International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
IJCS 2019; 7(5): 2682-2685

Received: 21-07-2019
Accepted: 25-08-2019

SJ Goswami
Department of Genetics and Plant Breeding, CPCA, SD Agricultural University, Sardarkrushinagar, Gujarat, India

PT Patel
Department of Seed Technology, SD Agricultural University, Sardarkrushinagar, Gujarat, India

AB Khatri
Department of Genetics and Plant Breeding, CPCA, SD Agricultural University, Sardarkrushinagar, Gujarat, India

RA Gami
Sorghum Research Station, SD Agricultural University, Deesa, Gujarat, India

KG Kugashiya
Department of Seed Technology, SD Agricultural University, Sardarkrushinagar, Gujarat, India

PO Vaghela
Department of Seed Technology, SD Agricultural University, Sardarkrushinagar, Gujarat, India

Corresponding Author:
AB Khatri
Department of Genetics and Plant Breeding, CPCA, SD Agricultural University, Sardarkrushinagar, Gujarat, India

Study of genetic divergence for forage and grain yield in sorghum [*Sorghum bicolor* (L.) Moench]

SJ Goswami, PT Patel, AB Khatri, RA Gami, KG Kugashiya and PO Vaghela

Abstract
The present investigation was carried out to study genetic divergence for fodder and grain yield in sorghum [*Sorghum bicolor* (L.) Moench] using torcher method. The genetic diversity analysis revealed that the formation of eight clusters suggested the presence of considerable genetic diversity among the 40 genotypes studied. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that 1000-grain weight, protein content, panicle length, leaf: stem ratio, dry fodder yield per plant and grain yield per plant contributed maximum towards total genetic divergence. It was observed that 1000-grain weight (30.64 g), protein content (29.49 %), panicle length (12.82 cm), leaf: stem ratio (9.62), dry fodder yield per plant (7.82 g) and grain yield per plant (5.13 g) were the main contributors to the total divergence. Days to flowering (2.05 day), panicle width (1.28 cm) and leaf width (1.15 cm) shown small contribution. Maximum number of genotype observed in cluster I with 33 genotype, while other seven cluster observed with single genotype in each. Maximum cluster distance was found between cluster VI and cluster VIII.

Keywords: genetic divergence, sorghum genotypes, fodder and grain yield, cluster analysis

1. Introduction
Sorghum or Great millet [*Sorghum bicolor* (L.) Moench] is one of the most important cereal crop in the world because of its adaptation to a wide range of ecological conditions, suitability for low input cultivation and diverse uses (Doggett, 1988) [5]. Sorghum belongs to family *Poaceae* and tribe Andropogoneae (Harlan & de wet, 1972) [6]. It is an often cross-pollinating, diploid crop (2n=20) with a genome size of 730mb (Paterson *et al.*, 2009) [13]. It is a C_4 plant with higher photosynthetic efficiency and higher abiotic stress tolerance (Nagy *et al*., 1995; Reddy *et al*., 2009) [11, 15]. Cultivated sorghum have been classified into 5 races *viz*., *Bicolor*, *Guinea*, *Caudatum*, *Durra* and *Kafir* and ten intermediate races corresponding to the pair wise combination of major races. These are identified according to the morphological traits, especially panicle, grain and glume traits (Harlan & de Wet, 1972) [6].
Sorghum is fifth most important cereal crop globally and is the dietary staple of more than 500 million people in 30 countries. It is grown on 40 million ha in 105 countries of Africa, Asia, Oceania and the Americas. Africa and India account for the largest share (Near about 70%) of global sorghum area while USA, Mexico, Nigeria, Sudan and Ethiopia are the major sorghum producers (Kumar *et al*., 2011) [8]. Worldwide, it is cultivated on 44.27 million ha with a production of 63.35 million metric tones and productivity of 1.43 metric tons/ha (USDA, 2017) [20]. It is the fourth important cereal in India after rice, wheat and pearl millet. The area under this crop in the country is about 5.14 million hectares with an annual production of 4.57 million tones and productivity of 889 kg/ha. The major states in the country where this cereal grain is produced are Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, Rajasthan and Gujarat. In Gujarat, area, production and productivity of sorghum is 0.10 million hectares, 0.15 million tonnes and 1408 kg/ha, respectively (Anonymous, 2017) [2].
In order to make sorghum as an enterprising and remunerative crop, obviously there is an urgent need to initiate research to develop varieties and hybrids having faster growth, early to medium maturity and higher grain and fodder yield with good quality parameters. To improving the genetic potential for grain and fodder yield in sorghum is prime concern for breeder. It is noted that cultivated sorghums are highly variable and suggested that to enhance the productivity levels of sorghum, prior information on the nature and the magnitude of

genetic variability present in germplasm collection is a pre-requisite. Assessment of genetic variability in the base population is the first step in any breeding programme. Variability should be determined with the help of certain parameters, such as genotypic and phenotypic coefficient of variation, heritability estimates and genetic advance.

