

*Full Length Research Paper*

# Correlation and path coefficient analysis of agronomic and quality traits in a bioenergy crop, sweet sorghum [*Sorghum bicolor* (L.) Moench]

Chalachew Endalamaw<sup>1,2</sup>, Asfaw Adugna<sup>3\*</sup> and Hussein Mohammed<sup>2</sup>

<sup>1</sup>Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agriculture Research Center, P. O. Box 436 Adama, Ethiopia.

<sup>2</sup>Department of Plant and Horticultural Sciences, Hawassa University, P. O. Box 05, Hawassa, Ethiopia.

<sup>3</sup>Advanta Seeds Ltd., P. O. Box 10438, Eldoret, Kenya.

Received 10 September 2017; Accepted 13 November, 2017

Sweet sorghum is considered one of the best sources of bioethanol due to its higher total reducing sugar content, which ferments completely to produce ethanol coupled with its adaptation to the changing climate. A study was carried out in Ethiopia, during the 2015/16 crop season, to determine the extent of phenotypic and genotypic relationships among 13 agronomic traits and six quality components of 28 sweet sorghum genotypes. Panicle weight and width, dry matter yield, thousand kernel weight and harvest index had significant positive correlation with grain yield and exerted favourable direct effects both at phenotypic and genotypic levels. Ethanol yield was also correlated with juice yield, sugar yield and fresh stalk yield. Therefore, these yield and quality components are suggested to receive due attention during sweet sorghum varietal selection. Moreover, days to maturity had negative correlation and imposed negative direct effect on grain yield, which may indicate the possibility to select high yielding, early maturing dual purpose varieties for dry environments where terminal drought is rampant. The studied genotypes were grouped into three clusters according to their  $D^2$  values, worthy of future breeding work considering the special merits in each cluster depending on the objectives of the breeding program. Some of the genotypes excelled as one of the two commercial sugarcane varieties used as controls for some quality traits. Therefore, considering their less water requirement, faster production cycle, and additional advantage of grain production over sugarcane, sweet sorghum stalks can serve as alternatives to sugarcane for use as feedstock in drier areas of the world under the changing climate.

**Key words:** Bioethanol, correlation, juice, path-coefficient, sweet sorghum.

## INTRODUCTION

Sorghum's ability to withstand drought and heat stresses and to give reasonable yields under adverse

\*Corresponding author. E-mail: [asfaw123@rediffmail.com](mailto:asfaw123@rediffmail.com).

Author(s) agree that this article remains permanently open access under the terms of the [Creative Commons Attribution License 4.0 International License](https://creativecommons.org/licenses/by/4.0/)

environmental conditions have raised its importance as a food security and bioenergy crop in arid and semi-arid tropics. In stress environments, pearl millet and sorghum are the dominant crops and receive fewer agricultural inputs than any other major cereals (McGuire, 2008). Sweet sorghum (*Sorghum bicolor*) is a natural variant of common grain sorghum with high stem sugar content, which can offer both food and fuel. The sugar content in the stalk juice of sweet sorghum reaches 10 to 25% at grain maturity (Pei et al., 2010). This sugar in the juice can be used to produce table sugar, syrup, wine or biofuel. The bagasse is used as forage or as raw material for the paper industry (Koeppen et al., 2009). Sweet sorghum ensures food and feed security and provides opportunities for additional income for small farmers serving as a feedstock for bioethanol production while protecting the environment (Almodare and Hadi, 2009). It requires 37% less nitrogen fertilizer and 17% less irrigation water than maize, and could yield more ethanol than maize during a dry year (Hills et al., 1990; Putnam et al., 1991). Its potential ethanol yield of 5000 L/ha/yr is more than that of sugarcane, maize, cassava and wood (Hodes, 2006).

There is an increasing interest in using sweet sorghum as source of bioethanol due to its various salient features including the higher total reducing sugar (glucose and fructose) and poor sucrose contents compared to sugarcane juice (Huligol et al. 2004), which prevent crystallization resulting in near complete fermentation efficiency to produce ethanol (Ratnavathi et al., 2004; Anderson, 2005). In general, alcohol as a fuel is clean, burning when used alone and when mixed with gasoline it acts to increase the octane rating (Schaffert and Gourley 1982), which may also mean that it contributes to climate change mitigation. Moreover, because of its efficient conversion of atmospheric CO<sub>2</sub> into sugar, sweet sorghum is a promising crop for use in the bio-energy industry and the ethanol production process from sweet sorghum is eco-friendly with less or no environmental pollution compared to that from molasses. However, information on the relationship of different agronomic and quality characters directly or indirectly involved in ethanol production is still meager. Therefore, the present study was carried out: to quantify the genetic correlations among various morpho-agronomic and quality traits in sweet sorghum genotypes; to identify the grain yield and bioethanol production potential among the genotypes; and to partition the correlation coefficients of various traits into direct and indirect effects.

## MATERIALS AND METHODS

### Description of the study site

Melkassa Agricultural Research Center (MARC) is located in the central Rift Valley of Ethiopia at a distance of 115 km from the capital Addis Ababa and 16 km south east of Adama town. The site is placed at an altitude of 1500 m above sea level on geographical

coordinates of 8° 30' latitude and 39° 21' longitude. The area receives mean annual rainfall of 763 mm and the mean maximum and minimum temperatures are 24.8 and 14.0°C, respectively. Agro-ecologically, the area is categorized as dry semiarid. The soil is a well-drained typical sandy loam Andosols with a pH of 8.0.

### Treatments and experimental design

The treatments consist of 28 genotypes including 26 accessions of sweet sorghum introduced from ICRISAT and preserved at MARC and two released grain sorghum varieties (Meko and Gambella 1107) as standard check (Appendix Table S1). The experiment was laid out in a Randomized Complete Block Design with three replications with each plot having 4 rows of 5 m length with row spacing of 0.75 m. Sowing was done by hand drilling on 4 July, 2015. Twenty days after planting (DAP), the seedlings were thinned to 0.15 m distance between plants. Phosphorus and nitrogen fertilizers were applied at the recommended rates of 100 and 50 kg-ha<sup>-1</sup> in the form of DAP (46%P<sub>2</sub>O<sub>5</sub>, 18%N) and Urea (46%N), respectively. The DAP was applied during planting in the seed furrows with all plots top-dressed with urea when the plants reached 30 cm height. The experiment was conducted under rain fed conditions. Moreover, two commercial sugarcane varieties, [NCO-334(Cip) and B52298 (Wonji-1) from Wonji Sugar Corporation Estate of Ethiopia were used for comparison.

