

STUDY OF GENETIC DIVERGENCE IN SWEET SORGHUM [SORGHUM BICOLOR (L.) MOENCH]

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ABSTRACT

Genetic diversity is an essential prerequisite for improving the genetic makeup of any cop. Inclusion of genetically diverse parents in hybridization programme helps in isolation of superior recombinants. So, an experiment was conducted to investigate the genetic diversity among 46 genotypes of Sweet Sorghum [*Sorghum bicolor* (L.) Moench] against the thirteen growth characters mostly at maturity that has effect on ethanol production. Present study reveals that the clustering pattern based on D² statistics grouped 46 genotypes into 11 clusters, out of which cluster I shows the highest intra cluster value (13.79) followed by cluster II (13.64) while maximum inter cluster distance (i.e. 34.72) was observed between cluster V and cluster IX, indicating there is presence of wide range of genetic diversity among the sweet sorghum genotypes. Such genotypes with wide genetic diversity based on their mean values can either be utilized for breeding programmes for genetic improvement in sweet sorghum or directly adopted as a variety.

INTRODUCTION

In any crop improvement programme, study of genetic diversity is an essential prerequisite for hybridization. Inclusion of genetically diverse parents in hybridization programme helps in isolation of superior recombinants (Rajashekhhar, 2008). In present investigation an effort has been made to study the genetic diversity amongst 46 genotypes of sweet sorghum [*Sorghum bicolor* (L.) Moench] for thirteen characters.

Genetic diversity can be worked out with the help of D² analysis which was given by Mahalanobis (1936). For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952). It is a very potent technique of measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence (Murthy and Arunachalam, 1966; Kadam *et al.*, 2001; Patankar *et al.*, 2005; Ganesamurthy, 2010).

Sweet sorghum is generally cultivated for grain and fodder purpose. Besides these traditional uses, it can be used for manufacturing of several other alternative products such as starch, silage, syrup, jaggery, alcohol, sugar, wine, vinegar, paper, sweeteners and natural pigments (Ratanavathi *et al.*, 2004). Sweet sorghum is similar to the grain sorghum but possess sweet juice in the stalk that can be fermented and distilled to produce ethanol (Mandke and Kapoor, 2004). Ethanol produced from Sweet sorghum is ecofriendly and profitability used as a biofuel in automobiles (Roman *et al.*, 1998; Woods, 2001; Dolciotti *et al.* (1998), Reddy and Reddy, 2003; Reddy *et al.*, 2005). Hence, Sweet sorghum is considered as a much promising biofuel crop that complements with other feedstocks for biofuel production.

Considering the present fuel crisis there will be great demand for biofuel in future. Therefore, there is great need of developing high ethanol yielding varieties and hybrids. As information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for breeding programme, more emphasis should be given on the study of genetic diversity among genotypes of sweet sorghum with respect to yield and ethanol production related growth characters.

So, present investigation was under taken according to its precision and versatility with an objective to study of genetic diversity in 46 popular genotypes of sweet sorghum, keeping in the view that it will provide systematic approach and basic information on which the success of breeding programme rests.

MATERIALS AND METHODS

A field experiment to investigate the genetic diversity in 46 genotypes of Sweet Sorghum [*Sorghum bicolor* (L.) Moench] was laid out in a randomized block design (RBD) with three replications (Panse and Sukhatme, 1967), during *kharif*-2008, at College farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari. The experimental material required for present investigation was obtained from the germplasm maintained at the Main Sorghum Research Station, Surat, M.P.K.V Rahuri, P.D.K.V. Akola and M.A.U. Parbhani. Each genotype was sown in three rows, each of three meter length with plant to plant distance of 15cm. The rows were spaced 45cm. All the recommended agronomical practices were carried out timely and appropriately. Qualitative and quantitative characters were recorded using minimal

descriptor developed by NBPGR (Mahajan *et al.*, 2000). Five randomly selected plants were used for recording the observations on thirteen growth characters mostly at maturity *i.e.* days to fifty per cent flowering, days to physiological maturity, plant height (cm) at physiological maturity, number of internodes at physiological maturity, stem girth at maturity, green cane yield at physiological maturity on an average of five plants (kg), and grain yield (g) at physiological maturity. Brix percentage (%) at sixty days after sowing, at fifty per cent flowering, and at physiological maturity were recorded by

$$\text{Juice extraction percentage} = \frac{\text{Volume of juice from five cones (mL)}}{\text{Weight of five canes (g)}} \times 100$$

hand refractometer while juice extraction per cent at physiological maturity were worked out by using formula:

