98	-0.09	-0.05	4.18	-3.51**	3.31	-1.29	-3.31*	-3.55*
Anthesis silking interval	Mean	4.00	4.00	4.00	3.50*	4.00	4.00	4.00	4.00	4.00	3.00**
	gca (line)	-0.31 **	-0.02 ns	0.33 **	0.07 ns	0.07 ns	-0.10 ns	-0.10 ns	0.07 ns	-0.43 **	0.40 *
	Mean R%	10.24	-2.50	-5.95	-18.06	5.56	-12.50	11.11	16.67*	4.17	-11.11
Plant height	Mean	148.75	192.50**	180.00**	193.25	178.25	165.75	163.00	186.75	221.25**	225.00**
	gca (line)	2.90 ns	0.22 ns	-3.11 ns	8.56 **	1.66 ns	8.73 **	14.84 **	-14.60 **	-17.31 **	-1.87 ns
	Mean R%	6.94**	11.41**	11.11*	-5.66	-3.34	-25.27	-14.82**	-5.26	-12.67**	-1.72
Cob length	Mean	14.85	19.70**	12.00	14.40	15.30	15.95	18.20*	14.35	17.25	17.25
	gca (line)	0.35 ns	-0.48 ns	0.13 ns	-0.41 ns	1.60 **	0.92 *	1.09 **	-0.71 ns	-0.58 ns	-1.92 **
	Mean R%	0.04	0.06	0.03	-0.06**	-0.04	-0.17*	-0.11	0.04	-0.07	0.13*
Cob girth	Mean	12.55	12.20	11.93	12.45	13.25	13.41	14.36	19.52**	12.25	13.25
	gca (line)	0.39 ns	-0.44 *	0.05 ns	0.18 ns	-0.20 ns	0.64 *	0.11 ns	-0.16 ns	0.06 ns	-0.63 *
	Mean R%	-1.81	3.31	-0.16	-1.88	1.11	-7.18*	2.22	1.29	-4.56	5.89*
Kernel rows per cob	Mean	14.00	14.50*	12.50	13.00	14.50	14.00	15.50	14.50	13.00	15.00
	gca (line)	0.18 ns	-0.05 ns	-0.12 ns	0.00 ns	-0.50 ns	0.83 *	1.50 **	0.17 ns	-1.50 **	-0.50 ns
	Mean R%	0.17	1.43	3.22	-12.67**	2.70	-7.47**	-3.09	3.95	6.30	-0.99
Kernels per row	Mean	32.00	42.50**	26.50	26.00	22.00	18.50	22.50	34.00**	27.00	33.00**
	gca (line)	-2.03 **	0.84 **	1.19 **	-2.95 **	-0.12 ns	0.71 *	3.71 **	1.38 **	-1.62 **	-1.12 **
	Mean R%	8.51	4.54	-4.75	11.98*	2.51	-4.05	-4.31**	-9.88	-19.95	4.33
Total sugars	Mean	15.16*	15.21*	14.34	13.53	12.05	14.16**	12.69	13.55	13.42	15.35**
	gca (line)	-0.49 **	1.23 **	-0.75 **	1.15 **	-2.01 **	-1.34 **	-0.12 ns	-0.50 **	2.65 **	0.17 ns
	Mean R%	0.83	-5.91	1.71	-2.51	17.94*	10.72*	10.69	0.48	-19.13	-10.32
Reducing sugars	Mean	1.53**	1.06	1.48**	1.63**	1.33**	1.66**	1.64**	0.15	1.13	1.42**
	gca (line)	-0.00 ns	-0.01 ns	0.01 ns	-0.09 **	-0.06 **	-0.42 **	0.13 **	0.25 **	0.13 **	0.04 **
	Mean R%	-9.27	-1.88	-3.36	6.77	10.29	30.25**	-4.05	-10.98*	-1.99	3.58
Green cob weight (g/cob)	Mean	122.74	137.36**	103.08	122.35	164.44	208.83**	167.25	155.4	166.91	198.13**
	gca (line)	30.79 **	-22.63 **	-8.16 *	-9.50 **	-9.26 **	14.55 **	50.13 **	-15.48 **	-14.94 **	-15.49 **
	Mean R%	-22.96**	5.28	-6.04	20.78**	24.76	-28.31*	3.96	22.94**	-15.27	26.48*

* = Significant at 0.05 probability level; ** = Significant at 0.01 probability level; R% = Reciprocal cross effects; gca = genetic combining ability effects.

Inbreds with significant *per se* performance paralleled with significant *gca* effects were ascertained as best lines. SCL$_2$ was the best combiner for days to 50% tasseling, days to 50% silking, kernels per row and total sugars. NCL$_4$ was the best combiner for cob length and cob girth. NCL$_3$ was the best combiner for green cob weight and NCL$_7$ for reducing sugars. NCL$_6$ and NCL$_5$ were good combiners for days to 50% silking and kernels per row respectively in addition to SCL$_2$ (**Table 4**). Mean reciprocal cross effects of common maternal parent genotype applied as a reliable measure to infer how good fit the best line could be for a maternal parent (Kalapakdee *et al.,* 2020; Ordas *et al.,* 2008). SCL$_2$ was thus a good fit as seed parent for days to 50% tasseling, days to 50% silking and total sugars; NCL$_4$ for cob length and cob girth; NCL$_5$ for kernels per row and NCL$_3$ for green cob weight (**Table 4**).