### Data recording and analysis

#### Agronomic characteristics

Data were recorded on days to 50% flowering (DTF), days to maturity (DTM), plant height (PH) (cm), stalk diameter (cm) (STD), number of productive tillers (NPT), panicle length (PL) and width (PW), panicle weight (PWT), fresh stalk yield (FSY), dry stalk yield (DSY), thousand kernel weight (TKW) (at 12% moisture) and grain yield (GY). Stalk diameter was recorded as the average width of the middle part of the stem from five randomly selected plants in a plot at maturity using vernier caliper and record in centimeters. Productive tillers were recorded as the number of tillers that bear grain recorded from five randomly taken plants at maturity. Fresh stalk yield (kg) was measured from the two central rows of 25 randomly selected plants in each plot before harvesting for juice extraction. Dry stalk yield (kg) was measured from the two central rows of five randomly selected plants in each plot after.

#### Quality characteristics

The juice was extracted from 25 plants randomly taken from the two central rows in each plot and the volume was measured at hard dough stage. The juice was extracted using roller mills at Wonji Sugar Corporation Estate of Ethiopia. Due to the relatively long distance from the trial site to the extracting machine, the sample juice volume was expected to be biased. Therefore, alternative method of Wortmann et al. (2010) was followed to adjust the lost juice and sugar yields as follows:

$$JY (80\% \text{ extracted}) = [FSY - (DSY - CSY)] \times 0.8;$$

$$CSY = (FSY - DSY) \times \text{Brix} \times 0.75;$$

$$SY = JY \times \text{Brix} \times 0.75;$$

Where, JY = juice yield (t ha<sup>-1</sup>), FSY = fresh stalk yield (t ha<sup>-1</sup>); DSY = dry stalk yield (t ha<sup>-1</sup>); CSY = conservative sugar yield (t ha<sup>-1</sup>) and SY = sugar yield (t ha<sup>-1</sup>).

Brix % (BRX) was measured in the field from five randomly selected plants at middle portions of the stem from two central rows using refractometer (Atago 2522; Atago USA Inc., Bellevue, WA). To measure pol percent (POL), 200 ml of juice was transferred into a 300-ml Erlenmeyer flask, after purification with dry lead (Hornes dry lead) through filter paper No. 42. The pol tube was filled with the filtrate juice, and the POL reading was recorded from the Saccharimeter. Purity percent of the juice (PTY) was computed as  $(POL/BRX)100$ . Sugar yield estimates were calculated following the approach of Wortmann et al. (2010) that assumes 75% of the BRX as fermentable sugars. Theoretical EY ( $L \cdot ha^{-1}$ ) was calculated from extracted juice as SY ( $kg \cdot ha^{-1}$ ) multiplied by a conversion factor ( $0.581 L \cdot kg^{-1}$  ethanol) (Teetor et al., 2011). The above ground parts of five plants were chopped and kept in an oven at  $70^{\circ}C$  for 72 h to get dry stalk yield (DSY). Moreover, harvest index (HI) was calculated using the formula of Donald (1968) and expressed as percent.

Ten full canes were randomly collected from each of the two commercial sugarcane varieties from two rows. The plants were 12 months old during the time of sampling and their FSY, JY, BRX, POL, PTY, SY and EY were recorded to compare with the sweet sorghums.

### Statistical analysis

The recorded data were subjected to analysis of variance using the procedures outlined by Gomez and Gomez (1984) using the GLM and PROC MIXED procedures implemented in SAS software v. 9.1.3 (SAS Institute 2003) and Program Genes (Cruz, 2006). Correlations among each pair of characters were also computed. The paired D-square value was computed based on the pooled mean of the genotypes and cluster analysis was obtained following the techniques of Tocher's (Rao, 1952).

## RESULTS

### Phenotypic and genotypic correlations among agronomic characters

Analysis of variance revealed highly significant differences among the genotypes for all the measured agronomic characters, except for number of tillers, indicating the existence of considerable genetic variability (data not shown). The comparative performance of sweet sorghum genotypes for agronomic traits is presented in Table 1. Phenotypic and genotypic correlations among agronomic characters are also presented in Appendix Table S2. Panicle weight, PW, HI, TKW and DMY were observed to have positive and significant correlations with GY at phenotypic and genetic levels, showing the inter-relationship of these traits. This was further confirmed by Path coefficient analysis (Appendix Tables S3 and S4). On the other hand, GY had significant negative correlation with DTM. Dry matter yield had significant positive correlation with DTF, PH, DSY and GY. Panicle weight and DMY had the highest positive direct effect on GY at phenotypic level, but only PWT and PL had the same effect at the genetic level. Days to maturity had negative direct effect on GY at both levels and their indirect effect via other characters was also mostly negative; thus, the relationship was mainly due to both direct and indirect effects.

### Correlations among quality characters

Analysis of variance also revealed highly significant differences among the genotypes for all the measured quality characters (data not shown). The comparative performance of the studied genotypes for quality traits are presented in Appendix Table S5. Phenotypic and genotypic correlations among the quality characters are presented in Table 2. Juice yield and SY were observed to have positive significant ( $p < 0.01$ ) correlations with EY at phenotypic and genotypic levels. Ethanol yield had positive correlation with JY and FSY, but its correlation with the rest of the characters was not significant. Moreover, JY was highly correlated with SY. Plants with greater FSY and JY also produced greater SY and EY. Accordingly, genotypes with higher FSW produced higher JY that can be immediately fermented to bioethanol. Sweet sorghum genotypes those had the highest SY and EY were due to increased juice and high and moderate BRX, but they had moderate GY. Genotypes with high and moderate BRX, and high JY produced high SY and EY, and moderate GY. Brix percentage was significantly ( $p < 0.01$ ) correlated with POL at both levels, but it had no significant associations with other characters. The phenotypic and genotypic direct and indirect effects of different characters on EY are presented in Appendix Tables S6 and S7, respectively. Six of the nine characters studied showed positive direct effects on EY, whereas juice yield had the highest direct effect on EY followed by BRX.

### Correlation among agronomic and quality characters

Wide genetic variability was found among the 28 genotypes for FSY, BRX, JY, SY and EY. Also, there were significant positive correlations among EY, FSY, and JY at phenotypic and genotypic levels, but the direct effect of FSY on EY was negligible. Phenotypic and genotypic path analysis showed that DTF, PH, BRX and POL had positive direct effect, but DTM, SW and DSY had negative direct effect and phenotypic and genotypic correlation with EY. Because their indirect effect via other characters was negligible, their phenotypic and genotypic correlation with EY was mainly due to direct effect.

