GENETIC VARIABILITY STUDIES IN SWEET SORGHUM (*Sorghum bicolor*L.) GENOTYPES FOR SUGAR AND BIOMASS RELATED TRAITS

ABSTRACT

Sorghum bicolor (L. Moench) is an important crop in the semi-arid tropics of Africa and Southern Asia. Sweet sorghum is characterized by more rapid growth, higher biomass production, wider adaptation and greater potential for ethanol production. The present study was conducted to evaluate 33 sweet sorghum genotypes including two check varieties for different yield and sugar related traits. Analysis of variance revealed the presence of significant difference for all characters under the study.The genetic variability study revealed the presence of greater phenotypic co-efficient of variation (PCV) than genotypic co-efficient of variation (GCV) for most of the characters indicating the presence of the environmental effect.Stem girth, nodes per plant, biomass weight, cane weight, juice content and total soluble solids, total sugars were recorded high PCV and GCV. Plant height and cane height recorded moderate PCV and GCV.Except for plant height at 30daysafter sowing (DAS) all other characters plant height at 60DAS, plant height at 90DAS, cane height, nodes per plant, stem girth, biomass weight, cane weight, total biomass yield, juice yield, total soluble solids, total sugars, total reducing sugars and total non-reducing sugars showed high heritability estimates coupled with high genetic advance as percent of mean suggesting that, these characters are under the control of additive genes and phenotypic selection will be effective for these traits.

Keywords:Genotypic co-efficient of variation (GCV), Phenotypic co-efficient of variation (PCV), Heritability, Genetic advance as a percentage of mean (GAM).

INTRODUCTION

The C4 crop sweet sorghum (Sorghum bicolor (L.) Moench) stands out by its great photosynthetic efficiency. It belongs to Plantae kingdom, Poaceae (grass) family and genus Sorghum.Sweet sorghum is a diploid with chromosome number 2n=2x=20, originated in Africa, just like grain sorghum.Sweet sorghum is the major cereal crop cultivated in tropical and subtropical areas of the world. And the total cultivated area, production and productivity in India is 5,281.5 ha, 6,214.4 t and 18,000 to 32,000 kg/ha (Doggett, 2020) respectively.

With a sugar content of 10–25% brix, sweet sorghum can grow up to 14 ft tall and, under favorable circumstances, produce 20–50 tonnes of biomass (fresh weight)per ac.Given its capacity to go dormant during the driest periods, it is frequently regarded as one of the most drought-resistant agricultural crops. Additionally, sweet sorghum is well suited to temperate areas like other sorghum varieties. Because of the ability to withstand dry conditions, requirement of less fertilizer, rapid growth rate, high biomass production capacity, ease of planting and lower cost of total fermentable sugars, sweet sorghum is one of the most promising sources of bioenergy (Rathnavathi*et al*., 2011).

Like sugar cane, sweet sorghum, often referred to as sweet-stemmed sorghum, has a sap that is high in sucrose.It was originally developed as a natural sweetener in the form of a syrup The fermentable sugars in the juice (sap) (53%–85% sucrose, 9%–33% glucose and 6%–21% fructose) can be directly fermented into bioethanol (Serna-Saldívar *et al*., 2012).Apart from the juice from the sweet sorghum stem, the grain in the head contains 60%–74% starch which can be hydrolyzed and fermented into bioethanol. The dry fibrous lignocellulosic stem material,bagasse and the residues from the head can also be used as biomass for bioethanol production (Taylor *et al*., 2019).

In the context of producing bioethanol, sweet sorghum has drawn interestsince it is a non-food feedstock that may supplement regional energy sources and reduce greenhouse gas emissions. Sweet sorghum is one of the most cost-effective sourcesfor producing high-quality bioethanol, according to characteristics like remarkable biologic productivity with few inputs, a brief growth period, a high tolerance to soil water deficit (water consumption is 2/3 less than that of sugarcane and 1/2 less than that of maize), a high tolerance to environmental stress and a high adaptability to a wide range of environments(Prasad *et al*.,2007).

In contrast to other feed stocks like sugar beet, sweet sorghum offers a great alternative. This crop is similar to sugarcane in that it accumulates sucrose and has juicy stems. Due to its four-month growing season and ability to be grown from seed, sweet

sorghum has an advantage over sugarcane. Ethanol production of sweet sorghum is more (12000-14000 L/ha) compared to sugarcane (8000-9000 L/ha). The by-product from sweet sorghum *i.e.*, its grain can also be utilized for ethanol production as currently sorghum grain is used for potable alcohol which has recovery capacityup to 400 litres per ton of grain.

