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Research Article

Development and genetic evaluation of single cross *super*-sweet (shrunken 2) sweet corn hybrids (*Zea mays* var. *saccharata* L.):A novel *choice* for commercial market

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Abstract
The present investigation was carried for developing sweet corn (shrunken 2) hybrids coupled with high yield and extended shelf life. The selected inbreds with *sh2* gene *viz.*, six lines and five testers were crossed in Line × Tester mating design and the hybrids were evaluated for important yield contributing traits. Relative proportion of GCA variance to SCA variance was less than unity, specifying the preponderance of non-additive gene action for all the traits studied. The lines SC 11-07, SC 11-2 and testers, MRCSC 11, WNDMRSCY 19R763 were identified as ideal parents for synthesizing high yielding hybrids with high mean and *gca* effects for green cob yield in addition to some of the yield contributing traits. The line SC 11-07 was identified as a potential parent with high total sugar content. Among the hybrids, SC 11-07 × MRCSC 11 followed by SC 11-07 × WNDMRSCY 19R763 and SC 11-2 × WNDMRSCY 19R763 were found to be the best performers with significant *per se* performance and *sca* effects and standard heterosis for green cob yield and contributing traits. Remarkably, SC 11-07 × MRCSC 11 also recorded superiority for quality traits. Hence, these hybrids could be subjected to further multi-location evaluation to assess the yield stability across varying environments and exploited for commercial cultivation.

Keywords: Line x tester analysis, combining ability, gene action, heterosis, shrunken sweet corn

INTRODUCTION

Sweet corn is grown as a vegetable in many countries like USA and Canada and is also known as Sugar corn or Pole corn. Sweet corn is harvested, when the kernels are at its milky stage (18- 22 days after pollination). In India, increasing urbanization, changing food habits, improved economic status and diverse uses of sweet corn demands a paradigm shift towards sweet corn cultivation (Datta *et al.,*2022). But, the national breeding programs mainly focus on maize and much more attention to sweet corn improvement is still essential. Though many composites *viz.,* Madhuri, Priya and Win-Orange are from the public sector, the farmers prefer only hybrids because of high yield and uniformity in hybrid cultivation. Currently, only a limited number of sweet corn hybrids are available to farmers. So it is necessary to develop suitable hybrids to exploit heterosis and strengthen the production technology to cope up with the growing demand. But the challenge associated with sweet corn breeding is that due to its high metabolic activity, corn has a limited shelf life.

Fresh sweet corn is a perishable vegetable with faster sugar catabolism and a higher respiration rate (Wang *et al.,*2023). Quantitative data available in literature shows that 40-60% of sucrose which is originally present in sweet corn, depletes after 24 hrs. of storage at 25^{0}C. Therefore, the development of sweet corn with enhanced shelf life

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is imperative. The identification and use of shrunken 2 (*sh2*) gene in sweet corn breeding has resulted in 'super sweet' or 'extra sweet' corn with increased sweetness and extended shelf life.

In general, starch is a storage polysaccharide made up of several glucose units. ADP- glucose is the donor for glucose residues. The rate-limiting step in starch biosynthesis pathway is the synthesis of ADP-Glucose from glucose - 1 - phosphate and adenosine diphosphate catalyzed by adenosine diphosphate glucose pyrophosphorylase (AGP) (Tsai and Nelson, 1966). AGP enzyme is a hetero tetramer with two subunits coded by two different genes. The largest subunit of the enzyme is encoded by functional *Sh2* and smallest subunit by *Bt2* genes (Hannah *et al.*, 1993). Loss of functional AGP enzyme results in reduced kernel starch. Biochemical studies by Tsai and Nelson (1966) concluded that in shrunken 2 mutant adenosine diphosphate glucose pyrophosphorylase (AGP) activity is completely reduced in endosperm and embryo tissue. Failure of shrunken mutants to make ADP-glucose pyrophosphorylase causes accumulation of sucrose and lipids instead of Water Soluble Polysachharide and starch (Coe Jr *et al.*, 1988). As a result, there is a reduction in total carbohydrate and the kernels are characterized by shrunken endosperm at maturity (Khanduri *et al.*, 2010). Super sweet corn contains two to three times higher sugar than traditional sugary sweet corn and six-fold higher sugar than field corn (Chhabra *et al.*, 2019). In super sweet corn, conversion of sugar to starch is much more slower than sugary type and it is preferred by shippers, grocers, and farmers. Because of comparatively high sugar, less total carbohydrate (less calories), high fiber and high protein, super sweet types are favored over sugary type. In the recent past, *sh2* mutants have transformed the sweet corn industry.