### Genetic divergence and cluster mean analysis

D-square analyses grouped the genotypes into three major clusters (Table 3), which may indicate that the tested genotypes were moderately divergent. The largest cluster (Cluster II) comprised of 16 genotypes (57.14%). Eight genotypes were grouped in Cluster III (28.57%) and the remaining four genotypes were included in Cluster I (12.29%). Cluster I was characterized by the highest PH, STD, DSY, DMY, POL, BRX and PTY, whereas Cluster II was characterized by the highest PWT, GY and HI. On

**Table 1.** Mean values of the 13 morpho-agronomic characters of the 28 genotypes studied at Melkassa during 2015/16.

Genotype	DF	DM	PH	PW	SWD	PL	PWT	FSY	DSY	GY	DMY	TKW	HI
104GRD	69.67	109.67	2.31	6.56	1.86	20.87	0.16	22.29	13.11	4.86	21.85	23.14	22.21
89MW 5073	60.33	105.33	1.79	8.28	1.83	22.53	0.23	17.40	9.56	8.90	22.37	30.41	39.84
E 36-1	59.00	107.00	1.61	7.51	1.51	22.07	0.21	16.96	7.56	7.40	19.52	36.74	38.33
Ent. # 64DTN	67.33	108.33	1.51	7.65	1.82	21.20	0.21	17.82	7.33	5.56	16.84	29.54	33.41
Gambella 1107	68.00	111.33	1.79	7.29	1.90	20.33	0.22	21.18	11.33	7.23	23.81	30.83	30.40
ICSB 324	69.00	113.67	1.70	4.81	2.19	25.93	0.14	18.58	13.30	5.37	22.81	25.35	23.91
ICSB 654	50.67	112.00	1.67	5.97	1.63	25.73	0.19	12.56	8.22	6.31	17.44	35.96	39.22
ICSR 93034	69.33	111.67	1.68	5.19	1.99	21.87	0.18	17.16	9.95	6.79	24.04	31.67	29.04
ICSV 700	68.67	116.33	2.25	4.87	2.05	18.07	0.22	26.00	22.89	6.51	32.96	29.02	19.83
ICSV 93046	62.67	106.33	1.73	8.07	1.96	21.73	0.18	19.20	9.04	6.61	20.37	30.12	33.55
IESV 91104 DL	67.67	106.33	1.79	7.86	1.82	19.73	0.24	22.89	13.83	8.43	27.69	28.07	30.82
IESV 92001 DL	65.00	107.67	1.75	9.19	2.08	19.93	0.21	20.27	12.56	8.29	25.67	34.35	32.50
IESV 92008 DL	65.00	106.00	1.64	8.80	1.63	21.20	0.21	14.44	8.89	7.18	20.63	33.89	34.99
IESV 92021 DL	67.00	110.00	1.60	8.09	1.71	19.73	0.19	20.56	10.59	6.22	21.30	27.99	31.70
IESV 92028 DL	66.33	112.67	1.75	7.00	1.77	21.40	0.21	23.78	11.74	6.81	22.37	31.05	30.57
IESV 92089 DL	61.00	106.00	1.65	7.79	1.80	21.00	0.19	14.64	7.96	7.31	19.74	29.99	38.05
IESV 92099 DL	61.67	107.67	1.69	7.91	2.11	21.20	0.19	16.22	8.37	6.28	17.93	33.80	34.86
IESV 92165DL	62.00	111.33	1.74	6.37	1.83	23.33	0.22	18.29	10.30	7.66	22.37	27.26	35.18
IESV 92207 DL	66.67	112.00	1.79	6.10	1.81	22.53	0.19	22.11	15.19	7.66	28.09	34.70	27.35
IS 2331	63.33	107.67	2.17	10.39	1.84	22.33	0.14	20.42	14.59	6.24	24.89	33.65	25.99
Kari Mtama 1	63.33	104.33	1.48	9.56	1.92	20.47	0.20	14.87	9.59	7.82	24.89	28.13	31.84
IESV 92022 DL	58.00	107.33	1.83	10.65	1.80	20.33	0.20	13.16	5.39	7.92	24.19	32.12	39.42
Meko	51.00	104.67	1.62	8.12	1.62	23.00	0.18	12.49	5.07	6.67	15.59	36.99	44.27
MR#22 X IS- 8613/1/2/5-2-1	69.33	112.67	1.60	6.63	1.89	19.13	0.11	14.11	5.67	4.22	13.87	23.54	30.99
MR #22 X IS- 8613/2/3-1-3	70.67	112.00	1.46	4.74	1.59	18.93	0.20	14.64	7.48	5.68	18.15	25.23	34.17
NTJ 2	62.67	105.00	1.74	8.57	1.88	20.33	0.18	19.60	8.74	7.16	20.93	33.17	34.22
S 35	59.33	104.00	1.58	8.32	1.80	20.13	0.17	17.71	6.22	6.57	16.59	33.69	40.27
SDSL 90167	66.33	108.33	1.74	9.14	1.89	19.00	0.22	22.62	9.93	7.30	22.04	27.76	33.63
Mean	63.96	108.83	1.74	7.55	1.84	21.22	0.19	18.28	10.16	6.82	21.75	30.65	32.88
LSD (5%)	9.0	12.5	0.5	5.7	0.4	4.3	0.1	9.1	7.8	2.2	14.9	9.9	23.9
CV%	4.4	3.6	8.1	23.5	6.3	6.4	15.0	15.6	24.1	10.1	21.4	10.1	22.8

\*\*, \* Significant at 1 and 5% probability levels, respectively.

DF= Days to 50% flowering, DM= Days to maturity, PHT= Plant height (m), PWD=Panicle width (cm), SD= Stalk diameter (cm), PL= Panicle length (cm), PWT= Panicle weight (kg), GY= grain yield (ton ha<sup>-1</sup>), DMY= Dry matter yield (ton ha<sup>-1</sup>), TSW= 1000 seed weight (g), HI= Harvest index.

the other hand, Cluster III was characterized by the highest JY, SY, and EY (Appendix Tables S6 and S7).

## DISCUSSION

### Phenotypic and genotypic correlations among agronomic characters

Similar to the present study, Tesso et al. (2011) reported that GY was positively associated with TKW, PW and PL among 200 sorghum accessions included in their studies. In the present study, GY had negative correlation with DM at phenotypic and genotypic levels, which was in agreement with the results of Patted et al. (2011). Furthermore, DM had negative direct effect on GY at

both levels, and their effect via other characters was also mostly negative. These negative correlations may help to select early maturing genotypes with high grain yield for moisture stressed areas where terminal drought is recurrent. Moreover DTF was negatively correlated with such characters as PL, TKW and HI, which was similar to the results of Gaikwad et al. (2013) and Sowmy et al. (2015). Tesso et al. (2011) also reported significant negative correlation between TKW and DTF. Thousand kernel weight was positively correlated with PW and HI. Panicle width and PL had the highest positive direct effect on GY at genetic level, which shows that the correlation explained the true relationship and suggests that direct selection for these traits could be effective. Meanwhile, similar results were previously reported by Sowmy et al. (2015). The phenotypic and genetic residual