The two main objectives of breeding projects for sweet sorghum with a bioenergy focus are to boost fresh biomass productivity and enhance the quantity and quality of sugars in the juicy stem. Information on genetic diversity, environmental adaptation, and genetic relationships between sorghum accessions are crucial for designing effective breeding programmes for the plant in order to choose parents which exhibit desirable features (Govindaraj *et al*., 2015).

Genetic variability is of greatest interest to the plant breeder as it plays a vital role in framing successful breeding programme. Heritability of a metric character is a parameter of particular significant to the breeder as it measures the degree of resemblance between the parents and the offsprings and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure. Study of variability, heritability and genetic advance will help to ascertain the real potential value of the genotypes. Since the material used in the present study has got novelty for various sugar and biomass related characters a study has been conducted to assess the variability for different traits.

MATERIAL AND METHODS

The study was carried out in the Department of Plant Biotechnology, UAS, GKVK, Bengaluru,Karnataka, India which consists of 30 sweet sorghum genotypes with two standard check varieties (SSV84 and SSV74) obtained from Indian Institute of Millets Research (IIMR), Hyderabad and one grain sorghum variety (Gundlupet local) procured from V.C. farm Mandya (Table 1).Experiment was carried out on sandy loam soil, during year 2022. The Randomized Complete Block Design (RCBD) was followed with three replications. All the recommended packages of practice were followed to raise the crop.

Table 1: List of Sweet Sorghum genotypes used in the study

Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source
1	*SSV 84	IIMR(HYD)	18	EC 21	IIMR(HYD)

2	*SSV 74	IIMR(HYD)	19	ES 27	IIMR(HYD)
3	Gundlupet local	(V. C Farm, Mandya)	20	PU 23	IIMR(HYD)
4	PU 12	IIMR(HYD)	21	EC 22	IIMR(HYD)
5	EC 15	IIMR(HYD)	22	EP 37	IIMR(HYD)
6	IS 4831	IIMR(HYD)	23	E 74	IIMR(HYD)
7	IS 686	IIMR(HYD)	24	IS 14861	IIMR(HYD)
8	IS178009	IIMR(HYD)	25	E 66	IIMR(HYD)
9	IS 4835	IIMR(HYD)	26	IS 7073	IIMR(HYD)
10	IS 9911	IIMR(HYD)	27	E 40	IIMR(HYD)
11	EC 20	IIMR(HYD)	28	ES 17	IIMR(HYD)
12	IS 1846	IIMR(HYD)	29	PU 22	IIMR(HYD)
13	EP 97	IIMR(HYD)	30	EP 45	IIMR(HYD)
14	EC 23	IIMR(HYD)	31	EP 113	IIMR(HYD)
15	EP 32	IIMR(HYD)	32	IS 9699	IIMR(HYD)
16	EP 68	IIMR(HYD)	33	IS 14904	IIMR(HYD)
17	EP 41	IIMR(HYD)			

IIMR (HYD) - Indian Institute of Millets Research, Hyderabad. (*)- check variety

All the genotypes were assessed for the 14physiological traits*viz.*,plant height (PH) at 30, 60, 90 DAS (Days after sowing), cane height (CH), nodes per plant (NPP), stem girth (SG), biomass weight (BMW), total biomass yield (TBY), cane weight (CW), juice content (JC), total soluble solids (TSS), total sugars (TS), total reducing sugars (TRS), total non-reducing sugars (TNS).

The mean values of genotypes in each replication were used for analysis of variance. This analysiswas carried out using the mean values of replications following the method given by Panse and Sukhatme (1967). The significance of the differences among all the genotypes was tested by F-test using the error variance. Further, Phenotypic variance, genotypic variance, heritability and genetic advance were estimated as per the formulae suggested by Lush (1949), Hanson et al. (1956) and Johnson et al. (1955).

Table 2: Results of ANOVA

Source of variation	DF	MSS	Cal F
Replication	(r-1)	RMSS	
Genotype	(g-1)	TMSS	TMSS/EMSS
Error	(r-1) (g-1)	EMSS	
Total	(rg-1)		

Where, r = number of replications

g = number of treatments (genotypes)

TMSS = Mean sum of square due to genotypes

EMSS = Mean sum of square due to error

RMSS= Mean sum of square due to replication

The standard error was calculated as

$$SEM = \frac{\sqrt{\text{EMSS}}}{\text{r}}$$

After testing for significance of the differences among the means of different genotypes for each character, further computations were done as detailed below.

Phenotypic and genotypic variance

Phenotypic variance and genotypic variance were estimated as per the formulae suggested by Lush (1949).