Therefore, the present objective is to synthesize single cross sweet corn hybrids with *sh2* allele. To formulate a relevant breeding strategy for crop improvement, a better understanding of nature and magnitude of gene action governing quality traits, yield and their component traits are essential and hence, this study was undertaken.

MATERIALS AND METHODS

The present investigation was carried out during 2019 – 2020 at the experimental fields of Department of Millets, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore. The sweet corn inbreds maintained at the Department of Millets were visually characterized for the shrunken nature of kernels at maturity and absence of anthocyanin pigments at the stem base. Six lines *viz.,* SC 11-07, SC 11-2, SC 1421-5-2-1, WNC 12069-2, WNC 12039-1 and USC 1-2-3-1 and five testers *viz.,* MRCSC 11, WNDMRSCY 19R763, DMSC 20, 951-7and DMSC 36 were selected and used as parents in crossing programme. Further, the selected inbreds were confirmed for the presence of *sh2* allele (recessive shrunken 2) using *M1-sh2*, a dominant marker (Chhabra *et al.*, 2019). CO 6 maize hybrid with dominant *Sh2* allele was used as a check to screen for the presence of the *sh2* allele since the maker used is dominant. The DNA of the genotypes was isolated by following the modified CTAB method (Saghai-Maroof *et al.*, 1984). *M1-sh2* primer sequence is GCAACTCTTAGAACGCTCACC (Forward) and TCCATCAGCAAAGTTGATCC (Reverse)

The crossing programme was carried out during *Kharif* 2019 using the selected six lines and five testers in Line × Tester mating design (Kempthorne, 1957). The resultant hybrids along with their parents and commercial check hybrid (Misthi) were evaluated during *Rabi* 2020 in Randomized complete block design (RBD) with two replications. In the experimental field, the length of rows formed was 4 m and each entry was raised in two rows in both the replications. For a good crop stand, the optimum plant population was maintained with proper spacing of 60 × 25 cm and required cultural and plant protection measures were followed.

Five plants were randomly selected and tagged from each entry in both the replications. Various biometrical observations *viz.,* plant height (cm), cob placement height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row and green cob weight (g), were recorded from the tagged plants, except for days to 50% tasseling, days to 50% silking, anthesis silking interval (ASI) and green cob yield (t/ha) which were noted on plot basis. Individual plot yield was recorded in terms of kilogram, from which yield per hectare was computed and expressed in tonnes/hectare. In addition, four grain quality traits were recorded after harvest in the immature kernels. Total soluble solids (TSS-per cent brix) was measured with hand refractometer, total sugar content (%) and reducing sugars were estimated as per Yemm and Willis (1954) and Somogyi (1952), respectively and non-reducing sugar (%) was calculated by deducing reducing sugar from total sugar.

The replicated mean data obtained were subjected to Line x Tester analysis as suggested by Kempthorne (1957) and it was accomplished by TNAUSTAT-statistical package (2014). The standard heterosis was computed based on the superiority of the hybrids over Misthi (commercial hybrid check).

RESULTS AND DISCUSSION

Parental selection – Morphological screening and molecular confirmation: Hunting for the morphological trait linked to the expression of genes will help the breeders in selection. In this context in sweet corn, the shrunken nature of kernels and absence of anthocyanin pigmentation are the two morphological markers available to screen for super sweet corn with shrunken (*sh2*) gene. The genes *viz., a1* (anthocyanin 1) and *sh2* (shrunken 2) controlling the above traits are physically linked in the coupling phase with a distance less than one centimorgan (i.e.140 kb) (Chhabra *et al.*, 2019). Both genes are located in chromosome 3.

With this backdrop, sweet corn inbreds maintained at the Department of Millets were phenotypically characterized for shriveled kernels at maturity and the absence of anthocyanin pigmentation at the stem base. As a result, eleven inbreds *viz*., SC 11-07, SC 11-2, SC 1421-5-2-1, WNC 12069-2, WNC 12039-1, USC 1-2-3-1, MRCSC 11, WNDMRSCY 19R763, DMSC 20, 951-7 and DMSC 36 with the above features were selected and used as parents in hybridization programme (**Plate 1, 2**).

Further, the parents selected for the shrunken (*sh2)* gene were validated using the *Sh2* gene-based dominant marker, *M1-sh2.* The genomic DNA from eleven parents, as well as DNA from CO 6 (with dominant *Sh2* gene), was amplified by PCR. The gene was found to be amplified in CO 6 maize hybrid. The absence of amplification for the recessive *sh2* (shrunken) allele in all the eleven parents confirmed that those selected inbreds were super sweet corn types (**Plate 3**). The marker used was based on the findings of Chhabra *et al.* (2019), in which three *Sh2* gene-based markers were designed and validated and *M1-sh2* was one among them.

