MadrasAgric.J.,2024; https://doi.org/10.29321/MAJ.10.0MMA24

RESEARCH ARTICLE

Assessment of Combining Ability in Sweet Corn Hybrids Targeting Yield and Sweetness

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Received: 16 Jan 2024
Revised: 27 Jan 2024
Accepted: 12 Feb 2024

ABSTRACT

The present study was carried out to determine the combining ability for yield and quality traits in sweet corn (*Zea mays con var saccharata*). Nine sweet corn inbred lines were crossed with three inbred testers, resulting 27 hybrids using Line × Tester mating design. These hybrids, along with their parents, were evaluated using a randomized complete block design. Combining ability studies revealed that specific combining ability (SCA) variances were greater than the general combining ability (GCA) variances, indicating the predominance of non-additive gene action for all the traits. The lines L_1, L_3, L_5 and the testers T_1 and T_3 recorded a significant positive *gca* effect coupled with higher mean performance for green cob weight without husk and sweetness traits. The hybrids with good specific combining ability were $L_1 \times T_1$, $L_1 \times T_3$, $L_2 \times T_1$, $L_3 \times T_1$, $L_5 \times T_1$, $L_7 \times T_3$ and $L_8 \times T_3$ for green cob weight without husk and sweetness traits. Overall, the hybrids $L_1 \times T_1$ (16.12%), $L_1 \times T_3$ (17.84 %) and $L_5 \times T_1$ (20.11 %) exhibited improved sugar content along with good agronomic performances. With further evaluation across different environments, they could be considered for large-scale cultivation and commercialization and would hold great significance in mitigating nutritional imbalances in both rural and urban communities.

Keywords: Sweet Corn, Gene Action, Combining Ability, General Combining Ability, Specific Combining Ability

INTRODUCTION

Sweet corn (*Zea mays* L. *saccharata*) has emerged as a highly popular vegetable crop in various nations, including the United States, Canada, India, and other Asian countries. Its inherent sweetness, tender texture, digestibility, and nutritional benefits make it a preferred choice for consumers (Mehta *et al.,* 2017). Unlike field corn, sweet corn is harvested at the milky stage and consumed fresh, canned, or frozen. Its sweetness and palatability are largely determined by specific recessive genes that limit the conversion of sugar into starch in the kernels, resulting in higher sugar accumulation. The sweetness of sweet corn kernels is regulated by six recessive mutant genes that are active in the endosperm *viz., brittle1* (*bt1*), *brittle2* (*bt2*), *shrunken1* (*sh1*), *shrunken2* (*sh2*), *sugary1* (*su1*), and *sugary enhancer1* (*se1*) (Tracy *et al.*, 1984). In the process of developing high-yielding and sweet cultivars, hybrid breeding plays a crucial role. Combining ability analysis provides essential insights into the genetic potential of inbred lines and their performance in hybrid combinations. A popular method for estimating the combining ability of inbred lines is Line × Tester analysis, an extension of the top cross method for crossing several testers with chosen inbred lines. Combining ability refers

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to the potential of a genotype to pass along improved performance to its progeny. Combining ability studies helps to determine the type and degree of gene interactions that affect the various polygenic traits that emerge. The General Combining Ability (GCA) measures the average performance of inbreds, while the Specific Combining Ability (SCA) explains the performance of hybrid combinations (Sprague and Tatum, 1942). Thus, the present study aims to assess the combining ability of various sweet corn inbred lines to identify promising parental combinations for hybrid development focusing on green cob weight and sweetness.

