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Rani Chapara

Scientist (Genetics and Plant Breeding), Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India

Umakanth AV

Principal Scientist (Plant Breeding), Indian Institute of Millet Research, Rajendranagar, Hyderabad, Telangana, India

Hariprasada Reddy K

Professor and Head, Department of Genetics & Plant breeding, S.V. Agricultural College, Tirupati, Andhra Pradesh, India

Eswara Reddy NP

Professor and Head, Regional Agricultural Research Station, Tirupati, Andhra Pradesh, India

Venkata Ramana Chapara

Ph.D., Assistant Research Professor/Plant Pathology, 9280 107th Ave NE, NDSU/Langdon Research Extension Centre, Langdon, North Dakota

Corresponding Author:**Rani Chapara**

Scientist (Genetics and Plant Breeding), Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India

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Heterosis, combining ability and stability analysis for Bioenergy traits in sweet sorghum [*Sorghum bicolor* (L.) Moench]

Rani Chapara, Umakanth AV, Hariprasada Reddy K, Eswara Reddy NP and Venkata Ramana Chapara

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Abstract

An investigation on assessment of heterosis, combining ability and G×E interaction in respect of ethanol yield and its attributing traits was carried out with 30 test hybrids of sweet sorghum developed by crossing five (5) low-sugar female lines with six (6) high-sugar male lines in Line x Tester mating design during *kharif* season of 2010 over three locations. The hybrids *viz.*, NSS 1007A × CSV 19SS and RS 1220A × SSV 74 are highly suitable for heterosis breeding as they exhibited significant positive standard heterosis for ethanol yield and its contributing traits. The parents, RS 1220B, CSV 19SS and SSV 74 were found to be good general combiners, while the cross combinations *viz.*, NSS 1007A × CSV 19SS and NSS 1016A × SSV 84 showed good specific combining ability coupled with high *per se* performance for ethanol yield hence highly suitable for heterosis breeding. Based on stability, the hybrids *viz.*, NSS 8A × SSV 84 and NSS 1007A × CSV 19SS for ethanol yield, juice yield and total biomass were found to be stable with well adaptation to all environments whereas NSS 8A × CSV 19SS showed specific adaptation to favourable environments for the traits like ethanol yield, juice yield, total soluble solids and total sugar index while NSS 8A × SSV 74 showed specific adaptation to unfavourable environments for ethanol yield. The hybrid NSS 1007A × CSV 19SS exhibited high mean, significant positive standard heterosis and *sca* effects along with *bi* near to unity and non-significant deviation from regression.

Keywords: Standard heterosis, combining ability, genotype × environment, stability, *Sorghum bicolor*

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) (2n=20) is the fifth major cereal crop in the world and occupies fifth position in acreage after wheat, rice, maize and barley. Major producers of sorghum in the world are Nigeria, USA, India, Mexico, Argentina, Sudan, Ethiopia, Brazil, China and Australia. It has been classified under family Graminae, subfamily Poaceae, tribe Andropogonae and genus *Sorghum*. It is a special type of sorghum that can be grown for food, fuel, fodder and fibre (a crop of 4 FFFF's). It is a new generation energy crop that has a potential to accumulate sugars 10 - 20% in its stalks as similar to sugarcane but also produce grains. Bagasse after extraction of juice can be used to cogenerate power. It has the potential to improve the rural livelihoods in India due to its potential industrial use for bioethanol production. However, its potential to stimulate rural growth due to its high biomass potential has been receiving attention of late in India. In recent years, there is increased interest in the utilization of sweet sorghum for ethanol production because of its shorter growing period (about four months), and low water requirement (8,000 cu m) for raising two crops, unlike sugarcane which has a growing period of 12 to 18 months and a water requirement of 36,000 cu m per crop. Besides these, the national biofuel policy of 2009 aims at promoting biofuels to meet India's energy needs in an environmentally-sustainable manner, while reducing its import dependence on fossil fuels. The policy also proposed an indicative target of 20 per cent blending of ethanol by 2017 from the 10 per cent ethanol blending with petrol. The traditional route of ethanol production through sugarcane molasses would not be meeting this huge demand because of the difficulties in increasing the sugarcane area beyond the current 4.4 million ha in the country.

Therefore, renewable sources of energy in the form of other biofuel crops would be promising options in view of the emerging trends in international energy markets as well as indigenous strengths. The significant advantage of sweet sorghum stalk as a source of biofuel is that it is not prone to the food-versus-fuel debate and the ethanol is produced from the non-molasses route which is environment friendly in the absence of any sulphur and has high octane rating. Research results and pilot studies on ethanol production from the juice of sweet sorghum stalks have affirmed its cost effectiveness vis-a-vis other feed stocks. Dayakar Rao *et al.* (2004) [4] suggested sweet sorghum as the best alternative feedstock for bioethanol production. Continuous supply of feed stock to the industries is one of the major constraints in sweet sorghum ethanol production. To encourage the distilleries to make sweet sorghum a major raw material in addition to sugarcane molasses in ethanol production, there is an urgent need to arrange for the supply of sweet sorghum stalks to the distilleries all round the year.

Sweet sorghum hybrids produce relatively higher biomass, besides being early and photo-insensitive than varieties under normal as well as water-limited environments. The requirement of photo and thermo-insensitiveness is essential to facilitate plantings at different dates for timely scheduling the supply of sweet sorghum stalks to distilleries for ethanol production. Therefore, development of sweet sorghum hybrids should receive high priority to produce more feedstock per drop of water and unit of energy invested. However, the availability of improved hybrids for developing high biomass and juice yielding sweet sorghum hybrids is a limiting factor. Increased productivity of sorghum can be achieved by adopting improved agronomic practices and using F₁ hybrid cultivars. Growing sweet sorghum hybrid with high cane juice, sweetness and the total fermentable sugars is consider to be a high efficiency in producing ethanol. Heterosis in sorghum was first reported in 1927, but commercial exploitation was not possible until the discovery of cytoplasmic genetic male sterility system by Stephens and Holland in 1954 [24]. Most of the sweet sorghum varieties mature between 115 and 125 days during rainy season. Stalks can be harvested along with grain. The wide range of variability for brix reading (from 13 to 24%), sucrose per cent (from 7.2 to 15.5), stalk yield (from 24 to 120 t ha⁻¹) and biomass yield (from 36 to 140 t ha⁻¹) in sweet sorghum under long growing seasons in Iran (Almodares *et al.*, 1997) [2] and brix readings (from 14.1 to 19.2%) and millable stalk yield (27.1 to 47.6 t ha⁻¹) under Indian conditions (DSR, 2004 and 2005) [6] indicates the high potential for genetic improvement to produce high sweet-stalk yield coupled with high sucrose per cent sweet sorghum lines.

Genotypic differences for extractable juice, total sugar content and fermentation efficiency and alcohol production have also been reported (Ratnavathi *et al.*, 2003) [4]. The predominant role of non-additive gene action for plant height, stem girth,

total soluble solids, millable sweet-stalk yield and extractable juice yield indicates the importance of breeding for heterosis for improving these traits (Sankarapandian *et al.*, 1994) [20]. Heterosis is of direct relevance for developing hybrids in cross pollinated as well as self-pollinated crops. Manifestation of heterosis for yield is expressed in the form of increased yield, which in turn depend up on the combination of its components (Grafius, 1959) [9]. Exploitation of heterosis on commercial scale for a particular location requires isolation of suitable inbreds and development of hybrids. To accomplish this task one has to know the genetic diversity of the available germplasm and the combining ability of the parents. The common approach of selecting parents based on their *per se* performance always may not lead to fruitful results. Hence, parents selected from combining ability studies would throw up more desirable segregants.

Line × Tester mating design as suggested by Kempthorne (1957) [13] is a modified form of the top cross and is an appropriate method to identify superior parents and hybrids based on general and specific combining ability respectively and to study the nature of gene action. To exploit commercially viable crosses, the crosses are compared with released hybrids so that the crosses with high heterotic potential would be identified. Genotype × Environment interactions are known to infer with evaluation of genotypes and reduce the progress of selection in a plant breeding programme (Allard and Bradshaw, 1964) [1]. Hence, estimation of the nature and magnitude of genotype × environment interaction for ethanol yield and its component traits is essential to identify stable genotypes over environments.

Keeping these views in consideration, the study was carried out at three locations *viz.*, Directorate of Sorghum Research, Hyderabad (Andhra Pradesh), Rahuri (Maharashtra) and Coimbatore (Tamil Nadu) with the objectives to estimate general combining ability of parents and specific combining ability of hybrids, to study nature and magnitude of gene action governing ethanol yield and its related traits, to estimate the extent and nature of heterosis among F₁ hybrids for ethanol yield and its related traits and to identify the high yielding hybrids of sweet sorghum suitable to different locations by assessing their stability.