Analysis of variance: All the fifteen agronomic and quality traits studied exhibited a highly significant genotypic effect, evincing the presence of genetic variability in the genotypes studied. Similarly, all the quantitative and quality attributes showed a significant difference among parents as well as hybrids. This observation has given a thrust to proceed further in to the study.

Analysis of variance for combining ability: On further partitioning of variance in terms of lines, testers and line × tester, it was noticed that the variance due to lines was significant for all the traits, representing the presence of substantial variability among lines. Variance due to testers was significant for most of the traits except anthesis silking interval, plant height and the number of kernels per row. Apart from total soluble solids, all other characters included in the study showed significant variation for line × tester interaction (**Table 1**). Thus, the genotypes included were diverse in nature. In agreement with this report, significant mean squares due to genotypes for all the yield and yield-related attributes studied were also reported by Chinthiya *et al.* (2019) and Sadaiah *et al.*(2013) for sugar traits in sweet corn.

Nature of gene action: The proportion of GCA variance to SCA variance was less than unity, specifying the preponderance of non-additive gene action for all the characters evaluated (**Table 1**). The predominance of dominance and epistatic gene action in the SCA variance opens up a wide scope for heterosis breeding to exploit hybrid vigor. The result of predominance of non-additive gene action was in complete agreement with the findings of Chinthiya *et al.* (2019), Ravikesavan *et al.* (2020) for all the observed traits and Niji *et al.* (2018) for all the characters considered except for days to 50% tasseling and anthesis silking interval in sweet corn. Duraes *et al.*(2017) reported non additive effects for yiled related traits in super sweet corn hybrids. With respect to the quality traits, Kumara *et al.* (2013) reported preponderance of non additive gene action for total sugars and non-reducing sugar, Bharathi (2018) for reducing sugar and Yuwono *et al.* (2017) for total soluble solids in sweet corn.

Evaluation of parents- Per se and general combining ability effects: Sweet corn breeding programme are mostly aimed at improving yield along with desirable sweetness and cob appearance coupled with economic value (Duraes *et al*., 2017**.** Evaluation of parents and hybrids are mainly based on these prime traits for crop improvement. While evaluating an inbred, two prime factors that should be taken into consideration are the performance of the line itself and the performance of a line in a series of hybrid combinations or in a particular cross combination.

The identification of potent parental inbreds for hybridization can be done by using *per se* values and general combining ability effects (**Table 2**). Parents with high mean performance need not associate always with high *gca* effects. Thus the knowledge on *gca* effects and mean performance would be useful in the proper selection of parents to derive a desirable hybrids.

Using both significant *per se* performance and significant *gca* effects, the lines SC 11-07 and SC 11-2 were excelling for higher green cob yield with the mean of 6.92 (t/ha) and 6.86 (t/ha), respectively. SC 11-07 also recorded superior performance for total sugars with mean of 16.39 %. SC 11-2 recorded superiority for cob length and green cob weight. For earliness in silking, WNC 12069-2 and WNC 12039-1 were the best lines. To improve the traits *viz.,* cob placement height and number of kernel rows, SC 1421-5-2-1 was found to be a promising line.

Within testers, MRCSC 11 and WNDMRSCY 19R763 recorded both significant *per se* and *gca* estimates for green cob yield with mean of 7.54 and 7.49 (t/ha), respectively. MRCSC 11 excelled for the traits *viz.,* cob length and the number of kernel rows. WNDMRSCY 19R763 excelled for the number of kernel rows and single plant green cob weight. DMSC 20 was the best tester to achieve earliness. 951-7 was observed to be superior in terms of mean (1.73%) and *gca* for reducing sugars.

In the present study, based on their desirable significant mean performance and significant *gca* effects, the inbreds, SC 11-07 , SC 11-2 , MRCSC 11 and WNDMRSCY 19R763 could be selected as parents for synthesizing high yielding hybrids. The tester, DMSC 20 could be used to develop early maturing hybrids that can escape drought in case of terminal drought stress. The inbreds, SC 11-07 and 951-7 could be utilized in breeding programmes to