MATERIALS AND METHODS

The experimental materials consisted of nine sweet corn inbred lines and three testers, which were obtained from Department of Plant Molecular Biology and Bioinformatics, Tamil Nadu Agricultural University, Coimbatore. The sweet corn parental inbreds used in this study contains *sh2* gene (shrunken) for sweetness. The nine inbred lines *viz.,* DBT-25-4-7-34-4-22 (L1), DBT-23-7-3-2-5-8 (L2), DBT-26-1-2-1-42-7 (L3), DBT-17-1-1-37-1-1 (L4), DBT-18-1-18-5-6-3 (L5), DBT-15-1-15-3-32-35 (L6), DBT-15-1-15-3-23-21 (L7), DBT-18-1-18-5-2-5 (L8) and DBT-18-1-18-5-1-5 (L9) were crossed with three testers *viz.,* DBT-15-1-15-3-12-11 (T1), DBT-16-1-11-22-7-9 (T2), and DBT-18-1-18-5-4-7 (T3) in Line × Tester (L × T) mating design. The resulting 27 crosses were grown during the *Kharif* 2023 along with nine lines and three testers in randomized block design with two replicates each. Five plants per genotype were randomly selected from each replication within the parental lines and the F_1 hybrids. Eighteen biometrical traits related to yield and quality traits *viz*., plant height (cm), cob placement height (cm), days to 50% tasseling, days to 50% silking, anthesis silkinginterval, tassel length (cm), number of tassel branches, leaf length (cm), leaf breadth (cm), cob length (cm), cob width (cm), number of kernel rows per cob (No‘s), number of kernels per row (No‘s), green cob weight without husk (g), total soluble solids (%), total sugars (%) by anthrone method (Yemm and Willis, 1954), reducing sugars (%)by Nelson and Somogyi method (Somogyi, 1952), and non – reducing sugars (%) were recorded. The mean values were calculated for each trait and used for the combining ability analysis.

RESULTS AND DISCUSSION

The significant differences were examined by analyzing the distinct components of variation for eighteen traits among the genotypes (Table 1). The results showed that variations due to genotypes were significant for all the studied traits, which implies the presence of substantial variation for crop improvement. Similar results had been previously reported by Chinthiya *et al.* (2019); and Sumalini (2023) for the traits of significant variance due to genotypes. Analysis of variance for combining ability revealed significant differences among the lines and testers for all the characters except leaf breadth (Table 2). SCA variance was found to be greater than GCA variance for all the traits, indicating the presence of non-additive gene action among the

Table 1. List of lines and testers used in the analysis

S. No.	Code No.	Name of lines
1	L_1	DBT-25-4-7-34-4-22
2	L_2	DBT-23-7-3-2-5-8
3	L_3	DBT-26-1-2-1-42-7
4	L_4	DBT-17-1-1-37-1-1
5	L_5	DBT-18-1-18-5-6-3
6	L_6	DBT-15-1-15-3-32-35
7	L_7	DBT-15-1-15-3-23-21
8	L_8	DBT-18-1-18-5-2-5
9	L_9	DBT-18-1-18-5-1-5
10	T_1	DBT-15-1-15-3-12-11
11	T_2	DBT-16-1-11-22-7-9
12	T_3	DBT-18-1-18-5-4-7

Table 2. ANOVA for L × T analysis in sweet corn

Source of variation	df	Mean squares								
		PH	CPH	DT	DS	ASI	LL	LB	TL	NTB
Replication	1	89.02	10.39	0.05	0.12	0.01	52.27	0.28	0.08	46.15
Genotypes	38	469.35**	304.25**	8.69**	13.39**	1.72**	65.69**	0.44**	23.44	37.86
Error	38	96.08	164.35	0.76	0.93	0.25	10.93	0.36	4.26	8.42
Source of variation	df	Mean squares								
		CL	CW	NKRC	NKR	GCW	TSS	TS	RS	NRS
Replication	1	0.12	0.18	0.12	2.04	0.84	1.04	15.35	0.09	13.02
Genotypes	28	6.93**	2.61**	79.54**	61.07**	2626.83**	3.71**	7.26**	0.13**	6.94**
Error	28	0.36	0.31	0.70	0.28	2.60	0.41	3.29	0.12	2.97

* - Significant at 5%, ** - Significant at 1%

Where, PH - plant height (cm), CPH - cob placement height (cm), DT - days to 50% tasseling, DS - days to 50% silking, ASI - anthesis silking interval, LL - leaf length (cm), LB - leaf breadth (cm), TL - tassel length (cm), NTB - number of tassel branches, CL - cob length (cm), CW - cob width (cm), NKRC - number of kernel rows per cob (No‘s), NKR - number of kernels per row (No‘s), GCW - green cob weight without husk (g), TSS - total soluble solids (%), TS - total sugars (%), RS - reducing sugars (%) and NRS - non – reducing sugars (%).

genotypes under study (Table 3). Similar results were already reported by Kuselan *et al.* (2017). Due to the predominance of non-additive gene action in the inheritance of the studied characteristics, heterosis breeding and recombination breeding with extending the duration of selection to later generations would be excellent for producing genotypes that are superior for these traits Kumara *et al.* (2013), Chinthiya *et al.* (2019), and Darshan *et al.,* (2019).

