Genetic Divergence Studies in Forage Sorghum
(*Sorghum bicolor* L. Moench)

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ABSTRACT

Fifty four lines of forage sorghum were evaluated for genetic diversity using D^2 and principal component analysis for fifteen characters during *kharif,* 2011. The genotypes under study were grouped into eight clusters. The cluster I was the largest with 27 genotypes followed by cluster II (15) and cluster VI (7). Remaining clusters were solitary. The clustering pattern of genotypes indicated that geographical distribution and genetic diversity were not related to each other. The inter cluster distances were higher than the average intra cluster distances indicating wider genetic diversity among the genotypes of different groups. Maximum inter cluster distance was observed between cluster VI and VIII followed by cluster II and VIII, I and VIII and V and VIII showing wide diversity among the groups. Based on the cluster means, the important clusters are cluster VI for stem weight, stem girth, biomass per plant and crude protein, cluster V for days to 50 per cent flowering, leaf length, green fodder yield, green fodder yield per day, dry fodder yield and brix per cent. Crude protein per cent, stem weight, days to 50 per cent flowering, leaf width, plant height, number of leaves per plant and dry fodder yield have contributed more towards divergence among the genotypes.

Key words : D^2 statistics, Forage sorghum, Genetic divergence, Principal component analysis.

Sorghum (*Sorghum bicolor* L. Moench) is a a highly diverse species grown for food, feed, fodder and fuel in different parts of the world because of its wider adaptability to varied soil and environmental conditions. It is one of the most important *kharif* fodder crop, further improvement in its plant type for forage will help to narrow down the gap between demand and supply of fodder for the increasing livestock population. Hybridization between genetically diverse parents is expected to produce transgressive segregants in the advanced generation (Kumar *et al., 2010*). The success and usefulness of multivariable techniques in quantification of genetic diversity has been demonstrated by many workers Agarwal *et al.* (2002), Yadav *et al.* (2003) and Rohman *et al.* (2004). Keeping in view that selection of elite genetic stocks based on genetic divergence studies is the key for the development of high yielding varieties, the present investigation was undertaken to study the nature and magnitude of genetic divergence for forage yield and its components in selected sorghum genotypes to provide a basis for selection of parents for hybridization.

MATERIAL AND METHODS

The material for the present study comprised of fifty four genotypes includes local forage lines from different states, sweet sorghum lines, brown midrib lines and dual purpose lines and evaluated in randomized block design with three replications during *kharif,* 2011 at Directorate of Sorghum Research Farm, Rajendranagar, Hyderabad. Each entry in each replication was sown in 2 rows of 4 m length spaced 45 cm apart from each other with plant to plant distance of 15 cm. Recommended package of practices were followed for raising a normal crop. Observations were recorded on five randomly selected plants for plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), stem weight (g), stem girth (mm), biomass per plant (kg), green fodder yield (Q ha^{-1}), green fodder yield per day (Q ha^{-1} day^{-1}), dry fodder yield (Q ha^{-1}), dry fodder yield per day (Q ha^{-1} day^{-1}), brix per cent and crude protein per cent. However, observations for the characters namely early vigour and days to 50 per cent flowering were recorded on plot basis. Genetic diversity was studied following Mahalanobis D^2

Table 1. Distribution of 54 genotypes of forage sorghum into different clusters.

Cluster	Number	Genotypes
I	27	CSV 15, CSV 20, CSV 21 F, Pant Chari 4, BJ 248, S541, UP Chari 2, URJA, GFS 5, Pant Chari 3, SEVS 4, HC 308, Pant Chari 5, Rampur Local, UP Chari 1, Ramkel, Kharif yellow sorghum, Katarkhatav, Rabi sorghum kasegaon, SSV 74, MP Chari, HC 171, CSV 19SS, PC 23, Pant Chari 6, NSSV 13, BMR 23369
II	15	BMR 23375, UPMC 512, BMR 23150, BMR 23158, EC 582510, Keller, PSC 1, Pant Chari 7, EC 582504, EC 582508, HJ 260, Pant Chari 8, Niz forage, UPMC 503, SL 44
III	1	HJ 513
IV	1	Sangola Hundi
V	1	SSRG 212
VI	7	SSRG 214, SSRG 222, Halyal Dt Afzalpur, SSRG 164, HC 136, SSV 84, SSRG 200
VII	1	SSG 59-3
VIII	1	CO (FS) 29