Plate 1. Kernel phenotype (Shrunken at maturity) in parents

Plate 2. Absence of anthocyanin pigmentation at stem base of parents

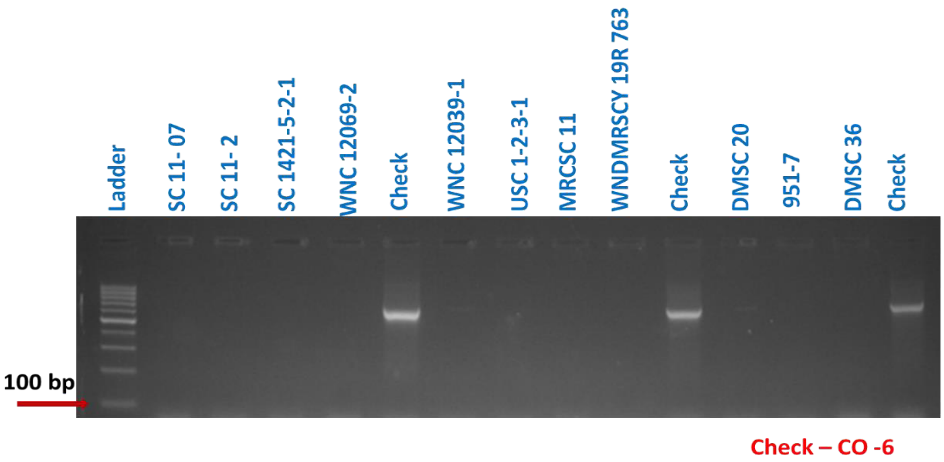

Plate 3. Molecular screening of parents with Dominant marker, *M1-sh2*

Table 1. Analysis of variances for combining ability in sweet corn genotypes for quantitative and quality traits

S.No	Characters	Sources of variation				Variance ratio (GCA/SCA)
		Lines	Testers	Line x Tester	Error	
1	Days to 50% tasseling	5.12**	11.15**	3.12**	1.0598	0.0464
2	Days to 50% silking	8.1867**	7.6083**	4.6283**	0.6115	0.0168
3	Anthesis Silking Interval	2.3467**	1.2083	1.8883**	0.5149	0.0007
4	Plant height	215.1542*	25.506	258.2809**	78.9511	0.0145
5	Cob placement height	232.2313**	120.6154**	101.5696**	14.0394	0.0189
6	Cob girth	1.7081**	1.7667**	1.4674**	0.4068	0.0051
7	Cob length	3.261*	8.8521**	3.8507**	1.2483	0.0148
8	Number of kernels per row	12.7439**	4.1023	18.7743**	3.4209	-0.0131
9	Number of kernel rows	0.6667**	6.3917**	5.0417**	0.0667	-0.0075
10	Total sugars	4.9733**	2.1552**	2.5833**	0.4547	0.0109
11	Reducing sugar	0.1359**	0.1215**	0.072**	0.0112	0.0197
12	Non reducing sugar	3.8296**	1.4968*	2.5402**	0.5303	0.0025
13	Total soluble solids	0.9144*	1.6398*	1.5165	0.3128	0.0048
14	Green cob weight	519.6685**	645.8667**	651.5796**	70.2428	-0.0027
15	Green cob yield	13.1024**	30.8173**	7.2552**	0.2577	0.0400

* Significant at 0.05 level. **Significant at 0.01 level.

develop hybrids with good quality traits. Favorably, line SC 11-07 was identified as potential parent in hybrid breeding with high yield and quality, as it is found to be a good performer and a combiner for most of the desirable traits (yield and total sugars).

Evaluation of hybrids- Per se, sca and standard heterosis: In sweet corn, hybrid breeding is a widely accepted strategy for yield enhancement through hybrid vigor exploitation. Prediction of single cross hybrid value in terms of mean, specific combining ability and heterosis over the commercial check hybrid available to farmers will be reliable (**Table 3**).

Sometimes, hybrids of parents with high *gca* effects are not with predicted favorable performance and this may be due to the interaction of parental *gca* effects. On the other hand, hybrids of parents with low *gca* effects were with desirable performance than expected. This could be measured by *sca* effects of hybrid (Kumar and Bharathi, 2009). In addition, it is imperative to note that the performance of the hybrid developed should preferentially exceed the best check hybrid available commercially. This can be measured in terms of standard heterosis. It occupies a vital role during hybrid evaluation and can be further used for commercial cultivation.