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{TMSS} - \text{EMSS}}{\text{r}}$$

Error of variance σe^2 = EMSS

Phenotypic variance $\sigma p^2 = \sigma g^2 + \sigma p^2$

Where,

TMSS = Mean sum of square due to genotypes

EMSS = Mean sum of square due to error

σg^2= Genotypic variance

σe^2 = Error variance

r = Number of replications

Heritability

Heritability in the broad sense was estimated by following the method suggested by Hanson *et al.* (1956).

$$\text{Heritability}(h^2) = \frac{\sigma g2}{\sigma p2} \times 10$$

Where,

h^2 = heritability (broad sense)

σg^2= genotypic variance

σp^2= phenotypic variance

Genetic advance

This was computed according to the method suggested by Johnson *et al.* (1955).

Genetic advance (GA) = K x σp x h^2

Where,

K = Selection differential at 5 per cent selection intensity

K=2.06 (Falconer *et al*., 1994).

σp = Phenotypic standard deviation and

h^2 = heritability (broad sense)

Character correlation analysis

Correlation co-efficient is the statistical measure used to estimate the association amongst the various quantitative characters. In the present investigation correlation co-efficient for characters were estimated using the formula given by Sunder Raj *et al.* (1972).

$$r_{xy} = \frac{CoV_{xy}}{(\sqrt{Var_x} \times \sqrt{Var_y}}$$

where,

r_{xy} = Phenotypic correlation coefficient between the characters x and y

CoV_{xy}= Phenotypic covariance between characters x and y

Var_x= Phenotypic variance of the character x

Var_y = Phenotypic variance of the character y

VY(p) = Phenotypic variance of Y.

Variance and covariance components were used to estimate phenotypic correlation coefficient between all the pairs of characters and the formula used is as mentioned below

$$rp_{(xy)} = \frac{P_x P_y}{\sqrt{Vp_x Vp_y}}$$

where,

PxP = Phenotypic covariance of x and y.

Vpx = Phenotypic variance of x.

Vpy = Phenotypic variance of y.

Rp(xy) = Phenotypic correlation of x and y.

Test of significance for correlation was done at n-2 degree of freedom using table from Fisher and Yates at 0.05 and 0.01 probability levels.

RESULTS AND DISCUSSION

Analysis of variance

In a field experiment, analysis of variance was conducted for sugar associated variables of sweet sorghum genotypes and the mean sum of squares for all the characters is provided in Table 3 and Table 4. The analysis of variance indicated a significant ($p < .05$) variation in all studied traits with considerable ranges in plantheight (PH) [PH at 30 DAS (28.18-40.96 cm), PH at 60 DAS (92.73-156.92 cm), PH at 90 DAS (136.19-264.07 cm)], cane height (78.52-214.07cm), nodes per plant (4.45-10.44), stem girth (6.16-37.79mm), biomass weight (116.51-652.62g/plant), cane weight (65.38-408.33g/plant), juice content (22.71-116.14ml/plant), total soluble solids (Brix%) (4.6-15.65%), total sugars (4.50-

17.03mg/100ml), total reducing sugars (2.77-9.75mg/100ml) and total non-reducing sugars (1.19-9.25mg/100ml) demonstrating that the investigation's material choice was acceptable. The fact that the range for all of the traits was substantially broader, highlighting extreme genotypes for selection, provided additional support for this(Table 1). Wide variations for the studied parameters were also recorded by Mani (2017), Soujanya, (2017) and Sandeep (2010) in their investigations on sweet sorghums, which produced the same outcomes.

Plant height at 30 DAS was higher in the genotype PU 23 (40.96 cm) while the genotypeIS 686 had showed the lowest plant height (28.18 cm). Plant height at 60 DAS was higher in EP 68 (156.92 cm) while the genotypes IS 4835 and check variety SSV 84 showed the lowest values (93.00 cm and 92.73 cm respectively).Plant height at 90 DAS was higher in the genotype EP 45 recorded the highest value (264.07cm) while it was least in IS 4835 (136.19 cm). Cane height was higher in the genotype EP 45 (214.07 cm) while the genotype IS 4835 (78.52 cm) showed lowest.EP 41 (10.44) showed highest nodes per plant while lowest was recorded for IS 686 (4.45).The character stem girth showed significantly highest width in IS 14861 (37.74 mm) and lowest in IS4835 (6.16mm). The highest biomass weight was recorded in IS 178009 (652.62g)whereas, the lowest biomass was recorded in GUNDLUPET LOCAL (116.51g).The highest total biomass yieldwas recorded in IS 178009 (96.69 t/ha)whereas, the lowest was recorded in Gundlupet local (17.26t/ha).The genotype EP 45 recorded significantly the highest cane weight (408.33 g) whereas, IS 4835 had recorded the lowest 65.38 g (Table 3 and Table 4).