Reducing sugar (%) at physiological maturity estimated using DNS method (Prabhakar, 2003) and non-reducing sugar (%) at physiological maturity was estimated by subtracting total sugars (Dubois *et al.*, 1956) from Reducing sugars. Analysis of variance for the individual character and analysis of co-variance for character pairs were carried out as described by Cochran and Cox (1957). Wilk criteria was used to test the significance of pooled differences (Wilk, 1932). Genetic divergence was estimated by Mahalanobis's (1936) D^2 statistics method and genotypes were clustered into different groups on the basis of minimum generalised distance using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variances for genetic divergence showed highly significant differences among the genotypes for all the thirteen growth characters studied, indicating appreciable amount of variability among the genotypes.

The clustering based on D^2 statistics grouped genotypes into eleven clusters, indicating the presence of wide range of genetic diversity among the genotypes under investigation (Table 1). The maximum numbers of genotypes were grouped into cluster I followed by cluster II and Cluster V, each comprising of 26, 9 and 3 genotypes respectively. While remaining clusters were solitary. Similar results were observed by Sarwate (1985); Barhate (1996); Shridher *et al.* (2003); Patankar *et al.* (2005); Ganesamurthy (2010) who has reported 14, 13, 23, 10 and 14 clusters respectively. Clustering pattern also reveals that

genotypes SSV-84, AKSSV-22, PVR-453 and SPV-422, from different sources M.P.K.V., Rahuri, P.D.K.V., Akola M.A.U., Parbhani and M.S.R.S., Surat respectively, were grouped into single cluster (*i.e.* cluster V), while genotypes RSSV-101, RSSV-96, RSSV-91, RSSV-82 and RSSV-157 from one single source (*i.e.* from M.P.K.V., Rahuri) grouped into different clusters. It signifies that cluster may contain the genotypes from different origins or genotypes from different origins may be grouped into single cluster. It confirms that geographic diversity is not fully reflected in genetic diversity. Such unparallelism between geographic and genetic diversity was also reported by Yadav *et al.* (2003); Kadam *et al.* (2001) and Ganesamurthy (2010).

The intra and inter cluster D^2 values among 46 genotypes (Table 2) revealed that cluster V recorded the lowest intra cluster value (12.03) suggesting that the genotypes within this cluster were less divergent. It might be due to unidirectional selection practiced in past that has resulted in uniformity and less divergence between these genotypes. Similar results were advocated by Vivekanandan and Subramanian (1993) in rice crop. Cluster I shows the highest intra cluster value (13.79) followed by cluster II (13.64). Selection among these clusters based on higher mean values of a concerned character related to ethanol production could be useful for improvement in sweet sorghum through inter varietal hybridization programme (Kadam *et al.*, 2001; Ganesamurthy, 2010). While null intra cluster distances were recorded by the clusters having single genotype (Shridher *et al.*, 2003; Patankar *et al.*, 2005; Ganesamurthy, 2010).

Maximum inter cluster distance (*i.e.* 34.72) was observed between cluster V and cluster IX, indicating that genotypes belonging to these groups were genetically most divergent. Simultaneously, cluster V recorded higher values of inter cluster distances with cluster VI (33.25), cluster VII (30.25) and cluster VIII (30.57). Similar higher value of inter cluster were recorded between cluster II and IX (32.20) which indicates that genotypes included in these clusters also possess considerable genetic diversity among themselves. Such genetically diverse sweet sorghum genotypes can be effectively utilized as parents in hybridization programme. This type of hybridization would be useful for obtaining highest number of valuable segregates along with maximized vigour. Similar instances for intra and inter cluster distances were recorded by Kadam *et al.* (2001); Shridher *et al.* (2003); Patankar *et al.* (2005) and Ganesamurthy (2010).