**Table 2.** Mean quality characters of sweet sorghum genotypes studied at Melkassa in 2015/16.

Genotype	JY	SY	EY	BRX	POL	PUR
104GRD	11.11	1.48	860.78	17.86	13.17	73.74
89MW5073	7.03	0.85	493.75	16.13	7.27	45.00
E36-1	9.62	1.24	721.08	17.15	10.87	63.01
Ent.#64DTN	9.44	1.18	688.47	16.85	10.86	64.43
Gambella 1107	11.36	1.28	744.81	15.10	10.36	68.83
ICSB324	6.30	0.84	487.48	17.72	14.57	82.44
ICSB654	5.70	0.77	448.23	18.05	13.17	73.06
ICSR93034	8.38	0.97	565.28	15.44	9.23	59.99
ICSV700	3.20	0.40	232.66	16.62	11.42	68.64
ICSV93046	7.51	0.85	496.38	15.17	8.91	59.04
IESV91104DL	10.60	1.30	752.65	16.16	9.87	61.03
IESV92001DL	5.59	0.73	426.89	17.53	7.02	40.13
IESV92008DL	5.04	0.68	393.47	17.95	11.89	66.17
IESV92021DL	7.11	0.73	425.10	13.71	8.09	58.91
IESV92028DL	10.82	1.34	778.14	16.50	10.05	60.88
IESV92089DL	8.38	0.84	489.37	13.40	6.94	51.78
IESV92099DL	5.52	0.72	416.25	17.45	11.70	67.44
IESV92165DL	4.74	0.58	336.82	16.31	11.41	69.84
IESV92207DL	8.41	1.05	608.32	16.61	8.17	49.38
IS2331	6.86	0.80	466.61	15.67	10.54	67.26
Kari Mtama1	4.72	0.56	323.97	15.71	10.95	69.70
IESV92022DL	5.66	0.64	374.53	15.18	11.04	72.75
Meko	8.32	0.89	519.77	14.38	8.04	55.87
MR#22XIS-8613/1/2/5-2-1	8.79	0.99	573.43	14.92	11.69	78.15
MR#22XIS-8613/2/3-1-3	6.42	0.77	448.38	16.03	11.11	69.49
NTJ2	11.39	1.54	892.17	17.97	14.01	77.94
S35	11.70	1.39	808.58	15.88	12.72	80.09
SDSL90167	12.39	1.50	870.31	16.08	10.14	63.17
Mean	7.93	0.96	558.70	16.20	10.54	64.94
LSD (5%)	4.7	0.6	350.9	2.2	5.6	33.4
CV%	18.5	19.7	19.6	4.3	16.6	16.1

\*\* , \* Significant at 1 and 5% probability levels, respectively.

value (0.218 and 0.04, respectively) showed that the characters in the path coefficient analysis accounted for 78.2 and 96% of the variation in GY at phenotypic and genetic levels, respectively (Appendix Tables S3 and S4). The positive associations among GY with PW and PW, TKW and DMY indicate that selecting for positively associated panicle related traits would have a positive effect on GY. Negative correlations were observed among some traits which could be utilized in breeding for negatively correlated traits.

### Correlation among quality characters

The significant ( $p < 0.01$ ) correlations of JY and SY with EY in this study was in agreement with the results of Makanda et al. (2009) and Rutto et al. (2013) and may indicate the usefulness of these characters to improve

EY. Thus, breeding for higher juice type genotypes might result in higher SY and EY than other traits. Brix was found to have no direct contribution to EY, which was against Gaikwad et al. (2013). Generally, correlation analyses indicated greater contribution of JY to higher SY and EY than BRX alone suggesting that improvement for high SY and EY could be achieved through selecting genotypes with high JY. Given the same BRX value, genotypes with greater JY produced higher sugar and ethanol yields (Table 2). Similar to this result, Makanda et al. (2009) reported that genotypes with higher JY and lower BRX had better SY than those genotypes with lower JY and higher BRX. The highest performing genotypes in the present study also confirmed that JY is an important trait for selection of higher SY and EY. Juice yield, which had positive and highly significant phenotypic correlation ( $r = 0.970^{**}$ ) with EY had also the highest direct effect at phenotypic and genotypic levels, which

**Table 3.** Distribution of 28 sweet sorghum genotypes in different clusters.

Cluster	Number of genotypes	Genotypes
Cluster –I	4	104GRD, ICSB324, ICSV700, MR#22 × IS8613/1/2/5-2-1
Cluster-II	16	89MW5073, ICSB654, ICSR93034, ICSV93046, IESV92001DL, IESV92008DL, IESV92021DL, IESV92089DL, IESV92099DL, IESV92165DL, IESV92207DL, IS2331, Kari Mtama 1, IESV92022DL, Meko, MR #22 X IS- 8613/2/3-1-3, MR #22xIS- 8613/2/3-1-3
Cluster-III	8	E36-1, Ent. # 64DTN, Gambella 1107, IESV91104 DL, IESV92028 DL, NTJ2, S35, SDSL90167

was in agreement with the results of Shinde et al. (2013).

### Correlation among agronomic and quality characters

The positive correlation between EY and FSY, and EY and JY at phenotypic and genotypic levels may indicate that sweet sorghum genotypes with improved SY and EY can be utilized for genetic improvement. The correlation between EY and FSY was in agreement with the findings of Alhajturki et al. (2014). Prasad et al. (2013) also reported significant correlations among EY, FSY, SY and JY. The positive correlation ( $r = 0.35^*$ ) of FSY with EY but negligible direct effect at both levels, may indicate that high FSY with high JY is a pre-requisite for high ethanol recovery (Rani and Umakanth, 2012). Hence, these traits could be utilized in the sweet sorghum breeding program. Critical analysis of character association and path analysis suggests that more focus needs to be given in selection programs for traits such as BRX, FSY, and JY. Phenotypic and genotypic path analysis showed that DTF, PH, BRX and POL had positive direct effect and phenotypic and genotypic correlation, but DTM, SW and DSY had negative values with EY. Because their indirect effect via other characters was negligible, their phenotypic and genotypic correlation with EY was mainly due to direct effect. The JY could also be directly related to FSY. Previous studies in sweet sorghum showed that FSY was correlated with PH, SD and JY (Audilakshmi et al., 2010) which it entails. Therefore, selection for FSY needs to take into consideration PH, SD, BRX and JY. Significant genotypic variability among sweet sorghum germplasm was also reported by Ali et al. (2008) and Murray et al. (2009) for PH and juice BRX.

### D-square and cluster mean analyses

It is essential to determine how the influential traits lead to an improved sweet sorghum cultivar. The present study showed significant variation among the genotypes for the traits considered. Improvement in EY and GY could be achieved by direct or indirect selection for high yielding genotypes and for yield components positively associated with these target traits. Genotypes were grouped into three clusters and the future breeding

program utilizing the studied accessions is suggested to be based on the genetic analysis of the various traits to which clusters are predominant. Hence, for future breeding work it could be useful to select individual genotypes from these clusters by considering the special advantages of each cluster and the objectives of the breeding program.

