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Short Communication

Genetic variability among Indian rainy season sorghum cultivars revealed by morpho-agronomic traits

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Abstract

Sorghum [*Sorghum bicolor* L. (Moench)] is an important crop for the semi-arid tropics. To protect varieties under Protection of Plant Varieties and Farmers Rights Act (PPV&FRA) 2001 the entries need to be tested for distinctiveness, uniformity and stability during the season of their adaptation itself. Fifteen parental lines and 32 varieties belonging to different categories of sorghum were characterized for DUS traits during the *kharif* seasons of 2006 and 2007. Among quantitative traits total plant height contributed >70% towards variability of the genotypes. Quantitative traits alone put the 47 genotypes into three clusters, while qualitative traits alone grouped the genotypes into four main clusters. Grouping based on qualitative traits corroborated more towards the total variability as against quantitative traits alone. Generated data clearly could establish distinctiveness among all the genotypes without any ambiguity. Combination of qualitative and quantitative traits in establishing distinctiveness was more effective than any type of trait alone.

Key words: Genetic variability, diversity, dendrogram, quantitative traits, DUS trait, euclidean distance, *Sorghum bicolor* L. (Moench)

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most important cereal crop to provide food, feed and fodder across semi-arid tropics including India. In India since 1969, 23 varieties (CSV 1 to CSV 23) and 25 hybrids (CSH 1 to CSH 25) along with 32 promising parental lines have been released. Out of these, 19 varieties, 20 hybrids and 26 parental lines are adapted to *kharif* season [1]. Characterization of these cultivars is needed to understand their genetic relationship so that they may be deployed effectively in breeding programme. Intra-specific diversity of sorghum has been studied using agro-morphological traits by various authors [2-4]. In most of the recent reports morphological markers have been supplemented with molecular data [5-7]. Using the accepted DUS testing guidelines of India for the first time establishment of distinctiveness among only 11 out of 26 varieties has been reported [3]. However, this study is restricted to forage sorghum varieties only. The present work was carried out (1) to establish the genetic variability among the extant kharif varieties/parental lines using DUS traits, and (2) to study the diversity among the kharif genotypes.

The study was focused on 47 kharif extant varieties and parental lines (Table 1). The experiments were conducted during Kharif seasons of 2006 and 2007 as per the DUS test guidelines [8] using randomized complete block design with four replications. Genotypes were sown in six rows of 6 m with 60 × 15 cm spacing. Data were recorded for 12 quantitative traits, namely, days to panicle emergence, plant height up to base of flag leaf, stigma length, anther length, total plant height, stem diameter, leaf blade length, leaf blade width, panicle length without peduncle, branch length in panicle, neck length of panicle visible above sheath and 1000 grain weight (g), and 21 qualitative traits *viz*., anthocyanin colouration of coleoptile, leaf sheath anthocyanin

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Table 1. Sorghum cultivars released for rainy season (*kharif*) of India subjected to phenotypic analysis determining the genetic diversity