The cluster mean values estimated over genotypes for thirteen

Table 1 Distribution of forty six genotypes of Sweet Sorghum in to different clusters

Cluster No.	No. of Genotypes	Name of Genotypes
I	26	RSSV-101, RSSV-120, RSSV-106, RSSV-119, RSSV-158, RSSV-138, KARS-95, IS-17814, BJ-248, RSSV-134, Phule-Mauli, NSSV-261, KARS-225, EG-25, RSSV-104, IS-14529, IS-5353, AKSSV-15, ICSV-93046, PAC52093, AKSSV-23, Urja, EG-23, NSSV-260, BAR-162, HES-4.
II	9	RSSV-91, RSSV-56, SPV-422, SPV-1595, SSV-84, RSSV-95, AKSSV-22, PVR-453, RSSV-96.
III	1	EC-532167
IV	1	IS-3556
V	3	BJ-248, SG-11, PVK-1050.
VI	1	RSSV-82
VII	1	Keller
VIII	1	RSSV-157
IX	1	CSV-1955
X	1	Waray
XI	1	NTJ-2

Table 2 Average Intra and Inter-cluster distance (D) value for thirteen growth characters in Sweet Sorghum

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	13.79	20.32	17.35	16.61	24.14	17.77	17.68	18.01	19.52	16.58	19.28
II		13.64	20.16	18.49	19.89	27.24	28.59	19.37	32.20	23.55	22.60
III			0.00	20.14	16.35	27.76	23.47	25.27	26.57	20.39	18.55
IV				0.00	23.70	23.45	16.98	22.43	25.36	16.53	22.14
V					12.03	33.25	30.25	30.57	34.72	27.35	22.46
VI						0.00	19.51	16.31	15.06	18.77	25.62
VII							0.00	26.30	13.30	16.50	24.35
VIII								0.00	25.35	22.76	21.73
IX									0.00	18.56	26.74
X										0.00	22.74
XI											0.00

growth characters in sweet sorghum related to ethanol production shows a wide range of variation (Table 3). Minimum cluster mean values for days to fifty per cent flowering was recorded in cluster V followed by cluster IX, while cluster X followed by cluster VI were recorded minimum cluster mean values for days to maturity. It reveals that genotypes included in these clusters are useful in inducing earliness in sweet sorghum varieties (Kadam *et al.*, 2001; Patankar *et al.*, 2005).

Maximum plant height was observed in genotypes of cluster V followed by cluster XI, VII, IV and VIII. Maximum number of internodes were exhibited by cluster VI followed by cluster IV and cluster VII. Study also reveals that clusters such as V and VII which are exhibiting higher mean values for plant height but lowest mean values for number of internodes are having longer internodes as compared to others. As hybridization between superior parents produce superior recombinants, such genotypes with longer internodes and genotypes having short internodes but more in numbers both are considered as a valuable material for increasing plant height (Rajashankar, 2007).

Maximum stem girth was recorded in cluster IV followed by X and VII. Brix at sixty days after sowing shows highest mean values for cluster XI followed by VII. While brix at fifty per cent flowering recorded highest mean values for cluster IV followed by VII. On the other hand brix at maturity exhibited highest mean values for cluster X followed by IV and II. Most of the clusters under study exhibit a trend of slight decrease in brix percentage from brix at fifty per cent flowering to maturity. Similar trend for brix values is recorded by Bapat *et al.* (1983); Channappagodouar *et al.* (2007) and Reddy *et al.* (2007). So, the genotypes in clusters such as II, V, X and XI showing trend

of continuous increase in brix percentage from brix at sixty days after sowing to maturity may play important role in increasing brix values in sweet sorghum crop. Simultaneously, cluster showing prolonged period between days to fifty per cent flowering and maturity may be valuable, as brix is generally recorded maximum at fifty per cent flowering stage than sixty days after sowing and maturity (Channappagodouar *et al.*, 2007; Ganesamurthy, 2010).

Characters such as juice extraction, reducing sugar and non-reducing sugar plays prominent and direct role in ethanol production for biofuel (Mandke and Kapoor, 2004; Almodares and Hadi, 2009). In present study higher mean values for juice extraction were recorded in cluster III followed by X, XI and V respectively. Similarly, highest values for reducing sugar and non-reducing sugar were observed in IX and cluster VII followed by IV respectively, while lowest values for reducing sugar and non-reducing sugar were recorded by cluster V and VII. Genotypes in above mentioned clusters scoring higher mean values in respective characters can be considered as a good source for genetic improvement of sweet sorghum in terms of ethanol production.