Material and Methods

The experimental material comprised of five cytoplasmic genetic male sterile lines (NSS 8B, NSS 10B, NSS 1007B, NSS 1016B and RS 1220B) used as females, six male-fertile lines (SSV 84, M 11, CSV 19SS, SSV 74, RSSV 76 and RSSV 120) and their 30 F₁ hybrids derived through line × tester mating design (during *rabi* 2009-10) and three promising checks (CSH 22SS, PAC 52093 and NSSV 13). The parents were selected based on the characters contributing to increased stalk and sugar yields (Table 1).

Table 1: Salient characteristic features of sweet sorghum parents used in the study

S. No.	Genotype	Important features	Status of brix
Lines			
1	NSS 8B	Tan pigmented, dwarf, high fresh stalk yielder	Low
2	NSS 10B	Tan pigmented, tall, late maturing and high grain yielder	Medium
3	NSS 1007B	Tan pigmented, late maturing but poor grain yielder	Low
4	NSS 1016B	Tan pigmented, early maturing with high juice extraction percent	Low
5	RS 1220B	Tan pigmented, medium tall with high grain yield	Medium
Testers			

1	SSV 84	Non-tan pigmented, late maturing, high sugar and grain yield, medium tall, early maturing and good grain yield	High
2	M 11	Non-tan pigmented, tall, pearly white	Medium
3	CSV 19SS	medium seed, good green cane yield, juice yield and tolerant to shoot fly	High
4	SSV 74	Non-tan pigmented, tall, high biomass, good head size, purple glume and white bold seed	High
5	RSSV 76	Non-tan pigmented with low fresh stalk yield, juice yield and grain head size, purple glume and white bold seed.	Medium
6	RSSV 120	Non-tan pigmented, tall, early maturing with good juice extraction	Medium
Checks			
7	CSH 22SS	High in total soluble sugars, juice yield and grain yield	High
8	PAC 5203	High in total soluble sugars, juice yield and grain yield	High
9	NSSV 13	High in total soluble sugars, juice yield and grain yield	High
High brix: >16%; Medium brix: 12-16%; Low brix: <12%			

Experimental site

The 30 F₁ hybrids, their corresponding 11 parents and three checks, (two hybrids (CSH 22SS, PAC 52093) and one variety (NSSV 13)) were evaluated at three different locations covering three states of India with semi-arid environments viz., Directorate of Sorghum Research (DSR) farm, Hyderabad, Andhra Pradesh (latitude 17_190N, longitude 78_230E), Centre for Plant Breeding and Genetics farm, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (latitude 11_00N, longitude 76_550E) and Sorghum Research Station farm, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra (latitude 19_200N, longitude 74_380E) during rainy season of 2010. The experiment was conducted in a Randomized Block Design with three replications at all the three locations. Each entry was sown and raised in two rows of 4 m length with 60×15 cm spacing. Recommended agronomic practices were followed throughout the crop season. In each replication, observations were recorded on 10 randomly selected competitive plants. At physiological maturity, data was recorded on following traits.

Days to 50 per cent flowering

The number of days taken from sowing to the day when 50 per cent plants in each replication exhibited flowering was recorded as days to fifty per cent flowering.

Days to maturity

Number of days taken from sowing to the day on which seed of most of the plants in a plot become hard i.e. appearance of black spot on the hilum of seed, were recorded as days to maturity.

Plant height (cm)

The height of the plant was measured from base of the plant to the tip of the panicle in centimeters before harvesting.

Brix per cent

Brix term used when a refractometer equipped with a scale, based on the relationship between refractive indices at 20°C and the percentage by mass of total soluble solids of a pure aqueous sucrose solution, is used instead of a hydrometer to test the solids concentration of a sucrose containing solution. It is a widely used approximation for sugar content. The values from the composite juice were recorded °brix, using an Atago PAL-1 digital hand-held pocket refractometer (with automatic temperature compensation ranging from 0 to 50°C) at the hard dough stage.

Total biomass (t ha⁻¹)

At physiological maturity, the selected ten plants with their leaves, stems, and panicles were weighed and recorded in kilograms and later converted to t ha⁻¹.

Fresh stalk yield (t ha⁻¹)

The leaves plus sheath and panicles were removed from the 10 selected plants carefully and the weight of the fresh (millable) stalk yield was recorded in kilograms and then converted to t ha⁻¹.

Juice yield (l ha⁻¹)

Juice extraction was done on an electrically operated three-roller stalk crusher (make: Rasraj No. 9, 15-HP, with resolution of 2100-2300 kg/ha) with a minimum of three passings of the selected stalk so that the last drop of juice came out from the stems. Juice extracted was measured in kilograms and later converted into litres by multiplying with conversion factor 0.9.

Juice extraction per cent

It was computed by dividing the juice weight by respective cane weight and multiplied the value by 100.

$$\text{Juice Extraction Per cent} = \frac{\text{Juice weight (kg)}}{\text{Fresh stalk weight (kg)}} \times 100$$

Total soluble solids (TSS) (%)

The term total soluble solids represents the total fermentable sugars such as glucose, fructose and sucrose etc., including starch in juice and it is measured by °brix in sweet sorghum juice. Total soluble solids were calculated following regression equation as reported by Reddy *et al.* (2005)^[19]. Total Soluble Solids (%) = 0.1516 + (Brix % × 0.8746)

Total sugar index (t ha⁻¹)

Total sugar index which was considered as total sugar yield calculated following regression equation as reported by Reddy *et al.* (2005)^[19].

$$\text{Total Sugar Index (t ha}^{-1}\text{)} = \left(\frac{\text{TSS (\%)}}{100} \right) \times \left(\frac{\text{Juice Yield (l ha}^{-1}\text{)}}{1000} \right)$$

Grain yield (t ha⁻¹)

All the panicles collected from the net plot were threshed, dried and the dry weight was recorded in kilograms at 14% seed moisture content and then converted to t ha⁻¹.

Ethanol yield

The ethanol yield was calculated from total sugar yield by using following formula as reported by Reddy *et al.* (2005)^[19].

$$\text{Ethanol Yield (t ha}^{-1}\text{)} = \left(\frac{\text{Total sugar yield (t ha}^{-1}\text{)}}{5.68} \right) \times 3.78 \times 1000 \times 0.8$$

Data analysis: Statistical evaluations were all conducted with INDOSTAT Software.

Combining ability

Combining ability analysis in Line $\times$ Tester design was carried out following Kempthorne (1957) [13]. The mathematical model for combining ability analysis is given below. Analysis of variance for heterosis (with parents and crosses) in RBD.

Table: ANOVA for line $\times$ tester analysis

Source of variation	Degrees of freedom	Mean sum of squares	F test
Replication	(r-1)	RMS	M ₁
Treatments	(t-1)	Tr. MS	M ₂
Parents (P)	(P-1)	PMS	M ₃
Crosses (C)	(C-1)	CMS	M ₄
Parents vs. Crosses	1	P vs. CMS	M ₅
Error	(t-1) (r-1)	EMS	M ₆

Where,

R: Number of replications

T: Number of treatments

P: Parents

C: Crosses

E: Error

M: Mean sum of squares

ANOVA for line $\times$ tester analysis

Table: Sources of variation

Sources of variation	Degrees of freedom	Mean sum of squares	
		Observed	Expectations of mean squares
Lines	(l-1)	M ₁	$\sigma^2_e + r [\text{COV. F.S}] - 2\text{COV. H.S} + rt [\text{COV. H.S}]$
Testers	(t-1)	M ₂	$\sigma^2_e + r [\text{COV(FS)}] - 2\text{COV. H.S} + rt [\text{COV. H.S}]$
Line $\times$ tester	(l-1) (t-1)	M ₃	$\sigma^2_e + r [\text{COV. F.S}] - 2\text{COV. H.S}]$
Error	(r-1) (lt-1)	M ₄	σ^2_e

i. Estimation of covariance

Covariance of full sibs and covariance of half sibs were estimated by using the formula (Kempthorne, 1957) [13] given below:

$$\text{Covariance of half sibs (COV. H.S)} = \frac{\left(\frac{(M_1 - M) + (M_2 - M)}{13} \right)}{r(f+m)}$$

Covariance of full sibs (COV. F.S) =

$$\frac{(M_1 - M) + (M_2 - M) + (M_3 - M)r}{4} \div \frac{r(f+m)}{4} \text{ COV. H.S}$$

Estimation of variances

Using the covariances of half sibs and full sibs variance due to general combining ability (σ^2_{gca}) and variance due to specific combining ability (σ^2_{sca}) were estimated as

$$\text{COV. H.S} = \sigma^2_{gca}$$

$$\text{COV. F.S} - 2 \text{ COV. H.S} = \sigma^2_{sca}$$

From the variances of *gca* and *sca*, the gene action was calculated as follows.

$$\text{Additive genetic variance } (\sigma^2_a)$$

$$\text{Non additive genetic variance } (\sigma^2_d)$$

$$= 2\sigma^2_{gca} (F=1)$$

$$= \sigma^2_{sca} (F=1)$$

Estimation of combining ability effects

The *gca* and *sca* effects of the *ijk*th observation was arrived at using the mathematical model given below:

$$X_{ijk} = \mu + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + \hat{e}_{ijk}$$

where,

X_{ijk} = Value of *ijk*th observation

μ = Population mean

$\hat{g}_i$ = *gca* effect of *i*th line

$\hat{g}_j$ = *gca* effect of *j*th tester

$\hat{s}_{ij}$ = *sca* effect of *ij*th combination

$\hat{e}_{ijk}$ = Error associated with the observation X_{ijk}

i = Number of male parents

j = Number of female parents

k = Number of replications

$$\text{Mean } (\mu) = \frac{X_{\dots}}{mfr}$$

where,

X = Total of all hybrid combinations over all replications

r = Number of replications

f = Number of female parents

m = Number of male parents

Analysis of variance for combining ability was carried out using mean values across environments (Kempthorne, 1957) [13] to test the significance of differences among the genotypes

including crosses and parents (Snedecor and Cochran, 1967; Panse and Sukhatme, 1984) ^[23, 16]. The sum of squares for hybrids was further partitioned into variation due to lines, testers and line $\times$ tester interactions. The mean squares due to lines and testers were tested against the mean squares due to line $\times$ tester, and the latter were tested against the pooled error. The mean squares due to environment, line and environment $\times$ tester were tested against the mean squares due to environment $\times$ tester $\times$ line, and the latter was tested against the pooled error. Estimate of *gca* variances and *sca* variances were obtained (Singh and Chaudhary, 1987) ^[87].