To select genotypes with desirable traits and determine relationships among the breeding materials, breeders can improve by understanding *gca* effects (Sprague and Tatum 1942). The *gca* effects of parents is presented in Table 4. Among the lines, L_1, L_2, L_3 and L_5 recorded significant positive *gca* effect for green cob weight without husk. In addition, L_1 was found to be the significant good combiners for plant height, cob placement height, tassel length, leaf length, total soluble solids, total sugars, reducing sugars and non-reducing sugars. Similarly, L_2 showed positively significant *gca* effect for tassel length, leaf length, cob length, cob width, number of kernel rows per cob and number of kernels per row. L_3 found to have negative significant *gca* effect for days to 50% tasseling, days to 50% silking, tassel length, number of tassel branches, leaf length, cob length, cob width, number of kernel rows per cob, number of kernels per row, total sugars, reducing sugars and non-reducing sugars. The line L_5 exhibited significant positive *gca* effect for plant height, cob width, number of kernel rows per cob, number of kernels per row, total soluble solids, total sugars, reducing sugars and non-reducing sugars along with negative significant *gca* effect for days to 50% tasseling, days to 50% silking and anthesis silking interval. Among the testers, T_1 and T_3 found to be significantly good combiners for green cob weight. The tester T_1 possessed positive significant *gca* effect for plant height, cob placement height, tassel length, leaf length, cob length, number of kernel rows per cob and number of kernels per row, total soluble solids, total sugars, reducing sugars and non-reducing sugars. Similarly, T_3 recorded significant negative *gca* effect for days to 50% silking and anthesis silking interval, plant height, number of tassel branches, cob width, number of kernel rows per cob, number of kernels per row, total sugars, reducing sugars and non-reducing sugars. Similarly, Mogesse *et al.* (2020) noted significant negative GCA values for days to 50% tasseling and days to 50% silking and Abd-Allah Ramadan *et al.* (2020) reported parents showed negative significant *gca* effect for ASI and days to 50% flowering while cob length, plant height exhibited positive *gca* effects. Assefa *et al.* (2017) observed positive significant *gca* effect for cob length; Gami *et al.* (2018) for cob width and cob length.

The *sca* effect of hybrids is presented in Table 5. The hybrids with good specific combining ability were

Table 3. ANOVA for combining ability in sweet corn

Sources of variation	df	Mean squares								
		PH	CPH	DT	DS	ASI	LL	LB	TL	NTB
Replication	1	134.58	45.26	0.00	-0.00	0.00	52.41	0.01	1.31	37.50
Crosses	26	453.09**	299.24	8.09**	11.44**	1.49**	56.03**	0.36	23.07 **	36.73**
Lines	8	691.24**	256.88	13.08**	11.07**	0.64*	103.71**	0.70	49.97**	69.42**
Testers	2	1523.20 *	1093.62*	35.39**	90.02**	13.02**	144.60**	0.38	25.27*	48.57**
L × T interaction	16	200.26**	221.12**	2.18*	1.81	0.47*	21.12*	0.19	9.35	18.91*
Error	26	111.91	207.13	0.88	1.04	0.23	8.96	0.47	4.58	8.31
Sources of variation	df	Mean squares								
		CL	CW	NKRC	NKR	GCW	TSS	TS	RS	NRS
Replication	1	0.08	0.07	1.22	0.43	3.90	1.50	7.60	0.11	5.86
Crosses	26	8.35**	2.66*	43.68**	6.33**	2835.87**	3.65**	7.47**	0.13	6.93 **
Lines	8	15.51**	4.21**	51.23**	5.93**	3870.53**	0.77**	0.99**	0.08**	1.03**
Testers	2	1.78*	0.94 **	27.25**	36.04**	2173.29**	1.41*	6.22**	0.06**	5.05**
L × T interaction	16	5.59**	2.11**	41.95**	2.82**	2401.36**	5.36**	10.86**	0.16	10.11**
Error	26	0.36	0.30	0.52	0.17	1.49	0.38	2.30	0.11	2.10