### Advantages of sweet sorghum over commercial sugarcane as sources of bioethanol

Among the 28 genotypes, seven (NTJ 2, SDSL 90167, 104GRD, E36-1, Ent.#64DTN, IESV 92028 DL and S 35) had sugar-rich juice (JY, SY and EY), comparable to one of the commercial sugarcane varieties, NCO334(Cip) but the other commercial sugarcane variety B52298(Wonji-1) was superior in all characters (Appendix Table S8). Sweet sorghum genotypes were harvested in less than four months of growth period at MARC, while sugarcane varieties were 12 months old at the time of sample collection. Sweet sorghum genotypes were grown with less rainfall, whereas sugarcane varieties used all available rain and a large amount of irrigation water. Previous reports by Soltani and Almodares (1994) showed that sweet sorghum grown for ethanol production in India took about four months and water requirement of 8000 m<sup>3</sup> over two cropping seasons, which was four times less than those of sugarcane (12 to 16 months and 36,000 m<sup>3</sup> crop<sup>-1</sup>, respectively). Similarly, it has been shown that the cost of cultivation of sweet sorghum is three times less than that of sugarcane (Dayakar Rao et al., 2004). In this study, sugarcane varieties had higher pol (sucrose), PTY, FSY and BRX than sweet sorghum genotypes (Appendix Table S9). However, in addition to sweet-stalk, which can be sold out to the distillers, grain yield of 4.22 to 8.9 t ha<sup>-1</sup> is an added advantage of sweet sorghum over sugarcane, which can be used as food or for sale by the small holder farmer.

### Conclusion

Those yield and quality components, which were significantly correlated in these study are suggested to receive due attention during sweet sorghum varietal

selection. The study has also shown the possibility of selecting high yielding, early maturing varieties for dry environments where terminal drought is rampant. Considering their less water requirement, faster production cycle, and additional advantage of grain production over sugarcane, sweet sorghums can serve as very good alternatives to sugarcane for use as feedstock to ethanol distillers in the drier areas of the world under the changing climate.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

## ACKNOWLEDGEMENTS

The authors thank the national sorghum coordination program at Melkassa Agricultural Research Center for providing with the seed of the sweet sorghum. The support in juice extraction and provision of test sugarcane by Wonji Sugar Estate is duly acknowledged.

## REFERENCES

- Alhajturki D, Aljamali M, Kanbar A, Azmah F (2014). Potential of Some Sweet Sorghum (*Sorghum bicolor* L) Genotypes under Two Water Regimes for Sugar and Bio-ethanol Production. *Int. J. Sug. Crops Rel. Indust.* 14:376-382.
- Ali ML, Rajewski JF, Baenziger PS, Gill KS, Estridge KM, Dweikat I (2008). Assessment of genetic diversity and relationship among a collection of US sweet sorghum germplasm by SSR markers. *Mol. Breeding* 21:497-509.
- Almodares A, Hadi MR (2009). Production of bio-ethanol from sweet sorghum: A review. *Afr. J. Agric. Res.* 4:772-780.
- Anderson IC (2005). Ethanol from sweet sorghum. Available at: <http://www.energy.iastate.edu/renewable/biomass/cs-anoerobic2.html>. (accessed 14/02/2008)
- Audilakshmi S, Mall AK, Swarnalatha M, Seetharama N (2010). Inheritance of sugar concentration in stalk (brix), sucrose content, stalk and juice yield in sorghum. *Biomed. Bioenerg.* 34:813-820.
- Cruz CD (2006). Program Genes: Biometrical. UFV. Viscose (MG), 382p.
- Dayakar Rao B, Ratnavathi CV, Karthikeyan K, Biswas PK, Rao SS, Vijay Kumar BS, Seetharama N (2004). Sweet sorghum cane for bio-fuel production: A SWOT analysis in Indian context. National Research Centre for Sorghum, Rajendranagar, Hyderabad, AP 500 030 India 20p.
- Donald C M (1968). The breeding of crop ideotypes. *Euphytica* 17:385-403.
- Gaikwad AR, Shinde MS, Repe SS, Dalvi US, Gadakh SR (2013). Physio-biochemical assessment of sweet sorghum genotypes during post rainy season. *J. Acad. Indus. Res.* 1(8).
- Gomez KA, Gomez AA (1984). *Statistical Procedures for Agricultural Research*. 2nd ed. John Wiley and Sons, New York. 680p.
- Hills F J, Lewellen R T, Skoyen I O (1990). Sweet Sorghum Cultivars for Alcohol Production. *Calif. Agric.* 44:14-16.
- Hodes GS (2006). Expanding Biofuels in Africa. Opportunities for South-South technological cooperation.
- Huligol RV, Ramakrishna, Govind M (2004). A trial with sweet sorghum. CFC and ICRISAT.; In Alternative uses of sorghum and pearl millet in Asia, proceedings of the Expert Meeting, ICRISAT, Andhra Pradesh, India. pp. 333-337
- Koeppen S, Reinhardt G, Gaertner S (2009). Assessment of Energy and Greenhouse Gas: Inventories of Sweet Sorghum for First and Second Generation Bioethanol. *FAO Environmental and Natural Resources Service Series*, No 30, FAO, Rome.
- Makanda I, Tongona P, Derera J (2009) Quantification of genotypic variability for stem sugar accumulation and associated traits in new sweet sorghum varieties. *Afr. Crop Sci. Conf. Proc.* 9:391-398.
- McGuire SJ (2008). Path-dependency in plant breeding: Challenges facing participatory reform in the Ethiopia sorghum improvement program. *Agric. Syst.* 96:139-149.
- Murray SC, Rooney WL, Martha T, Hamblin MT, Sharon E, Mitchell SE, Kresovich S (2009). Sweet sorghum genetic diversity and association mapping for brix and height. *Plant Genome* 2:48-62.
- Patted VS, Lakkundi BS, Dandagi MR, Kamatar MY, Hakkalappanavar SS (2011). Correlation and path analysis in F3 material for grain yield and grain mold resistance. *Int. J. Plant Prot.* 4:292-297.
- Pei Z, Gao J, Chen Q, Wei J, Li Z, Luo F, Shi L, Ding B, Sun S (2010). Genetic diversity of elite sweet sorghum genotypes assessed by SSR markers. *Biol. Plant.* 54:653-658.
- Prasad S, Kumar A, Muralikrishna KS (2013). Assessment of ethanol yield associated characters in sweet sorghum. Centre for Environment, Science, and Climate Resilient Agriculture, Indian Agricultural Research Institute, New Delhi-110012, India Maydica electronic publication 58:299-303.
- Putnam D H, Lueschen W E, Kanne B K, Hoverstad T R (1991). A Comparison of Sweet Sorghum Cultivars and Maize for Ethanol Production. *J. Prod. Agric.* 4:377-381.
- Rani Ch, Umakanth AV (2012). Genetic variation and trait inter-relationship in F1 hybrids of sweet sorghum (*Sorghum bicolor* (L) Moench). *J. Trop. Agric.* 50:80-83.
- Rao CR (1952). *Advanced Statistical Methods in Biometrics Research*. John Wiley and Sons, New York.
- Rutto LK, Xu Y, Brandt M, Ren S, Maru K (2013). Juice, Ethanol, and Grain Yield Potential of Five Sweet Sorghum (*Sorghum bicolor* [L] Moench) Cultivars. *J. Sust. Bioen. Syst* 3:113-118.
- Schaffert RE, Gourley LM (1982). Sorghum as an energy source. In: Mertin JV (ed.), *Sorghum in the eighties*, Proc. Int. Symp. Sorghum, 2-7 Nov 1981, ICRISAT, Patancheru, AP, India; pp. 605-624.
- Shinde MS, Repe SS, Gaikwad AR, Dalvi US, Gadakh SR (2013). Physio-biochemical assessment of sweet sorghum genotypes during post rainy season. *J. Acad. Indus. Res.* 1(8).
- Soltani A, Almodares A (1994). Evaluation of the investments in sugar beet and sweet sorghum production. National Convention of Sugar Production from Agriculture Products, 13-16 March 1994, Shahid Chamran University, Ahwaz, Iran.
- Sowmy HH, Brunda SM, Deepakkumar GS, Vidya G, Kamatar MY (2015). Estimation of Correlation Coefficients and Path for Yield Traits in Grain Mold Tolerant F3 Progenies of Sorghum. *Int. J. Sci. Res. (IJSR) ISSN (Online)* pp. 2319-7064.
- Teetor V H, Duclos D V, Wittenberg E T, Young K M, Chawhuaymak J, Riley M R, Ray D T (2011). Effects of Planting Date on Sugar and Ethanol Yield of Sweet Sorghum Grown in Arizona. *Indus. Crops Prod.* 34:1293-1300.
- Tesso T, Tirfessa A, Mohammed H (2011). Association between morphological traits and yield components in the durra sorghums of Ethiopia. *Hereditas* 148:98-109.
- Wortmann C S, Liska A J, Ferguson R B, Lyon D J, Klein R N, Dweikat I (2010). Dry land Performance of Sweet Sorghum and Grain Crops for Biofuel in Nebraska. *Agron. J.* 102:319-326.