S.No.	Cultivar name	Nature of cultivar	Pedigree	Year of release	Central/ state release	Source/centre
1.	2077B	Parental line (B) of CSH 5	IS 2046 × 3677B	1974	Central	DSR, Hyderabad, Andhra Pradesh
2.	2219B	Parental line (B) of CSH 3 and CSH 6	Selection from Kharif Shallu	1970 & 1977	Central	DSR, Hyderabad, Andhra Pradesh
3.	296B	Parental line (B) of CSH 9, CSH 10, CSH 11, CSH 12R, CSH 13K & CSH13R	IS 3922 x Karad local	1981, 1984, 1986 & 1992	Central	DSR, Hyderabad, Andhra Pradesh
4.	27B	Parental line (B) of CSH 16	83B x 199B	1997	Central	DSR, Hyderabad, Andhra Pradesh
5.	AKMS 14B	Parental line (B) of CSH 14 and CSH 17	(MR 760 x BT 632) x AKMS 2B	1992 & 1999	Central	PDKV, Akola, Maharashtra
6.	7B	Parental line (B) of CSH 23	Selection from AKMS14A	2005	Central	DSR, Hyderabad, Andhra Pradesh
7.	IMS 9B	Parental line (B) of CSH 18	2077A x (MA9B x Vidisha 60-1) 11-4-2-5-5A	1999	Central	RVSKVV, Indore
8.	CS 3541	Parental line (R) of CSH 5 & CSH 9	IS 3675 x IS 3541	1974 & 1981	Central	DSR, Hyderabad, Andhra Pradesh
9.	RS 29	Parental line (R) of CSH 13K & CSH 13R	SC 108 x SPV 126	1986 & 1992	Central	DSR, Hyderabad, Andhra Pradesh
10.	C43	Parental line (R) of CSH 16	CS3541 x IS23549	1997	Central	DSR, Hyderabad, Andhra Pradesh
11.	RS 673	Parental line (R) of CSH 17	SPV 544 x K 24-1	1998	Central	DSR, Hyderabad , Andhra Pradesh
12.	MR 750	Parental line (R) of CSH 11	Sel. MR 841 (SC 108-3 x CS 3541-27)	1986	Central	ICRISAT, Hyderabad, Andhra Pradesh
13.	AKR 150	Parental line (R) of CSH 14	CS 3541 x 900	1992	Central	PDKV, Akola, Maharashtra
14.	Indore 12	Parental line (R) of CSH 18	(SSV 53 x SPV 475-7-1-1-1)	1999	Central	RVSKVV, Indore, Madhya Pradesh
15.	AKR73	Parental line (R) of AKSH 73 (SPH 388)	—	1990	State	PDKV, Akola, Maharashtra
16.	CSV 13	Grain sorghum variety	(IS 12622 × 555) x S 3612 x 2219B x E 35-1	1988	Central	ICRISAT, Hyderabad, Andhra Pradesh
17.	CSV 15	Grain sorghum variety	SPV 475 x SPV 462	1996	Central	DSR, Hyderabad, Andhra Pradesh
18.	CSV 17	Grain sorghum variety	SPV 946 x SPV 772	2002	Central	MAUA&T, Udaipur, Rajasthan
19.	CSV 20	Grain sorghum variety	SPV 946 x Kh 89-246	2006	Central	DSR, Hyderabad, Andhra Pradesh
20.	ICSV 745	Grain sorghum variety	(PM 11344 x A6250- 4-1-1-1)	1990	Central	ICRISAT, Hyderabad, Andhra Pradesh

Table 1 contd.

Table 1 contd.

21.	APK 1	Grain sorghum variety	TNS 30 x Co-26	1996	State	TNAU, Arupukottai, Tamil Nadu
22.	BSR 1	Grain sorghum variety	Multiple cross (CSC 108-3 x CSV 4) 16-3-1 x (MR 801x R2751)	1990	State	TNAU, Bhavanisagar, Tamil Nadu
23.	GJ 9	Grain sorghum variety	Pure line selection from local Brooch Dist.	1979	Central	GAU, Surat, Gujarat
24.	GJ 37	Grain sorghum variety	(2077 x M 28) x Cuandri	1986	State	GAU, Surat, Gujarat
25.	GJ 38	Grain sorghum variety	GJ 35 x E 35-1	1994	State	GAU, Surat, Gujarat
26.	GJ 40	Grain sorghum variety	(2077 A x M 25) x Malvan	1995	State	GAU, Surat, Gujarat
27.	JJ 741	Grain sorghum variety	CSV 4 x E 35-1	1991	Central	RVSKVV, Indore, Madhya Pradesh
28.	JJ 938	Grain sorghum variety	SPV 221 x E 602	1995	State	RVSKVV, Indore, Madhya Pradesh
29.	JJ 1022	Grain sorghum variety	(SPV 475 x SPV 462) 21-3-3	2006	State	RVSKVV, Indore, Madhya Pradesh
30.	JJ 1041	Grain sorghum variety	(SPV 475 x SPV 462) 7-1-2	1997	State	RVSKVV, Indore, Madhya Pradesh
31.	PVK 400	Grain sorghum variety	SDS 2650 x CS 3541	1993	State	MAU, Parbhani, Maharashtra
32.	PVK 801	Grain sorghum variety	Sel. From ICRISAT population GD 34-5-5-3	1999	State	MAU, Parbhani, Maharashtra
33.	PVK 809	Grain sorghum variety	PVK 801 x SOV 881	2004	State	MAU, Parbhani, Maharashtra
34.	PSV 1	Grain sorghum variety	MS-827 x IS-3691	1996	State	ANGRAU, Palem, Andhra Pradesh
35.	PVR 453	Grain sorghum variety	Selection from local, Parbhani Jyoti		2001	State MAU, Parbhani, Maharashtra
36.	K 8	Grain sorghum variety	IS 12611 C x SC 108	1990	Central	TNAU, Kovilpatti, Tamilnadu
37.	Co(S) 28	Grain sorghum variety	Co 25 x SPV 942	2001	State	TNAU, Coimbatore, Tamilnadu
38.	CSV 19SS	Sweet sorghum variety	RSSV 2 x SPV 462	2004	Central	MPKV, Rahuri, Maharashtra
39.	SSV 84	Sweet sorghum variety	Selection from Zera-Zera sorghum IS 23568	1992	Central	MPKV, Rahuri, Maharashtra
40.	Pant chari 3	Forage sorghum variety	Visarada 61-1 x IS 6953	1990	State	GBPUA&T, Pantnagar, Uttarakhand
41.	Pant chari 4	Forage sorghum variety	IS 4776 x RIO	1995	State	GBPUA&T, Pantnagar, Uttarakhand
42.	Pant chari 5	Forage sorghum variety	CS 3541 x IS 6935	1999	Central	GBPUA&T, Pantnagar, Uttarakhand
43.	Pant chari 6	Forage sorghum variety	SDSL 92140-MCT-36-93, Selection from Zimbabwe germplasm line	2006	Central	GBPUA&T, Pantnagar, Uttarakhand
44.	HC 136	Forage sorghum variety	IS 3214 (bicolor) x PC 7R	1982	Central	CCSHAU, Hisar, Haryana
45.	HC 171	Forage sorghum variety	SPV 8 x IS 4776	1987	Central	CCSHAU, Hisar, Haryana
46.	SSG 59-3	Forage sorghum variety	Non-sweet Sudan grass x JS 263	1977	Central	CCSHAU, Hisar, Haryana
47.	UP chari 2	Forage sorghum variety	Vidisha 60-1 x IS 6953	1984	Central	GBPUA&T, Pantnagar, Uttarakhand