The Highest juice yield per plantwas recorded in IS 14861 (116.14ml/plant)while the lowest was recorded in ES 27 (22.71ml/plant).The genotypes EC 22 and E 66 recorded highest TSS 15.50% and 14.27% respectively, the genotype IS 14861 has showed the lowest TSS value (4.6 %).The genotype IS 9699 and EC 15 showed highest total sugars 17.51mg and 17.03mg respectively,IS 14861 genotype has showed the lowest total sugars (4.6mg).The genotype IS 9699 and EC 15 showed highest total reducing sugars 9.05mg and 7.78mg respectively,IS 14861 genotype has showed the lowest total reducing sugars (2.77mg).The genotypes EC 15 and E 66 showed highest total non-reducing sugars 9.26mg and 9.14mg respectively, IS 4831 genotype has showed the lowest total non-reducing sugars 1.19mg (Table 4 and Table 5).

Estimation of Genetic variability parameters

For each trait under consideration, the range, mean, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (h^2), and genetic advance as a percentage of mean (GAM) were calculated and are displayed in Table 7to show the extent to which observed variation is caused by genetic factors. Results revealed a minimal difference in GCV and PCV values, suggesting that environmental influences on genotypes were less significant.

Stem girth, nodes per plant, biomass weight, cane weight, juice content and total soluble solids, total sugars were recorded high PCV and GCV (Table 7) suggesting that the genotypes have a strong potential to react well to selection for cane and sucrose production as they have wide genetic basis.Plant height and cane height recorded moderate PCV and GCV indicating limited scope for direct selection for these characters.Similar results were obtained by Tomar *et al*. (2012), Wu *et al*. (2010) and Kachapur and Salimath(2009).

To have a knowledge of the heritable portion of the variability, it is essential to determine the heritability of each character. Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences.The discrepancy between PCV and GCV estimates demonstrated the proportional impact of environment on characteristics, which determined that their heritability of the difference for any character is minimal, resulting in high heritability,while significant discrepancies between GCV and PCV estimations suggested that environmental factors had a significant role in the low heritability estimates.High broad sense heritabilitywas observed for all fourteen traits (plant height at 30DAS, plant height at 60DAS, plant height at 90DAS, cane height, nodes per plant, stem girth, biomass weight, cane weight, total biomass yield, juice yield, total soluble solids, total sugars, total reducing sugars and total non-reducing sugars) in the genotypes under study indicating that selection for these characters will be rewarding, as they were least influenced by environment.High heritability estimates indicate that these variation is generated by high additive gene effects, which increases the potential for increasing yield through selection. Similar results were obtained by Tomar *et al*. (2012), Chethan (2016) and Sadashiva (2015) in his study regarding the screening of sweet sorghum genotypes for higher ethanol production.

The amount of genetic advancement that would occur from the selection of the fittest individuals cannot be determined by heritability value alone. Johnson *et al*. (1995) in their paper said that estimates of heritability combined with genetic gain would be more effective

in evaluating the success of choosing the best candidates than the former by itself. Therefore, in order to improve the effectiveness of the selection process, it is crucial to include the expected genetic advance together with the heritability estimate as a pool in the selection approach.A general picture of the type of gene action influencing a given trait can be gained from a relative comparison of heritability values and predicted genetic advance expressed as a percentage of mean. Low environmental effect and a predominance of additive gene action in their expression are revealed by high heritability and high genetic advance (Panse and Sukhatme, 1967).

Except for plant height at 30DAS all other characters plant height at 60DAS, plant height at 90DAS, cane height, nodes per plant, stem girth, biomass weight, cane weight, total biomass yield, juice yield, total soluble solids, total sugars, total reducing sugars and total non-reducing sugars showed high heritability estimates coupled with high genetic advance as percent of mean suggesting that, these characters are under the control of additive genes and phenotypic selection will be effective for these traits.Similar results were obtained by Tomar *et al*. (2012) and of Kulkarni (2016), whose research focused on genetic variability and correlation investigations in genotypes of sweet sorghum.

Information is of greater value when the GCV is high and combined with high heritability and genetic advance. Based on the present study except for plant height at 30DAS, plant height at 60DAS, plant height at 90DAS & cane height all other traits were having high GCV combined with high heritability and high genetic advance.