Estimation of standard heterosis: Heterosis of F_1 over standard heterosis (SH) was calculated as per Turner (1953) ^[25] and Hayes *et al.* (1955) ^[10].

Standard heterosis

$$\text{Standard Heterosis (SH) \%} = \frac{(\bar{F}_1 - \bar{SC})}{\bar{SC}} \times 100$$

where,

$\bar{SC}$: Mean of standard check

Test of significance for standard heterosis

$$\text{Standard heterosis} = \frac{\bar{F}_1 - \bar{SC}}{\sqrt{\frac{Me}{t} \times 2}}$$

Where,

r: Number of replications M_e : Error variance

Significance of “t” is tested by referring to “t” table at the appropriate error degrees of freedom.

Genotype $\times$ Environment Interaction

The data obtained on all the characters over three environments was subjected to two-way analysis of variance using the method outlined by Sharma (2003) ^[21]. This was done for each character in order to find out the variation due to genotypes and environments and to reveal the existence of genotype $\times$ environment interaction, if any. Only after ascertaining that genotype $\times$ environment interaction was significant in the two-way analysis of variance, the data was further subjected to stability analysis. The stability analysis was done using the linear regression model suggested by Eberhart and Russell (1966) ^[7] and the model is presented below.

$$Y_{ij} = \mu_j + \beta_i I_j + \delta_{ij}$$

Where Y_{ij} is the mean grain yield of the i^{th} genotype in the j^{th} environment, μ_i is the mean of the i^{th} genotype, β_i the coefficient which measures the regression of the i^{th} genotype on different environments (linear response predictive), δ_{ij} is the deviation from regression of the genotype in the j^{th} environment, and I_j is the environmental index calculated as the mean of all genotype at the j^{th} environment less the grand mean over all environments.

Table: Analysis of variance for stability parameters as proposed by Eberhart and Russell (1966) ^[7]

Source	Degree of freedom	Sum of squares	Mean sum of squares
Total (Treatment combining)	ge-1	$\sum_i \sum_j Y_{ij}^2 - C.F.$	MS_1
Genotype Environments (Genotype $\times$ Environment)	(g-1) (e-1) (g-1) (e-1)	$1/e \sum_i Y_i^2 - C.F.$	
(Genotype $\times$ Environment) Environment linear	g (e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_i^2 / e \quad 1/g (\sum_i Y_{ij})^2 / \sum_j I_j^2$	
Environment (linear)	L		
Genotype $\times$ Environment (Linear)	g-1	$\sum_i [(\sum_j Y_{ij} I_j)^2 / \sum_j I_j] - \text{Env. (Linear) S.S.}$	MS_2
Pooled deviation	g(e-2)	$\sum_i \sum_j \delta_{ij}^2 I_j$	MS_3
Deviations due to genotypes...1	e-2	$[\sum_j Y_{ij}^2 (Y_i^2) / e] - (\sum_j Y_{ij}^2)^2 / \sum_j 2I_j = \sum_j \sigma^2 w$	$MS_3 - 1$
Genotypes ....g	e-2	$[\sum_j Y_{ij}^2 - (Y_i^2) / e] - 22 = \delta_g (\sum Y_{ij}) / \sum_j I_j$	$MS_3 - g$
Pooled error		$e(r-1) (g-1)$	
g = genotype		e = environment	r = replication

The phenotypic stability is based on regression analysis. The environment and genotype $\times$ environment interactions were partitioned into three components *viz.*, environment (linear), genotype $\times$ environment (linear) and deviation from regression (pooled deviation over the genotypes).

Estimation of stability parameters

Since the sum of I_j over all environments is zero, the yield of a variety in a given environment can be predicted as follows: $Y_{ij} = \mu_i + \beta_i I_j$. Where μ_i and β_i are estimates of μ_i and β_i , respectively. The mean squares due to deviations from regression (S_2 d) indicate the degree of reliance that can be placed upon linear regression. In fact, S^2 d reveals a non-linear response of varieties (non-predictive). When the deviations are significant, the genotype stability is specified by a joint consideration of both μ and β . The significance of

means squares was tested against the pooled error. The t-test based on the standard error of regression value was used to test the significant deviation of b from 1.0. To determine whether deviations from regression were significantly different from zero, the F-test was employed (*i.e.*, comparing the mean squares due to deviations from regression with pooled error mean squares). The estimate of deviations from regressions suggests the degree of reliance that should be put to linear regression in interpretation of the data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted significantly. When deviations are not significant, the conclusion may be drawn by the joint consideration of mean yield and regression values (Finlay and Wilkinson, 1963 and Eberhart and Russell, 1966) ^[8, 7] as given below.

Table: Type of Remarks

Regression	Stability	Mean yield	Remarks
b = 1	Average	High	Well adapted to all environments
b = 1	Average	Low	Poorly adapted to all environments

b > 1	Below average	High	Specifically adapted to favourable environments
b < 1	Above average	High	Specifically adapted to unfavourable environments

Regression values of unity are interpreted as average stability.

Results and Discussion

Pooled analysis of variance for heterosis in line $\times$ tester analysis of sweet sorghum for different characters is given in Table 2. It revealed considerable genetic variation among the parents and hybrids for all the characters except grain yield in case of hybrids over the three environments. Thus material studied was fairly diverse for the characters. The parents vs. hybrids component also exhibited significance for all the characters except for juice extraction per cent indicating presence of heterosis in F_1 hybrids.

Pooled analysis of variance for line $\times$ tester analysis in respect of twelve characters over three environments is presented in Table 3. It indicated significant mean sum of squares due to lines, testers and line $\times$ tester interaction for almost all the characters under study except brix per cent, total sugar index and juice extraction per cent in case of lines. This indicates that the variation in hybrids was largely influenced by the interaction between lines and testers. Greater diversity was found among the testers than the lines for traits of interest like brix per cent, fresh stalk yield, juice yield and ethanol yields as indicated by the larger mean sum of squares. This was an indicative of the larger contribution of testers to greater *gca* effects than that of lines for these characters as also noticed by Itai *et al.*, (2009), Kenga *et al.*, (2004), Mohammed and Mohamed (2009), Indhubala *et al.*, (2010), Vinay kumar *et al.* (2011), Umakanth *et al.*, (2012) and Bahadure *et al.*, (2015) [12, 14, 15, 11, 27, 26 3]. Further, pooled analysis of variance revealed significant variation for the environments for all the traits. The testers were important for improving brix per cent, total sugar index, total biomass, fresh stalk yield, juice yield, juice extraction per cent and ethanol yield (as seen by magnitude of tester mean sum of squares) while lines contributed more for days to 50 per cent flowering, days to maturity, plant height, total soluble solids and grain yield in sweet sorghum hybrid breeding programme. The significant line $\times$ tester mean squares for all the traits indicated the significant contribution of *sca* variance components and heterosis.

Estimates of general combining ability variances of parents were presented in Table 4. The lines had a higher *gca* variance as compared to testers for plant height, brix per cent, total soluble sugars and total biomass whereas the testers had a higher *gca* variance for days to 50 per cent flowering, days to maturity, fresh stalk yield, juice yield, juice extraction per cent, grain yield and ethanol yield. The *gca* variance due to lines and testers were same for total sugar index (sugar yield). With respect to *sca* variance the lines had a higher *sca* variance than the testers for all the traits (Table 5). Evaluation based on *sca* effects disclosed that the hybrid NSS 1007A $\times$ CSV 19SS was found to be superior for days to 50 per cent flowering, days to maturity, total soluble solids, total biomass, fresh stalk yield, juice yield, juice extraction per cent and ethanol yield followed by NSS 1016A $\times$ SSV 84 for total sugar index, total biomass, fresh stalk yield, juice yield and ethanol yield. The hybrids viz., NSS 8A $\times$ CSV 19SS, NSS 8A $\times$ RSSV 76, NSS 10A $\times$ CSV 19SS and NSS 10A $\times$ RSSV 120 were the next best hybrids. Hence these hybrids are highly suitable for heterosis breeding.

