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GENETIC DIVERSITY STUDIES IN SWEET SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH], A CANDIDATE CROP FOR BIOFUEL PRODUCTION

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SUMMARY

A field experiment was conducted at IIMR during *rabi* 2016-17 to study the nature and magnitude of genetic diversity and identify promising parents in sweet sorghum for biofuel related traits like brix (%), green cane yield and related characters in 68 sweet sorghum genotypes. Depending on the D2 values, these were grouped into 9 clusters. Cluster II was the largest consisting of 17 genotypes and cluster IX was the least with one genotype. Among the 13 characters studied, days to 50% flowering contributed the most followed by 100 seed weight towards the divergence of genotypes. The highest intra cluster distance was observed for cluster VIII while the maximum inter cluster distance was observed between clusters IV and IX. Based on the D2 values, the genotypes from diverse clusters would be derived and used in the hybridization program to generate wide range of transgressive segregants for genetic enhancement of sweet sorghum for biofuel related traits.

Key words : sweet sorghum, genetic diversity, brix, green cane yield

Sweet sorghum is promising as a multifunctional crop not only for its high economic value but also due to its high sustainable productivity (40-50 t/ha of green cane yield) and to the wide range of its products (grains, sucrose and lignocelluloses).

Sweet sorghum thus can be considered a crop of universal value, because it can be grown in all continents, in tropical subtropical and temperate regions as well as poor quality soils and in semi arid regions (Reddy and Sanjana, 2003). Recently, interest in utilization of sweet sorghum for ethanol production has been increased in India as sweet sorghum has other benefits over sugarcane and maize as feedstock for ethanol production. It requires only one half of the water required to grow maize and around one eighth of the water required to grow sugarcane; and has the least cost of cultivation which is around one fifth of the cost for growing sugarcane. It grows in short duration (115-120 days) when compared with sugarcane which takes 12-18 months. The ethanol production through sweet sorghum will help boost bio fuel production at a lesser cost than the sugarcane molasses-based ethanol thus benefiting farmers. Hence there is a need to intensify research on sweet sorghum. For any effective breeding programme, choice of divergent parents is of prime importance because the level of heterosis exhibited by a hybrid is a function of genetic divergence between parents. Therefore, a meaningful classification of germplasm and other available material will enable the sweet sorghum breeder to identify the best parents with wide genetic divergence and to utilize the selected divergent parents in hybridization programme. Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Among the several multivariate analyses, the Mahalonobis D^2 (1936) technique is a unique tool for identifying the degree of genetic divergence in a biological population. An attempt in the present study has been made to study the nature and magnitude of genetic divergence and identify promising parents for biofuel related traits like brix (%), green cane yield and other characters in sweet sorghum genotypes.

MATERIALS AND METHODS

The material for the present study comprised

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of 68 sweet sorghum genotypes which included germplasm from different countries, advanced breeding stocks and varieties. The experiment was conducted at the IIMR farm (Indian Institute of Millets Research), Rajendranagar, Hyderabad during *rabi* 2016-17. Each genotype was raised in 2 rows of 4 m length spaced at 60 cm with inter plant distance of 15 cm. The experiment was laid out in a Randomized Block Design with three replications. In each entry, five randomly selected plants were utilized to collect data on different characters *viz.*, plant height (cm), days to 50 per cent flowering, number of leaves per plant, leaf length (cm), leaf width (cm), number of nodes per plant, stem girth (cm), green cane yield (t ha^{-1}), juice volume (L/ha), brix content (%), juice extraction (%), 100 seed weight (g) and grain yield per plant (g) and the data was subjected to statistical analysis. Wilk's criterion was used to test the significance of pooled differences in mean values for all characters. Genetic diversity was studied using Mahalanobis D^2 and clustering of genotypes was done according to Tocher's method as per Rao (1952) while principal component analysis was carried out as per Rao (1964).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on D^2 statistics, the 68 genotypes were grouped into 9 clusters with variable number of genotypes revealing the presence of considerable amount of genetic diversity in the material (Table 1). Cluster II had the maximum number of 17 genotypes followed by cluster III with 16 genotypes and cluster I with14 genotypes. Cluster IV had 7 genotypes while cluster V had 5 genotypes. Clusters VI to IX were distinct from the rest with each one of them having less number of genotypes indicating their uniqueness from breeding point of view.

The intra and inter cluster D^2 values among 68 genotypes (Table 2) revealed highest intra cluster distance for cluster VIII (82.86) followed by cluster VI (78.42) and cluster V (71.04). Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past history of selection in developmental traits and degree of general combing ability (Dikshit and Swain, 2000). The least intra cluster distance was exhibited by cluster VII followed by cluster II, indicating the similarity of genotypes. The inter cluster D^2 values ranged from 47.48 to 573.07, the maximum inter cluster distance was observed between IV and IX (573.07) followed by I and IX (561.25) and III and IX (497.71) which indicated that the crosses among the genotypes included in these clusters may give high heterotic response and thus better segregants. The minimum inter cluster distance was observed between cluster II and III (47.48) indicating the close relationship among the genotypes in these clusters which are mostly from India and Sudan. Rohman *et al* (2004) in a genetic diversity study involving 35 sorghum genotypes observed that the inter cluster distance in most cases was higher than the intra cluster distance, indicating wider genetic diversity between the genotypes of different clusters.