CONCLUSION

In this study, 31 sweet sorghum genotypes were evaluated for morphological traits and yield-related characteristics to assess genetic variation and divergence. Genotypes with high total soluble solids (TSS) are recommended for ethanol and syrup production, while those with high juice yield and biomass weight are suitable for bioethanol production and

fodder purposes. Stem girth, nodes per plant, biomass weight, cane weight, juice content, and total soluble solids exhibited high genetic potential for selection, indicating their suitability for cane and sucrose production. Heritability estimates were high for most traits, suggesting effective phenotypic selection. Biomass yield showed significant positive correlation with stem girth, while fresh cane weight correlated strongly with biomass weight. Total sugars correlated positively with total non-reducing sugars and total reducing sugars. Ethanol yield was positively correlated with juice yield, cane weight, biomass weight, and total reducing sugars. Improving these correlated traits could enhance overall yield.

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Table3:Comparision ofmeanperformancesofallthegenotypesfor plant height at 30, 60, 90 DAS, cane height at 110 DAS and nodes per plant.

GENOTYPES	PH (30DAS)	PH (60DAS)	PH (90DAS)	CH(110DA)	NPP
***SSV-84**	30.34^{jklmn}	92.73^{k}	196.32^{j}	149.75^{hi}	5.33^{hijk}
***SSV-74**	31.11^{ijklmn}	113.56^{efghij}	204.89^{hi}	174.73^{b}	5.78^{fghijk}
GUNDLUPET LOCAL	33.04^{hijk}	119.5^{defg}	154.44^{o}	110.2^{n}	5^{jk}
PU 12	36.59^{bcdefg}	111.5^{efghij}	208.69^{ghi}	132.61^{l}	7.33^{cde}
EC 15	32.66^{hijk}	107.08^{hij}	184.58^{lm}	167.65^{c}	4.89^{jk}
IS 4831	34.04^{efghi}	109.68^{fghij}	195.26^{jk}	153.32^{fghi}	5.11^{jk}
IS 686	28.18^{n}	119.81^{defg}	174.8^{n}	107.99^{n}	4.45^{k}
IS 178009	29.38^{lmn}	108.02^{ghij}	242.63^{bc}	139.59^{jk}	6.89^{defg}
IS 4835	31.91^{ijklm}	93^{k}	136.19^{p}	78.52^{o}	5.33^{hijk}
IS 9911	33.89^{fghi}	116.71^{defgh}	224.01^{d}	156.59^{ef}	9.22^{ab}
EC 20	37.06^{bcdef}	104.22^{ijk}	218.44^{de}	161.98^{cde}	5.56^{ghijk}
IS 1846	35.38^{defgh}	115.17^{defghi}	187^{lm}	125.44^{m}	5.22^{ijk}
EP 97	33.15^{hij}	107.67^{hij}	190.64^{jkl}	126.44^{m}	5.78^{fghijk}
EC 23	32.26^{hijkl}	109.37^{fghij}	218.48^{de}	176.1^{b}	7.78^{cd}
EP 32	33.62^{ghij}	120.2^{def}	203.24^{i}	153.4^{fghi}	6.78^{defg}
EP 68	33.49^{ghij}	156.92^{a}	219.7^{de}	141.03^{jk}	7.67^{cd}
EP 41	37.22^{bcde}	106.96^{hij}	246.64^{b}	151.52^{fghi}	10.44^{a}
EC 21	29.72^{klmn}	132.2^{bc}	262.06^{a}	211.2^{a}	6.78^{defg}
ES 27	38.71^{abc}	110.56^{efghij}	239.51^{c}	164.28^{cd}	8.33^{bc}
PU 23	40.96^{a}	107.5^{hij}	244.51^{bc}	167^{cd}	7.11^{cdef}
EC 22	39.15^{ab}	115.47^{defghi}	214.98^{efg}	154.31^{fgh}	6.67^{defgh}
EP 37	40.62^{a}	116.49^{defgh}	211.06^{fgh}	147.69^{i}	7.44^{cde}
E 74	36.76^{bcdefg}	136.92^{b}	189.35^{klm}	135.97^{kl}	5.56^{ghijk}
IS 14861	32.94^{hijk}	111.54^{efghij}	202.14^{i}	156.2^{efg}	5.67^{ghijk}
E 66	38.14^{abcd}	102.67^{jk}	183.58^{m}	142.11^{j}	6.56^{defghi}
IS 7073	28.85^{mn}	120.21^{def}	215.82^{ef}	166.17^{cd}	5.33^{hijk}
E 40	39.67^{ab}	126.55^{bcd}	206.01^{hi}	161.6^{de}	6.22^{efghij}
ES 17	39.58^{ab}	122.16^{cde}	208^{hi}	141.43^{jk}	6.67^{defgh}
PU 22	35.48^{cdefgh}	101.87^{jk}	184.06^{m}	141.6^{jk}	7.22^{cde}
EP 45	32.83^{hijk}	126.82^{bcd}	264.07^{a}	214.07^{a}	9.89a
EP 113	32.9^{hijk}	126.41^{bcd}	246.17^{b}	153.41^{fghi}	7.22^{cde}
IS 9699	38.08^{abcd}	93.46^{k}	174.75^{n}	122.7^{m}	4.56^{k}
IS 14904	40.8^{a}	148.31^{a}	214.69^{efg}	150.21^{ghi}	9.56^{ab}
Mean	34.80	115.49	208.08	149.60	6.65
CD at 5%	2.83	9.85	5.79	5.32	1.18
CV	4.98	5.23	1.71	2.18	10.92