Based on the significant mean performance of inbred and *gca* of the tester, SCT$_2$; NCT$_6$ and NCT$_1$were good combiners as pollen parent for days to 50% tasseling. SCT$_2$; NCT$_6$ and NCT$_7$ were good combiners as male parents for days to 50% silking and NCT$_1$ for anthesis silking interval and SCT$_2$ and NCT$_1$ for plant height. SCT$_2$was a good combiner for kernels per row and total sugars, while SCT$_3$; NCT$_2$, NCT$_3$ and NCT$_7$were for reducing sugars and NCT$_7$ for green cob weight. However, when favored mean reciprocal cross effect of the common paternal parent was included as the basis for the screening inbreds with a good fit as a pollen parent, SCT$_2$ was identified good fit as a pollen parent for days to 50% tasseling, days to 50% silking and total sugars. While NCT$_7$was for plant height and SCT$_3$ for reducing sugars (**Table 5**). Conclusively, mean reciprocal cross effects would narrow down the top performing parents

Table 5. Comparision of mean; *gca* (tester) and mean reciprocal cross effect (%) of common paternal parent genotypes for yield and quality related traits

Traits		SCT$_1$	SCT$_2$	SCT$_3$	NCT$_1$	NCT$_2$	NCT$_3$	NCT$_4$	NCT$_5$	NCT$_6$	NCT$_7$
Days to 50% tasseling	Mean	52.50	49.50**	50.50	57.00	58.50	58.00	60.50	50.50**	50.00**	51.50**
	gca (tester)	0.00 ns	-0.29 *	0.29 *	-0.10 ns	1.57 **	0.07 ns	1.24 **	-0.60 **	-1.43 **	-0.76 **
	Mean R%	-0.66	-1.73	-0.49	-0.33	-3.55	3.36*	-2.51	2.81	3.84	3.09
Days to 50% silking	Mean	56.50	53.50**	54.50	60.50	62.50	62.00	64.50	54.50**	54.00**	54.50**
	gca (tester)	0.00 ns	-0.50 **	0.50 **	-0.48 *	1.86 **	-0.31 ns	1.52 **	0.02 ns	-1.81 **	-0.81 **
	Mean R%	-0.92	-0.98	0.09	0.05	-4.18	3.5**	-3.31	1.29	3.31*	3.55*
Anthesis silking interval	Mean	4.00	4.00	4.00	3.50*	4.00	4.00	4.00	4.00	4.00	3.00**
	gca (tester)	0.02 ns	-0.19 ns	0.17 ns	-0.38 **	0.29 **	-0.38 **	0.29 **	0.62 **	-0.38 **	-0.05 ns
	Mean R%	-10.24	2.50	5.95	18.06	-5.56	12.50	-11.11	-16.67*	-4.17	11.11
Plant height	Mean	148.75	192.50**	180.00**	193.25	178.25	165.75	163.00	186.75	221.25**	225.00**
	gca (tester)	-2.44 ns	3.99 **	-1.55 ns	15.39 **	15.35 **	-19.69 **	2.35 ns	-5.37 *	-22.31 **	14.28 **
	Mean R%	-6.94**	-11.41**	-11.11*	5.66	3.34	25.27	14.82**	5.26	12.67**	1.72
Cob length	Mean	14.85	19.70**	12.00	14.40	15.30	15.95	18.20*	14.35	17.25	17.25
	gca (tester)	0.40 ns	-0.26 ns	-0.15 ns	-0.90 ns	1.45 *	-1.34 *	-0.08 ns	0.64 ns	-1.16 ns	1.39 *
	Mean R%	-0.04	-0.06	-0.03	0.06**	0.04	0.17*	0.11	-0.04	0.07	-0.13*
Cob girth	Mean	12.55	12.20	11.93	12.45	13.25	13.41	14.36	19.52**	12.25	13.25
	gca (tester)	0.07 ns	-0.05 ns	-0.02 ns	-0.06 ns	0.01 ns	-0.34 ns	0.52 ns	0.09 ns	-0.52 ns	0.30 ns
	Mean R%	1.81	-3.31	0.16	1.88	-1.11	7.18*	-2.22	-1.29	4.56	-5.89*
Kernel rows per cob	Mean	14.00	14.50*	12.50	13.00	14.50	14.00	15.50	14.50	13.00	15.00
	gca (tester)	-0.07 ns	-0.07 ns	0.14 ns	-1.64 **	0.20 ns	-0.17 ns	1.33 **	1.00 *	-0.30 ns	-0.40 ns
	Mean R%	-0.17	-1.43	-3.22	12.67**	-2.70	7.47**	3.09	-3.95	-6.30	0.99
Kernels per row	Mean	32.00	42.50**	26.50	26.00	22.00	18.50	22.50	34.00**	27.00	33.00**
	gca (tester)	-0.07 ns	1.14 **	-1.07 **	2.04 **	1.38 **	-0.12 ns	2.38 **	-0.46 ns	-6.09 **	0.88 ns
	Mean R%	-8.51	-4.54	4.75	-11.98*	-2.51	4.05	4.31**	9.88	19.95	-4.33
Total sugars	Mean	15.16*	15.21*	14.34	13.53	12.05	14.16**	12.69	13.55	13.42	15.35**
	gca (tester)	-0.13 *	0.51 **	-0.38 **	0.50 **	0.50 **	-0.05 ns	1.32 **	-0.63 **	-0.13 ns	-1.52 **
	Mean R%	-0.83	5.91	-1.71	2.51	-17.94*	-10.72*	-10.69	-0.48	19.13	10.32
Reducing sugars	Mean	1.53**	1.06	1.48**	1.63**	1.33**	1.66**	1.64**	0.15	1.13	1.42**
	gca (tester)	-0.08 **	0.05 **	0.03 **	-0.06 **	0.04 **	0.02 *	-0.02 *	-0.02 ns	0.01 ns	0.02 **
	Mean R%	9.27	1.88	3.36	-6.77	-10.29	-30.25**	4.05	10.98*	1.99	-3.58
Green cob weight	Mean	122.74	137.36**	103.08	122.35	164.44	208.83**	167.25	155.4	166.91	198.13**
	gca (tester)	0.90 ns	3.88 ns	-4.77 *	11.42 *	28.50 **	-44.58 **	40.16 **	7.37 ns	-56.89 **	14.03 **
	Mean R%	22.96**	-5.28	6.04	-20.78**	-24.76	28.31*	-3.96	-22.94**	15.27	-26.48*