Pooled ANOVA for combining ability for twelve characters over three locations is presented in Table 6. The magnitude of *sca* variance was greater than their corresponding *gca* variance for the characters days to 50 per cent flowering, days

to maturity and total soluble solids and was highly significant for brix per cent and grain yield indicating the preponderance of non-additive gene action for those characters.

The selection of parents not only based on *sca* effects alone, but also consider mean and *gca* effects in identification of different sets of parents as promising ones (Itai *et al.*, (2009), Umakanth *et al.* (2012) and Bahadure *et al.* (2015) [12, 26, 3]. Hence, evaluating the parents using both these criteria would be more appropriate than using either one of them. Based on *per se* performance, significant positive standard heterosis and *sca* effects the hybrid, NSS 1007A $\times$ CSV 19SS for total soluble solids, total biomass, fresh stalk yield, juice yield, juice extraction percent and ethanol yield; NSS 8A $\times$ CSV 19SS for brix per cent, total biomass and fresh stalk yield and NSS 1016A $\times$ SSV 84 and NSS 8A $\times$ CSV 19SS for total biomass and fresh stalk yield were identified as promising for commercial exploitation (Table 7). It is also observed that the hybrids NSS 1007A $\times$ CSV 19SS for total soluble solids, juice yield and ethanol yield; NSS 10A $\times$ CSV 19SS for total sugar index, total biomass and fresh stalk yield; NSS 8A $\times$ CSV 19SS for brix percent; NSS 8A $\times$ RSSV 120 for juice extraction per cent and NSS 8A $\times$ SSV 84 for grain yield were involved either both or at least one high *gca* parent produced hybrids with high *sca* effects for the respective characters. However, low $\times$ low and average $\times$ low and average $\times$ average parental combinations also produced significant positive *sca* effects. Hence, it is evident that hybrids performance is independent of parent's performance. It was observed that almost all types of *sca* effects (significantly positive, significantly negative or non-significant) were obtained from all combinations of *gca* effects (high $\times$ high, high $\times$ low and high $\times$ average) for all most all characters studied. The hybrid NSS 1007A $\times$ CSV 19SS and NSS 1016A $\times$ SSV 84 were found to be good specific combiner for ethanol yield and its essential component characters such as total biomass, fresh stalk yield and juice yield indicating that these hybrids can be utilized for commercial exploitation. The hybrids involved one or both of high, low or average combiners for various traits. For instance, out of 30 hybrids, one hybrid displayed average $\times$ high and the other hybrid exhibited low $\times$ average combiners for ethanol yield. Majority of superior specific combinations, however, involved the parents with low $\times$ high combinations for most of the traits. Finally it can be concluded that the hybrids having at least one parent with high *gca* effect and the other with low or average *gca* is desirable to get high *sca* effect in their cross combinations.

Critical evaluation based on the *per se* performance, *sca* effects, and standard heterosis, it is concluded that for days to 50 per cent flowering five hybrids; for days to maturity seven hybrids; for plant height and brix per cent two hybrids; for total soluble solids and total sugar index three hybrids; seven for total biomass and fresh stalk yield hybrids; for juice yield and juice extraction per cent one hybrid; for grain yield ten hybrids and for ethanol yield one hybrid were promising with significant standard heterosis and *sca* effects in desirable direction for commercial exploitation (Table 7).

Analysis of variance for G $\times$ E interactions revealed that considerable variability was existed in the experimental material and environments (Table 8). The pooled analysis of variance for stability revealed that G $\times$ E interaction was

significant for TSS, TSI, total biomass, juice yield, grain yield and bioethanol yield. Partitioning of sum of squares revealed the significant variation due to environment (linear) for all the characters revealing the linear contribution of environmental effects and additive environment variance on these characters. The linear component of $G \times E$ interaction was highly significant for plant height, total biomass, total soluble solids, total sugar index, juice yield, grain yield and ethanol yield suggesting that the genotypes differed for their linear response to environments. The mean sum of squares for pooled deviation was significant for all the characters except for total sugar index and grain yield indicating the non-linear response and unpredictable nature of the genotypes by significantly differing for stability (Prabhakar and Patil (2002) [17]. Low mean and unit regression value and non-significant deviation were exhibited by NSS 1016A $\times$ M 11 for juice yield and ethanol yield; NSS 1016A $\times$ SSV 84 for total soluble solids and total sugar index and NSS 8A $\times$ SSV 84 for total biomass. Hence, these could be considered as average stable hybrids with poor adaptation to a range of environments. The hybrid NSS 8A $\times$ CSV 19SS for total soluble solids, total sugar index, juice yield and ethanol yield;

NSS 8A $\times$ SSV 84 for ethanol yield, juice yield and total biomass; NSS 8A $\times$ SSV 74 for total sugar index and total biomass; NSS 8A $\times$ SSV 76 for total soluble solids and total sugar index had high mean, b_i more than unity and non-significant deviation from regression indicating that these hybrids perform better under favourable environments. Under unfavorable environments like drought, salt and low temperature stress the hybrid NSS 8A $\times$ SSV 74 for ethanol yield; NSS 8A $\times$ M11 for total sugar index and NSS 10A $\times$ RSSV 120 for juice yield perform better with above average stability as these possessed high mean, b_i less than unity and non-significant deviation from regression (Table 9).

Based on this study, the hybrid NSS 1007A $\times$ CSV 19SS (Table 10) was stable with high *per se* performance, significant positive *sca* effects and standard heterosis for ethanol yield, total soluble solids, total biomass, and juice yield. Hence, this hybrid may be further tested in multilocation trials across India and can be recommended for commercial release. The knowledge and material generated in the present investigation could be utilized in future breeding programmes.

Table 2: Pooled analysis of variance for heterosis for different characters in sweet sorghum over three environments

Source of Variation	df	DF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
Replications	2	0.33	0.205962	1800.52	0.23	4.49***	0.24***	147.81***	79.72***	296073.7	38.77	648939.60***	16446.15
Genotypes	40	127.35***	135.7339***	20042.94***	9.29***	7.63***	0.33***	1634.11**	470.12***	52117332.00***	55.19**	7258071.00***	384043.40**
Parents	10	369.24***	383.2626***	40725.74***	9.87***	12.14***	0.50***	1860.55**	909.93***	89951704.00***	59.97**	1685735.00***	780883.10**
Hybrids	29	47.22***	52.51***	6600.09***	8.80***	4.69***	0.26***	1193.06**	224.06***	24761374.00***	53.91**	666421	189550.0***
Parents vs. Hybrids	1	32.13*	73.76***	203057.40***	17.63**	47.98***	0.59***	12160.10**	3207.68***	467096288.00***	44.74	80203256.00**	205594.00**
Error	240	5.37	6.49	601.29	1.63	0.59	0.02	20.038	10.16	2412365.00**	14.98	85741.21***	26735.69

*Significant at 5% level; ** Significant at 1% level and *** Significant at 0.1% levels

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent; GY: Grain yield.

Table 3: Pooled analysis of variance for line $\times$ tester analysis for different traits of sweet sorghum over three environments

Source of variation	df	Mean sum of squares											
		DF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
Environments	2	3569.37**	13822.62**	376623.10**	25.82**	148.06**	9.02**	96133.80**	16129.10**	2730377561.55*	18744.29**	5898487.00***	19117944.00***
Rep $\times$ Environments	4	30.94***	32.47***	1578.79*	7.76**	10.54***	0.27**	49.46*	26.37*	8644625.00**	50.93**	100468.90	100225.40*
Hybrids	29	47.22***	52.51***	6600.09***	8.80***	4.69***	0.26**	1193.06***	224.06***	24761374.00***	53.91***	666421.00	189550.0**
Lines	4	200.05***	181.50***	17498.91***	3.42	9.59***	0.03	232.30***	101.87***	15141757.00***	7.74	1499532.00***	104440.90**
Testers	5	33.39***	23.31**	4125.51***	9.04***	3.88***	0.29**	376.69***	265.79***	34843044.00***	85.51***	491640.20***	122088.90**
Line $\times$ Tester effect	20	31.28***	36.87***	3791.73***	6.57***	4.76***	0.21**	1247.25***	180.16***	11310427.00***	32.85**	6973906.00***	108116.50**
Lines $\times$ Environments	8	40.90***	53.76***	919.14	1.82	13.44***	0.01	80.22***	31.90**	9683616.00***	103.49***	34340.36	53777.06*
Testers $\times$ Environments	10	6.99	16.41**	1930.94**	1.22	1.99***	0.18**	214.00***	115.13***	27968416.00***	105.64***	14404.59	173483.50**
L $\times$ T $\times$ Environments effect	40	19.35***	20.87***	1356.76***	1.74	1.21***	0.16**	1169.00***	166.46***	17850344.00***	51.60***	209080.10***	113809.80**
Error	240	5.37	6.49	601.29	1.635	0.59	0.02	20.03	10.163	2412365.00	14.98	85741.21	26735.69

Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent; GY: Grain yield; EY: Ethanol yield.