Legend: PH-Plantheight(cm),**DAS**- Day AfterSowing,**CH-** Cane Height(cm),**NPP**-Nodes Per Plant

Table4:Comparision ofmeanperformancesofallthegenotypesforstem girth, biomass weight, total biomass yield, cane weight, juice content and total soluble solids (brix) after 110DAS (Days after sowing)

GENOTYPES	SG (110DAS)	BMW	TBY	CW	JC	BRIX (TSS)
***SSV-84**	14.27^{fghij}	339.96^{f}	50.37^{f}	207.6^{def}	75.07^{e}	15.65^{a}
***SSV-74**	16.64^{defg}	512.82^{c}	75.97^{c}	343.16^{b}	106.23^{bc}	14.63^{b}
GUNDLUPETLOCAL	8.57^{lm}	116.51^{l}	17.26^{l}	66.52^{k}	22.88^{j}	10.03^{m}
PU12	15.36^{defgh}	491.29^{c}	72.78^{c}	219.1^{de}	95.77^{d}	12.19^{f}
EC 15	14.08^{fghij}	506.77^{c}	75.08^{c}	224.54^{d}	95^{d}	11.76^{gh}
IS 4831	12.06^{hijkl}	289.73^{ghi}	42.92^{ghi}	146.41^{hi}	42.21^{gh}	12.43^{ef}
IS 686	11.76^{hijkl}	447.31^{d}	66.27^{d}	205.4^{def}	79.3^{e}	10.1^{m}
IS 178009	22.06^{b}	652.63^{a}	96.69^{a}	363.62^{ab}	109.38^{b}	5.6^{q}
IS 4835	6.16^{m}	172.42^{k}	25.54^{k}	65.28^{k}	22.74^{j}	10.07^{m}
IS 9911	17.28^{cdef}	410.59^{e}	60.83^{e}	275.93^{c}	111.57^{ab}	10.13^{lm}
EC 20	9.84^{klm}	282.66^{hi}	41.88^{hi}	166.8^{efgh}	40.46^{hi}	12.5^{ef}
IS 1846	11.8^{hijkl}	282.77^{hi}	41.89^{hi}	165.72^{efgh}	55.31^{f}	10.34^{klm}
EP97	12.7^{ghijk}	269.9^{i}	39.99^{i}	$150.97^{f\ hi}$	47.1^{g}	11.7^{h}
EC 23	17.32^{cdef}	449.22^{d}	66.55^{d}	251.11^{cd}	77.45^{e}	12.13^{fg}
EP32	12.76^{ghijk}	312.78^{fgh}	46.34^{fgh}	205.42^{def}	78.7^{e}	11.07^{j}
EP68	11.95^{hijkl}	260^{i}	38.52^{i}	204.78^{def}	75.93^{e}	14.07^{c}
EP41	12.44^{hijkl}	208.09^{j}	30.83^{j}	103.04^{ijk}	35.38^{i}	13.23^{d}
EC 21	15.79^{defgh}	326.05^{fg}	48.3^{fg}	205.71^{def}	78.54^{e}	8.7^{o}
ES27	14.96^{efghi}	225.72^{j}	33.44^{j}	104.48^{ijk}	22.71^{j}	10.57^{k}
PU23	11.11^{ijkl}	317.77^{fgh}	47.08^{fgh}	211.07^{de}	77.23^{e}	10.2^{klm}
EC 22	19^{bcd}	519.85^{c}	77.01^{c}	375.01^{ab}	106.58^{bc}	15.5^{a}
EP37	12.88^{ghijk}	313.73^{fgh}	46.48^{fgh}	210.62^{de}	75.73^{e}	11.23^{ij}
E 74	11.08^{ijkl}	133.77^{l}	19.82^{l}	72.55^{k}	26^{j}	12.3^{ef}
IS 14861	37.79^{a}	630.41^{a}	93.39^{a}	398.59^{a}	116.14^{a}	4.6^{r}
E 66	10.3^{jklm}	280.53^{hi}	41.56^{hi}	132.83^{hij}	45.46^{gh}	14.27^{bc}
IS 7073	18.26^{cde}	315.11^{fgh}	46.68^{fgh}	203.59^{defg}	80.42^{e}	12.63^{e}
E 40	9.02^{klm}	191.62^{jk}	28.39^{jk}	65.73^{k}	24.22^{j}	9.23^{n}
ES17	12.23^{hijkl}	216.48^{j}	32.07^{j}	80.38^{jk}	27.47^{j}	11.47^{hi}
PU22	11.87^{hijkl}	259.98^{i}	38.52^{i}	90.42^{jk}	24.54^{j}	13.27^{d}
EP45	20.77^{bc}	632.46^{a}	93.7^{a}	408.33^{a}	108.52^{b}	7.67^{p}
EP113	14.21^{fghij}	587.31^{b}	87.01^{b}	335.48^{b}	102.16^{c}	10.53^{kl}
IS 9699	12.35^{hijkl}	331.29^{f}	49.08^{f}	204.03^{def}	80.24^{e}	10.13^{lm}
IS 14904	14.8^{efghi}	214.59^{j}	31.79^{j}	85.69^{jk}	21.77^{j}	13.53^{d}
Mean	14.35	348.55	51.6	198.48	66.31	11.19
CD at5%	3.37	32.30	4.78	48.14	5.29	0.37
CV	14.41	5.68	5.68	14.87	4.89	2.03