## APPENDIX

**Table S1.** List of the 28 Sweet sorghum genotypes used in the evaluation study at Melkassa in 2015.

SN	Genotype	Source
1	ICSV 93046	ICRISAT
2	IESV 92008 DL	ICRISAT
3	Kari Mtama 1	ICRISAT
4	NTJ 2	ICRISAT
5	IESV 91104 DL	ICRISAT
6	104GRD	ICRISAT
7	IESV 92165DL	ICRISAT
8	MR #22 X IS 8613/2/3-1-3	ICRISAT
9	ICSR 93034	ICRISAT
10	MR # 22 X IS 8613/1/2/5-2-1	ICRISAT
11	S 35	ICRISAT
12	IESV 92028 DL	ICRISAT
13	ICSB 654	ICRISAT
14	ICSB 324	ICRISAT
15	ICSV 700	ICRISAT
16	IESV 92022 DL	ICRISAT
17	IS 2331	ICRISAT
18	IESV 92021 DL	ICRISAT
19	IESV 92001 DL	ICRISAT
20	Ent. # 64DTN	ICRISAT
21	SDSL 90167	ICRISAT
22	E 36-1	ICRISAT
23	89MW 5073	ICRISAT
24	IESV 92099 DL	ICRISAT
25	IESV 92089 DL	ICRISAT
26	IESV 92207 DL	ICRISAT
27	Gambella 1107	Released variety
28	Meko	Released variety

**Table S2.** Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 11 agronomic characters from 28 sweet sorghum genotypes.

Trait	DF	DM	PHT	PWD	SD	PL	PWT	GY	DMY	TSW	HI
DF	1	0.48**	0.19	-0.36*	0.40*	-0.46**	-0.07	-0.3	0.36*	-0.68**	-0.77**
DM	0.59**	1	0.28	-0.76**	0.23	0.06	-0.15	-0.43*	0.28	-0.38*	-0.62**
PHT	0.23	0.48**	1	-0.02	0.3	-0.08	-0.09	-0.06	0.58**	-0.12	-0.61**
PWD	-0.44*	-0.87**	-0.11	1	-0.09	-0.21	0.12	0.43*	-0.03	0.34*	0.39*
SD	0.51**	0.32	0.39*	-0.1	1	-0.04	-0.18	-0.07	0.38*	-0.3	-0.54**
PL	-0.54**	0.03	-0.15	-0.23	-0.02	1	-0.2	-0.02	-0.18	0.3	0.16
PWT	-0.08	-0.14	-0.22	0.16	-0.25	-0.3	1	0.73**	0.38*	0.17	0.24
GY	-0.32	-0.61**	-0.09	0.50**	-0.12	0.02	0.79**	1	0.48**	0.43*	0.35*
DMY	0.55**	0.59**	0.79**	-0.01	0.43*	-0.23	0.52**	0.61**	1	-0.05	-0.61**
TSW	-0.79**	-0.58**	-0.22	0.38*	-0.41*	0.37*	0.09	0.40*	-0.11	1	0.49**
HI	-1.00**	-1.00**	-1.00**	0.63**	-0.79**	0.28	0.28	0.47**	-0.37*	0.76**	1

\*\*, \*: Significant at 1 and 5% probability levels, respectively. DF= Days to 50% flowering; DM= days to maturity; PHT= plant height (m); PWD=panicle width (cm); SD= stalk diameter (cm); PL= panicle length (cm); PWT= panicle weight (kg); GY= grain yield (ton ha<sup>-1</sup>); DMY= dry matter yield (ton ha<sup>-1</sup>); TSW= 1000 seed weight (g); HI= harvest index.



**Table S3.** Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of ten traits on grain yield in 28 sweet sorghum genotypes tested at MARC.

Trait	DF	DM	PHT	PWD	SD	PL	PWT	DMY	TSW	HI	r <sub>p</sub>
DF	<b>0.406</b>	-0.077	0.002	-0.025	0.024	-0.103	-0.009	0.353	-0.044	-0.821	<b>-0.298</b>
DM	0.196	<b>-0.160</b>	0.003	-0.053	0.013	0.014	-0.020	0.277	-0.024	-0.666	<b>-0.435*</b>
PHT	0.075	-0.044	<b>0.009</b>	-0.001	0.018	-0.017	-0.013	0.566	-0.008	-0.654	<b>-0.060</b>
PWD	-0.147	0.122	0.000	<b>0.070</b>	-0.005	-0.047	0.017	-0.033	0.022	0.421	<b>0.430*</b>
SD	0.164	-0.036	0.003	-0.006	<b>0.058</b>	-0.010	-0.025	0.374	-0.019	-0.575	<b>-0.071</b>
PL	-0.187	-0.010	-0.001	-0.014	-0.003	<b>0.224</b>	-0.028	-0.174	0.019	0.167	<b>-0.019</b>
PWT	-0.027	0.023	-0.001	0.008	-0.011	-0.045	<b>0.138</b>	0.368	0.011	0.252	<b>0.727**</b>
DMY	0.146	-0.045	0.005	-0.002	0.022	-0.040	0.052	<b>0.982</b>	-0.003	-0.651	<b>0.475**</b>
TSW	-0.277	0.060	-0.001	0.023	-0.018	0.067	0.024	-0.045	<b>0.065</b>	0.528	<b>0.427*</b>
HI	-0.312	0.100	-0.006	0.027	-0.031	0.035	0.033	-0.597	0.032	<b>1.071</b>	<b>0.352*</b>

Residual= 0.218. DF= Days to 50% flowering; DM= days to maturity; PHT= plant height (m); PWD=panicle width (cm); SD= stalk diameter (cm); PL= panicle length (cm); PWT= panicle weight (kg); GY= grain yield (ton ha<sup>-1</sup>); DMY= dry matter yield (ton ha<sup>-1</sup>); TSW= 1000 seed weight (g); HI= harvest index.