Source: Tonapi *et al*. [1].

colouration, leaf mid rib colour (5th fully developed leaf), yellow colouration of flag leaf midrib, presence of arista, stigma anthocyanin colouration, stigma yellow colouration, length of pedicellate spikelet, colour of dry anthers, glume colour, panicle density, panicle shape, glume length, threshability score, caryopsis colour after threshing, grain shape in dorsal view, grain shape in profile view, size of mark of germ, endosperm texture, colour of vitreous albumen and grain lustre. Ten competitive plants were randomly selected from middle four lines of each replication for recording the field observations for all the traits except days to panicle emergence, which was observed on plot basis. For the quantitative data, variance components were estimated with restricted likelihood method (REML) using SAS Mixed Procedure (SAS 9.2). Genotypes were considered fixed, while other factors as random. SAS code for the analysis as given by [8] was followed. The quantitative and qualitative data were transformed into binary data according to [6]. The binary data were used to calculate Jaccard's similarity coefficients and were used to construct dendrogram employing UPGMA (Unweighted Paired Group Method using Arithmetic Average) using NTSYSpc 2.02e [10].

Analysis of variance showed significant differences among the 47 genotypes, for all the quantitative traits studied (data not shown). Maximum variability as represented by panicle neck length followed by plant height up to base of flag leaf, panicle branch length and other traits. This observation is in complete agreement with earlier report [4]. However, Elangovan *et al*. [11] reported much higher variation for all the traits than what we and Reddy *et al.* [10] have observed. This may be due to the fact that the earlier studies included landraces, while the present investigation study is restricted to released cultivars. Significant genotype x year interactions were recorded for all the traits except plant height up to base of flag leaf, while year effect was insignificant for plant height up to base of flag leaf, stigma length, leaf length and panicle length (data not shown). This supported earlier report by Reddy *et al*. [4]. High broad sense heritability (>90%) was recorded for majority of traits except leaf blade length (66%), stem diameter (72%), leaf blade width (80%) and anther length (86%). This is partially in agreement with earlier results [4], which reported low heritability for days to panicle emergence (55%) and grain weight (72%).

High positive genetic correlations ($\geq$0.70) were recorded between plant height up to base of flag leaf and total plant height (0.99), followed by panicle length-panicle branch length (0.86), leaf length-panicle length (0.75), days to panicle emergence-plant height up to base of flag leaf (0.72), and others (Table 2). Moderate negative correlations were recorded between leaf length-anther length (–0.67), plant height up to base of flag leaf/total plant height-leaf length among others. This is not in agreement with earlier findings, who reported predominance of positive correlation among quantitative traits in sorghum [2, 11]. The high genetic as well as phenotypic correlation between total plant height and plant height up to base of flag leaf suggested that these are highly correlated traits and one may be dropped as DUS trait. Like Ayana and

Table 2. Broad-sense genotypic (above diagonal) and phenotypic (below diagonal) correlations between quantitative traits