The choice of parents for hybridization is one of the crucial decisions that a plant breeder has to take for further improvement of the crop. Sabharwal *et al.* (1995) [16] emphasized that sorghum parents with more diversity among them are expected to exhibit a higher amount of heterotic expression and a broad spectrum of variability in segregating generations. There are various methods for identifying such material. Among them Mahalanobis's D^2 technique is one of the efficient tools for estimating genetic divergence and identifying the desirable parents for any crossing programme.

The assessment of genetic diversity using quantitative traits is very important for differentiating the well-defined populations. Several methods of divergence analysis based on quantitative traits have been proposed to various objectives, of which Mahalanobis's generalized distance occupy a unique place and an efficient method to judge the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

2. Material and Methods

The experimental material consisting of 40 genotypes were grown in Randomized Block Design (RBD) with three replications. The experimental material was planted in field during *kharif* 2018. The observation on five randomly selected plants were recorded for days to flowering, days to maturity, plant height (cm), Number of leaf per plant, stem girth (mm), leaf width (cm), leaf area (cm^2) (Model No.: LI-310006), leaf: stem ratio, panicle length (cm), panicle width (cm), dry fodder yield per plant (g), grain yield per plant (g), Protein content (%) (by micro Kjeldahl's method). The mean of the data recorded were used for statistical analysis. The analysis of variance was calculated with the method suggested by Panse and Sukhatme, 1985 [12]. Mahalanobis's D^2 statistics was followed for genetic divergence study. Grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952) [14]. The inter-cluster distance was calculated by measuring the distance between clusters I and cluster II, between clusters I and cluster III, between clusters II and cluster III and so on. Likewise, one by one cluster was taken and their distances from other clusters were calculated. For graphical presentation average intra-cluster values were used to obtain manual relationship between clusters.

3. Results and Discussion

3.1 Genetic divergence

The selection of parents based on individual attributes may be advantageous as compared to base on a number of important components collectively, especially if the aim is to seek improvement in complex quantitative traits such as grain yield and dry fodder yield. The genetic diversity existing in the population helps in selection of suitable parents for breeding programme. Mahalanobis's D^2 statistics is therefore employed to assess the amount of genetic diversity and a rational choice of potential parents for breeding programme. The results of genetic diversity are presented below.

In the present study, D^2 statistic estimated on 40 genotypes of sorghum for 15 characters showed that the generalized distance ($\sqrt{D^2}$) between two populations varied from 60.21 to 627.57 which was an indicator of high diversity available in the material evaluated. On the basis of D^2 values, eight clusters were formed from 40 genotypes. The clustering pattern indicated that the geographical diversity need not necessarily be related to the genetic divergence. This could be evidenced from the study that genotypes from the same eco-geographical region did scatter in eight clusters. The results obtained in the present study are in accordance to the findings of Kadam *et al.* (2001) [7] and Asthana *et al.* (2002) [3] who also reported that varieties from the same state did not form the single cluster.

The cluster I was the largest one containing 33 genotypes. The cluster II, III, IV, V, VI, VII and VIII had single genotype. In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster distance was in cluster II, III, IV, V, VI, VII and VIII (D = 0), whereas the highest intra-cluster distance was in cluster I (D=112.36). The maximum inter-cluster distance (D) was observed between clusters VI and VIII (D = 627.57) followed by clusters IV and VI (D=518.27). The genotypes belonging to different clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster VIII can be crossed with clusters IV and VI in hybridization programme for obtaining a wide range of variation among the segregants. Maximum and minimum inter-cluster divergence within different clusters also reported by Chittapur *et al*. (2013) [4], Umadevi *et al.* (2009) [19], Mahajan and Wadikar (2012) [9], Ahamad *et al.* (2015) [1], Sujatha *et al. (*2015) [18], Sinha and Kumaravadivel (2016) [17] and More *et al.* (2018) [10]. All the genotypes evaluated in the present investigation were developed at Sorghum Research Station, S.D.A.U, Deesa and Indian Institute of Millets Research, Hyderabad. Thus, the observed clustering pattern of genotypes was independent of their geographical origin. , Kadam *et al.* (2001) [7], Asthana *et al.* (2002) [3] and Chittapur *et al*. (2013) [4] did agree with this view and pointed out that geographical diversity need not result in genetic divergence.