Legend: SG- StemGirth(mm),**BMW-**BiomassWeight(g/plant),**TBY**-Total biomass yield(t/ha), **CW-**CaneWeight(g/plant),**JC-**JuiceContent(ml/plant),**TSS-**TotalSoluble Solids(%)

Table 5: Average concentration of total sugars, total reducing sugars and total non-reducingsugarsofsweetsorghumgenotypes after 110DAS (Days after sowing)

GENOTYPES	TS	TRS	TNS
***SSV-84**	9.04^{jk}	4.62^{fghi}	4.42^{gh}
***SSV-74**	16.66^{abc}	9.75^{a}	6.91^{de}
GUNDLUPETLOCAL	10.75^{i}	3.55^{jklm}	7.2^{bcde}
PU12	14.04^{ef}	5.17^{ef}	8.87^{a}
EC 15	17.03^{ab}	7.78^{b}	9.26^{a}
IS 4831	4.96^{o}	3.76^{ijklm}	1.19^{l}
IS 686	7.74^{klm}	3.35^{jklm}	4.39^{gh}
IS 178009	6.42^{mn}	2.94^{lm}	3.48^{ghij}
IS 4835	7.46^{lm}	4.77^{fgh}	2.69^{ijkl}
IS 9911	6.63^{m}	3.36^{jklm}	3.27^{hij}
EC 20	12.31^{gh}	3.77^{ijklm}	8.54^{ab}
IS 1846	9.12^{j}	3.18^{klm}	5.94^{ef}
EP97	7.7^{klm}	3.51^{jklm}	4.19^{gh}
EC 23	13.84^{ef}	4.86^{fgh}	8.97^{a}
EP32	7.72^{klm}	5.14^{efg}	2.58^{ijkl}
EP68	5.26^{no}	3.63^{ijklm}	1.63^{kl}
EP41	15.98^{bcd}	7.18^{b}	8.8^{a}
EC 21	6.78^{m}	4.15^{ghijk}	2.62^{ijkl}
ES27	7.53^{lm}	3.18^{klm}	4.35^{gh}
PU23	6.56^{mn}	4.29^{fghij}	2.27^{jkl}
EC 22	11.56^{ghi}	3.6^{jklm}	7.96^{abcd}
EP37	6.43^{mn}	3.44^{jklm}	2.99^{hijk}
E 74	8.27^{jkl}	4.36^{fghij}	3.91^{ghi}
IS 14861	4.5^{o}	2.77^{m}	1.73^{kl}
E 66	15.38^{cd}	6.24^{cd}	9.14^{a}
IS 7073	14.76^{de}	5.97^{de}	8.79^{a}
E 40	7.61^{lm}	2.85^{m}	4.76^{fg}
ES17	10.55^{i}	4.15^{ghijk}	6.4^{e}
PU22	10.79^{i}	3.48^{jklm}	7.31^{bcde}
EP45	12.82^{fg}	3.89^{hijkl}	8.93^{a}
EP113	15.57^{cd}	6.98^{bc}	8.59^{ab}
IS 9699	17.51^{a}	9.05^{a}	8.46a^{bc}
IS 14904	11.3^{hi}	4.19^{fghijk}	7.1^{cde}
Mean	10.32	4.63	5.69
CD at5%	1.22	0.85	1.25
CV	7.27	11.22	13.45