Table 2. Best parents based on significant *gca* effects and *per se* for different traits

Characters	Lines				Testers			
	Lines with significant *gca* effects	*gca* values	*Per se*	*gca* and *per se*	Testers with significant *gca* effects	*gca*	*Per se*	*gca* and *per se*
D50%T	WNC 12039-1	-0.80*	52.00	-	DMSC 20 DMSC 36	-1.20** -0.62*	48.00** 54.50	DMSC 20
D50%S	WNC 12069-2 WNC 12039-1	-0.97** -0.97**	54.00** 53.50*	WNC 12069-2 WNC 12039-1	DMSC 20 DMSC 36	-1.03** -0.62*	53.00** 57.00**	DMSC 20, DMSC 36
ASI	SC 11-2	-0.67**	2.00	-	-	-	-	-
PH	WNC 12039-1	6.23*	132.07	-	-	-	-	-
CPH	SC 1421-5-2-1	5.19**	67.33**	SC 1421-5-2-1	MRCSC 11 WNDMRSCY 19R763	2.61* 3.02**	64.00 69.50	-
CG	USC 1-2-3-1	0.78**	14.78**	USC 1-2-3-1	DMSC 36	0.53**	8.90	-
CL	SC 11-2	0.87*	16.60*	SC 11-2	MRCSC 11	1.24**	16.70**	MRCSC 11
NKPR	SC 1421-5-2-1	1.65**	23.50	-	-	-	-	-
NKR	SC 1421-5-2-1	0.47**	15.00**	SC 1421-5-2-1	MRCSC 11 WNDMRSCY 19R763 DMSC 20	0.57** 0.32** 0.32**	16.00** 16.50** 13.50	MRCSC 11, WNDMRSCY 19R763
TS	SC 11-07 SC 1421-5-2-1	0.58* 0.51*	16.39** 13.88	SC 11-07	DMSC 20	0.50*	15.25	-
RS	SC 11-07 SC 1421-5-2-1	0.17** 0.07*	1.01 1.01	-	DMSC 20 951-7	0.11** 0.08*	1.45 1.73**	951-7
NRS	-			-	-	-	-	-
TSS	SC 11-07	0.43*	15.15	-	951-7	0.42*	17.00	-
GCW/P	SC 11-2	11.80**	127.98	SC 11-2	WNDMRSCY 19R763	7.52**	142.20	WNDMRSCY 19R763
GCY	SC 11-07 SC 11-2 WNC 12039-1	1.42** 0.88** 0.58**	6.92* 6.86* 5.80	SC 11-07 SC 11-2	MRCSC 11 WNDMRSCY 19R763 DMSC 36	1.20** 1.42** 0.46**	7.54** 7.49* 6.75	MRCSC 11 WNDMRSCY 19R763

* Significant at 0.05 level. **Significant at 0.01 level

D50% T - Days to 50% tasseling, D50% S - Days to 50% silking, ASI- Anthesis Silking Interval, PH- Plant height (cm), CPH- Cob placement height (cm), CG - Cob girth (cm), CL- Cob length (cm), NKPR- Number of kernels per row, NKR- Number of kernel rows, TS- Total sugar (%), RS- Reducing sugar (%), NRS- Non - reducing sugar (%), TSS- Total soluble solids (% brix), GCW - Green cob weight per plant (g), GCY – green cob yield (t/ha)

Therefore, comparative evaluation of hybrids based on significant - mean, *sca* and standard heterosis helps in the accurate selection of better performing hybrids (**Table 3**). Those hybrids selected will be highly valuable for heterosis breeding. In this study, the hybrid SC 11-07 × MRCSC 11 was outstanding in all three decisive factors (mean, *sca* and standard heterosis) for cob length, the number of kernel rows per cob, total sugars, non-reducing sugar, green cob weight and green cob yield . SC 11-07 × MRCSC 11 recorded mean for green cob weight and green cob yield were 215.18 (g) and 15.07 (t/ha), respectively and standard heterosis of 12.40 % and 11.76 %, respectively. It was followed by SC 11-07 × WNDMRSCY 19R763 and SC 11-2 × WNDMRSCY 19R763 for number of kernel rows per cob, green cob weight and green cob yield. The mean values recorded by SC 11-07 × WNDMRSCY 19R763 for green cob weight and green cob yield were 221.78 (g) and 14.91 (t/ha), respectively and standard heterosis of 15.84 % and 10.61 %, respectively. The mean values recorded by SC 11-2 × WNDMRSCY 19R763 for green cob weight and green cob yield were 218.33(g) and 14.65 (t/ha), respectively and standard heterosis of 14.04% and 8.72%, respectively.