* = Significant at 0.05 probability level; ** = Significant at 0.01 probability level; R% = Reciprocal cross effects; gca = genetic combining ability effects.

Table 6. Comparison of mean; specific combining ability effects and reciprocal cross effects (%) of hybrids for yield and quality related traits.

Crosses	DFT	DFS	ASI	PH	CL	CG	KR	K	TS	RS	GCW
SCL$_1$ × NCT$_1$	49.00	51.00**	2.00**	234.39*	18.74	15.44	14.00	38.50	16.66**	1.56	246.30**
NCL$_1$ × SCT$_1$	48.00**	51.00**	3.00	264.94**	20.06	15.12	15.50	31.00	15.35**	1.67	169.47
sca effects(DC)	-0.48 ns	-1.17 **	-0.69 **	-6.53 ns	0.21 ns	0.25 ns	-0.38 ns	2.03 *	2.25 **	-0.10 **	10.78 ns
sca effects(RC)	-1.17 **	-1.33 **	-0.36 ns	15.84 **	0.37 ns	-0.03 ns	-0.43 ns	-2.76 **	0.30 ns	0.21 **	8.71 ns
R%	-2.04*	0.00	50.00**	13.03**	7.04	-2.07	10.71*	-19.48**	-7.86**	7.05**	-31.20**
SCL$_1$ × NCT$_2$	50.00	53.00	3.00	254.42**	18.69	15.20	17.10	35.50	12.63	1.77*	250.80**
NCL$_2$ × SCT$_1$	50.50	54.00	4.00	245.07	22.00	15.05	15.50	41.00**	12.55	1.45	120.34
sca effects(DC)	-1.14 **	-1.50 **	-0.36 *	13.55 **	-2.19 ns	-0.07 ns	0.89 ns	-0.30 ns	-1.80 **	0.02 ns	-1.79 ns
sca effects(RC)	1.33 **	1.67 **	0.64 *	2.87 ns	0.29 ns	0.28 ns	0.07 ns	4.40 **	0.67 **	-0.04 ns	-40.65 **
R%	1.00	1.89*	33.33**	-3.68*	17.71**	-0.99	-9.36*	15.49**	-0.63	-18.08**	-52.02**
SCL$_1$ × NCT$_3$	50.00	53.00	3.00	223.94	20.00	15.55	17.00	32.50	13.09	1.75	219.19*
NCL$_3$ × SCT$_1$	50.50	53.50	3.00	243.08	21.00	15.64	18.00*	36.00	12.63	0.84	220.45**
sca effects(DC)	0.36 ns	0.67 ns	0.31 ns	18.11 **	1.91 ns	0.63 ns	1.16 ns	-1.80 *	-0.77 **	0.01 ns	39.68 **
sca effects(RC)	-0.67 *	-0.83 *	-0.19 ns	-6.19 ns	-0.03 ns	0.04 ns	1.24 *	-1.43 *	0.08 ns	-0.29 **	35.66 **
R%	1.00	0.94	0.00	8.55**	5.00	0.58	5.88	10.77**	-3.51*	-52.00**	0.57
SCL$_1$ × NCT$_4$	51.00	55.00	4.00	217.31	21.65	16.43*	18.50*	38.50	16.48**	1.70	261.19**
NCL$_4$ × SCT$_1$	48.50**	51.50**	3.00	246.75	20.26	15.20	16.00	40.50**	12.89	1.39	213.54**
sca effects(DC)	0.19 ns	0.83 *	0.64 **	-10.57 *	2.30 *	0.65 ns	1.16 ns	1.70 *	1.24 **	0.01 ns	-3.06 ns
sca effects(RC)	-0.83 *	-1.00 **	-0.19 ns	-8.63 *	-0.93 ns	0.13 ns	-1.43 *	0.07 ns	-0.88 **	-0.29 **	-6.84 ns
R%	-4.90**	-6.36**	-25.00**	13.55**	-6.42	-7.49*	-13.51**	5.19**	-21.78**	-18.23**	-18.24**
SCL$_1$ × SCT$_5$	51.50	55.50	4.00	219.51	19.95	14.35	16.50	29.00	12.65	1.66	215.51
NCL$_5$ × SCT$_1$	51.50	55.50	4.00	242.32	17.81	14.80	16.00	37.50	14.97**	1.95**	147.64
sca effects(DC)	2.52 **	2.83 **	0.31 ns	-0.64 ns	-0.12 ns	-1.00 ns	-0.51 ns	-4.97 **	-0.64 **	-0.03 *	-15.96 ns
sca effects(RC)	1.33 **	2.00 **	0.64 *	16.39 **	-1.59 *	-0.01 ns	-0.10 ns	-0.60 ns	1.58 **	0.15 **	-7.14 ns