* - Significant at 5%, ** - Significant at 1%

Where, PH - plant height (cm), CPH - cob placement height (cm), DT - days to 50% tasseling, DS - days to 50% silking, ASI - anthesis silking interval, LL - leaf length (cm), LB - leaf breadth (cm), TL - tassel length (cm), NTB - number of tassel branches, CL - cob length (cm), CW - cob width (cm), NKRC - number of kernel rows per cob (No's), NKR - number of kernels per row (No's), GCW - green cob weight without husk (g), TSS - total soluble solids (%), TS - total sugars (%), RS - reducing sugars (%) and NRS - non – reducing sugars (%)

Table 4. Magnitude of Additive and Dominance Variances

S. No.	Characters	Additive Variances	Dominance Variances	Additive: Dominance ratio
1	Days to 50% tasseling	0.37	1.30	0.28
2	Days to 50% silking	0.60	0.77	0.77
3	Anthesis silking interval	0.06	0.25	0.26
4	Plant height	15.65	88.35	0.18
5	Cob placement height	4.84	13.99	0.35
6	Tassel length	0.85	4.77	0.18
7	Number of tassel branches	1.10	10.60	0.10
8	Leaf length	2.16	12.16	0.18
9	Leaf breadth	0.01	0.28	0.04
10	Cob length	0.17	5.23	0.03
11	Cob width	0.03	1.81	0.02
12	Number of kernel rows per cob	0.11	41.43	0.00
13	Number of kernels per row	0.22	2.65	0.08
14	Green cob weight without husk	26.90	2399.87	0.01
15	Total soluble solids	0.11	4.98	0.02
16	Total sugar	0.21	8.56	0.02
17	Reducing sugar	0.00	0.05	0.04
18	Non-reducing sugar	0.20	8.01	0.02

Table 5. Combining ability effects of parents (*gca*)

PARENTS	PH	CPH	DT	DS	ASI	LL	LB	TL	NTB
L_1	9.39 *	14.25 **	-0.61 ns	-0.80 ns	-0.19 ns	6.91 **	0.20 ns	3.64 **	-0.07 ns
L_2	8.48 ns	2.19 ns	-0.44 ns	-0.30 ns	0.15 ns	2.58 *	0.55 ns	3.56 **	1.93 ns
L_3	2.99 ns	-3.95 ns	-2.28 **	-1.63 **	0.65 **	4.36 **	0.26 ns	3.15**	3.93 **
L_4	1.04 ns	11.67ns	1.06 *	1.20 **	0.15 ns	-2.02 ns	-0.18 ns	-1.95 *	-0.24 ns
L_5	5.41 **	3.16 ns	-0.78 **	-1.30 **	-0.52 *	-1.14 ns	-0.21 ns	-0.19 ns	-1.91 ns
L_6	-14.83 **	-3.70 ns	-0.44 ns	-0.46 ns	-0.02 ns	-6.19 **	-0.19 ns	-4.75 **	-1.57 ns
L_7	-18.58 **	-7.83 ns	-0.78 ns	-0.63 ns	0.15 ns	1.08 ns	-0.62 *	-1.55 ns	-7.24 **
L_8	-5.27 ns	-8.65 ns	-2.06 **	1.87 **	-0.19 ns	-4.27 **	0.03 ns	-0.70 ns	3.43 **
L_9	11.38 *	2.85 ns	2.22 **	2.04 **	-0.19 ns	-1.32 ns	0.17 ns	-1.20 ns	1.76 ns
SE	4.32	5.88	0.38	0.42	0.20	1.22	0.28	30.96	1.18
CD (5%)	12.58	17.12	1.12	1.21	0.57	3.56	0.81	2.55	3.43
CD (1%)	16.98	23.10	1.51	1.64	0.77	4.80	1.10	3.44	4.63
T_1	9.77 **	8.73 *	-1.17 **	-1.69 **	-0.52 **	3.19 **	-0.08 ns	1.32 *	-1.80 *
T_2	-1.28 ns	-2.46 ns	1.56 **	2.54 **	0.98 **	-2.23 **	0.17 ns	-0.98 ns	0.37 ns
T_3	8.49 **	-6.27 ns	-0.39 ns	-0.85 **	-0.46 **	-0.96 ns	-0.09 ns	0.74 ns	1.43 *
SE	2.49	3.39	0.22	0.24	0.11	0.71	0.16	31.30	0.68
CD (5%)	7.26	9.88	0.65	0.70	0.33	2.06	0.47	1.47	1.98
CD (1%)	9.80	13.34	0.87	0.94	0.45	2.77	0.63	1.98	2.67

Table 5. Continued.