The cluster mean for 15 characters are presented in Table 3. Greater range of mean values among the clusters was recorded for different traits. The cluster II was better for plant height (259.73 cm). The cluster III got desirable rating in respect of number of leaf per plant (11.20) and leaf length (88.13 cm) and 1000-grain weight (34.92 g). The cluster IV was better stem girth (11.49 mm) and protein content (9.98 %). The cluster V got desirable rating in respect of panicle length (25.32 cm), panicle width (9.47 cm) and grain yield per plant (95.87 g). The cluster VI got desirable rating in respect of days to flowering (87.67), days to maturity (123.67), leaf width (8.18 cm), leaf area (2633.68 cm^2) and dry fodder yield per plant (182.80 g). The cluster VIII got desirable rating in respect of leaf: stem ratio (0.52).

3.2 Contribution of different characters to divergence

The components of D^2 due to each character variable were ranked I being assigned to the highest value. The total of these ranks over all possible n (n-1)/2 = 780 combinations would provide indirect information about the order of priority in terms of percentage contribution of the character to the total divergence. These percentages are presented in Table 4. It was observed that 1000-grain weight (30.64 g), protein content (29.49 %), panicle length (12.82 cm), leaf: stem ratio (9.62), dry fodder yield per plant (7.82 g) and grain yield per plant (5.13 g) were the main contributors to the total

divergence. Days to flowering (2.05), panicle width (1.28 cm) and leaf width (1.15 cm) shown small contribution. While, characters like days to maturity, plant height, number of leaves per plant, stem girth, leaf length and leaf area showed no contribution towards total genetic divergence. High cluster means for various characters were also reported by Ahamad *et al.* (2015) [1], Sujatha *et al. (*2015) [18], Sinha and Kumaravadivel (2016) [17] and More *et al.* (2018) [10].

4. Conclusion

The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement. It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations. So based on study crossing between clusters VI and VIII. In the present study will have more chances of delivering sergeants as maximum inter-cluster distance (D) was observed between them. 1000- grain weight, protein content, panicle length, leaf: stem ratio, dry fodder yield per plant and grain yield per plant were the main contributors and days to flowering, panicle width and leaf width were small contributors for grain yield per plant. These all characters may be used for selection, evaluation and utilization in crossing programme for yield and fodder sorghum as well by selecting desirable segregants in F_2 and subsequence advance generations to further improvement in sorghum.

Table 1: Grouping of 40 genotypes of sorghum in various clusters on the basis of D^2 – statistics

Cluster	No. of Genotypes	Name of the genotypes
I	33	EJN 1, EJN 14, EJN 20, EJN 22, EJN 24, EJN 26, ER 23, DS 1054, DS 1055, DS 1060, DS 1073, DS 1067, EC 483113, EC 484215, EC 484286, EC 488239, EC 843004, IC 484618, IC 485031, IC 485202, DS 0105, DS 0137, DS 0156, DS 0157, DS 0159, DS 0164, DS 0167, DS 0169, DS 0148, DS 0171, DS 0182, GJ 39, CSV 27
II	1	DS 1101
III	1	DS 0149
IV	1	DS 1053
V	1	ER 25
VI	1	EC 842912
VII	1	Malwan
VIII	1	IC 289489

Table 2: Average inter and intra-cluster distance ($D=\sqrt{D^2}$) values in 40 genotypes of sorghum

	I	II	III	IV	V	VI	VII	VIII
I	112.36	202.56	206.36	274.66	233.08	189.14	210.33	344.47
II		0	321.03	60.21	273.15	406.14	192.93	279.22
III			0	307.67	103.16	455.82	169.78	429.27
IV				0	224.7	518.27	235.98	308.64
V					0	454.82	147.21	449.95
VI						0	411.39	627.57
VII							0	197.11
VIII								0