R%	0.00	0.00	0.00	10.39**	-10.73	3.14	-3.03	29.31**	18.34**	17.47**	-31.49**
SCL$_1$ × NCT$_6$	47.00**	49.50**	2.50**	199.56	17.53	14.85	14.60	28.00	14.22	1.77*	160.97
NCL$_6$ × SCT$_1$	51.00	53.00	2.00**	218.14	20.05	13.97	13.50	36.00	16.71**	1.97**	144.60
sca effects(DC)	-1.14 **	-1.33 **	-0.19 ns	-3.65 ns	-0.74 ns	0.11 ns	-1.11 ns	-0.34 ns	0.42 *	0.05 **	-6.24 ns
sca effects(RC)	1.17 **	0.33 ns	-0.86 **	-5.10 ns	0.52 ns	-1.06 *	-0.93 ns	0.90 ns	0.17 ns	0.29 **	-10.71 ns
R%	8.51**	7.07**	-20.00	9.31**	14.38	-5.93	-7.53	28.57**	17.51**	11.30**	-10.17
SCL$_1$ × NCT$_7$	48.50	51.50*	3.00	229.53	19.45	14.99	14.40	39.00*	11.69	1.77*	214.72
NCL$_7$ × SCT$_1$	49.00	53.00	4.00	223.50	19.55	15.00	17.00	35.00	12.13	1.55	175.74
sca effects(DC)	-0.31 ns	-0.33 ns	-0.02 ns	-10.27 *	-1.37 ns	-0.57 ns	-1.21 ns	3.70 **	-0.71 **	0.03 *	-23.41 *
sca effects(RC)	-1.17 **	-0.83 *	0.31 ns	-15.18 **	1.36 *	0.66 ns	1.57 **	-0.60 ns	-1.93 **	-0.04 *	20.97 **
R%	1.03	2.91**	33.33**	-2.63	0.51	0.07	18.06**	-10.26**	3.76*	-12.43**	-18.15**
SCL$_2$ × NCT$_1$	50.00	54.00	4.00	250.03**	18.45	14.36	14.60	37.00	14.21	1.69	202.71
NCL$_1$ × SCT$_2$	49.00	52.00*	3.50	261.93**	19.15	15.25	16.50	36.00	14.66**	1.10	168.42
sca effects(DC)	1.31 **	2.33 **	1.02 **	11.79 **	0.75 ns	-0.01 ns	0.45 ns	-2.34 **	-1.92 **	0.04 **	20.61 *
sca effects(RC)	0.12 ns	0.17 ns	0.36 ns	6.40 ns	0.12 ns	0.23 ns	0.57 ns	1.02 ns	-1.02 **	-0.49 **	4.68 ns
R%	-2.00**	-3.70**	-12.50	4.76**	3.79	6.20	13.01*	-2.70	3.17*	-34.91**	-16.92**
SCL$_2$ × NCT$_2$	51.50	55.50	4.00	216.22	20.85	14.05	17.00	42.50**	14.73	1.75	177.90
NCL$_2$ × SCT$_2$	47.00**	50.00**	3.00	247.51	20.53	14.47	16.00	37.50	11.22	1.88**	183.84
sca effects(DC)	1.14 **	1.50 **	0.36 *	-21.96 **	0.80 ns	-0.39 ns	1.02 ns	3.82 **	-1.42 **	0.00 ns	-21.28 *
sca effects(RC)	-1.88 **	-1.83 **	-0.14 ns	-1.12 ns	-0.51 ns	-0.18 ns	0.57 ns	-0.31 ns	-1.32 **	0.26 **	19.87 **
R%	-8.74**	-9.91**	-25.00**	14.47**	-1.53	2.99	-5.88	-11.76**	-23.83**	7.43**	3.34
SCL$_2$ × NCT$_3$	48.50	50.50**	2.00**	201.47	16.00	13.55	16.00	36.00	17.12**	1.72	147.85
NCL$_3$ × SCT$_2$	50.00	53.00	3.00	244.56	20.76	15.55	17.50	40.50**	13.63	1.36	228.54**
sca effects(DC)	-0.36 ns	-1.33 **	-0.98 **	-1.68 ns	-1.25 ns	-0.54 ns	0.39 ns	-1.18 ns	1.54 **	-0.01 ns	21.75 *
sca effects(RC)	-0.88 *	-0.83 *	0.02 ns	-11.14 **	0.40 ns	0.07 ns	0.74 ns	1.86 **	0.44 **	0.10 **	40.76 **
R%	3.09**	4.95**	50.00**	21.39**	29.75**	14.76**	9.38*	12.50**	-20.39**	-20.93**	54.58**
SCL$_2$ × NCT$_4$	48.50	52.50	4.00	215.17	17.25	15.60	15.00	38.50	17.87**	1.74	189.01
NCL$_4$ × SCT$_2$	50.00	53.00	3.00	261.18**	21.35	14.90	18.00*	40.50**	15.92**	1.94**	220.63**