About quality, based on desirable significance of mean, *sca* and standard heterosis, WNC 12069-2 × WNDMRSCY 19R763 was proven to be an elite hybrid with increased total sugar (*per se* and standard heterosis of 18.48 % and 20.78%, respectively), non-reducing sugar (*per se* and standard heterosis of 17.32% and 22.27%, respectively), and total soluble solids (*per se* and standard heterosis of

Table 3. Best hybrids based on significant *sca* effects, *per se* and standard heterosis

Characters	Hybrids with significant *sca* effects	*sca* values	*Per se*	Standard heterosis (%)	Superior cross selected based on mean, *sca* and standard heterosis
D50%T	SC 11-2 × 951-7	-2.18**	49.50	-8.33**	USC 1-2-3-1 × DMSC 20
	USC 1-2-3-1 × DMSC 20	-1.60*	48.00**	-11.11**	
D50%S	SC 11-07 × MRCSC 11	-1.48*	55.00	-1.79	WNC 12069-2 × 951-7 USC 1-2-3-1 × DMSC 20
	SC 11-2 ×MRCSC 11	-1.68**	53.50	-4.46**	
	SC 11-2 ×951-7	-1.60**	53.00	-5.36**	
	WNC 12069-2 × 951-7	-1.70**	52.00**	-7.14**	
	USC 1-2-3-1 × WNDMRSCY 19R763	-1.27*	53.50	-4.46**	
	USC 1-2-3-1 × DMSC 20	-1.27*	52.00**	-7.14**	
ASI	SC 11-07 × DMSC 20	-1.07*	2.50	25.00	-
	SC 1421-5-2-1 × 951-7	-2.22**	2.00	0.00	
PH	SC 11-2 ×MRCSC 11	17.87**	215.33**	8.39	SC 11-2 × MRCSC 11
	SC 1421-5-2-1 ×DMSC 20	15.09*	207.52	4.45	
CPH	SC 11-07 ×WNDMRSCY 19R763	8.60**	97.58**	23.00**	SC 11-07 × WNDMRSCY 19R763 SC 11-07 × 951-7 SC 11-2 × MRCSC 11
	SC 11-07 ×951-7	10.60**	95.94*	20.94**	
	SC 11-2 ×MRCSC 11	14.91**	102.83*	29.62**	
	WNC 12069-2 ×DMSC 20	5.99*	76.58	-3.47	
	WNC 12039-1 × DMSC 36	6.44*	92.25	16.28**	
	USC 1-2-3-1 × DMSC 36	5.51*	90.95	14.64**	
CG	USC 1-2-3-1 × DMSC 36	2.32**	16.84**	18.14**	USC 1-2-3-1 × DMSC 36
CL	SC 11-07 × MRCSC 11	3.65**	23.87**	25.63**	SC 11-07 × MRCSC 11
NKPR	SC 11-2 × MRCSC 11	3.71**	43.25*	1.86	SC 1421-5-2-1 × DMSC 36
	SC 1421-5-2-1 × 951-7	3.53*	43.45*	7.95	
	SC 1421-5-2-1 × DMSC 36	4.10**	44.00**	9.30*	
	WNC 12069-2 × DMSC 36	2.87*	39.50	-1.86	
	WNC 12039-1 × WNDMRSCY 19R763	3.11*	42.50	5.59	
	USC 1-2-3-1 × DMSC 20	4.66**	43.00**	6.83	
NKR	SC 11-07 × MRCSC 11	1.03**	17.50**	9.38*	SC 11-07 × MRCSC 11 SC 11-07 × WNDMRSCY 19R763 SC 11-2 × MRCSC 11 SC 11-2 × WNDMRSCY 19R763 SC 1421-5-2-1 × DMSC 20 SC 1421-5-2-1 × DMSC 36 WNC 12069-2 × MRCSC 11 WNC 12039-1 × WNDMRSCY 19R763 USC 1-2-3-1 × DMSC 20
	SC 11-07 ×WNDMRSCY 19R763	1.78**	18.00**	12.50**	
	SC 11-2 ×MRCSC 11	1.03**	17.50**	9.38*	
	SC 11-2 × WNDMRSCY 19R763	1.78**	18.00**	12.50**	
	SC 1421-5-2-1 ×DMSC 20	1.28**	14.00	12.50**	
	SC 1421-5-2-1×951-7	0.87**	16.00	0.00	
	SC 1421-5-2-1 × DMSC 36	1.53**	18.00**	12.50**	
	WNC 12069-2 × MRCSC 11	1.83**	18.00**	12.50**	
	WNC 12039-1 × WNDMRSCY 19R763	1.28**	17.50**	9.38*	
	WNC 12039-1 × 951-7	1.37**	16.00	0.00	
	USC 1-2-3-1 × DMSC 20	1.28**	17.50**	9.38*	
TS	SC 11-07 × MRCSC 11	1.33**	17.93*	17.16**	SC 11-07 × MRCSC 11 SC 1421-5-2-1 × 951-7 WNC 12069-2× WNDMRSCY 19R763
	SC 1421-5-2-1 × 951-7	1.05*	18.30**	19.64**	
	WNC 12069-2 × WNDMRSCY 19R763	2.22**	18.48**	20.78**	
	USC 1-2-3-1 × DMSC 36	1.32**	17.11	11.83*	
RS	SC 11-07 × DMSC 36	0.16*	1.59*	40.09**	SC 1421-5-2-1 × WNDMRSCY 19R763 SC 11-07 × DMSC 36
	SC 1421-5-2-1×WNDMRSCY 19R763	0.31**	1.75**	54.19**	
	WNC 12069-2×MRCSC 11	0.23**	1.39	22.91	
	WNC 12039-1 × DMSC 20	0.24**	1.57	38.77**	
	USC 1-2-3-1 × DMSC 36	0.27**	1.45	27.75*	
NRS	SC 11-07 × MRCSC 11	1.48**	16.66**	17.61**	SC 11-07 × MRCSC 11 WNC 12069-2 × WNDMRSCY 19R763 SC 11-07 × DMSC 20
	SC 11-07 × DMSC 20	0.99 *	16.06**	18.43**	
	WNC 12069-2 × WNDMRSCY 19R763	2.36 **	17.32**	22.27**	
	WNC 12039-1 × 951-7	1.03*	15.22	7.48	
	USC 1-2-3-1 × DMSC 36	1.05*	15.66**	10.55*	