PARENTS	CL	CW	NKRC	NKR	GCW	TSS	TS	RS	NRS
L_1	0.39 ns	0.28 ns	0.17 ns	-0.20 ns	17.28 **	0.22 **	0.44 **	0.19 **	0.35 **
L_2	3.66 **	0.91 **	4.64 **	0.80 **	45.82 **	0.19 ns	0.35 ns	0.15 ns	0.20 ns
L_3	0.77 **	0.48 *	1.22 **	1.27 **	18.40 **	-0.15 ns	0.34 **	0.17 **	0.50 **
L_4	-2.13 **	]-1.04 **	-6.15 **	-1.37 **	-40.23 **	0.19 ns	0.24 ns	0.05 ns	0.19 ns
L_5	-0.33 ns	0.73 **	-1.93 **	0.97 **	8.64 **	0.32 **	0.35 **	0.35 **	0.30 **
L_6	-0.26 ns	-0.95 **	1.25 **	-1.20 **	-18.49 **	-0.15 ns	-0.68 ns	-0.09 ns	-0.59 ns
L_7	-1.19 **	-1.05 **	-0.83 **	-1.03 **	-15.38 **	-0.81 **	0.53 **	0.14 ns	2.66 **
L_8	-0.53 *	0.88 **	1.12 **	0.30 ns	-4.56 **	0.35 ns	-0.27 ns	-0.04 ns	-0.22 ns
L_9	-0.39 ns	-0.25 ns	0.52 ns	0.47 **	-11.49 **	0.35 ns	-0.05 ns	0.02 ns	-0.07 ns
SE	0.24	0.23	0.29	0.17	0.50	0.25	0.62	0.14	0.59
CD (5%)	0.71	0.66	0.86	0.49	1.45	0.74	1.80	0.40	1.72
CD (1%)	0.96	0.89	1.16	0.66	1.96	1.00	2.43	0.54	2.33
T_1	0.36 *	-0.17 ns	1.27 **	1.31 **	13.44 **	1.04 *	2.32 **	0.23 **	2.30 **
T_2	-0.20 ns	-0.09 ns	-1.18 **	-0.19 ns	-8.86 **	-0.26 ns	-0.68 ns	-0.17 *	-0.61 ns
T_3	-0.16 ns	0.26 **	2.09 **	1.50 **	12.30 **	0.30 ns	1.35 **	0.28 **	1.31**
SE	0.14	0.13	0.17	0.10	0.29	0.15	0.36	0.08	0.34
CD (5%)	0.41	0.38	0.50	0.28	0.84	0.43	1.04	0.23	1.00
CD (1%)	0.56	0.51	0.67	0.38	1.13	0.58	1.41	0.31	1.34

* - Significant at 5%, ** - Significant at 1%

Where, PH - plant height (cm), CPH - cob placement height (cm), DT - days to 50% tasseling, DS - days to 50% silking, ASI - anthesis silking interval, LL - leaf length (cm), LB - leaf breadth (cm), TL - tassel length (cm), NTB - number of tassel branches, CL - cob length (cm), CW - cob width (cm), NKRC - number of kernel rows per cob (No's), NKR - number of kernels per row (No's), GCW - green cob weight without husk (g), TSS - total soluble solids (%), TS - total sugars (%), RS - reducing sugars (%) and NRS - non – reducing sugars (%).

Table 6. Specific Combining ability effects of sweet corn hybrids (*sca*)