Table 2. Average intra-(diagonal and bold) and inter-cluster D^2 estimates in forage sorghum.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**27.206**	59.142	40.758	46.380	42.899	64.110	99.138	242.229
II		**38.649**	93.302	58.503	113.227	134.095	97.568	266.512
III			**0.000**	83.154	49.698	64.064	90.412	196.250
IV				**0.000**	76.107	115.804	70.199	180.805
V					**0.000**	59.894	123.587	227.359
VI						**47.850**	184.795	307.411
VII							**0.000**	76.979
VIII								**0.000**

statistics described by Mahalanobis (1936). Clustering of genotypes was done according to Tocher's method and principal component analysis as described by Rao (1952). All the statistical analysis was carried out using Windostat Version 8.6 computer software.

RESULTS AND DISCUSSION

Analysis of variance revealed the significant differences among the genotypes for the traits studied indicating a considerable amount of genetic variability for the characters and therefore divergence analysis was carried out.

Based on D^2 values the genotypes were grouped into eight clusters given in Table 1. Out of the eight clusters obtained, cluster I was the largest with 27 genotypes followed by cluster II and cluster VI with 15 and 7 genotypes, respectively. Remaining clusters were solitary. The clustering pattern observed in the present study revealed that, genetic diversity was not necessarily parallel to geographic diversity (For example the genotypes HJ 513 of cluster III and CO(FS) 29 of cluster VIII are from Haryana and Tamilnadu respectively). Genotypes evolved in the same area were grouped into different clusters. Similar results were reported by Narkhede *et al.* (2001), Singh *et al.* (2001), Kadam *et al.* (2001) and Veerabadhiran and Kennedy (2002), Yadav *et al.* (2002), Umakanth *et al.* (2003), Patankar (2005), Khapre *et al.* (2007) and Ganesamurthy *et al.* (2010).

Table 3. Cluster mean values for different characters in forage sorghum.

Character	I	II	III	IV	V	VI	VII	VIII	Times Ranked Ist	Contri bution %
Early vigour	2.94	2.93	3.16	3.00	2.50	3.09	3.50	1.66	20	1.40
Days to 50% flowering	71.04	62.22	75.66	62.33	79.66	78.28	67.66	72.66	193	13.49
Plant height (cm)	326.20	253.40	448.00	297.60	337.30	341.50	351.60	345.60	112	7.83
Number of leaves/plant	14.17	11.91	17.80	24.66	16.75	17.01	27.44	48.11	92	6.43
Leaf length (cm)	86.50	79.55	94.46	78.41	104.20	94.35	79.66	81.80	21	1.47
Leaf width (cm)	8.44	7.85	7.84	9.52	8.10	8.78	4.21	3.65	168	11.74
Stem weight (g)	416.07	230.81	435.33	293.33	470.00	639.87	161.16	152.00	288	20.13
Stem girth (mm)	1.634	1.45	1.86	1.44	1.77	2.11	1.16	1.15	7	0.49
Biomass/plant (kg)	0.675	0.44	0.59	0.55	0.87	0.98	0.28	0.28	22	1.54
Green fodder yield (Q ha^{-1})	369.28	236.97	302.77	386.45	509.02	398.08	347.91	277.08	42	2.94
Green fodder yield/day (Q ha^{-1} day^{-1})	5.22	3.833	4.01	6.20	6.38	5.08	5.13	3.81	10	0.70
Dry fodder yield (Q ha^{-1})	99.26	61.47	111.61	104.45	133.61	101.74	113.26	106.62	82	5.73
Dry fodder yield/day (Q ha^{-1} day^{-1})	1.402	0.99	1.47	1.67	1.67	1.30	1.67	1.46	57	3.98
Brix (%)	12.08	11.70	13.70	9.56	14.74	8.98	10.55	11.42	12	0.84
Crude protein (%)	8.18	9.49	9.08	6.69	6.37	9.72	8.08	8.47	305	21.31

The average D^2 values within (intra) and between (inter) clusters were given in Table 2. The inter cluster distances were higher than the average intra cluster distances, which indicated wide genetic diversity among the genotypes of different groups than those of the same cluster. Maximum differences among the genotypes within the same cluster were shown by cluster VI (47.850) and minimum by cluster I (27.206). Maximum inter cluster value was observed between cluster VI and VIII (307.411) followed by cluster II and VIII (266.512), cluster I and VIII (242.229) and cluster V and VIII (227.359) and the minimum between cluster I and III (40.758). Thus, it can be suggested that, genotypes included in these clusters are genetically diverse and may give rise to high heterotic response. This findings supports with findings of Agarwal *et al.* (2002), Sridhar *et al.* (2003), Rohman *et al.* (2004), Sridhar *et al.* (2007), Kumar *et al.* (2010) and Ganesamurthy *et al.* (2010).

