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Genetic divergence analysis of sorghum [*Sorghum bicolor* (L.) Moench] germplasm lines

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Abstract
This study was performed at Instructional dairy farm, Govind Ballabh Pant University of agriculture and technology during *Kharif* season, 2017 to evaluate and characterize 96 sorghum accessions for various morphological and fodder yield parameters. On the basis of Hierarchical cluster analysis, 96 genotypes were classified into seven clusters. Maximum number of genotypes were found in cluster II (42) followed by cluster number V. The pattern of group clusters proved that geographical diversity need not necessarily be related to the genetic diversity. The generalized intra cluster distance ranged from 0.00 (cluster VI and cluster VII) to 116.756 (cluster II). The relative distance of each cluster from cluster (inter cluster distance) indicated high degree of divergence between cluster I and cluster VII (895.34) followed by cluster VI and cluster VII (757.58). So the genotypes of cluster I and cluster VII can be used as parents in yield improvement programmes.

Keywords: Accessions, genetic diversity, cluster, sorghum, morphological

Introduction
Agriculture systems are time dependent and dynamic. Agriculture, with its related sectors, is the largest livelihood providers in India, especially in the rural areas of the country. In a country like India, traditional agriculture, either in the form of growing sole crops or mixed crops, provides greater survival value rather than confer advantage of greater productivity.
Sorghum [*Sorghum bicolor* (L.) Moench] also known as Jowar has originated in Northeastern Africa about 5000 – 8000 years ago (De Candolle 1884) [11]. The five different races of sorghum were distributed to wide range of places due better quality, high yielding capacity and palatability. The demand for fodder sorghum is increasing at a faster rate. To meet the demand there is need of increase in the production and it should come from it or even less area in the present situation of shrinking agricultural land (Prakash *et al*., 2010) [8]. For better animal performance it is necessary to improve the nutritional quality and fodder sorghum yield. Improving the genetic potential of the crop for maximizing the economic gain per unit of input is the most various sorghum growing states and agro climatic region have been developed with research efforts taken under the All India Coordinated Sorghum Improvement Project. It is found that the impact of sorghum hybrid has not been felt in country. This calls for a much needed up thrust in the productivity levels of better quality sorghum along with the necessary production technology. Indian Institute of Millets Research (IIMR) is engaged in basic and strategic research on millets including sorghum under Indian Council of Agricultural Research (ICAR). Sorghum research is coordinated at national level by IIMR through All India Coordinated Research Projects on Pearl Millet, Sorghum and Small Millets and it also provides linkages with various national as well as international agencies.
Development of broad genetic base, stable and high yielding sorghum cultivars requires a continuous supply of new germplasm as a source of desirable genes in breeding programs. The primary sources of such genes are introductions, weedy species, landraces, and wild relatives of crop plants. Therefore, comprehensive knowledge of germplasm diversity and genetic relationships among cultivated sorghum will remain an in important aid in the crop improvement strategies for breeding programs (Mohammadi and Prasanna, 2003) [15]. Many studies are done to assess patterns of genetic variation based on morphology or pedigree (Agrama and Tuinstra, 2003) [1]. Sorghum has 42,000 accessions which makes it one of the largest crop germplasm collections (Huang, 2004; Dahlberg *et al*., 2002) [13, 5]. The diverse germplasm is a great source for improvement of the plant adaptation and other agronomic traits (Huang, 2004) [13].
Proper exploitation of the available variability in the crop is done to identify and select superior genotypes having desirable trait from a broad range of breeding material is genotypes

will serve as an important tool to exploit the genetic variability for the rapid progress in hybrid breeding programmes.

Material and method

Ninty six sorghum genotypes were used for the present study. The trial was grown at the Instructional Dairy Farm of the Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India during *Kharif* 2017. Pantnagar is located at an altitude of 243.84 meters above mean sea level and 29ºN latitude. Falls under the humid subtropical zone and is situated in the Tarai region at the foothills of Shivalik range of Himalayas. The experiment was carried out in an Augmented Block Design with each block containing 24 test entries and 5 checks (randomly allocated) with the total of 29 treatment in each block. Each genotype were sown in two rows of 3 metre length with a row spacing of 45cm. Recommended package of practices were followed to grow the normal healthy crop. An average rainfall of 948.6mm is experienced annually.