Highest mean values for green cane yield were recorded in genotypes of cluster II followed by genotypes of cluster V. As green cane yield play important role in obtaining maximum ethanol production, genotypes with higher green cane production are beneficial in breeding point of view. While highest mean values for grain yield were recorded in cluster IV followed by VII; also, clusters IX, X and XI shows average mean values for grain yield. Genotypes having higher green cane yield along with higher or average grain production (*i.e.* genotypes included in X, XI, I and IV clusters) can be utilized for improvement in

Table 3: Cluster means for thirteen growth characters in Sweet Sorghum

Clusters	DF	DM	PH	NI	SG	B60	B50	BM	JE	RS	NRS	GY	GCY
I	86.47	121.35	280.24	12.23	1.93	11.39	15.79	14.49	21.58	2.19	12.84	31.68	0.25
II	88.19	122.48	293.83	11.76	1.96	11.39	16.63	18.07	18.00	0.96	9.85	30.81	0.29
III	88.67	123.00	276.00	10.93	1.12	11.07	14.13	13.84	46.96	1.67	15.70	27.00	0.14
IV	106.33	127.33	288.00	13.40	2.17	12.77	20.20	19.30	9.72	1.74	15.81	56.00	0.25
V	72.67	115.33	317.98	8.87	1.83	11.67	12.20	15.41	21.21	0.83	15.11	29.22	0.26
VI	79.00	114.67	226.93	14.07	1.80	9.77	13.01	13.91	7.10	2.83	8.78	41.33	0.14
VII	81.67	121.00	315.33	9.33	2.07	13.17	20.07	16.05	14.39	2.84	16.61	50.00	0.08
VIII	90.33	123.33	308.53	13.27	1.86	12.08	16.07	13.99	19.70	1.91	5.01	27.33	0.25
IX	72.00	141.00	315.07	11.27	1.88	10.07	16.14	13.43	18.88	3.45	13.45	48.40	0.18
X	76.00	111.33	291.27	12.87	2.15	11.10	15.04	25.18	28.42	2.61	13.71	48.40	0.24
XI	93.67	135.33	317.73	11.60	1.78	18.06	11.09	15.18	25.61	1.92	11.67	46.67	0.23

DF: Days to fifty per cent flowering; DM: Days to maturity; PH: Plant height (cm); NI: Number of internodes; SG: Stem girth (cm); B50: Brix (%) at fifty per cent flowering; B60: Brix (%) at sixty days after sowing; BM: Brix (%) at maturity; JE: Juice extraction per cent; RS: Reducing sugar (%); NRS: Non-Reducing sugar (%); GY: Grain yield per plant (g); GCY: Green cane yield per plant (kg); Note: All the characters were recorded at physiological maturity except for DF, B60 and B50

sweet sorghum. Similar results were found by Kadam *et al.* (2001); Shridher *et al.* (2003) and Patankar *et al.* (2005).

Characters such as green cane yield, juice extractability, type and content of sugar in stalk and grain yield has been proved to be major contributors to its economic superiority (Bala *et al.*, 1996; Almodares *et al.*, 2008). Genetic diversity instigated in present study among these characters can be a base for genetic improvement in sweet sorghum.

From present study it can be concluded that there is presence of wide range of genetic diversity in sweet sorghum genotypes. Further, the genotypes which are most genetically diverse (e.g. genotypes of cluster vth among themselves and genotypes of cluster vth with CSV-1955); exhibiting earliness in flowering and maturity (e.g. genotypes of cluster vth and CSV-1955); prolonged period for maturity (e.g. RSSV-82, CSV-1955); maximum plant height (e.g. IS-3556, NTJ-2); trend of continuous increase in brix percentage from brix at sixty days after sowing to maturity along with higher brix value (e.g. genotypes of cluster IInd and Waray); higher juice extraction percentage (e.g. EC-532167, Waray); lower reducing sugars (e.g. genotypes of cluster vth) and higher green cane yield (e.g. genotypes of cluster IInd and vth) along with higher or average grain yield (e.g. IS-3556, Keller) may sever as good source of breeding material. Such more diverse genotypes in accordance with their mean values on any cluster as per desire can be used in hybridization programme for sweet sorghum improvement in terms of ethanol production. While, the cluster contributing maximum to the divergence were given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization.

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