Crosses	PH	CPH	DT	DS	ASI	LL	LB	TL	NTB
$L_1 \times T_1$	15.01 *	11.91 **	-0.50 ns	0.35 ns	0.85 *	1.74 ns	0.06 ns	0.74 ns	1.46 ns
$L_1 \times T_2$	-2.59 ns	3.74 ns	-0.22 ns	-0.37 ns	-0.15 ns	-3.79 ns	0.11 ns	-1.16 ns	-5.20 *
$L_1 \times T_3$	-12.43 ns	-8.65 ns	0.72 ns	0.02 ns	-0.70 *	2.05 ns	-0.17 ns	0.42 ns	3.74 ns
$L_2 \times T_1$	-11.67 ns	-9.13 ns	0.33 ns	-0.15 ns	-0.48 ns	1.78 ns	-0.14 ns	1.42 ns	-0.54 ns
$L_2 \times T_2$	10.63 ns	11.71 ns	-0.39 ns	0.13 ns	0.52 ns	-0.21 ns	-0.28 ns	-1.84 ns	4.30 *
$L_2 \times T_3$	10.63 ns	-2.58 ns	0.06 ns	0.02 ns	-0.04 ns	-1.57 ns	0.42 ns	0.42 ns	-3.76 ns
$L_3 \times T_1$	14.04 **	-0.04 ns	0.17 ns	0.19 ns	0.02 ns	3.74 ns	0.20 ns	2.73 **	-1.04 ns
$L_3 \times T_2$	-4.94 ns	-10.46ns	-0.56 ns	-0.54 ns	0.02 ns	-5.34 *	0.11 ns	-2.87ns	-0.70 ns
$L_3 \times T_3$	8.97 **	10.50 ns	0.39 ns	0.35 ns	-0.04 ns	1.60 ns	-0.31 ns	0.14 ns	1.74 ns
$L_4 \times T_1$	9.11 ns	22.69 *	-1.17 ns	-0.65 ns	0.52 ns	-1.37 ns	-0.11 ns	-1.87ns	-1.87 ns
$L_4 \times T_2$	-8.49 ns	-12.43ns	1.11 ns	1.13 ns	0.02 ns	0.24 ns	-0.10 ns	0.58 ns	1.46 ns
$L_4 \times T_3$	-0.62 ns	-10.26ns	0.06 ns	-0.48 ns	-0.54 ns	1.13 ns	0.21 ns	1.29ns	0.41 ns
$L_5 \times T_1$	9.36 **	-12.23ns	-0.67 **	0.35 ns	-0.31 ns	-1.81 ns	-0.22 ns	-1.55 ns	0.80 ns
$L_5 \times T_2$	5.00 ns	5.08 ns	-0.56 ns	-0.37 ns	0.19 ns	0.71 ns	-0.12 ns	-0.88 ns	0.13 ns
$L_5 \times T_3$	4.36 ns	7.15 ns	-0.11 ns	0.02 ns	0.13 ns	1.10 ns	0.34 ns	2.43 ns	-0.93 ns
$L_6 \times T_1$	12.88 ns	-2.89 ns	-1.17 ns	-1.48 ns	-0.31 ns	2.29 ns	0.20 ns	1.58 ns	0.46 ns
$L_6 \times T_2$	0.28 ns	3.39 ns	1.11 ns	1.30 ns	0.19 ns	1.36 ns	0.09 ns	1.88 ns	1.80 ns
$L_6 \times T_3$	-1.16 ns	-0.50 ns	0.06 ns	0.19 ns	0.13 ns	-3.65 ns	-0.29 ns	-3.46 *	-2.26 ns
$L_7 \times T_1$	1.81 ns	-5.26 ns	-0.33 ns	-0.31 ns	0.02 ns	-5.92 **	0.18 ns	-2.42 ns	2.13 ns
$L_7 \times T_2$	-1.66 ns	1.22 ns	-0.06 ns	-0.04 ns	0.02 ns	4.69 *	-0.17 ns	1.03 ns	-2.04 ns
$L_7 \times T_3$	-0.15 ns	4.04 ns	0.39 ns	0.35 ns	-0.04 ns	1.23 ns	-0.01 ns	1.39 ns	-0.09 ns
$L_8 \times T_1$	-12.02 ns	-5.69 ns	-0.17 ns	-0.31 ns	-0.15 ns	-1.07 ns	0.33 ns	0.23 ns	-3.54 ns
$L_8 \times T_2$	-0.12 ns	1.14 ns	-0.39 ns	-0.54 ns	-0.15 ns	0.79 ns	-0.02 ns	1.19 ns	3.80 ns
$L_8 \times T_3$	12.14 ns	4.55 ns	0.56 ns	0.85 ns	0.30 ns	0.28 ns	-0.31 ns	-1.42 ns	-0.26 ns
$L_9 \times T_1$	10.28 **	7.66 ns	2.17 **	2.02 **	-0.15 ns	0.63 ns	-0.51 ns	-0.87 ns	2.13 ns
$L_9 \times T_2$	1.88 ns	-3.41 ns	-0.06 ns	-0.70 ns	-0.65 ns	1.54 ns	0.40 ns	2.08 ns	-3.54 ns
$L_9 \times T_3$	-12.16 ns	-4.25 ns	-2.11 **	-1.31 ns	0.80 *	-2.17 ns	0.11 ns	-1.21 ns	1.41 ns
SE	7.48	10.18	0.67	0.72	0.34	2.12	0.48	1.51	2.04
CD (5%)	21.79	29.65	1.94	2.1	0.99	6.17	1.41	4.41	5.94
CD (1%)	29.41	40.01	2.61	2.83	1.34	8.32	1.9	5.95	8.01