It was gratifying to note that groups IV, I and

TABLE 1
Clustering pattern of 68 sweet sorghum genotypes based on D2 statistics

Cluster	Number of genotypes	Genotypes
I	14	IS 686, IS 9901, IS 17814, IS 19214, ICSV 700, NSSV 13, NSSV 255, IS10050, IS 11152, IS 14529, IS 19674, IS 21100, IS 5362,Wray
II	17	IIS 271, IS 2135, IS 2337, IS 4755, IS 5361, IS 6962, IS 20963, IS 21005, IS 21410, Seredo, APP 3, EG 25, ES 21, GGUB 29, IS 7073, IS 9639, RSSV 76
III	16	IS 15102, AKSSV 15, AKSSV 21, AKSSV 24, NSSV 6, RSSV 138, S-35, SSV 74, APP 1, GGUB 49, IS 6936, KARS 225, Zande Anjan, NTJ 2, SSV 84, CSV 19 SS S-35, SSV 74, APP 1, GGUB 49, IS 6936, KARS 225, Zandc Anjan, NTJ 2, SSV 84, CSV 19 SS
IV	7	IS 5352, IS 7546, IS 7553, IS 7554, IS 14904, IS 7550, IS 7551
V	5	IS 5356, IS 20888, IS 20984,IS 21991, EG 19
VI	3	IS 11161, SPV 422, NSSV256
VII	2	IS 7541, IS 7543
VIII	3	IS 21036, IS 18164, IS 21460
IX	1	Urja

TABLE 2
Average intra (along diagonal) and inter cluster values of D2 among different clusters in sorghum

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**32.06**	87.16	129.26	122.89	196.02	211.23	358.73	282.36	561.25
II		**25.47**	47.48	67.08	81.89	130.55	210.39	187.79	444.41
III			**33.43**	79.34	117.35	195.67	274.73	250.38	497.71
IV				**49.90**	123.20	140.98	310.43	331.98	573.07
V					**71.04**	141.41	127.70	179.62	428.29
VI						**78.42**	264.23	244.17	316.89
VII							**25.10**	138.15	416.16
VIII								**82.86**	253.83
IX									**0.00**

III mostly included African (Nigeria, Sudan, Ethiopia and Cameroon) and Indian germplasm and their derivatives while group IX included a selection from temperate germplasm. This suggests hybridization between genotypes (tropical x temperate) from the above distantly related clusters for better exploitation of heterosis.

The cluster means (Table 3) estimated over the genotypes for all the characters revealed considerable inter cluster variation. Cluster IX recorded highest means for important sweet sorghum traits *viz.*, Green cane yield (35 t/ha), brix content (20.3 %) and juice volume (13819 L/ha) while cluster VI was promising for grain yield per plant (215 g/plant), 100-seed weight (3.8 g) and leaf width (7.8 cm). Cluster III which included most of the released and *kharif* adapted sweet sorghum genotypes like SSV 84, CSV 19SS, SSV 74 etc. recorded least plant height, green cane yield, stem girth and juice volume. This reduction in yields may be due to the influence of photo period i.e., shorter day lengths and low temperatures prevailing during *rabi* season on the growth of these *kharif* genotypes.

Among the 13 characters studied, days to 50% flowering contributed the most (32.9%) followed by 100 seed weight (28.8%) towards the divergence of genotypes. Singh *et al.* (2008) in a genetic diversity study involving 32 genotypes of forage sorghum found that the number of leaves per plant had the greater contribution towards genetic divergence while Jhansi Rani (2004) observed plant height to be contributing maximum to genetic divergence followed by grain yield/plant. Rohman *et al.* (2004) further reported days to maturity and 1000 grain weight to be exhibiting greatest contribution towards genetic diversity in sorghum. Jain *et al* (2016) also reported similar results in a genetic diversity study involving 32 sorghum genotypes.

The principal component analysis based on correlation matrix yielded the eigen roots (values) and eigen vectors. These values and associated cumulative percentage of variation as explained by eigen roots

TABLE 3
Cluster means for 13 different characters in Sweet sorghum

Cluster	Plant height (cm)	Days to 50% flowering	No. of leaves/ plant	Leaf length (cm)	Leaf width (cm)	Nodes/ plant	Stem girth (cm)	Green cane yield (t/ha)	Juice volume (l/ha)	Brix content (%)	Juice extr'n (%)	100-seed weight (g)	Grain yield/ plant (g)
I	188	81	9	54.3	5.7	8	4.9	11	4844	11.5	42	2.24	148
II	194	87	10	66.1	6.4	9	5.4	13	2949	16.1	23	2.59	164
III	172	81	8	56.2	5.5	7	4.2	8	1246	15.7	16	2.46	117
IV	176	81	9	58.2	6.4	8	4.8	12	3236	15.2	25	3.50	155
V	247	98	11	75.2	6.8	10	5.1	15	2914	17.2	19	3.43	154
VI	177	99	11	71.7	7.8	9	6.4	25	8449	17.4	34	3.80	215
VII	315	113	14	97.0	6.5	11	6.5	19	2812	13.7	14	3.33	76
VIII	235	114	14	76.0	6.8	11	5.3	21	4618	17.4	20	1.93	117
IX	221	111	13	80.3	6.2	9	5.6	35	13819	20.3	39	2.06	102