Legend:TS- Total Sugars(mg/100ml), **TRS-** Total Reducing Sugars(mg/100ml),**TNS-** Total Non-ReducingSugars(mg/100ml)

Table 6: Analysisofvarianceforyieldattributingcharactersin sweet sorghum

Source ofvariance	Meansumofsquares											
	PH	**CH**	**NPP**	**SG**	**BMW**	**TBY**	**CW**	**JC**	**BRIX(TSS)**	**TS**	**TRS**	**TNS**
Treatments	2505.8*	2051.3*	7.2*	89.10*	66081.5*	1450.34*	30844.5*	3110.1*	16.60*	46.0*	9.3*	22.0*
Replication	9.42	5.02	0.44	1.25	34.78	0.76	1333.99	7.17	0.07	2.60	0.09	3.10
Error	12.61	10.62	0.52	4.27	392.22	8.60	871.14	10.52	0.05	0.56	0.27	0.58
SED	2.05	1.88	0.41	1.19	11.43	1.69	17.04	1.87	0.13	0.433	0.30	0.44
CD at5%	5.79	5.31	1.18	3.37	32.30	4.78	48.14	5.29	0.37	1.22	0.84	1.24

*Significant at 5% = Greater than 3.14

Legend:PH-PlantHeight(cm),**DAS**-DayAfterSowing,**CH-**CaneHeight(Cm),**NPP-**NodesPerPlant,**SG-**StemGirth(mm),**BMW-**BiomassWeight(g/plant), **CW-** Cane Weight(g/plant), **JC-** Juice Content(ml/plant), **TSS-** Total Soluble Solids(%), **TS-** Total Sugars(mg/100ml), **TRS-** Total ReducingSugars(mg/100ml),**TNS-**Totalnon-ReducingSugars(mg/100ml)

Table 7: Estimatesofgeneticvariabilityparametersfor fourteen charactersin sweetsorghum

Sl.No	Traits	Range		Mean	GCV%	PCV%	H^2%	GAM%
		Max	Min					
1	PH@30DAS(cm)	40.95	28.18	34.8	10.23	11.38	80.78	18.94
2	PH@60DAS(cm)	156.9	92.73	115.49	11.94	13.03	83.9	22.52
3	PH@90DAS(cm)	264.1	136.1	208.08	13.85	14.15	97.51	28.33
4	CH(cm)	214.6	78.52	149.6	17.02	17.95	98.31	35.64
5	NPP	10.44	4.44	6.64	22.45	24.97	80.87	41.59
6	SG(mm)	37.79	6.15	14.34	37.06	39.77	86.86	71.16
7	BMW (g/plant)	652.6	116.51	348.54	42.32	42.99	98.24	86.68
8	TBY (t/ha)	96.68	17.26	51.63	42.45	43.83	98.24	86.68
9	CW(g/plant)	408.3	65.27	198.48	50.36	52.51	91.98	99.49
10	JC(ml/plant)	116.1	22.71	66.30	48.48	49.25	98.35	99.25
11	^{o}Brix	15.5	4.6	11.19	20.98	21.08	99.07	43.03
12	TS(mg/100ml)	17.03	4.5	10.32	37.73	38.42	96.42	76.31
13	TRS(mg/100ml)	9.75	2.77	4.63	37.54	39.18	91.80	74.10
14	TNS(mg/100ml)	9.25	1.19	5.68	47.04	48.93	92.44	93.17

Legend: **PH**-PlantHeight(cm),**DAS**-DayAfterSowing,**CH**-CaneHeight(Cm),**NPP**-NodesPerPlant,**SG**-StemGirth(mm),**BMW**-BiomassWeight(g/plant), **CW**- Cane Weight(g/plant), **JC**- Juice Content(ml/plant), **TSS**- Total Soluble Solids(%), **TS**- Total Sugars(mg/100ml),

TRS- TotalReducingSugars(mg/100ml),**TNS-**Totalnon-ReducingSugars(mg/100ml), **GCV**-genotypic co-efficient of variation, **PCV**- phenotypic co-efficient of variation, $\mathbf{H^2}$-heritability, **GAM**-genetic advance as a percentage of mean.