Cluster means for different traits are presented in Table 3. Based on the cluster means, the important clusters are cluster VI for stem weight, stem girth, biomass per plant and crude protein, cluster V for leaf length, green fodder yield, green fodder yield per day, dry fodder yield and brix per cent. However, entries in cluster V and VI appeared to be late maturing than the genotypes from other clusters as evident from days to fifty per cent flowering which suggested that lines in these clusters produce high biomass. The prominent traits in cluster IV were leaf width and dry fodder yield per day, cluster III for plant height, cluster VIII had higher number of leaves per plant, and cluster VII had maximum early vigour. Thus involving the genotypes of outstanding mean performance from these clusters in the intervarietal and interspecific crosses will be useful in the development of high fodder yield with better quality. Their segregating progenies are also likely to yield good recombinants for economic traits. Crude

Table 4. The eigene values, per cent variance and per cent cumulative variance for six principal components (PCs) and factor loading between PCs and traits studied in forage sorghum.

|	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector
Eigene Value (Root)	5.35	2.66	1.33	1.22	1.02	0.69
% Var. Exp.	35.69	17.76	8.91	8.16	6.81	4.63
Cum. Var. Exp.	35.69	53.45	62.37	70.53	77.35	81.98
Traits			**Factor loading**			
Early vigour	0.063	0.187	0.626	0.364	0.011	0.280
Days to 50% flowering	0.394	-0.087	0.016	-0.043	0.069	-0.063
Plant height (cm)	0.293	-0.290	0.152	0.319	-0.048	-0.268
Number of leaves/plant	0.067	-0.472	0.023	-0.127	0.386	-0.371
Leaf length (cm)	0.308	0.153	-0.128	-0.274	-0.238	0.205
Leaf width (cm)	0.195	0.357	-0.204	-0.117	-0.332	-0.040
Stem weight (g)	0.371	0.110	-0.016	-0.003	0.105	-0.060
Stem girth (mm)	0.291	0.167	-0.318	-0.103	0.288	-0.037
Biomass/plant (kg)	0.305	0.013	0.145	-0.061	0.226	0.426
Green fodder yield (Q ha^{-1})	0.309	-0.182	0.082	-0.281	-0.219	-0.159
Green fodder yield/day (Q ha^{-1} day^{-1})	0.348	0.038	0.314	0.095	0.009	-0.096
Dry fodder yield (Q ha^{-1})	0.181	-0.167	-0.190	0.433	-0.558	-0.126
Dry fodder yield/day (Q ha^{-1} day^{-1})	-0.171	0.404	0.181	0.036	-0.072	-0.575
Brix (%)	-0.140	-0.479	-0.031	-0.051	-0.295	0.295
Crude protein (%)	0.067	0.068	-0.477	0.605	0.281	0.103
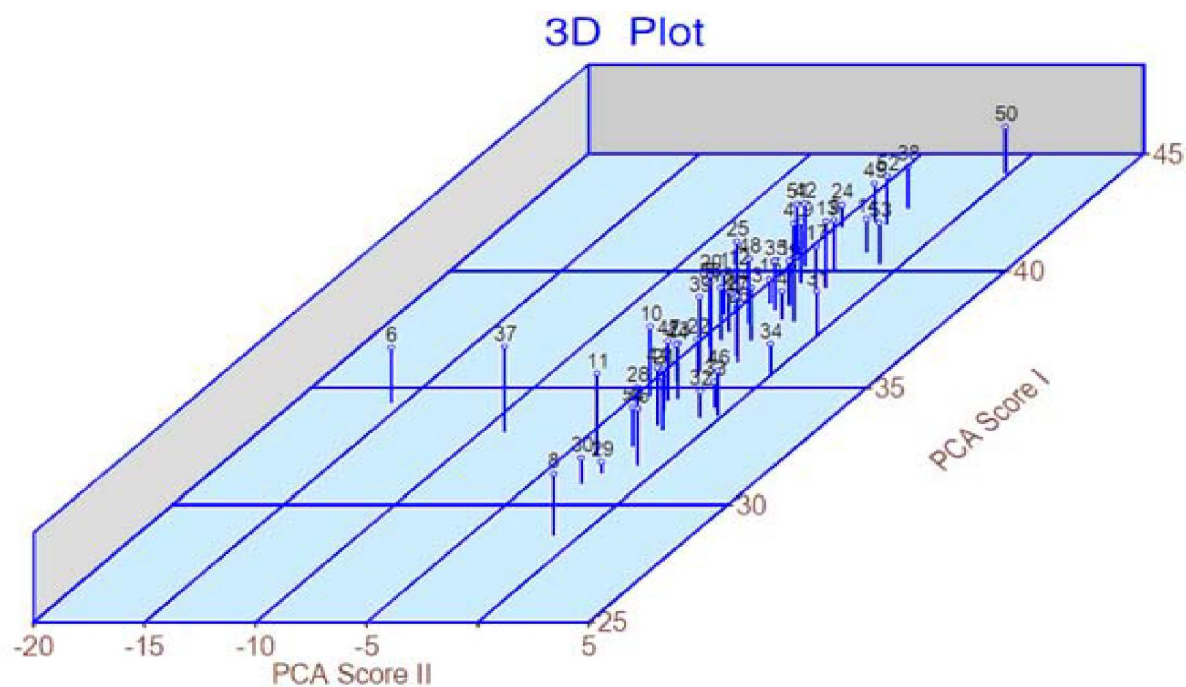
Figure 1. Three dimensional principal component scatter plot