Table 4: Pooled estimates of general combining ability effects of parents for 12 characters in sweet sorghum

S. No.	Parents	DFF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
Females													
1.	NSS 8B	0.196	0.174	-5.485	0.519***	0.058	0.184***	0.236	1.000*	327.973	0.720	-103.226*	45.493*
2.	NSS 10B	0.678*	0.822**	22.681***	-0.633***	-0.233*	-0.079***	-4.982***	-1.634***	-524.24	-0.266	289.367***	-66.563**
3.	NSS 1007B	0.696*	0.896**	-25.689***	0.548***	0.525***	-0.075***	-3.541***	-2.073***	-683.401**	-0.353	-69.856	-28.378
4.	NSS 1016B	-1.304***	-1.326***	-6.911*	-0.735***	-0.514***	-0.006	-0.657	-1.052*	-316.212	1.051*	378.607***	-52.396*
5.	RS 1220B	-0.267	-0.567	15.404***	0.302*	0.163	-0.024	8.944***	3.759***	1195.880***	-1.152*	-494.893***	101.844***
	S. Em ±	0.299	0.314	3.489	0.149	0.100	0.020	0.651	0.452	224.255	0.526	42.329	20.255
	CD at 5 %	0.590	0.621	6.887	0.294	0.198	0.041	1.285	0.892	442.611	1.038	83.544	39.977
	CD at 1 %	0.779	0.819	9.088	0.388	0.262	0.054	1.695	1.177	584.045	1.370	110.240	52.751
Males													
1.	SSV 84	2.096***	1.856***	-2.919	0.788***	0.318**	-0.048*	-1.616*	-0.939	-608.487*	-0.496	319.881***	-21.470
2.	M 11	0.763*	0.811*	-10.030**	-0.312	-0.111	-0.059*	-4.329***	-1.490**	-820.805**	-0.297	373.148***	-82.440***
3.	CSV 19SS	-0.748*	-0.389	21.037***	0.021	0.089	0.117***	5.595***	4.809***	1945.773***	0.148	-244.163***	155.640***
4.	SSV 74	0.696*	0.767*	1.726	-0.230	-0.127	0.003	3.807***	1.307**	999.572**	1.945***	168.592***	72.400**
5.	RSSV 76	-0.126	-0.167	-14.341***	-0.026	-0.133	-0.024	-1.673*	-2.777***	-1498.520***	-3.036***	-96.674*	-112.890***
6.	RSSV 120	-2.681***	-2.878***	4.53	-0.241	-0.036	0.011	-1.784*	-0.910	-17.538	1.736**	-520.785***	-11.240
	S. Em ±	0.328	0.344	3.822	0.163	0.110	0.022	0.713	0.495	245.659	0.576	46.369	22.188
	CD at 5 %	0.647	0.680	7.545	0.322	0.217	0.044	1.407	0.977	484.856	1.137	91.518	43.792

*Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent, GY: Grain yield; EY: Ethanol yield.

Table 5: Pooled estimates of specific combining ability effects of F₁ hybrids for 12 characters in sweet sorghum

S. No.	F ₁ Hybrid	DFF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
1	NSS 8A × SSV 84	1.293	1.404	-5.248	-0.601	-0.796**	-0.003	-0.009	0.823	576.842	-0.015	935.137***	13.485
2	NSS 8A × M 11	0.293	0.004	-3.804	-0.49	-0.216	0.018	-13.358***	-2.837*	-143.195	0.4	-10.129	-27.426
3	NSS 8A × CSV 19SS	-0.641	-0.352	-7.426	1.144**	0.541*	-0.006	3.366*	4.507***	-1.961	-2.924*	-413.263***	53.93
4	NSS 8A × SSV 74	0.915	1.159	3.663	-0.239	-0.426	0.137**	5.956***	-0.069	467.082	-0.078	-280.130**	20.396
5	NSS 8A × RSSV 76	-1.707*	-1.685*	14.063	0.59	0.768**	0.026	6.821***	1.871	-189.428	0.194	96.47037	-3.537
6	NSS 8A × RSSV 120	-0.152	-0.53	-1.248	-0.405	0.13	-0.172***	-2.776	-4.295***	-709.339	2.423	-328.085**	-56.848
7	NSS 10A × SSV 84	-1.411	-1.578*	21.363*	0.384	0.246	-0.066	-1.662	-0.022	361.322	-0.444	6.544	52.874
8	NSS 10A × M 11	-0.3	0.133	13.474	1.184**	0.814**	-0.128*	-2.156	0.774	128.906	-0.662	1579.722***	66.296
9	NSS 10A × CSV 19SS	-0.9	-1.0	6.852	-0.927*	-0.624*	0.188***	19.280***	4.396***	1028.684	-0.974	304.811**	7.43
10	NSS 10A × SSV 74	-2.122**	2.711***	2.941	-0.187	-0.570*	0.033	5.290**	-1.28	-179.104	1.125	668.944***	-24.77
11	NSS 10A × RSSV 76	1.700*	1.889*	4.119	-1.224***	-1.176***	-0.264***	-15.572***	-6.273***	1439.520* *	1.815	1549.340***	-159.259**
12	NSS 10A × RSSV 120	3.033***	3.267***	48.748* **	0.769*	1.310***	0.236***	-5.180**	2.405*	99.706	-0.86	1010.680***	57.43
13	NSS 1007A × SSV 84	0.904	0.904	20.156*	-0.375	-0.371	-0.154**	-9.336***	-4.572***	1412.360*	2.138	-633.344***	-148.756**
14	NSS 1007A × M 11	1.015	0.726	-8.711	-0.397	-0.445	0.084	12.995***	-0.965	-707.41	-0.374	-124.056	-90.556
15	NSS 1007A × CSV 19SS	-1.585*	-2.185**	15.222	0.481	0.756**	0.095	8.256***	4.346***	1976.323* **	2.972*	-914.856***	210.689***

*Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent, GY: Grain yield; EY: Ethanol yield.

Table 5: Cont....

S. No.	F ₁ Hybrid	DFF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
16	NSS 1007A × SSV 74	2.193**	2.659***	-5.578	0.021	0.277	-0.035	1.539	-0.541	-1058.120	-1.619	11.166	-70.844
17	NSS 1007A × RSSV 76	1.237	1.259	-21.733*	0.250	0.129	0.069	-8.799***	0.121	741.667	0.897	730.544***	69.667
18	NSS 1007A × RSSV 120	-	-	40.956***	0.021	-0.346	-0.060	-4.655**	1.61	459.901	-	930.544***	29.800
19	NSS 1016A × SSV 84	-0.763	-0.652	12.289	-0.136	-0.044	0.216***	19.155***	7.963***	1801.117**	-1.365	1037.140***	150.819**
20	NSS 1016A × M 11	1.126	1.393	15.844	0.397	0.397	-0.010	-3.258*	0.926	452.678	1.259	-58.629	63.463
21	NSS 1016A × CSV 19SS	2.193**	2.259**	-9.444	0.731*	0.096	-0.030	-17.157***	-4.297***	1469.330**	-0.759	185.459	-85.848
22	NSS 1016A × SSV 74	-0.696	-0.452	-23.800**	0.426	0.068	-0.063	-4.186**	-2.517*	-142.554	1.032	-186.963	-9.826
23	NSS 1016A × RSSV 76	-0.652	-0.852	6.933	-0.045	0.246	0.050	5.666***	0.223	-59.109	-0.625	832.081***	-3.426
24	NSS 1016A × RSSV 120	-1.207	-1.696*	-1.822	-	-0.763**	-0.163**	-0.221	-2.299*	-582.799	0.458	265.192*	-115.182*
25	RS 1220A × SSV 84	-0.022	-0.078	-8.248	0.727*	0.965***	0.007	-8.148***	-4.192***	-1326.920*	-0.314	728.803***	-68.422
26	RS 1220A × M 11	-2.133**	-2.256**	-16.804	-0.695	-0.549*	0.035	5.778***	2.103	269.019	-0.623	-	-11.778

												1386.910***	
27	RS 1220A × CSV 19SS	0.933	1.278	-5.204	-1.429***	-0.769**	-0.247***	-13.745***	-8.952***	-1533.710**	1.684	837.8481***	-186.200***
28	RS 1220A × SSV 74	-0.289	-0.656	22.774**	-0.022	0.652**	-0.072	-8.600***	4.406***	912.697	-0.460	-213.019*	85.044
29	RS 1220A × RSSV 76	-0.578	-0.611	-3.381	0.429	0.033	0.118*	11.883***	4.057***	946.386	2.281	-109.752	96.556
30	RS 1220A × RSSV 120	2.089**	2.322**	10.863	0.989**	-0.331	0.159**	12.832***	2.579*	732.530	1.994	143.025	84.800
	S.Em ±	0.733	0.771	8.548	0.365	0.246	0.050	1.595	1.107	549.312	1.288	103.684	49.614
	CD at 5 %	1.447	1.521	16.871	0.721	0.486	0.100	3.148	2.186	1084.171	2.543	204.641	97.923

*Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent, GY: Grain yield; EY: Ethanol yield.