Traits[$]	DPE	PHFL	SL	AL	TPH	SD	LL	LW	PL	PBL	PNL	GW
DPE	-	0.72	0.41	0.29	0.70	0.42	–0.49	0.04	–0.43	–0.23	–0.49	–0.21
PHFL	0.61	-	0.64	0.50	0.99	–0.20	–0.58	–0.36	–0.44	–0.19	–0.24	–0.18
SL	0.33	0.60	-	0.71	0.65	–0.16	–0.39	–0.30	–0.11	0.18	–0.16	–0.26
AL	0.15	0.42	0.59	-	0.51	–0.26	–0.67	–0.43	–0.25	0.07	–0.06	–0.14
TPH	0.60	0.97	0.62	0.43	-	–0.25	–0.52	–0.40	–0.34	–0.09	–0.15	–0.20
SD	0.26	–0.12	–0.13	–0.18	–0.16	-	–0.38	0.62	–0.28	–0.49	–0.44	0.19
LL	–0.40	–0.37	–0.23	–0.29	–0.35	–0.04	-	0.23	0.75	0.46	0.42	0.04
LW	–0.05	–0.28	–0.20	–0.29	–0.32	0.46	0.33	-	–0.16	–0.52	–0.32	0.44
PL	–0.35	–0.41	–0.10	–0.19	–0.32	–0.20	0.47	–0.13	-	0.86	0.63	–0.24
PBL	–0.19	–0.17	0.17	0.08	–0.09	–0.30	0.31	–0.38	0.78	-	0.53	–0.42
PNL	–0.34	–0.21	–0.12	–0.04	–0.11	–0.26	0.20	–0.27	0.50	0.43	-	–0.08
GW	–0.15	–0.16	–0.24	–0.10	–0.18	0.10	–0.03	0.33	–0.20	–0.37	–0.07	-

[$] DPE: days to panicle emergence; PHFL: plant height up to base of flag leaf, (cm); SL: stigma length (mm); AL: anther length (mm) ; TPH: total plant height (cm); SD: stem diameter (at lower one third height of plant) (cm); LL: leaf blade length (the third leaf from top including flag leaf) (cm); LW: leaf width (the third leaf from top including flag leaf) (cm); PL: panicle length without peduncle (cm) ; PBL: panicle branch length (middle third of panicle) (cm); PNL: panicle neck length above sheath (cm) ; GW: 1000 grain weight (g)

Bekele [2] we also recorded very high correlation between panicle length and panicle branch length, which they explained by 'multiplication and condensation' hypothesis.

Cluster analysis was carried out separately using quantitative and qualitative data separately, which put the genotypes into three and four clusters, respectively (data not shown). Jacard's similarity coefficient based on combined data (12 qualitative and 21 quantitative traits) as suggested by Geleta *et al*. [6] ranged from 0.08-0.93 with an average of 0.44. Clustering pattern put the genotypes under study into four main clusters (Fig. 1). Cluster I, was represented by three B lines (2077B, 27B and 296B). Cluster II was the biggest with four sub-clusters, represented by 33 genotypes. Sub-cluster IIa contained two R lines (RS29 and RS673), three B lines (2219B, AKMS14B and 7B) and remaining grain sorghum varieties. Sub-clusters IIb and IId were smallest with two varieties each. Sub-cluster IIc represented majority of R lines (5 out of 8). Majority of forage varieties (7 out of 8) were represented in two clusters, III and IV. Cluster III contained eight genotypes, of which four were forage sorghum varieties (HC 136, Pant Chari 3, HC 171, UP Chari 2), two grain sorghum varieties (GJ 9, PVR 453), and two sweet sorghum varieties (CSV 19SS and SSV 84). Cluster V was represented by only forage sorghum varieties (Pant Chari 4, Pant Chari 6, SSG 59-3). The PCA fully did not support the clustering pattern, as obtained by UPGMA. However, most of the forage sorghum varieties and sweet sorghum variety, CSV 19SS remained distinctly different from rest of the genotypes based on qualitative traits. The clustering pattern remained much similar to that obtained using qualitative traits alone with some differences in term of similarity values (Fig. 1). The product moment correlation coefficients through Mentel's test between the clustering patterns using qualitative data and quantitative data alone to that of combined data set were 0.93 and 0.83, respectively. This suggests that there was very good fit to the trees obtained by qualitative data and the combined data set, while good correlation could be obtained between quantitative data and combined data set.