protein per cent, stem weight, days to 50 per cent flowering, leaf width, plant height, number of leaves per plant and dry fodder yield have contributed more towards divergence, so the direct selection for these traits would be helpful as evident from number of times these traits appeared or ranked first during contribution to diversity.

The principal component analysis revealed that first six vectors accounted for 81.98 per cent of the total variability produced by all the characters under study are given in Table 4. The mean scores of first two canonical vectors were used to obtain graphical depiction of the genetic distance of the 54 genotypes. Using these scores, all the genotypes (numbers assigned to them) were plotted for PC I and PC II which cumulatively explained 53.45 per cent variability and accounted for the most important forage characters. The scatter plot of PC scores of first two PC axes is presented in Figure 1. Most of the entries accumulated towards the middle of PC I axis and the remaining entries towards right of PC I axis which accounts for the most important characters like days to 50 per cent flowering (0.394), leaf length (0.308), stem weight (0.371), stem girth (0.291), green fodder yield (0.309) and green fodder yield per day (0.348). Along PC II axis most of the entries accumulated towards the negative side of the axis as it accounts for the traits *viz.,* leaf width (0.357) which had positive contribution towards genetic divergence, while days to 50 per cent flowering (-0.087), plant height (-0.290), number of leaves per plant (-0.472) and brix per cent (-0.479) had negative contribution towards genetic divergence.

Tocher's method. The 24 genotypes belonging to cluster I in D^2 analysis were located closely towards the right side of PCA I axis. The 15 genotypes of cluster II in D^2 analysis were located nearer to each other towards left of PC I axis and positive side of PC II axis. The genotypes namely, SSRG 200 (50), SSV 84 (38), SSRG 164 (49), SSRG 214 (52), HC 136 (24), SSRG 222 (53) and Halyal Dt Afzalpur (14) were located on positive right side of PC I axis were found superior through principal factor analysis and these are the same genotypes which were also found better through D^2 analysis included in cluster VI with prominent characters like stem weight, stem girth,

biomass per plant and crude protein. Five lines HJ 513, Sangola Hundi, SSRG 212, SSG 59-3 and COFS 29 assigned with numbers 25, 10, 51, 37 and 6 appeared separately and could be easily marked which fall in five different clusters III, IV, V, VII and VIII, respectively. Such confirmatory results were also obtained by Yadav *et al.* (2003) in forage sorghum, Rohman *et al.* (2004) in sorghum and Ahmed *et al.* (2010) in fodder maize. Therefore, the present study helps in determining the diversity present among the genotypes and selection of desirable types of individuals for particular trait that will help in forage yield improvement programme.

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