Table 6: Pooled ANOVA for combining ability for twelve characters in sweet sorghum over three locations

Source of variation	DFF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
σ^2 Environments	21.09***	82.21***	2537.20***	0.05	0.16	0.07***	725.56***	123.59***	22001387.07***	136.93***	67834.51***	138991.08***
σ^2 gca	0.26	-0.18	183.91*	0.16	-0.06	0.00	8.79	3.74	247811.88	0.07	-17748.76	1774.48
σ^2 sca	1.33	1.78	270.55**	0.53***	0.39	0.00	8.69	1.52	-726657.45	-2.08	751647.2600***	-632.59
σ^2 gca/ σ^2 sca	0.20	-0.10	0.68	0.299	-0.14	0.75	1.01	2.455	-0.34	-0.031	-0.024	-2.81
σ^2 gca × Environments	2.05	3.37	40.72	0.002	0.18	0.00	-33.79	-2.69	1746812.76*	3.5634*	-3561.436	10004.93*
σ^2 sca × Environments	4.84	5.18	233.04***	0.18	0.22	0.04***	382.03***	51.80***	5044882.68***	12.22***	37441.70***	30551.75***
σ^2 a (F = 1)	0.52	-0.37	367.83	0.32	-0.12	0.01	17.57	7.47	495623.76	0.13	-35497.51	3548.96
σ^2 d (F = 1)	1.33	1.78	270.55	0.54	0.39	0.00	8.69	1.52	-726657.45	-2.08	751647.26	-632.59
σ^2 a/ σ^2 d	0.40	-0.21	1.36	0.60	-0.30	1.53	2.02	4.91	-0.68	-0.06	-0.05	-5.61
h^2_{ns} (%)	4.63	-2.64	35.85	27.34	-12.53	11.78	5.12	13.19	5.76	0.69	-4.69	6.34
GA at 5 %	0.20	-0.10	0.68	0.30	-0.15	0.77	1.01	2.46	-0.34	-0.03	-0.02	-2.81

* Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent; GY: Grain yield; EY: Ethanol yield.

Table 7: Mean, standard heterosis, sca effects and gca status of the parents of promising hybrids in sweet sorghum

Hybrid	Mean	Standard heterosis				
		CSH 22SS	PAC 52093	NSSV 13	sca effects	gca status of parents
Days to 50 per cent flowering						
NSS 1007 × RSSV 120	64	-19.21**	-11.32**	-12.67**	-3.763***	L × H
RS 1220A × M 11	68	-13.98**	-5.58**	-7.02**	-2.133**	A × L
NSS 8A × RSSV 76	68	-13.98**	-5.58**	-7.02**	-1.707*	A × A
NSS 1007A × CSV 19SS	68	-13.98**	-5.58**	-7.02**	-1.585*	L × H
NSS 10A × SSV 74	69	-12.85**	-4.34**	-5.80**	-2.122**	L × L
Days to maturity						
NSS 1007A × RSSV 120	102	-12.40**	-7.18**	-7.65**	-3.363***	L × H
NSS 10A × SSV 74	106	-8.78**	-3.34**	-3.82**	-2.711***	L × L
RS 1220A × M 11	105	-9.54**	-4.15**	-4.63**	-2.256**	A × L
NSS 1007A × CSV 19SS	106	-9.26**	-3.84**	-4.33**	-2.185**	L × L
NSS 1016A × RSSV 120	101	-12.88**	-7.68**	-8.15**	-1.696*	H × H
NSS 8A × RSSV 76	106	-9.26**	-3.84**	-4.33**	-1.685*	A × A
NSS 10A × SSV 84	108	-6.87**	-1.31	-1.81	-1.578*	L × L
Plant height (cm)						
NSS 10A × SSV 84	349	5.02	13.24**	9.19*	21.363*	H × A
RS 1220A × SSV 74	347	4.65	12.85**	8.80*	22.774**	H × A
NSS 1007A × RSSV 120	327	-1.41	6.32	2.51	40.956***	L × A
Brix per cent						
RS 1220A × SSV 84	19.07	9.72**	5.08	-0.92	0.727*	H × H
NSS 1016A × CSV 19SS	17.27	-0.64	-4.84	-10.28**	0.731*	L × A
Total soluble sugars (%)						
NSS 8A × CSV 19SS	15.39	4.21	3.28	-7.20**	0.541*	A × A
RS 1220A × SSV 74	15.39	4.21	3.27	-7.21**	0.652**	A × A
NSS 1007A × CSV 19SS	16.07	8.83**	7.86**	-3.09	0.756**	H × A
NSS 8A × RSSV 76	15.39	4.24	3.31	-7.17	0.768**	A × A
NSS 10A × M 11	15.17	2.73	1.81	-8.52**	0.814**	L × A
RS 1220A × SSV 84	16.14	9.35**	8.36**	-2.63	0.965***	A × H
NSS 10A × RSSV 120	15.74	6.61**	5.65*	-5.07*	1.310***	L × A

* Significance at 5% level; ** Significance at 1% level *** Significance at 0.1% level

L: low, H: high and A: average

Table 7: Cont....

Hybrid	Mean	Standard heterosis				
		CSH 22SS	PAC 52093	NSSV 13	sca effects	gca status of parents

Total sugar index (t ha ⁻¹)						
RS 1220A × RSSV 76	1.05	-5.21	4.42	-24.98**	0.118*	A × A
NSS 8A × SSV 74	1.21	17.74**	29.69**	-6.82	0.137**	H × A
RS 1220A × RSSV 120	1.13	12.03	-19.51**	-11.97*	0.159**	A × A
NSS 10A × CSV 19SS	1.21	8.92	19.98**	-13.80**	0.188***	L × H
NSS 1016A × SSV 84	1.14	3.11	13.58	-18.40**	0.216***	L × L
NSS 10A × RSSV 120	1.15	3.61	14.13*	-18.00**	0.236***	L × A
Total biomass (t ha ⁻¹)						
NSS 8A × CSV 19SS	72	-11.26**	12.19**	-2.1	3.366*	A × H
NSS 10A × SSV 74	67	-17.52**	4.27	-9.00**	5.290**	L × H
NSS 1016A × RSSV 76	66	-18.48**	3.06	-10.06**	5.666***	A × L
RS 1220A × M 11	73	-9.78**	14.05**	-0.47	5.778***	H × L
NSS 8A × SSV 74	73	-10.27**	13.44**	-1	5.956***	A × H
NSS 8A × RSSV 76	68	-15.96**	6.25	-7.28*	6.821***	A × L
NSS 1007A × CSV 19SS	73	-9.88**	13.92**	-0.58	8.256***	L × H
RS 1220A × RSSV 76	82	1.02	27.70**	11.44**	11.883***	H × L
RS 1220A × RSSV 120	83	1.02	27.70**	11.44**	12.832***	H × A
NSS 1007A × M 11	68	2.05	29.01**	12.58**	12.995***	L × L
NSS 1016A × SSV 84	80	-1.78	24.16**	8.35**	19.155***	A × L
NSS 10A × CSV 19SS	83	1.93	28.85**	12.45**	19.280***	L × H
Fresh stalk yield (t ha ⁻¹)						
NSS 10A × RSSV 120	43	-10.81**	5.8	-3.69	2.405*	L × A
RS 1220A × RSSV 120	49	0.69	19.43**	8.72*	2.579*	H × A
RS 1220A × RSSV 76	48	-0.11	18.48**	7.85*	4.057***	H × L
NSS 1007A × CSV 19SS	50	4.11	23.48**	12.41**	4.346***	L × H
NSS 10A × CSV 19SS	51	5.12	24.68**	13.50**	4.396***	L × H
RS 1220A × SSV 74	53	9.04**	29.33**	17.74**	4.406***	H × H
NSS 8A × CSV 19SS	54	10.78**	31.40**	19.62**	4.507***	H × H
NSS 1016A × SSV 84	49	1.81	20.76**	9.93**	7.963***	L × A

* Significance at 5% level; ** Significance at 1% level *** Significance at 0.1% level

L: low, H: high and A: average

Table 7: Conti.....