Data was recorded on time to 50% flowering (days), plant height (cm), number of nodes per plant, leaf length (cm), leaf width (cm), stem girth (cm), flag leaf length(cm), flag leaf width (cm), panicle length (cm), panicle width(cm), protein content (%), HCN content (ppm), days to maturity, Brix%, dry matter %, 1000 grain weight per panicle(gm), Dry fodder yield (g/plant) and green fodder yield (g/plant).

Hierarchical cluster analysis was performed on the basis of Euclidean distance between the genotypes.

Result and discussion

Analysis of variance indicated significant differences among genotypes for13 traits out of all the traits studied, indicating thereby the presence of wide range of variability.

On the basis of Hierarchical cluster analysis, 96 genotypes were classified into seven clusters. The detail of the genotypes in different clusters is given in Table 1. Maximum number of genotypes were found in cluster II (42) followed by cluster V (32), cluster I (14), cluster IV (7), cluster III (4) cluster VI (1) and cluster VII (1). The pattern of group clusters proved that geographical diversity need not necessarily be related to the genetic diversity. Similar study was conducted where 119 sorghum accessions were grouped into thirteen different clusters using hierarchical cluster analysis by Tesfaye, K. (2017) [9] and the clustering pattern indicated the existence of a significant amount of variability among the sorghum species. Badigannavar *et al.* (2017) [4] evaluated 141 exotic germplasm lines and 36 popular varieties for eight agro-morphological traits cluster analysis resolved all the genotypes into four major clusters.

Intra and inter cluster distance is measured to determine the degree of divergence between the clusters (Table 2). The maximum intra cluster distance was recorded for cluster II (116.756) followed by cluster V (115.07), cluster I (99.26), cluster IV (98.20), cluster III (73.48) while minimum distance was observed for cluster VI and cluster VII which indicates that these were less divergent. The maximum inter cluster distance was perceived between cluster I and cluster VII (895.34) followed by cluster VI and cluster VII (757.58). The relative distance of each cluster from cluster (inter cluster distance) indicated high degree of divergence between cluster I and cluster VII (895.34) followed by cluster VI and cluster VII (757.58). So the genotypes of cluster I and cluster VII can be used as parents in yield improvement programmes. The genotypes within the same cluster considered to have the similar phenotypic characters and are more related as compared to the genotypes of the other clusters whereas the genotypes between the clusters are more diverse ones. Therefore, the genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties. This finding supports with the finding of Nirubana *et al*. (2019) [6], Amarnath *et al*. (2019) [2], Flajsman *et al*. (2019) [12], Anteneh *et al*. (2019) [3] and Kumar *et al*. (2019) [14]. Table 3 shows the cluster means for different traits which indicates considerable differences between the clusters. The lowest cluster mean for Days to 50% flowering was observed in cluster IV (52.71), for maximum plant height in cluster III (347.62). Highest cluster mean for number of nodes was observed in cluster III (18.10), for leaf length in cluster III (82.11), leaf width cluster IV (6.40), green fodder yield in cluster VII (1142.18) for Dry matter% in cluster VI (126.04) and for Dry fodder was observed in cluster VI (629.79).

Table 1: Distribution of Sorghum accessions into different clusters based on hierarchical cluster analysis.