Table 6. continued

Crosses	DFT	DFS	ASI	PH	CL	CG	KR	K	TS	RS	GCW
sca effects(DC)	-1.52 **	-1.17 **	0.36 *	-10.03 *	-1.26 ns	0.65 ns	-2.11 **	-1.18 ns	0.91 **	0.05 **	-21.83 *
sca effects(RC)	0.95 **	1.00 **	0.02 ns	-0.64 ns	0.82 ns	-0.05 ns	0.57 ns	-1.14 *	1.50 **	0.13 **	-2.73 ns
R%	3.09**	0.95	-25.00**	21.38**	23.77**	-4.49	20.00**	5.19*	-10.91**	11.49**	16.73**
SCL$_2$ × NCT$_5$	47.50**	51.50*	4.00	229.56	20.00	14.40	17.00	45.50**	15.84**	1.68	155.78
NCL$_5$ × SCT$_2$	52.00	55.00	3.00	226.49	18.77	14.37	14.50	37.50	12.89	1.94**	127.48
sca effects(DC)	-0.69 ns	-0.67 ns	0.02 ns	12.08 **	0.76 ns	-0.13 ns	0.22 ns	8.66 **	0.83 **	-0.01 ns	-22.27 *
sca effects(RC)	2.12 **	2.00 **	-0.14 ns	-5.89 ns	0.04 ns	-0.32 ns	-1.60 **	-1.81 **	-1.15 **	0.01 ns	-30.28 **
R%	9.47**	6.80**	-25.00**	-1.34	-6.15	-0.21	-14.71**	-17.58**	-18.62**	15.48**	-18.17**
SCL$_2$ × NC T$_6$	47.00**	49.50**	2.50**	197.97	17.38	13.40	15.00	26.10	16.84**	1.69	126.40
NCL$_6$ × SCT$_2$	47.00**	50.00**	3.00	229.15	19.81	15.35	15.50	38.50*	16.81**	1.56	186.44*
sca effects(DC)	-0.36 ns	-0.83 *	-0.48 **	-2.56 ns	-0.06 ns	-0.51 ns	-0.48 ns	-5.11 **	1.33 **	-0.02 ns	12.60 ns
sca effects(RC)	-2.55 **	-2.17 **	0.36 ns	-0.52 ns	0.95 ns	0.45 ns	1.07 ns	2.19 **	-0.38 *	-0.24 **	28.14 **
R%	0.00	1.01	20.00	15.75**	13.98*	14.55**	3.33	47.50**	-0.18*	-7.69**	47.50**
SCL$_2$ × NCT$_7$	48.50	51.50*	3.00	249.47**	20.24	15.67	15.90	35.50	12.86	1.69	195.13
NCL$_7$ × SCT$_2$	52.00	55.00	3.00	258.01**	15.70	14.00	13.50	35.00	16.64**	1.96**	97.30
sca effects(DC)	0.48 ns	0.17 ns	-0.31 ns	12.35 **	0.26 ns	0.94 ns	0.52 ns	-2.68 **	-1.26 **	-0.05 **	10.42 ns
sca effects(RC)	2.12 **	1.67 **	-0.48 ns	12.91 **	-1.82 **	-0.21 ns	-1.93 **	-1.81 **	1.93 **	0.24 **	-60.44 **
R%	7.22**	6.80**	0.00	3.42	-22.43**	-10.66**	-15.09**	-1.41	29.39**	15.98**	-50.14**
SCL$_3$ × NCT$_1$	49.00	52.00	3.00	229.64	17.35	14.63	14.00	40.00**	13.82	1.72	165.19
NCL$_1$ × SCT$_3$	50.50	54.00	3.50	227.75	18.65	14.85	16.00	34.50	15.51**	1.85**	141.69
sca effects(DC)	-0.83 *	-1.17 **	-0.33 *	-5.27 ns	-0.96 ns	-0.24 ns	-0.08 ns	0.31 ns	-0.33 ns	0.06 **	-31.39 **
sca effects(RC)	1.05 **	1.17 **	-0.00 ns	-22.24 **	-0.49 ns	-0.20 ns	-0.14 ns	1.74 **	0.72 **	0.28 **	-13.39 *
R%	3.06**	3.85**	16.67	-0.82	7.49	1.50	14.29*	-13.75**	12.23**	7.56**	-14.23
SCL$_3$ × NCT$_2$	51.50	55.50	4.00	243.28**	22.05	15.40	14.00	35.50	17.38**	1.73	236.72**
NCL$_2$ × SCT$_3$	50.00	53.00	3.00	241.35	21.38	14.58	15.00	31.50	12.28	1.38	176.11
sca effects(DC)	0.00 ns	0.00 ns	-0.00 ns	8.42 *	1.39 ns	0.46 ns	-1.91 *	-3.52 **	3.21 **	-0.03 ns	23.07 *
sca effects(RC)	0.55 ns	0.17 ns	-0.50 ns	-1.74 ns	0.22 ns	-0.10 ns	-0.64 ns	-4.10 **	0.65 **	-0.23 **	20.79 **
R%	-2.91**	-4.50**	-25.00**	-0.79	-3.04	-5.32	7.14	-11.27**	-29.34**	-20.23**	-25.60**
SCL$_3$ × NCT$_3$	50.00	54.00	4.00	183.39	17.20	14.50	14.00	40.50**	12.84	1.74	79.15
NCL$_3$ × SCT$_3$	53.00	56.50	3.50	267.50**	20.10	15.40	15.00	36.00	11.78	1.43	102.71
