

Rationale and Objectives

In recent years, energy security, climate change and sustaining rural economies has become an important priority for researchers. Bioenergy has an unique place and can play an important role in energy security, environment and rural development. Most of the bioenergy at present is based on ethanol production from grains. However, new dedicated feed-stocks are needed for sustained biofuel production and minimize competition between fuel, food and feed production. Dry matter production, grain yield and composition of plants are important for potential use as biofuel crop. Sorghum (*Sorghum bicolor* L. Moench) exploits all these possibilities due to inherent capacity to produce high biomass and store sugars in stalks (sweet sorghum). Sweet sorghum has high potential for biomass and sugar production with relatively low inputs compared to other bioenergy crops. There is a wide array of genetic diversity and germplasm collections in sweet sorghum. However, at present we do not have detailed knowledge about the morphological, physiological and genetic traits associated with improved efficiency of biofuel production. Such knowledge is necessary for crop selection and development of sustained and efficient bioenergy cropping systems.

The objectives of this research were (a) to characterize and evaluate sweet sorghum germplasm for traits associated for improved sugar yield and biofuel production; and (b) to identify high yielding genotypes that can be used in breeding programs for hybrid production and crop improvement.

Materials and Methods

Sweet sorghum germplasm consisting of 280 genotypes were grown under field conditions in Manhattan, Kansas during 2007 (irrigated) and 2008 (irrigated and rainfed conditions). Each genotype was grown in 3-m long rows. Two representative plants for each genotype were tagged for measuring physiological and yield traits. Data on physiological traits (chlorophyll content, SPAD meter, Spectrum Technologies, Plainfield, IL); chlorophyll fluorescence, pulse modulated fluorometer, OptiScience, Hudson, NH) were measured at flowering and seed-filling stages. At final harvest, data on plant height, stem girth, brix value, and juice volume were measured. The juice volume was obtained by subtracting stem dry weight from stem fresh weight and expressed in milliliter plant⁻¹. Juice volume and brix values were used to estimate sugar yield. Based on data for brix value and juice volume over three seasons, only 78 genotypes were identified to have extractable juice, thus, only these genotypes were used for analyses of sugar yield. Relative sugar yield reduction due to water stress was estimated as the difference between the mean of two irrigated seasons (2007 and 2008) and one rainfed season (2008) and expressed as percentage. The experimental design was a randomized complete block design. The three seasons were used as replications and genotype means were separated using LSD.

Figure 1. Field evaluation of sweet sorghum germplasm under rainfed (left) and irrigated (right) conditions during 2008 at Manhattan, KS.



Experimental Results

There was significant variation in genotypes for physiological (SPAD and fluorescence values) and yield traits (plant height, stem girth, brix percentage, juice volume and sugar yield) (Table 1). The average percent reduction in sugar yield in rainfed conditions compared to irrigated was 61% (range 1 to 98%).

Table 1. Mean and range for different traits of sweet sorghum germplasm averaged across three seasons (2007 irrigated, 2008 irrigated and rainfed). Least Significant Differences based on three replications (seasons) was used to separate genotype means. [*,** Significant at P<0.05 and 0.01, respectively].

Trait	Genotypes	Mean	Range	CV (%)	LSD
SPAD	280	52.6	31.5-73.5	12.2	10.28**
Fo /Fm (Thylakoid membrane damage)	280	0.25	0.21-0.40	16.2	0.065**
Fv/Fm (PS II photochemical efficiency)	280	0.75	0.49-0.80	6.4	0.077*
Plant height (cm)	280	284	93 – 427	18.3	83.31**
Stem girth (mm)	280	16.6	7.0 - 29.6	14.3	3.81**
Brix (%)	78	13.4	6 - 21	24.6	5.35**
Juice volume (ml plant ⁻¹)	78	436	85- 1185	40.5	285.1**
Sugar yield (ml plant ⁻¹)	78	56	17-118	9.5	40.9**
Relative sugar yield reduction due to water stress (%)	78	60.6	1.0- 98.1	23.6	28.7**

Based on three seasons of data the entire sweet sorghum panel was ranked for brix, juice and sugar yield. Highest brix value was observed in genotype Dura Huria (20.8 %) followed by Smith, Masuda Blackseed, Leoti-pelier, Tracy, Top-76-6 and Dale (ranging from 18.0 – 18.7 %) (Table 2). Lowest brix was recorded in genotypes Iswa, followed by Sairwa, MN 1540, MN 2386, MN 2238, MN 2363 and MN 1921 (<7.0 %).