TABLE 4
Matrix of principal components for 13 characters in 68 Sweet sorghum genotypes

Trait	PCI	PC II	PC III	PC IV	PC V	PC VI
Plant Height (cm)	0.363	0.272	0.316	0.041	0.081	0.285
Days to 50% Flowering	0.485	0.041	-0.070	0.127	0.110	-0.166
Leaf Length (cm)	0.426	0.030	0.365	-0.118	-0.019	-0.164
Leaf Width (cm)	-0.268	-0.390	-0.073	0.081	0.106	-0.385
No. of leaves/ Plant	0.278	-0.241	-0.128	0.383	-0.114	-0.110
Nodes/ Plant	0.104	-0.065	-0.258	0.638	0.521	0.130
Stem Girth (cm)	0.162	-0.367	0.327	0.035	-0.076	-0.535
Green Cane Yield (t/ha)	0.358	-0.367	-0.065	-0.217	-0.084	0.190
100 Seed Weight (g)	-0.108	-0.170	0.498	-0.090	0.572	0.164
Grain Yield/plant (g)	-0.290	-0.173	0.274	0.171	-0.125	0.053
Juice Volume (L/ha)	0.169	-0.414	-0.283	-0.136	-0.227	0.358
Juice Extraction (%)	-0.109	-0.209	0.395	0.439	-0.402	0.391
Brix Content (%)	-0.019	-0.407	-0.058	-0.333	0.342	0.231
Eigene Value (Root)	3.499	2.600	1.366	1.222	0.986	0.830
% Variation	26.917	19.997	10.504	9.404	7.583	6.385
Cumulative variation	26.917	46.914	57.418	66.822	74.405	80.790

are presented in Table 4. Principal component analysis gave supplementary information on usefulness of the characters for defining the groups. The six vectors were responsible for 80.7 per cent of the total variability. Kang-Jung Hoon and Lee-HoJin (1996) in a similar study for 11 characters in introduced forage sorghum germplasm observed 82% of the total variation to be accounted for by the first four principal components. The first vector (PC1) accounted for 26.91 per cent of total variability and the major characters responsible for genetic divergence were days to 50 per cent flowering followed by leaf length, plant height and green cane yield. The second vector (PC2) accounted for 19.99 per cent of the total variance and the characters plant height, days to 50 per cent flowering and leaf length contributed positively towards genetic divergence while there was negative contribution from the remaining characters. In the third vector (PC 3) which accounted for 10.50 per cent of total variance, the characters 100 seed weight and juice extraction per cent contributed maximum towards genetic divergence.

Clustering pattern observed from the present study revealed that genetic diversity was not necessarily parallel to geographic diversity. Genotypes evolved in the same area were grouped into different clusters. Patankar *et al* (2005) in a study on the genetic divergence in 41 sweet sorghum genotypes grouped the genotypes into ten clusters and observed that the clustering patterns of these genotypes did not follow the geographical distribution. Sujata *et al* (2015) also reported similar results in a genetic diversity study involving 62 sorghum genotypes. Maximum heterosis is expected from crosses with parents belonging to most divergent clusters.

The major constraint in commercialization of sweet sorghum for biofuel production includes the non-availability of required quantity of feedstock during the lean crushing period of sugarcane industries. The *rabi* grown (Oct-Nov planted) crops will give almost 30-35% less yield than kharif and summer ones because of short day length and low night temperatures (Rao *et al* 2008) as was evident in the present study. In order to meet the industrial demand for feedstock after crushing of sugarcane crop, there is a need to develop sweet sorghum cultivars that are photo-and thermo-insensitive and which can be grown throughout the year with high stalk and sugar yields.

On the basis of inter cluster distances and *per se* performance observed in the present study, a hybridization programme involving IS 5352, IS 7546, IS 7553, IS 7554, IS 14904, IS 7550, IS 7551 (clusters IV), IS 11161, SPV 422, NSSV256 (cluster VI) and Urja (cluster IX) is suggested targeting characters like high brix content and high green cane and grain yields. These parents hold good promise for genetic enhancement of sweet sorghum by spinning off superior genotypes with all the desired traits from the segregating generations.

Coming to the specific combinations, the cross Urja x IS 11161 appears promising for important traits like green cane yield, juice volume and brix content and this cross can be exploited for development of parents for the *rabi* season especially as current

emphasis is on increasing the harvest window thereby ensuring continuous feed stock supply to industry.

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