Cluster number	No. of genotypes	Genotypes
I.	14	IS-313, Pant elite line 2001, SSG 59-3, Pant elite line 2004, Pant elite line 2022, IS-3314, IS-6193, IS-699, IS-1219, IS-4307, IS-23586, IS-14241, Pant elite line 2015 and Pant elite line 2042.
II.	42	IS-608, IS-3313, IS-4726, IS-3145, Pant elite line 2026, Pant elite line 2033, IS-3345, IS-6953, Pant elite line 2032, Pant elite line 2039, Pant elite line 2035, IS-1478, IS-3199, IS-3353, IS-3865, IS-21622, IS-2363, IS-14298, IS25733, Pant elite line 2014, IS-3359, Pant elite line 2003, IS-3318, Pant elite line 2037, Pant elite line 2006, IS29691, Pant elite line 2007, IS-639, IS23988, IS-3237, IS31861, CSV33MF, IS-7002, IS-20782, Pant elite line 2016, IS-14816, Pant elite line 2012, CSV30F, Pant elite line 2038, Pant elite line 2020, IS33096, SGL-87.
III.	4	IS-3821,IS-12743,IS-5434,IS-20740
IV.	7	IS-4613, IS-15008, IS-20399, IS-14278, Pant elite line 2024, Pant elite line 2030, Pant elite line 2018
V.	32	IS-4925, IS-21021, Pant elite line 2008, Pant elite line 2011, Pant elite line 2002, Pant elite line 2017, CSV 21F, Pant elite line 2019, Pant elite line 2023, Pant elite line 2025, Pant elite line 2028, Pant elite line 2009, PC-5, Pant elite line 2031, Pant elite line 2010, IS-6045, IS-9162, IS-21602, IS-14333, IS25419, IS-22241, IS23948, IS-20703, Pant elite line 2005, IS-21461, IS-14756, Pant elite line 2013, IS-6090, Pant elite line 2034, Pant elite line 2036, Pant elite line 2027, Pant elite line 2029
VI.	1	IS23992
VII.	1	Pant elite line 2021

Table 2: Intra and inter cluster distances between the clusters based on hierarchical cluster analysis of Sorghum germplasm.

Clusters	I.	II.	III.	IV.	V.	VI.	VII.
I.	99.26	212.71	495.31	584.49	399.10	616.61	895.37
II.		116.756	331.67	400.87	223.67	537.91	707.16
III.			73.48	229.19	211.17	407.28	465.52
IV.				98.20	208.83	602.03	331
V.					115.07	539.11	508.61
VI.						0.00	757.58
VII.							0.00

Table 3: Cluster means for different characters studies on Sorghum germplasm

cluster	Days to 50% flowering	Plant height (cm)	Stem girth (cm)	Number of nodes	Leaf length (cm)	Leaf width (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Panicle length (cm)	Panicle width (cm)	Days to maturity	HCN (ppm)	Protein content%	Brix %	IVDMD	Dry matter %	1000 seed weight	Dry fodder yield (g/plant)	Green fodder yield (g/plant)
I	58.70	332.96	1.29	16.68	76.60	5.57	35.95	4.90	27.01	6.27	95.42	58.78	4.69	7.40	46.98	26.37	19.44	72.80	269.91
II	58.61	292.20	1.39	16.05	74.12	6.27	36.87	5.64	24.34	6.00	99.00	60.63	4.62	9.42	48.33	24.06	20.77	110.57	454.44
III	75.35	347.62	1.47	18.10	82.11	5.84	48.98	6.09	24.61	5.80	108.2	66.00	4.38	7.57	48.13	43.17	22.14	303.24	700.92
IV	52.71	309.42	1.42	15.30	77.05	6.40	34.97	5.43	22.82	5.72	86.54	65.26	4.23	10.26	48.88	18.80	21.89	154.02	841.50
V	56.20	302.89	1.44	15.54	74.43	6.30	40.51	5.79	24.22	5.54	95.08	60.81	4.47	11.47	49.53	20.40	22.76	129.32	645.96
VI	74.05	267.21	0.74	14.10	51.43	5.16	27.85	4.12	24.42	4.92	93.05	57.92	3.95	9.81	36.39	126.04	22.46	629.79	497.65
VII	53.25	232.81	1.18	13.70	67.63	5.91	33.45	6.70	16.63	7.23	89.05	71.64	7.75	14.81	52.13	23.04	19.26	248.46	1142.18

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