Juice volume significantly varied among genotypes. Highest juice volume was observed in genotype MN 4566 (914 ml plant⁻¹), followed by MN 4564, MN 2109, Co-1, MN 4553, MN 2238, Wray, Sanyagie, MN 2386 and MN 2063 (< 700 ml plant⁻¹). The lowest juice yield was observed in Ames Amber (125 ml plant⁻¹) followed by HC 41-13, MN 2894, Luel, N111, Darso-28, Red-Amber, IS 2352 and Collier (<200 ml plant⁻¹).

Similarly, maximum sugar yield was recorded in genotype Wray (118 ml plant⁻¹), followed by MN 4564, Caxa, IS2131, Top-76-6, MN 4553, Smith, Dale, MN 4566, and No-6 Gambela, Co1, Sanyagie and Wad-fur-white (<81 ml plant⁻¹) (Table 3). The lowest sugar yield was observed in Ames Amber (17 ml plant⁻¹) followed by IS 2352, Luel, MN 2894, HC41-13, Red-amber, Darso 28, Iswa (<30 ml plant⁻¹).

Table 2. Ranking of genotypes (highest and lowest) for brix values.

High Brix (%)	Origin	Low Brix (%)	Origin
Dura Huria (20.8)	Zaire	Iswa (6.2)	Tanzania
Smith (18.7)	USA	Sairwa (6.2)	Nigeria
Masuda Black Seed (18.7)	Japan	MN 1540 (6.4)	Sudan
Leoti-Peltier (18.5)	*	MN 2386 (6.7)	Tanzania
Tracy (18.4)	*	MN 2238 (6.8)	*
Top 76-6 (18.2)	USA	MN 2363 (7.2)	Tanzania
Dale (18.0)	*	MN 1921 (7.3)	Malawi
Brawley (18.0)	*	MN 2161 (7.3)	Malawi
MN 4135 (17.8)	Yugoslavia	IS 2109 (8.0)	Ethiopia
N 111 (17.7)	USA	MN 1644 (8.1)	Tanzania

Table 3. Ranking of genotypes (highest and lowest) for sugar yield.

High Sugar Yield (ml plant ⁻¹)	Origin	Low Sugar Yield (ml plant ⁻¹)	Origin
Wray (118.4)	*	Ames Amber (17.1)	*
MN 4564 (105.0)	Ethiopia	IS 2352 (19.3)	Pakistan
Caxa (100.7)	Mexico	Luel (19.6)	Sudan
IS 2131(98.9)	Ethiopia	MN 2894 (20.8)	Syria
Top 76-6 (98.2)	USA	H.C 41-13 (22.2)	*
MN 4553 (93.9)	India	Red Amber (26.3)	Australia
Smith (89.6)	USA	Darso 28 (28.6)	Guadeloupe, Basse-Terre
Dale (88.3)	*	Iswa (30.5)	Tanzania
MN 4566 (88.0)	Ethiopia	N 111 (32.0)	USA
No. 6 Gambela (85.1)	Ethiopia	MN 1540 (32.2)	Sudan

* Origin unknown

There were about 20 genotypes which consistently ranked higher for both sugar and juice yield across seasons. Likewise there were about 6 genotypes with high brix and sugar yield. Similarly, there were about 25 genotypes which consistently had lower sugar and juice yields across seasons. Based on this research we identified 20 best and worst performers in terms of traits associated with biofuel production.

There were differences in performance of genotypes under rainfed and irrigated conditions, suggesting that some genotypes performed better than others. Based on relative sugar yield reduction (comparing two irrigated and one rainfed season) genotypes MN 2386, IS 2131, MN 2238, Opemba-nonpha, MN 600 and Atlas (>80%) were identified as susceptible to water stress. Minimum yield reduction due to water stress (rainfed conditions) was observed in genotypes MN 818, Red Amber, Wenabu, Leoti-Peltier, Brawley and Nlolongu (<5%).

Conclusions

The evaluation of the sweet sorghum germplasm showed a large and significant variation in physiological (chlorophyll content, chlorophyll fluorescence), morphological (plant height and stem girth) and sugar yield traits (brix, juice volume and dry matter production) associated with biofuel production. Irrigated conditions produced significantly higher sugar yields compared to rainfed conditions. However, genotypes differed in their response to water stress. Genotypes with greater potential for bioenergy and drought tolerance were identified and are being further investigated.

Future Research

The selected genotypes for varying sugars, brix, and juice characters will be further evaluated in replicated field tests. Furthermore, these genotypes will be used to identify QTL markers using bulk line analysis.

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