Existence of wide variability among extant varieties and parental lines was observed in the present investigation. Reddy *et al*. [4] first reported the variability among the released sorghum cultivars in India. The findings of present study are in broad agreement with their results. Relatively less variability among the male sterile (MS) lines was observed. Unlike the previous report, we found that IMS 9B was quite divergent from the remaining MS lines. The R lines were also relatively similar majority being grouped in sub-cluster IIc. More divergent R lines, like RS 29 or RS 673 may be hybridized with other R lines to derive new R lines. Genotypes in cluster I or II and III or IV were quite divergent. However, these may not

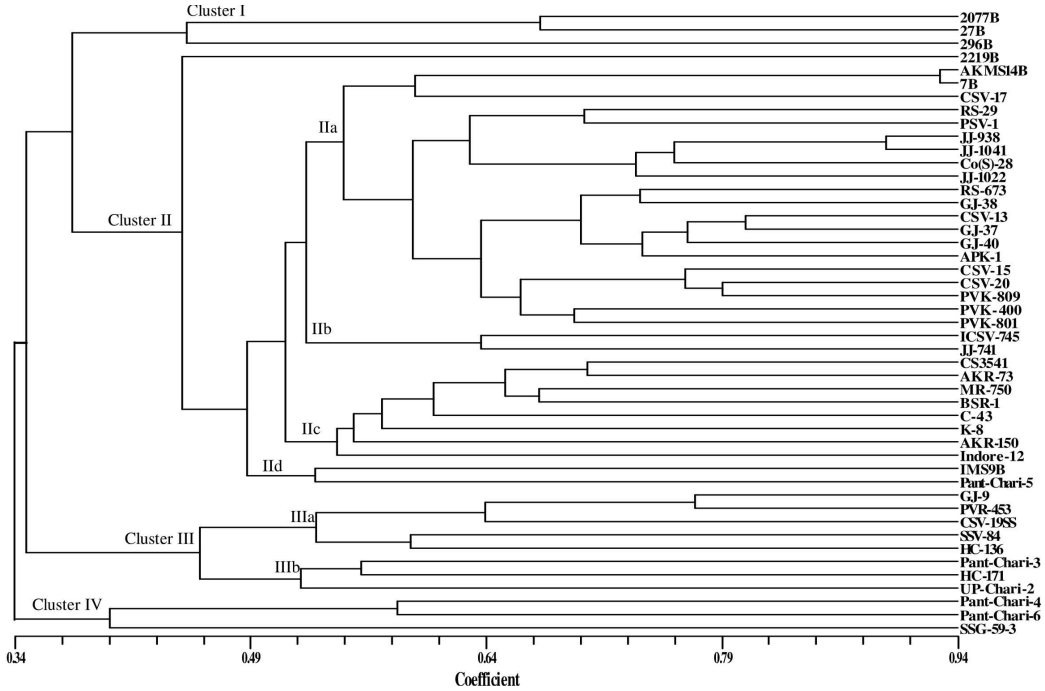

Fig. 1. Dendrogram based on Jaccard's coefficient using combined data (R = 0.88)

readily be used in crossing programme as they are predominantly quite different (grain types and forage types). Some of the grain type genotypes which are present in cluster III may be used in crossing programme with genotypes in cluster I or II to bring in wider variability among the progenies. Similarly, much diverse forage genotype, Pant Chari 5 (IId) may be crossed with other forage varieties in Cluster IIIb or IV to create more genetic variability for various morphological traits. In addition towards parental line development of grain sorghum genotypes belonging to Cluster I may be hybridized with genotypes belonging to Cluster IIb or IIc to derive new parental lines. Reddy *et al*. [4] also suggested crossing between genotypes from diverse clusters for improvement of female parents for DUS traits.

In the present study a considerable variability among genotypes was observed. However, few genotype combinations like AKMS14B-7B or JJ938-JJ1041 are much similar (Fig. 1). Pedigree information suggests that 7B is a selection from AKMS14B (Table 1). Thus, their morphological closeness is expected, which is certainly due to their similar genetic architecture. Similar was the case with JJ1022 and JJ1041. Some combinations were quite similar in terms of qualitative traits, as was the case with RS673 and GJ38. However, they were diverse in terms of quantitative traits. On the other hand several combinations, like CSV 15-CSV 20 or JJ 1041-PKV 809 came very close for quantitative values, but were diverse enough qualitatively (data not shown). So rightly these both are part of the DUS testing guidelines across crop species. It may be noted that in spite of existence of much variability for morphological traits some genotypes came much closer to each other (Fig. 1). Thus, it is imperative that efforts are needed continuously to search for new morphological traits to supplement existing traits as available in DUS testing guidelines in sorghum. Efforts are also needed to explore the application of DNA markers in such testing.

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