Table 3: Cluster mean for 15 different characters in 40 genotypes of sorghum

Clusters	Days to Flowering	Days to maturity	Plant height (cm)	Number of leaf per plant	Stem girth (mm)	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)	Leaf: Stem ratio	Panicle length (cm)	Panicle width (cm)	Dry fodder yield per plant (g)	1000-grain weight (g)	Grain yield per plant (g)	Protein content (%)
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)
I	76.57	112.30	237.07	9.72	10.93	76.37	6.30	1859.88	0.19	18.24	6.68	88.38	25.14	56.38	7.08
II	87.33	122.67	259.73	10.87	10.18	79.40	5.64	1935.64	0.13	19.91	7.73	93.40	25.43	31.73	9.55
III	74.00	110.00	244.07	11.20	11.05	88.13	5.42	2123.27	0.33	22.01	7.05	75.30	34.92	68.27	6.29
IV	81.00	116.67	240.60	10.07	13.17	81.87	6.51	2071.00	0.17	16.01	7.75	101.60	30.90	36.27	9.98
V	72.00	107.67	250.67	8.53	12.49	77.33	7.86	2015.23	0.26	25.32	9.47	127.83	33.68	95.87	7.31
VI	87.67	123.67	240.80	10.13	12.35	83.07	8.18	2633.68	0.11	14.23	5.89	182.80	21.11	59.73	6.43
VII	83.67	119.33	228.47	10.40	11.14	66.80	6.31	1770.62	0.40	21.59	9.28	142.97	28.24	56.67	7.65
VIII	66.67	103.00	209.93	8.80	10.61	63.93	6.81	1562.44	0.52	10.03	5.31	60.23	23.30	44.57	9.17
Mean	78.614	114.414	238.918	9.965	11.49	77.113	6.629	1996.47	0.264	18.418	7.395	109.064	27.840	56.186	7.933
SD	7.570	7.395	14.914	0.930	0.331	8.154	0.972	313.908	0.144	4.878	1.480	39.987	4.968	20.225	1.439
S.Em. ±	2.676	2.615	5.273	0.329	0.117	2.883	0.344	110.983	0.051	1.725	0.523	14.137	1.756	7.151	0.509
C.V.%	9.63	6.46	6.24	9.33	9.17	10.57	14.67	15.723	54.45	26.48	20.02	36.66	17.84	35.99	18.14

Table 4: Relative contribution of different characters towards genetic diversity in sorghum genotypes evaluated for grain yield

Sr. No.	Characters	Time ranked 1st	Contribution to divergence%
1	Days to flowering	16	2.05
2	Days to maturity	0	0
3	Plant height (cm)	0	0
4	Number of leaf per plant	0	0
5	Stem girth (mm)	0	0
6	Leaf length (cm)	0	0
7	Leaf width (cm)	9	1.15
8	Leaf area (cm^2)	0	0
9	Leaf: Stem ratio	75	9.62
10	Panicle length (cm)	100	12.82
11	Panicle width (cm)	10	1.28
12	Dry fodder yield per plant (g)	61	7.82
13	1000- Grain weight (g)	239	30.64