sca effects(DC)	-0.00 ns	0.67 ns	0.67 **	-16.43 **	-0.66 ns	-0.09 ns	-1.54 *	2.98 **	-0.77 **	-0.00 ns	-61.43 **
sca effects(RC)	1.55 **	1.67 **	0.17 ns	17.33 **	-0.38 ns	-0.11 ns	-1.98 **	-0.43 ns	-0.52 **	0.19 **	-76.42 **
R%	6.00**	4.63**	-12.50	45.86**	16.86*	6.21	7.14	-11.11**	-8.26**	-17.82**	29.77*
SCL$_3$ × NCT$_4$	52.50	55.50	3.00	242.46**	18.07	14.15	18.00*	39.50*	12.83	1.64	250.21**
NCL$_4$ × SCT$_3$	49.50	53.00	3.50	265.54**	20.75	14.90	18.50**	40.50**	12.91	1.95**	224.28**
sca effects(DC)	1.33 **	0.33 ns	-1.00 **	20.60 **	-1.04 ns	-1.29 *	0.96 ns	-0.52 ns	-2.15 **	-0.06 **	24.89 **
sca effects(RC)	-0.12 ns	0.00 ns	0.17 ns	9.27 *	0.11 ns	-0.08 ns	0.86 ns	1.07 ns	-0.62 **	0.16 **	9.57 ns
R%	-5.71**	-4.50**	16.67	9.52**	14.83*	5.30	2.78	2.53	0.62	18.90**	-10.36**
SCL$_3$ × NCT$_5$	47.50**	51.50*	4.00	202.69	19.20	16.15	17.00	33.50	12.85	1.75	230.75**
NCL$_5$ × SCT$_3$	47.00**	50.00**	3.00	216.33	20.40	15.05	18.00*	39.50**	12.70	1.75**	186.52*
sca effects(DC)	-1.83 **	-2.17 **	-0.33 *	-11.45 **	-0.64 ns	1.13 *	0.29 ns	-3.69 **	-0.19 ns	0.04 **	38.23 **
sca effects(RC)	-3.45 **	-4.00 **	-0.50 ns	-10.50 **	1.55 *	0.33 ns	1.69 **	2.40 **	-0.44 **	-0.16 **	37.41 **
R%	-1.05	-2.91**	-25.00**	6.73**	6.25	-6.81	5.88	17.91**	-1.17	0.00	-19.17**
SCL$_3$ × NCT$_6$	50.00**	54.00	4.00	203.41	18.85	14.80	17.00	37.00	11.78	1.70	121.90
NCL$_6$ × SCT$_3$	51.50	55.00	3.50	229.75	17.50	15.55	14.50	31.00	16.50**	1.74**	132.22
sca effects(DC)	1.50 **	2.17 **	0.67 **	6.21 ns	0.80 ns	0.40 ns	1.59 *	5.45 **	-1.75 **	-0.03 *	-6.37 ns
sca effects(RC)	1.38 **	1.83 **	0.50 ns	5.62 ns	-1.48 *	0.61 ns	-0.14 ns	-3.10 **	0.21 ns	-0.05 *	-17.43 **
R%	3.00**	1.85*	-12.50	12.95**	-7.16	5.07	-14.71**	-16.22**	40.07**	2.35	8.47
SCL$_3$ × NCT$_7$	49.00	53.00	4.00	231.72	21.70	14.85	16.00	37.50	14.12	1.75	212.19
NCL$_7$ × SCT$_3$	49.50	53.50	4.00	241.84	18.10	13.80	16.00	37.00	13.81	1.50	188.56*
sca effects(DC)	-0.17 ns	0.17 ns	0.33 *	-2.07 ns	1.11 ns	-0.37 ns	0.69 ns	-1.02 ns	1.97 **	0.01 ns	13.00 ns
sca effects(RC)	-0.95 **	-0.83 *	0.17 ns	2.27 ns	0.46 ns	-0.45 ns	0.36 ns	2.40 **	-0.00 ns	-0.20 **	39.47 **
R%	1.02	0.94	0.00	4.37*	-16.59**	-7.07	0.00	-1.33	-2.20	-14.29**	-11.14**

DC = direct cross; RC = reciprocal cross; DFT = days to 50% tasseling; DFS = days to 50% silking; ASI = anthesis silking interval; PH = plant height; CL = cob length; CG = cob girth; KR = kernel rows; K = kernels per row; TS = total sugars; RS = reducing sugars; GCW = green cob weight; * = significant at 0.05 probability level; ** = significant at 0.01 probability level; R% = Reciprocal cross effects.

to more promising ones. Similar results of the varying performance of hybrids based on mean reciprocal cross effects of common parental genotypes had been recorded in the study of reciprocal effects for biomass yield in switch grass by Bhandari *et al.* (2014).