Hybrid	Mean	Standard heterosis				
		CSH 22SS	PAC 52093	NSSV 13	sca effects	gca status of parents
Juice yield (l ha ⁻¹)						
NSS 1016A × SSV 84	11076	-11.87	-0.54	-4.78	1801.117**	A × L
NSS 1007A × CSV 19SS	13438	6.92	20.67**	15.53*	1976.323***	L × H
Juice extraction per cent						
NSS 1007A × CSV 19SS	39.99	12.10*	-8.53*	-2.47	2.972*	A × A
Grain yield (t ha ⁻¹)						
NSS 8A × SSV 84	4	163.44**	95.95**	424.30**	935.137***	L × H
NSS 10A × M 11	5	242.85**	155.01**	582.33**	1579.722***	H × H
NSS 10A × CSV 19SS	3	105.06**	52.52**	308.10**	304.811**	H × L
NSS 10A × SSV 74	4	161.63**	94.60**	420.69**	668.944***	H × H
NSS 1007A × RSSV 76	3	120.64**	64.11**	339.11**	730.544***	A × L
NSS 1007A × RSSV 120	1	104.32**	51.97**	306.63**	930.544***	A × L
NSS 1016A × RSSV 76	4	160.69**	93.90**	418.82**	832.081***	H × L
NSS 1016A × RSSV 120	3	88.53**	40.23**	275.20**	265.192*	H × L
RS 1220A × SSV 84	3	119.90**	63.56**	337.63**	728.803***	L × H
RS 1220A × CSV 19SS	3	86.76**	38.91**	271.69**	837.848***	L × L
Ethanol yield (l ha ⁻¹)						
NSS 1007A × CSV 19SS	1150	15.26*	23.55**	10.94	210.689***	A × H
NSS 1016A × SSV 84	889	-10.91	-4.5	-14.25*	150.819***	L × A

*Significance at 5% level; ** Significance at 1% level *** Significance at 0.1% level

L: low, H: high and A: average

Table 8: Pooled analysis of variance for stability in sweet sorghum hybrids

Source of variation	df	MSS											
		DFF	DM	PH (cm)	Brix (%)	TSS (%)	TSI (t ha ⁻¹)	TB (t ha ⁻¹)	FSY (t ha ⁻¹)	JY (l ha ⁻¹)	JE (%)	GY (t ha ⁻¹)	EY (l ha ⁻¹)
Genotypes (G)	43	46.12***	48.14***	6371.14***	3.26***	2.68***	0.12**	552.97***	149.73***	17230730.00***	21.35	2448889.75**	129059.91***
Environments (E)	2	1247.92**	4810.87**	134750.55**	7.72**	46.63**	3.63**	36792.80**	5929.32***	1033019584.00**	6874.78***	1863184.38**	7206927.00***
Genotype × Environments (G × E)	86	8.71	11.51	662.55	0.95	1.97***	0.08**	322.62***	58.68	11402291.0***	37.48	69067.23***	70012.79**
Total	13	39.91	96.81	4583.51	1.81	2.88	0.14	955.03	178.2	28912654	136.57	877621.5	198355.19

Env. + (Genotype × Environmen t)	88	36.87***	120.59***	3710.01***	1.11	2.98***	0.16**	1151.49***	192.11***	34620868.00***	192.87***	109842.63***	232215.39***
Environmen ts (Lin.)	1	2495.85**	9621.73**	269501.09**	15.43**	93.25**	7.26**	73585.59**	11858.65**	2066039168.00**	13749.57**	3726368.75**	14413854.00**
Geno. × Env. (Lin.)	43	9.62	13.71	891.00**	0.85	3.60***	0.15**	561.27***	71.56	18172024.00***	39.74	138018.52***	104933.39***
Pooled Deviation	44	7.62***	9.10***	424.23***	1.04***	0.33**	0	82.06***	44.76***	4527272.50***	34.42***	113.31	34294.63***
Pooled Error	258	1.73	2.13	199.24	0.52	0.19	0.01	6.35	3.25	791732.75	4.75	27471.97	8779.36

*Significance at 5% level; ** Significance at 1% level and *** Significance at 0.1% level

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent, GY: Grain yield; EY: Ethanol yield.

Table 9: Stability parameters for total soluble solids and total sugar index over three locations in 44 genotypes of sweet sorghum

S. No.	Hybrids	Total soluble solids (%)			Total sugar index			Total Biomass (t ha ⁻¹)			Juice Yield (l ha ⁻¹)		
		μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di
1	NSS 8A × SSV 84	14.28	2.07	-0.02	1.11	1.29*	-0.01	61	0.92	-1.16	10496	1.01	-737971
2	NSS 8A × M 11	14.43	1.26	-0.16	1.12	0.55*	-0.01	45	0.23	25.06*	9563	0.53	-365441
3	NSS 8A × CSV 19SS	15.39	1.58	-0.2	1.28	3.08*	-0.01	72	1.48	118.69***	12471	1.24	12788473
4	NSS 8A × SSV 74	14.2	1.05	-0.02	1.31	2.04*	-0.01	73	1.52*	-4.97	11994	0.91	9590299
5	NSS 8A × RSSV 76	15.39	1.96	-0.2	1.17	1.41*	-0.01	68	1.53*	135.53***	8839	0.25	911031.9
6	NSS 8A × RSSV 120	14.85	0.73	-0.18	1	1.03*	-0.01	58	0.79	2.62	9800	1.02	-830356
7	NSS 10A × SSV 84	15.03	0.03	0.89*	0.79	0.34*	-0.01	55	0.47	192.76***	9428	1.39	2757318
8	NSS 10A × M 11	15.17	-0.20*	-0.26	0.72	-0.31*	-0.01	51	0.27	263.97***	8983	1.54	13935478
9	NSS 10A × CSV 19SS	13.93	-0.81	1.46*	1.21	1.66*	-0.01	83	2.01	167.69***	12649	1.33	2268273
10	NSS 10A × SSV 74	13.77	0.72	-0.09	0.94	1.24*	-0.01	67	1.28	11.94	10495	1.16	-470441
11	NSS 10A × RSSV 76	13.16	0.65	-0.18	0.61	-0.52*	-0.01	41	0.15	34.88*	6737	0.71	10297054
12	NSS 10A × RSSV 120	15.74	-0.47	-0.15	1.15	2.31*	-0.01	51	0.58	45.15**	9757	0.52	14566051
13	NSS 1007A × SSV 84	15.17	0.65	0.36	0.71	0.03*	-0.01	48	0.56	-6.36	7495	0.86	4116344
14	NSS 1007A × M 11	14.67	0.36	-0.25	0.93	1.00*	-0.01	68	1.74	321.02***	7988	0.4	504458.2
15	NSS 1007A × CSV 19SS	16.07	0.98	-0.24	1.12	1.32*	-0.01	73	1	-2.71	13438	0.98	-3714299
16	NSS 1007A × SSV 74	15.37	0.54	-0.16	0.88	1.66*	-0.01	65	1.37	45.80**	9457	1.11	726692.8

*Significance at 5% level; ** Significance at 1% level; *** Significance at 0.1% level

Table 9: Conti....

S. No.	Hybrids	Total soluble solids (%)			Total sugar index			Total Biomass (t ha ⁻¹)			Juice Yield (l ha ⁻¹)		
		μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di
17	NSS 1007A × RSSV 76	15.22	1.34	-0.14	0.95	1.32*	-0.01	49	0.56	16.09	8759	0.86	-72870.2
18	NSS 1007A × RSSV 120	14.84	-0.41	0.15	0.86	-0.46*	-0.01	53	0.48	184.05***	9958	1.51	14921501
19	NSS 1016A × SSV 84	14.46	0.92	-0.13	1.14	1.87*	-0.01	80	1.99	243.08***	11076	1.01	5105686
20	NSS 1016A × M 11	14.47	0.41	-0.24	0.91	1.45*	-0.01	55	0.86	-6.02	9515	1.01	1169458
21	NSS 1016A × CSV 19SS	14.37	0.78	-0.09	1.06	1.38*	-0.01	51	0.55	28.50*	10359	1.05	1379558
22	NSS 1016A × SSV 74	14.13	0.71	-0.25	0.92	1.50*	-0.01	62	1.21	26.30*	10740	1.34	-526710
23	NSS 1016A × RSSV 76	14.3	0.51	0.57	1	1.01*	-0.01	66	1.53*	127.06***	8325	0.34	3075356
24	NSS 1016A × RSSV 120	13.39	-0.05	1.32	0.82	0.74*	-0.01	60	1.03	-2.4	9283	0.95	-298052
25	RS 1220A × SSV 84	16.14	-0.01	-0.25	0.92	0.30*	-0.01	62	0.91	73.14***	9460	1.37	3069097
26	RS 1220A × M 11	14.2	-0.38	-0.24	0.93	1.01*	-0.01	73	1.5	6.37	10843	1.43*	-834018
27	RS 1220A × CSV 19SS	14.18	0.2	0.1	0.83	0.17*	-0.01	64	0.85	218.15***	11807	2.05	16933710
28	RS 1220A × SSV 74	15.39	-0.11	0.37	0.89	1.74*	-0.01	67	0.84	699.83***	13307	2.48	971849.3
29	RS 1220A × RSSV 76	14.76	0.53	1.2	1.05	1.51*	-0.01	82	2.01*	14.05	10843	1.25	2225161
30	RS 1220A × RSSV 120	14.49	0.52	-0.11	1.13	1.78*	-0.01	83	2.07*	20.03*	12110	1.59	2649407
31	NSS 8B	13.13	2.23	-0.19	0.72	-0.68*	-0.01	35	0.21	10.74	4367	-0.27	2134657
32	NSS 10B	13.68	1.08	-0.15	0.7	-0.20*	-0.01	42	0.35*	-3.88	5869	0.2	1986131

*Significance at 5% level; ** Significance at 1% level; *** Significance at 0.1% level

Table 9: Conti....