**Table S4.** Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of ten traits on grain yield in 28 sweet sorghum genotypes tested at Melkassa (2015).

Trait	DF	DM	PHT	PWD	SD	PL	PWT	DMY	TSW	HI	r <sub>g</sub>
DF	<b>0.605</b>	-0.240	-0.011	-0.126	-0.101	-0.505	-0.057	0.119	-0.048	0.064	<b>-0.315</b>
DM	0.358	<b>-0.405</b>	-0.023	-0.252	-0.064	0.032	-0.100	0.128	-0.035	0.070	<b>-0.612**</b>
PHT	0.137	-0.192	<b>-0.048</b>	-0.032	-0.078	-0.141	-0.159	0.172	-0.013	0.052	<b>-0.092</b>
PWD	-0.265	0.354	0.005	<b>0.288</b>	0.021	-0.219	0.115	-0.002	0.023	-0.031	<b>0.500**</b>
SD	0.307	-0.130	-0.019	-0.030	<b>-0.200</b>	-0.018	-0.178	0.094	-0.025	0.039	<b>-0.120</b>
PL	-0.324	-0.014	0.007	-0.067	0.004	<b>0.941</b>	-0.215	-0.051	0.022	-0.014	<b>0.017</b>
PWT	-0.049	0.057	0.011	0.046	0.050	-0.284	<b>0.712</b>	0.113	0.006	-0.014	<b>0.789**</b>
DMY	0.332	-0.240	-0.038	-0.003	-0.087	-0.221	0.372	<b>0.216</b>	-0.006	0.018	<b>0.612**</b>
TSW	-0.477	0.234	0.010	0.110	0.082	0.344	0.065	-0.023	<b>0.061</b>	-0.037	<b>0.404*</b>
HI	-0.793	0.579	0.051	0.182	0.157	0.259	0.200	-0.079	0.047	<b>-0.049</b>	<b>0.474**</b>

Residual =0.04. DF= Days to 50% flowering; DM= days to maturity; PHT= plant height (m); PWD=panicle width (cm); SD= stalk diameter (cm); PL= panicle length (cm); PWT= panicle weight (kg); GY= grain yield (ton ha<sup>-1</sup>); DMY= dry matter yield (ton ha<sup>-1</sup>); TSW= 1000 seed weight (g); HI= harvest index.

**Table S5.** Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among eight quality characters from 28 sweet sorghum genotypes.

Trait	FSY	DSY	JY	SY	EY	BRX	POL	PUR
FSY	1	0.80**	0.3	0.35*	0.35*	0.16	-0.06	-0.14
DSY	0.93**	1	-0.21	-0.15	-0.15	0.24	-0.01	-0.12
JY	0.31	-0.2	1	0.97**	0.97**	-0.08	0.04	0.08
SY	0.35*	-0.13	0.97**	1	1.00**	0.16	0.18	0.14
EY	0.35*	-0.13	0.97**	1.00**	1	0.16	0.18	0.14
BRX	0.16	0.26	-0.09	0.15	0.15	1	0.59**	0.24
POL	-0.15	-0.02	0.01	0.18	0.18	0.67**	1	0.92**
PUR	-0.29	-0.17	0.05	0.14	0.14	0.32	0.92**	1

\*\* , \* : Significant at 1 and 5% probability levels, respectively. FSY= Fresh stalk yield (ton ha<sup>-1</sup>); DST= Dry stalk yield (ton ha<sup>-1</sup>); JUY= Juice yield (ton ha<sup>-1</sup>); SUY= Sugar yield (ton ha<sup>-1</sup>); ETY = Ethanol yield (L ha<sup>-1</sup>); BRX= Brix%; POL= POL juice.

**Table S6.** Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of nine traits on ethanol yield in 28 sweet sorghum genotypes tested at Melkassa.

Trait	DTF	DTM	PH	SD	FSY	DSY	JY	BRX	POL	$r_p$
DTF	<b>0.016</b>	-0.010	0.004	-0.007	0.022	-0.017	0.135	0.011	0.001	<b>0.155</b>
DTM	0.008	<b>-0.021</b>	0.005	-0.004	0.014	-0.019	-0.198	0.030	0.004	<b>-0.181</b>
PH	0.003	-0.006	<b>0.020</b>	-0.005	0.023	-0.026	-0.030	0.045	0.002	<b>0.027</b>
SD	0.006	-0.005	0.006	<b>-0.016</b>	0.015	-0.016	-0.152	0.033	0.002	<b>-0.128</b>
FSY	0.009	-0.007	0.012	-0.006	<b>0.040</b>	-0.029	0.292	0.037	-0.001	<b>0.346*</b>
DSY	0.008	-0.011	0.014	-0.007	0.032	<b>-0.037</b>	-0.200	0.054	0.000	<b>-0.147</b>
JY	0.002	0.004	-0.001	0.003	0.012	0.008	<b>0.959</b>	-0.018	0.001	<b>0.970**</b>
BRX	0.001	-0.003	0.004	-0.002	0.006	-0.009	-0.077	<b>0.226</b>	0.010	<b>0.157</b>
POL	0.001	-0.004	0.002	-0.002	-0.002	0.000	0.035	0.134	<b>0.017</b>	<b>0.182</b>

Residual = 0.049. DTF= Days to 50% flowering; DM= Days to maturity; PHT= plant height (m); SD= stalk diameter (cm); FSY= fresh stalk yield (ton ha<sup>-1</sup>); DST= dry stalk yield (ton ha<sup>-1</sup>); JUY= juice yield (ton ha<sup>-1</sup>); SUY=sugar yield (ton ha<sup>-1</sup>); BRX= Brix%; POL= Pol % juice.

**Table S7.** Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of nine traits on ethanol yield in 28 sweet sorghum genotypes tested at Melkassa Agricultural Research Center (2015/2016).