Crosses with desirable specific combining ability were not necessarily having a parallel advantage in reciprocal cross mean differences.SCL$_2$ × NCT$_6$ had been a potential heterotic combination for days to 50% silking, anthesis silking interval and total sugars. Whereas, NCL$_6$ × SCT$_2$ had been a potential heterotic cross combination for days to 50% tasseling, kernels per row and green cob weight. Thereby implying the advantage of both the combinations for improving the respective traits. SCL$_1$, SCL$_2$ and SCL$_3$ had contributed well for the hybrid vigour as maternal and paternal parents as well. NCL$_5$ gave appreciably good hybrids on par with the heterotic hybrids of direct crosses when used as a seed parent with SCL$_3$ as pollen parent. Reciprocal cross effect (advantage or disadvantage) ranged from 0.57 to 54.58 per cent for green cob weight and -0.18 to 40.07 per cent for total sugars (**Table 6**). Positive mean difference represents the favoured reciprocal direction of the cross and negative mean difference denotes the advantage of the direct cross in developing superior hybrids. The indispensable heterotic hybrids identified through alternating crossing direction unfolds the opportunities to explore the complex genetics behind the maternal effect patterns specific to cross combinations for target trait improvement (Bhandari *et al.,* 2014).

Plant height estimates had marked positive reciprocal cross mean differences (**Table 7**). This positive trend in the performance of reciprocal crosses denotes the better maternal attributes of normal corn inbreds for good crop stature. Mean green cob weight and reducing sugar values declined in the reciprocal crosses, emphasizing

Table 7. Traits with significant reciprocal cross effects (%)

Traits	Direct cross mean	Reciprocal cross mean	Reciprocal mean difference	Reciprocal cross effect (%)	SEd	t_{cal}
Days to 50% tasseling	49.43	49.86	0.43	0.87	0.4693	0.9132
Days to 50% silking	52.81	53.07	0.26	0.50	0.5047	0.5189
Anthesis silking interval	3.38	3.26	-0.12	-3.52	0.2948	-0.4038
Plant height (cm)	222.63	242.99	20.36**	9.15	5.2060	3.9109
Cob length (cm)	19.08	19.70	0.62	3.27	1.2531	0.4974
Cob girth (cm)	14.87	14.90	0.02	0.16	0.6415	0.0373
Kernel rows per cob	15.84	16.00	0.16	1.02	0.8654	0.1871
Kernels per row	36.46	36.79	0.33	0.90	0.9406	0.3493
Total sugars (%)	14.40	14.02	-0.38	-2.63	0.2314	-1.6404
Reducing sugars (%)	1.71	1.63	-0.08**	-4.99	0.0241	-3.5418
Green cob weight (g/cob)	193.31	169.36	-23.96*	-12.39	9.9418	-2.4095

SEd= standard error difference; t_{cal} = calculated t value; **= significance @ 0.01 probability level (t_{tab} = 2.528);
*= significance @ 0.05probability level (t_{tab} = 1.725).

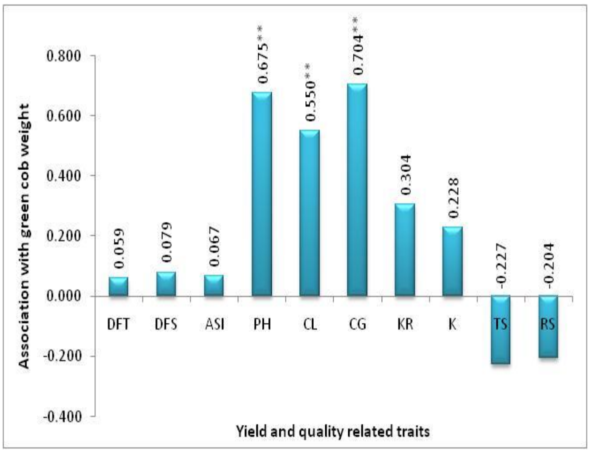

Fig. 1. Correlation of reciprocal cross effects of yield and quality related traits with green cob weight.