Crosses	CL	CW	NKRC	NKR	GCW	TSS	TS	RS	NRS
$L_1 \times T_1$	0.04 ns	1.64 *	-1.94 **	0.14 ns	29.88 **	0.87 **	0.85 **	0.22 **	1.97 *
$L_1 \times T_2$	-0.95 *	-0.43 ns	-0.49 ns	-1.48 **	-12.94 **	-0.41 ns	0.02 ns	0.15 ns	-2.04 ns
$L_1 \times T_3$	0.91 *	1.07 *	2.43 **	1.33 **	32.81 **	-0.46 ns	0.83 **	0.17 **	3.01**
$L_2 \times T_1$	0.67 ns	0.22 ns	5.49 **	0.64 *	31.25 **	1.70 **	2.01 **	-0.26 ns	2.27 *
$L_2 \times T_2$	0.68 ns	0.04 ns	1.55 **	-0.48 ns	-16.82 **	-1.07 *	-1.37 ns	0.29 **	-1.08 ns
$L_2 \times T_3$	-1.35 **	-0.26 ns	-7.04 **	-0.17 ns	-14.43 **	-0.63 ns	0.63 ns	0.56 *	-1.19 ns
$L_3 \times T_1$	-0.70 ns	0.46 ns	-1.24 *	0.68 *	15.38 **	1.04 *	1.91 ns	0.10 *	1.80 ns
$L_3 \times T_2$	0.66 ns	0.42 ns	2.76 **	1.16 **	-30.19 **	-1.74 **	-1.79 ns	0.11 ns	-1.81 ns
$L_3 \times T_3$	0.03 ns	0.88 *	-1.52 **	-1.83 **	-24.81 **	0.70 ns	0.41 **	0.32**	2.42 **
$L_4 \times T_1$	-0.25 ns	-1.48 **	-3.87 **	-1.19 **	-47.29 **	-2.30 **	-1.21 ns	0.12**	-1.23 ns
$L_4 \times T_2$	-2.49 **	1.24 **	-3.77 **	1.19 **	-1.63 ns	1.93 **	2.06 ns	0.20 **	1.86 ns
$L_4 \times T_3$	2.73 **	0.24 ns	7.64 **	-0.00 ns	-18.92 **	0.37 ns	0.86 ns	-0.22 ns	-0.63 ns
$L_5 \times T_1$	1.85 **	0.96 **	5.76 **	-1.52 **	21.24 **	1.37 **	3.43 **	0.24 **	3.19 **
$L_5 \times T_2$	1.11 *	-0.18 ns	-4.99 **	0.86 **	-10.69 **	1.09 *	1.10 ns	-0.14 ns	1.24 ns
$L_5 \times T_3$	-2.97 **	0.12 ns	-0.77 ns	0.67 *	-10.55 **	-2.46 **	-4.52 **	-0.10 ns	-4.43 **
$L_6 \times T_1$	0.44 ns	0.34 ns	1.98 **	0.64 *	-20.21 **	0.54 ns	0.24 ns	-0.09 ns	0.33 ns
$L_6 \times T_2$	-1.20 **	-0.85 *	-4.32 **	-0.48 ns	-4.48 **	0.26 ns	-0.83 ns	0.13 ns	-0.96 ns
$L_6 \times T_3$	0.76 ns	0.51 ns	2.34 **	-0.17 ns	-24.70 **	-0.80 ns	0.59 ns	-0.14 ns	0.63 ns
$L_7 \times T_1$	-0.78 ns	0.39 ns	-1.04 ns	0.48 ns	-14.06 **	-2.30 **	2.77 *	0.32 **	-2.45 *
$L_7 \times T_2$	-0.67 ns	-0.75 ns	0.71 ns	-0.14 ns	-20.08 **	1.43 **	2.20 ns	0.49 **	1.71 ns
$L_7 \times T_3$	1.45 **	0.36 ns	0.33 ns	-0.33 ns	6.02 **	0.87 ns	2.57 ns	0.17 **	0.74 ns
$L_8 \times T_1$	-0.45 ns	1.51 **	-2.64 **	1.14 **	-22.24 **	-0.96 *	2.51 ns	0.09 ns	-2.60 *
$L_8 \times T_2$	0.96 *	-1.18 **	3.86 **	-1.48 **	-30.19 **	-0.24 ns	0.46 ns	0.13 ns	1.59 ns
$L_8 \times T_3$	-0.52 ns	-0.33 ns	-1.22 *	0.33 ns	32.05 *	1.20 *	2.05 ns	0.24 **	2.01 ns
$L_9 \times T_1$	-0.83 ns	-0.86 *	-2.49 **	-1.02 **	-46.44 **	0.04 ns	2.24 **	0.10 ns	2.34 **
$L_9 \times T_2$	1.88 **	1.70 **	4.66 **	0.86 **	-57.67 **	-1.24 **	-1.84 ns	-0.32 ns	-1.52 ns
$L_9 \times T_3$	-1.05 *	-0.84 *	-2.17 **	0.17 ns	-11.22 **	1.20 *	2.08 ns	0.22 **	1.86 ns
SE	0.42	0.39	0.51	0.29	0.86	0.44	1.07	0.24	1.03
CD (5%)	1.23	1.14	1.49	0.84	2.52	1.28	3.12	0.69	2.99
CD (1%)	1.67	1.53	2.01	1.14	3.4	1.72	4.22	0.94	4.03