Trait	DTF	DTM	PH	SD	FSY	DSY	JY	BRX	POL	$r_g$
DTF	<b>0.059</b>	-0.044	0.006	-0.014	-0.049	0.048	0.179	0.020	0.002	<b>0.207</b>
DTM	0.035	<b>-0.074</b>	0.012	-0.009	-0.037	0.063	-0.310	0.062	0.006	<b>-0.252</b>
PH	0.013	-0.035	<b>0.024</b>	-0.011	-0.044	0.069	-0.034	0.053	0.003	<b>0.040</b>
SD	0.030	-0.024	0.010	<b>-0.028</b>	-0.031	0.039	-0.191	0.032	0.004	<b>-0.160</b>
FSY	0.042	-0.040	0.016	-0.013	<b>-0.069</b>	0.079	0.305	0.036	-0.003	<b>0.354*</b>
DSY	0.033	-0.054	0.020	-0.013	-0.064	<b>0.085</b>	-0.197	0.059	0.000	<b>-0.130</b>
JY	0.011	0.023	-0.001	0.005	-0.021	-0.017	<b>0.990</b>	-0.020	0.000	<b>0.970**</b>
BRX	0.005	-0.020	0.006	-0.004	-0.011	0.022	-0.086	<b>0.225</b>	0.015	<b>0.152</b>
POL	0.007	-0.021	0.003	-0.004	0.010	-0.002	0.009	0.151	<b>0.022</b>	<b>0.176</b>

Residual = 0.030. DTF= Days to 50% flowering; DM= Days to maturity; PHT= Plant height (m); SD= Stalk diameter (cm); FSY= Fresh stalk yield (ton ha<sup>-1</sup>); DST= Dry stalk yield (ton ha<sup>-1</sup>); JUY= Juice yield (ton ha<sup>-1</sup>); SUY= Sugar yield (ton ha<sup>-1</sup>); BRX= Brix%; POL= Pol % juice.

**Table S8.** The summary of cluster means of 19 quantitative traits for the sweet sorghum genotypes based on data set.

Characters	Cluster means			Overall Mean
	I	II	III	
Days to 50% flowering	69.17	62.35	64.58	65.37
Days to maturity	113.09	108.25	107.87	109.74
Plant height	1.97	1.71	1.69	1.79
Panicle width	5.72	7.83	7.92	7.16
Stem diameter	2.00	1.82	1.80	1.87
Panicle length	21.00	21.62	20.52	21.05
Panicle weight	0.16	0.19	0.21	0.19
Fresh stalk yield	20.25	16.78	20.32	19.12
Dry stalk yield	13.74	9.55	9.59	10.96
Grain yield	5.24	7.10	7.06	6.47
Juice yield	7.35	6.59	10.92	8.29
Sugar yield	0.93	0.78	1.35	1.02
Ethanol yield	538.59	452.07	782.03	590.90
Brix	16.78	15.92	16.46	16.39
Pol	12.71	9.72	11.11	11.18
Purity	75.74	60.99	67.42	68.05
Dry matter yield	22.87	21.73	21.22	21.94
Thousand seed weight	25.26	31.64	31.36	29.42
Harvest index	24.24	34.50	33.96	30.90

**Table S9.** Yield in bio energy traits for 28 sweet sorghum genotypes and two commercial sugarcane varieties.

<b>Sweet sorghum genotypes</b>	<b>FSY</b>	<b>JY</b>	<b>SY</b>	<b>EY</b>	<b>BRX</b>	<b>POL</b>	<b>PUR</b>
<b>104GRD</b>	<b>3.34</b>	<b>1.25</b>	<b>0.16</b>	<b>0.1</b>	<b>17.86</b>	<b>13.17</b>	<b>73.74</b>
89MW 5073	2.61	1.06	0.13	0.07	16.13	7.27	45
<b>E 36-1</b>	<b>2.54</b>	<b>1.28</b>	<b>0.17</b>	<b>0.1</b>	<b>17.15</b>	<b>10.87</b>	<b>63.01</b>
<b>Ent. # 64DTN</b>	<b>2.67</b>	<b>1.42</b>	<b>0.18</b>	<b>0.1</b>	<b>16.85</b>	<b>10.86</b>	<b>64.43</b>
Gambella 1107	3.18	1.31	0.15	0.09	15.1	10.36	68.83
ICSB 324	2.79	0.72	0.1	0.06	17.72	14.57	82.44
ICSB 654	1.88	0.59	0.08	0.05	18.05	13.17	73.06
ICSR 93034	2.57	0.97	0.11	0.07	15.44	9.23	59.99
ICSV 700	3.9	0.29	0.04	0.02	16.62	11.42	68.64
ICSV 93046	2.88	1.36	0.15	0.09	15.17	8.91	59.04
IESV 91104 DL	3.43	1.22	0.15	0.09	16.16	9.87	61.03
IESV 92001 DL	3.04	1.05	0.14	0.08	17.53	7.02	40.13
IESV 92008 DL	2.17	0.76	0.1	0.06	17.95	11.89	66.17
IESV 92021 DL	3.08	1.32	0.14	0.08	13.71	8.09	58.91
<b>IESV 92028 DL</b>	<b>3.57</b>	<b>1.62</b>	<b>0.2</b>	<b>0.12</b>	<b>16.5</b>	<b>10.05</b>	<b>60.88</b>
IESV 92089 DL	2.2	0.88	0.09	0.05	13.4	6.94	51.78
IESV 92099 DL	2.43	1.06	0.14	0.08	17.45	11.7	67.44
IESV 92165DL	2.74	1.08	0.13	0.08	16.31	11.41	69.84
IESV 92207 DL	3.32	0.94	0.12	0.07	16.61	8.17	49.38
IS 2331	3.06	0.78	0.1	0.06	15.67	10.54	67.26
Kari Mtama 1	2.23	0.71	0.08	0.05	15.71	10.95	69.7
IESV 92022 DL	1.97	1.04	0.12	0.07	15.18	11.04	72.75
Meko	1.87	0.99	0.11	0.06	14.38	8.04	55.87
MR # 22 X IS 8613/1/2/5-2-1	2.12	1.13	0.13	0.07	14.92	11.69	78.15
MR #22 X IS 8613/2/3-1-3	2.2	0.96	0.12	0.07	16.03	11.11	69.49
<b>NTJ 2</b>	<b>2.94</b>	<b>1.48</b>	<b>0.2</b>	<b>0.12</b>	<b>17.97</b>	<b>14.01</b>	<b>77.94</b>
<b>S 35</b>	<b>2.66</b>	<b>1.54</b>	<b>0.18</b>	<b>0.11</b>	<b>15.88</b>	<b>12.72</b>	<b>80.09</b>
<b>SDSL 90167</b>	<b>3.39</b>	<b>1.71</b>	<b>0.21</b>	<b>0.12</b>	<b>16.08</b>	<b>10.14</b>	<b>63.17</b>
<b>NCO-334(Cip)</b>	<b>26</b>	<b>1.55</b>	<b>0.21</b>	<b>0.12</b>	<b>18.49</b>	<b>17.08</b>	<b>92.4</b>
B52/298(Wonji-1)	30	2.8	0.42	0.25	20.13	18.68	92.8