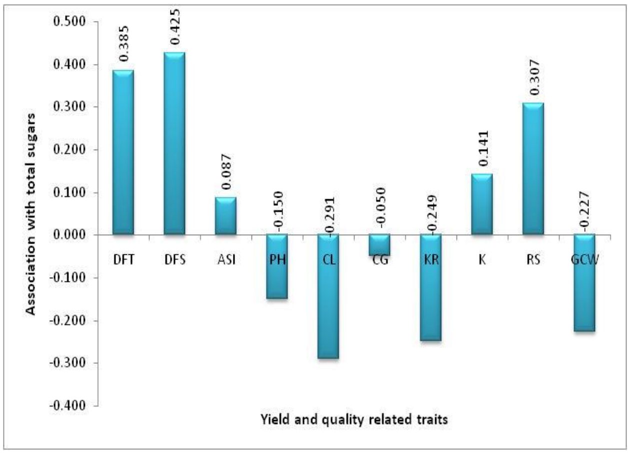

Fig. 2. Correlation of reciprocal cross effects of yield and quality related traits with total sugars.

the feasibility of quality and yield improvement with sweet corn inbreds as seed parents (**Table 7**). However, if the specific cross combinations were scrutinized for reciprocal cross effects, it widens the possibilities of exploiting the heterotic potential left unexplored before. These results of a limited number of traits expressing significant reciprocal cross effects had been reported in the study of Ordas *et al.* (2008).

Remarkably, reciprocal cross effects of cob girth were strongly associated with that of green cob weight, followed by the effects of plant height and cob length with r = 0.704; r = 0.675 and r = 0.550, respectively (**Fig.1**). None of the traits had a significant correlation with total sugars with respect to reciprocal cross effects (**Fig. 2**). Not much information could be inferred from the association results which could be an area of investigation in future studies on maternal effect.

Hybrids with superior heterotic potential based on favorable mean, *sca* effects and reciprocal cross effects are listed in **Table 8**. Favoured direct crosses for green cob weight were SCL_3 X NCT_4; SCL_3 X NCT_2; SCL_3 X $NCT_5$and favoured reciprocal cross was NCL_3 X SCT_2. Favoured direct crosses for total sugars were SCL_3 X NCT_2; SCL_1 X NCT_4; SCL_2 X NCT_3; SCL_1 X NCT_1; SCL_2 X $NCT_6$and favoured reciprocal cross was NCL_7 X SCT_2 (**Table 8**).Parental inbreds better fit as seed and pollen parents are listed in **Table 9**. Though the limited number of crosses were favoured in the reciprocals, the amount of variation contributed was appreciable to be pocketed for hybrid development and further commercialization.

Table 8. Best hybrids for important yield and quality related traits

Traits of importance	Sweet corn x Normal corn crosses	Normal corn x Sweet corn crosses
Early traits	Favored mean and sca effects associated with +ve R%	Favored mean and sca effects associated with -ve R%
Days to 50% tasseling	SCL_1 X NCT_6	NCL_6 X SCT_2; NCL_5 X SCT_3; NCL_2 X SCT_2; NCL_4 X SCT_1; NCL_1 X SCT_1
Days to 50% silking	SCL_1 X NCT_6; SCL_2 X NCT_3	NCL_2 X SCT_2; NCL_4 X SCT_1; NCL_5 X SCT_3; NCL_1 X SCT_1
Good cob traits	Favored mean and sca effects associated with -ve R%	Favored mean and sca effects associated with +ve R%
Kernel rows per cob	SCL_3 X NCT_6	NCL_7 X SCT_1
kernels per row	SCL_2 X NCT_5; SCL_1 X NCT_1; SCL_2 X NCT_2; SCL_3 X NCT_3; SCL_1 X NCT_7	NCL_6 X SCT_2; NCL_5 X SCT_3; NCL_2 X SCT_1; NCL_3 X SCT_2
Green cob weight	SCL_3 X NCT_4; SCL_3 X NCT_2; SCL_3 X NCT_5	NCL_3 X SCT_2
Sweetness traits	Favored mean and sca effects associated with -ve R%	Favored mean and sca effects associated with +ve R%
Total sugars	SCL_3 X NCT_2; SCL_1 X NCT_4; SCL_2 X NCT_3; SCL_1 X NCT_1; SCL_2 X NCT_6	NCL_7 X SCT_2
Reducing sugars	SCL_2 X NCT_1; SCL_1 X NCT_7	NCL_5 X SCT_1; NCL_7 X SCT_2; NCL_6 X SCT_1; NCL_4 X SCT_2; NCL_2 X SCT_2; NCL_1 X SCT_3

R% = reciprocal cross effects; sca = specific combining ability.

Table 9. Inbreds better fitting as maternal parents and paternal parents

Traits of importance	Inbreds with good fit for maternal parent	Inbreds with good fit for paternal parent
Early traits	Favored mean and gca effects associated with +ve R%	Favored mean and gca effects associated with -ve R%
Days to 50% tasseling	SCL_2; NCL_1; NCL_2; NCL_4	SCT_2
Days to 50% silking	SCL_2; NCL_1; NCL_2; NCL_4; NCL_6	SCT_2
Good cob traits	Favored mean and gca effects associated with -ve R%	Favored mean and gca effects associated with +ve R%
Kernel rows per cob	NCL_3; NCL_4	-
kernels per row	SCL_3; NCL_3; NCL_4; NCL_5	SCT_2
Green cob weight	SCL_1; NCL_3	NCT_7
Sweetness traits	Favored mean and gca effects associated with -ve R%	Favored mean and gca effects associated with +ve R%
Total sugars	SCL_2; NCL_4; NCL_6	SCT_2
Reducing sugars	NCL_4; NCL_5; NCL_6	SCT_3

R% = reciprocal cross effects; gca = general combining ability.

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