Table 3. Continued.

Characters	Hybrids with significant *sca* effects	*sca* values	*Per se*	Standard heterosis (%)	Superior cross selected based on mean, *sca* and standard heterosis
TSS	SC 11-07 × MRCSC 11	0.99*	18.00	8.27*	SC 1421-5-2-1 × 951-7 WNC 12069-2 ×WNDMRSCY 19R763
	WNC 12069-2×WNDMRSCY 19R763	1.06*	18.50*	11.28**	
	SC 1421-5-2-1×951-7	1.65**	18.63*	12.03**	
	USC 1-2-3-1 × DMSC 36	1.11v	18.25	9.77**	
GCW/P	SC 11-07 ×MRCSC 11	25.70**	215.18**	12.40**	SC 11-07 × MRCSC 11 SC 11-07× WNDMRSCY 19R763 SC 11-2 × WNDMRSCY 19R763
	SC 11-07 ×WNDMRSCY 19R763	28.02**	221.78**	15.84**	
	SC 11-2 ×WNDMRSCY 19R763	14.67*	218.33**	14.04**	
	SC 1421-5-2-1×DMSC 36	16.80**	184.42	-3.67	
	WNC 12069-2×DMSC 20	16.66**	205.25*	7.21	
	WNC 12069-2×951-7	21.61**	196.75	2.77	
	USC 1-2-3-1 ×DMSC 20	16.59**	201.00*	4.99	
	USC 1-2-3-1 ×DMSC 36	12.84*	185.17	-3.28	
GCY	SC 11-07 × MRCSC 11	1.52**	15.07**	11.76**	SC 11-07 × MRCSC 11 SC 11-07 × WNDMRSCY 19R763 SC 11-2 × WNDMRSCY 19R763
	SC 11-07 ×WNDMRSCY 19R763	1.15**	14.91**	10.61**	
	SC 11-07 ×DMSC 20	1.48**	13.24**	-1.78	
	SC 11-2 × MRCSC 11	1.22**	14.22**	5.49	
	SC 11-2 ×WNDMRSCY 19R763	1.44**	14.65**	8.72*	
	SC 11-2 ×DMSC 36	1.32**	13.58**	0.74	
	SC 1421-5-2-1 × DMSC 20	1.53**	10.76	-20.22**	
	SC 1421-5-2-1×DMSC 36	1.61**	11.88	-11.91**	
	WNC 12069-2×DMSC 36	3.03**	12.96**	-44.40**	
	WNC 12039-1 × MRCSC 11	0.80*	13.50**	0.15	
	WNC 12039-1 × WNDMRSCY 19R763	1.12**	14.03**	4.12	
	USC 1-2-3-1 × 951-7	1.97**	10.07	-25.30	

* Significant at 0.05 level; **Significant at 0.01 level.

D50% T - Days to 50% tasseling, D50% S - Days to 50% silking, ASI- Anthesis Silking Interval, PH- Plant height (cm), CPH- Cob placement height (cm), CG - Cob girth (cm), CL- Cob length (cm), NKPR- Number of kernels per row, NKR- Number of kernel rows, TS- Total sugar (%), RS- Reducing sugar (%), NRS- Non - reducing sugar (%), TSS- Total soluble solids (% brix), GCW - Green cob weight per plant (g), GCY – green cob yield (t/ha).