* - Significant at 5%, ** - Significant at 1%

Where, PH - plant height (cm), CPH - cob placement height (cm), DT - days to 50% tasseling, DS - days to 50% silking, ASI - anthesis silking interval, LL - leaf length (cm), LB - leaf breadth (cm), TL - tassel length (cm), NTB - number of tassel branches, CL - cob length (cm), CW - cob width (cm), NKRC - number of kernel rows per cob (No's), NKR - number of kernels per row (No's), GCW - green cob weight without husk (g), TSS - total soluble solids (%), TS - total sugars (%), RS - reducing sugars (%) and NRS - non – reducing sugars (%).

$L_1 \times T_1$, $L_1 \times T_3$, $L_2 \times T_1$, $L_3 \times T_1$, $L_5 \times T_1$, $L_7 \times T_3$ and $L_8 \times T_3$ for green cob weight without husk. The $L_1 \times T_1$ hybrid displayed significant *sca* effect for plant height, cob placement height, TSS, total sugars, reducing sugars and non-reducing sugars along with green cob weight without husk. The next best hybrid $L_1 \times T_3$ possessed good *sca* effect for cob width, number of kernel rows per cob, number of kernels per row, total sugars, reducing and non-reducing sugars along with significantly less anthesis silking interval. The cross $L_2 \times T_1$ exhibited positive significant SCA for number of kernel rows per cob, number of kernels per row, TSS, total sugars and non-reducing sugars. Followed by the cross $L_3 \times T_1$ showed significant *sca* effect for tassel length, number of kernels per row, TSS and reducing sugars while $L_8 \times T_3$ for TSS and reducing sugars. The other best hybrid $L_5 \times T_1$ had recorded good SCA for the traits like plant height, cob length, cob width, number of kernel rows per cob, TSS, total sugars, reducing sugars and non-reducing sugars. The higher SCA showed that the crosses have higher dominance effects. Chinthiya *et al.* (2019) reported predominance of non-additive gene action for all the traits and reported positive significant *sca* effect for green cob weight and other quality traits. Similarly Arsode *et al.* (2017) noted significant negative SCA values for days to 50% tasseling and days to 50% silking. Kuselan *et al.* (2017) observed for rows per cob, number of grains per cob and cob girth. Similarly, Mousa *et al.* (2021) were also reported that the best combiners were selected based on the estimates of *sca* effects. The hybrids with strong *sca* effects were produced by an array of high × low, low × high and high × high parental *gca* combinations. These positive *sca* effects could be the result of non-additive gene activation combined with promising genes from relating parents.

CONCLUSION

Thus, based on green cob weight without husk and sweetness traits, the hybrids *viz.,* $L_1 \times T_1$ (16.12 %), $L_1 \times T_3$ (17.84 %), $L_5 \times T_1$ (20.11 %) were promising. These hybrids, once rigorously evaluated for yield and sweetness traits across various locations, have the potential for commercialization.

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