14	Grain yield per plant (g)	40	5.13
15	Protein content (%)	230	29.49

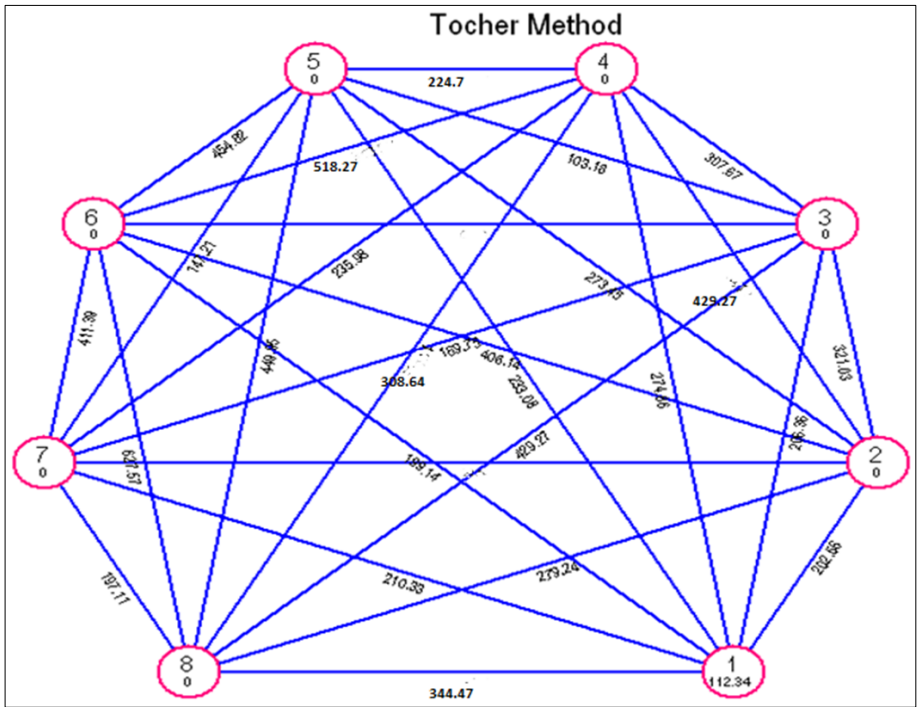

Fig 1: Cluster diagram of 8 clusters for 40 genotypes of sorghum

5. Acknowledgement
The research funded as well as facilitate by Sardarkrushinagar Dantiwada Agricultural University.

6. References

1. Ahamad KU, Akhter B, Islam MR, Alam MK, Hssain MM. Assessment of genetic divergence in sorghum [*Sorghum bicolor* (L.) Moench] germplasm. Bulletin of the Institute of Tropical Agriculture. 2015; 38(1):47-54.
2. Anonymous. Agriculture statistics at a glance (2017), Ministry of Agriculture, Department of Agriculture and Cooperation, Directorate of Economics and Statistics, New Delhi, India, 2017, pp.99.
3. Asthana OP, Asthana N, Sharma RL. Genetic divergence studies in exotic sorghums [*Sorghum bicolor* (L.) Moench] using cluster/principal component analysis. Advances in Plant Sciences. 2002; 15:579-587.
4. Chittapur R, Biradar BD, Salimath PM, Sajjanar GM. Genetic divergence for grain quality and productivity traits in *rabi* sorghum. International Journal of Agriculture Innovations and Research. 2013; 1(5):132-135.
5. Doggett H. "Sorghum" Second edition. New York, USA: John Wiley and Sons, 1988, pp.512.
6. Harlan JR, de Wet JMJ. A simple classification of cultivated sorghum. Crop Science. 1972; 12:172-176.
7. Kadam DE, Patil FB, Bhor TJ, Harer PN. Genetic diversity studies in sweet sorghum. Journal of Maharashtra Agricultural Universities. 2001; 26:140-143.
8. Kumar AA, Reddy BVS, Ramaiah B, Sharma R. Heterosis in white grained grain mold resistant sorghum hybrids. SAT Journal. 2011; 9:1-9.
9. Mahajan RC, Wadikar PB. Genetic divergence analysis in sorghum [*Sorghum bicolor* (L.) Moench]. Agricultural Science Digest. 2012; 32(3):244-246.
10. More AW, Kalpande HV, Dhutmal RR. Genetic Divergence Studies in Sorghum (*Sorghum bicolor* L.) Land Races for Yield and Yield Parameters. International Journal of Current Microbiology and Applied Sciences. 2018; 6:393-399.
11. Nagy ZZ, Tuba F, Soldos Z, Erdei L. CO_2 exchange and water relation responses of sorghum and maize during water and salt stress. Journal of Plant Physiology. 1995; 145:539-544.
12. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, ICAR, New Delhi, 1985.
13. Paterson AH, Bowers JE, Rokhsar DS. The *Sorghum bicolor* genome and the diversification of grasses. Nature. 2009; 457:551-556.
14. Rao CR. Adavanced Statistical Methods in Biometrical Research. John Willy and Sons Inc.; New York, 1952, pp.390.
15. Reddy BVS, Ramesh S, Reddy PS, Kumar AA. Genetic enhancement for drought tolerance in sorghum. Plant Breeding Reviews. 2009; 31:189-222.
16. Sabharwal PS, Pahunja SK, Lodhi GP. Germplasm evaluation for different fodder traits in forage soghum. Haryana agricultural Universities Journal. 1995; 25:207-210.
17. Sinha S, Kumaravadivel N. Understanding genetic diversity of sorghum using quantitative traits. Hindawi Publishing Corporation Scientifica, 2016, 1-8.
18. Sujatha K, Pushpavalli S. Genetic divergence for yield attributing trails in the *Rabi* sorghum germplasm. Electrenic Journal of Plant Breeding. 2015; 6(2):521-527.
19. Umadevi M, Kumaravadivel N. Variability and genetic diversity studies in sorghum germplasm. Plant Archives. 2009; 9:31-35.
20. USDA. United States Department of Agriculture, Foreign agricultural service, 2017, pp.18.