18.5% and 8.27%, respectively). SC 11-07 × MRCSC 11 was superior for total sugars (*per se* and standard heterosis of 17.93% and 17.16 %, respectively) and non-reducing sugars (*per se* and standard heterosis of 16.66% and 17.61%, respectively) and SC 1421-5-2-1 × 951-7 for total sugars(*pe rse* and standard heterosis of 18.30% and 19.64%, respectively) and total soluble solids (*per se* and standard heterosis of 18.63% and 12.03%, respectively). On the other hand, considering reducing sugar alone, SC 11-07 × DMSC 36 (*per se* and standard heterosis of 1.59% and 40.09%, respectively) and SC 1421-5-2-1 × WNDMRSCY 19R763 (*per se* and standard heterosis of 1.75% and 31.58%, respectively) were found to be the best hybrids. Yuwono *et al.* (2017) and Chinthiya *et al.* (2019) have reported hybrids with significant *sca* effects and significant standard heterosis for for all the fifteen important biometrical and quality traits studied in sweet corn.

The outstanding hybrid identified based on combined results of significant mean, significant *sca* and significant standard heterosis were SC 11-07 × MRCSC 11 followed by SC 11-07 × WNDMRSCY 19R763 and SC 11-2 × WNDMRSCY 19R763 for high yield. For quality, the elite hybrids were WNC 12069-2 × WNDMRSCY 19R763 followed by SC 11-07 × MRCSC 11 and SC 1421-5-2-1 × 951-7. Remarkably, SC 11-07 × MRCSC 11 recorded superiority for green cob yield and quality traits. The selection of hybrids with earliness could be useful in abiotic stress breeding programme owing to the association of drought escape mechanism (Shavrukov *et al.*, 2017). Precocity of such hybrids could be utilized for planting more than one crop in a year. Among all the hybrids evaluated, USC 1-2-3-1 × DMSC 20 displayed earliness.

It is not an easy task for a breeder to pyramid all the desirable traits into an inbred and make them to express its heterotic potential in the developing hybrids for the traits of interest. In the study also, none of the hybrids recorded desirable significant *sca* effects for all the traits studied. Some of them do not report high *sca* effects though the parents are good general combiners. The characterized best specific combining hybrids was from high × high (SC 11-07 × MRCSC 11, SC 11-07 × WNDMRSCY 19R763, SC 11-2 × MRCSC 11, SC 11-2 × WNDMRSCY 19R763, WNC 12039-1 × WNDMRSCY 19R763), low × high (SC 1421-5-2-1 × DMSC 36) and high × low (SC 11-07 × DMSC 20) general combiners. These crosses involved at least one parent with high *gca*. Similar findings of hybrids with high *sca* derived from low × high and high × low *gca* combinations were reported by Niji *et al.* (2018), Chinthiya *et al.* (2019) in sweet corn.

Based on the study, it was concluded that elite inbreds for synthesizing high yielding hybrids were lines SC 11-07 , SC 11-2 and testers, MRCSC 11, WNDMRSCY 19R763, since the above inbreds registered desirable mean and *gca* effects for green cob yield and some of the yield contributing traits. In addition, SC 11-07 was found to be potent inbred with higher yield and total sugar content. The outstanding hybrid identified based on combined results of performance *per se*, *sca* and standard heterosis was SC 11-07 × MRCSC 11 with desirable performance in terms of cob length, the number of kernel rows per cob, total sugars, non-reducing sugar and green cob weight and green cob yield. This was followed by SC 11-07 × WNDMRSCY 19R763 and SC 11-2 × WNDMRSCY 19R763 for high green cob yield and some yield attributing traits. On the whole, the outstanding hybrid, SC 11-07 × MRCSC 11 was with lengthier cob with more number of kernels in a row which resulted in increased green cob weight and green cob yield (t/ha). It was considerably sweet with significant amount of total sugars and non-reducing sugars. This particular cross combination can be promoted as a commercial hybrid for sweet corn improvement.With respect to synchrony in reproductive phase, all the hybrids recorded synchrony with the narrow difference in days to 50% silking of respective lines and days to 50% tasseling in respective testers *i.e.,* 1.5 days in SC 11-07 × MRCSC 11, 7.5 days in SC 11-07 × WNDMRSCY 19R763 and 6.5 days in SC 11-2 × WNDMRSCY 19R763 . These hybrids could be subjected to further multi-location evaluation to assess the yield stability for commercial exploitation.

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