S. No.	Hybrids	Total soluble solids (%)			Total sugar index			Total Biomass (t ha ⁻¹)			Juice Yield (l ha ⁻¹)		
		μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di	μ Mean	βi	σ ² di
33	NSS 1007B	11.84	6.24	-0.17	0.63	-0.44*	-0.01	29	-0.09	-0.69	3583	-0.36	1018766
34	NSS 1016B	12.1	4.22	-0.06	0.62	-0.67*	-0.01	34	0.16	5.55	3787	-0.2	2220120
35	RS 1220B	14.28	2.31	0.17	0.76	-0.44*	-0.01	40	0.23*	-1.57	6501	0.5	6593086
36	SSV 84	15.18	1.82	0.37	1.18	1.46*	-0.01	64	1.08	-4.54	10704	1.1	-689527
37	M 11	13.95	2.19	-0.21	0.92	-0.27*	-0.01	50	0.62	-0.99	6667	0.08	1488720
38	CSV 19SS	15.52	1.34	-0.24	1.07	1.44*	-0.01	68	1.26*	-6.83	11787	1.64	-518571
39	SSV 74	14.84	1.47	-0.16	0.78	1.11*	-0.01	57	0.78	39.15*	9443	1.33	32762.55

40	RSSV 76	14.16	1.68	-0.21	1.13	1.60*	-0.01	63	1.12	3.14	9542	0.37	2959407
41	RSSV 120	14.04	3.37	-0.18	1.28	2.30*	-0.01	65	1.23	109.19***	12011	1.05	3521693
42	CSH 22SS (Check)	14.76	-0.41	0.01	1.11	1.26*	-0.01	81	1.63*	-5.78	12568	1.64*	-778648
43	PAC 52093 (Check)	14.9	0.62	0.62	1.01	1.05*	-0.01	64	1.05	70.59***	11136	1.52*	-774933
44	NSSV 13 (Check)	16.58	0.09	0.14	1.4	3.02*	-0.01	74	1.68*	97.16***	11632	0.98	19767482
	Mean	14.54	1		0.97	1		60	1		9672	1	
	S.Em±	0.4			0			6.4					
	S.E b _i	0.39			0			0.22			0.3		

*Significance at 5% level; ** Significance at 1% level; *** Significance at 0.1% level

Table 9: Conti.....

S. No.	Hybrids	Grain yield (t ha ⁻¹)			Bioethanol yield (l ha ⁻¹)		
		μ Mean	β _i	σ ² di	μ Mean	β _i	σ ² di
1	NSS 8A × SSV 84	4	2.21*	-29024.19	849	0.92	-4769.46
2	NSS 8A × M 11	3	0.34*	-29034.92	747	0.55*	-9259.5
3	NSS 8A × CSV 19SS	2	0.39*	-29035.03	1067	1.33	106726.4
4	NSS 8A × SSV 74	2	0.79*	-29034.36	950	0.89	43650.88
5	NSS 8A × RSSV 76	2	0.76*	-29033.56	741	0.36	31500.79
6	NSS 8A × RSSV 120	2	0.38*	-29034.7	789	0.97	-9044.12
7	NSS 10A × SSV 84	3	2.73*	-29018.36	776	1.42	36748.13
8	NSS 10A × M 11	5	5.27*	-28970.37	729	1.44	108989.8
9	NSS 10A × CSV 19SS	3	1.45*	-29031.01	908	0.99	10954.02
10	NSS 10A × SSV 74	4	3.10*	-29016.04	793	1.08	-8519.56
11	NSS 10A × RSSV 76	1	-0.17*	-29035.19	473	0.59	42735.75
12	NSS 10A × RSSV 120	1	-0.30*	-29034.66	791	0.55	108287.1
13	NSS 1007A × SSV 84	2	0.97	-29032.17	613	0.93	26842.15
14	NSS 1007A × M 11	3	1.16*	-29031.64	610	0.43	6638.04
15	NSS 1007A × CSV 19SS	1	0.19*	-29035.11	1150	1.01	-16628.4
16	NSS 1007A × SSV 74	4	1.98*	-29025.54	785	1.16	51.01
17	NSS 1007A × RSSV 76	3	1.32*	-29030.08	740	0.83	-1429.26
18	NSS 1007A × RSSV 120	2	2.68*	-29017.93	802	1.42	131389.1
19	NSS 1016A × SSV 84	2	1.46*	-29030.96	889	1.01	20633.13
20	NSS 1016A × M 11	2	1.91*	-29026.94	740	0.95	1348.56
21	NSS 1016A × CSV 19SS	2	1.07	-29032.18	829	0.99	-2415.96
22	NSS 1016A × SSV 74	3	2.07*	-29024.69	822	1.23	-7065.32

*Significance at 5% level; ** Significance at 1% level; *** Significance at 0.1% level

Table 9: Conti...

S. No.	Hybrids	Grain yield (t ha ⁻¹)			Bioethanol yield (l ha ⁻¹)		
		μ Mean	β _i	σ ² di	μ Mean	β _i	σ ² di
23	NSS 1016A × RSSV 76	4	3.28*	-29013.07	643	0.38	7286.19
24	NSS 1016A × RSSV 120	3	1.83*	-29027.89	633	0.74*	-9260.41
25	RS 1220A × SSV 84	3	2.65*	-29019.37	824	1.36	32725.36
26	RS 1220A × M 11	1	-0.27*	-29035.19	819	1.23	-6920.39
27	RS 1220A × CSV 19SS	3	2.24*	-29023.97	883	1.77	93604.53
28	RS 1220A × SSV 74	2	1.32*	-29030.05	1071	2.29	3041.53
29	RS 1220A × RSSV 76	2	1.11*	-29032.83	897	1.27	-6631.53
30	RS 1220A × RSSV 120	2	0.620*	-29033.75	987	1.46	-4591.39
31	NSS 8B	2	1.12*	-29032.35	320	-0.22	-488.65
32	NSS 10B	2	0.10*	-29035.17	418	0.23	-3287.03
33	NSS 1007B	2	0.30*	-29034.84	257	-0.25*	-8469.28
34	NSS 1016B	2	-0.16*	-29035.13	273	-0.14	-789.42
35	RS 1220B	1	-0.10*	-29035.17	513	0.47	22846.43
36	SSV 84	1	-0.68*	-29034.39	909	1.04	-2814.36
37	M 11	1	-0.48	-24307.63	861	1.57	114208.5
38	CSV 19SS	4	-0.36*	-29035.02	1017	1.69	-6083.89
39	SSV 74	3	-0.09*	-29035.19	762	1.32	-7479.21
40	RSSV 76	3	0.08*	-29035.13	741	0.41	40094.2
41	RSSV 120	1	-0.73*	-29034.27	1002	1.1	42876.09
42	CSH 22SS (Check)	3	-0.14*	-29035.07	997	1.55	-5553.9
43	PAC 52093 (Check)	2	1.11*	-29032.83	930	1.55	-862.72
44	NSSV 13 (Check)	2	-0.60*	-29034.94	1036	0.96	157036.9
	Mean	2	1		782	1	
	S.Em±	7.5			130.9		
	S.E b _i	0			0.3		

*Significance at 5% level; ** Significance at 1% level; *** Significance at 0.1% level

Table 10: Performance of top hybrid NSS 1007A × CSV 19SS with respect to various ethanol yield and its related traits

Character	Mean	gca status of parents	sca effects	Standard heterosis (%)			Stability parameters		
				Check 1	Check 2	Check 3	μ (Mean)	β_i	σ^2_{di}
				(CSH 22SS)	(PAC 52093)	(NSSV 13)			
TSS (%)	16.07	High × low	0.756**	8.83**	7.86**	-3.09	16.07	0.98	-0.24
TB (t ha ⁻¹)	73	Low × high	8.256***	-9.88**	13.92**	-0.58	73	1	-2.7
JY (l ha ⁻¹)	13438	Low × high	1976.323***	6.92	20.67**	15.53*	13438	0.98	-3714298.50
EY (l ha ⁻¹)	1150	Low × high	210.689***	15.26*	23.55**	10.94	1150	1.01	-16628

*Significance at 0.05 level** Significance at 0.01 level *** Significance at 0.001 level

TSS: Total soluble solids; TB: Total biomass; JY: Juice yield, JE: Juice extraction per cent, EY: Ethanol yield.

Abbreviations: SH: Standard Heterosis; gca: general combining ability; sca: specific combining ability; DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; TSS: Total soluble sugars; TSI: Total sugar index; TB: Total biomass; FSY: Fresh stalk yield; JY: Juice yield; JE: Juice extraction per cent, GY: Grain yield; EY: Ethanol yield.

Declaration

The authors declare no conflict of interest.

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