Biological Forum – An International Journal **14(1): 800-803(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Assessment of Genetic Diversity in *rabi* Sorghum [*Sorghum bicolor* (L.) Monech] using D^2 Statistics

Lokesh Kumar Verma[1*], B.D. Biradar[2] and A.K. Meena[1]
[1]Ph.D. Scholar, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, (Karnataka), India.
[2]Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, (Karnataka), India.

(Corresponding author: Lokesh Kumar Verma)*
(Received 02 November 2021, Accepted 04 January, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Genetic diversity is a necessary part of a successful hybrid breeding programme. One of the reasons why the *rabi* hybrids programme hasn't had much success is that there hasn't been a systematic assessment of genetic variation before incorporating into a hybrid combination. In the present experiment, 75 sorghum genotypes, including two checks, were evaluated for genetic diversity using twenty quantitative traits. After the D^2 and Tochar methods, the studied genotypes were distributed into ten clusters. Cluster I to VI had various numbers of genotypes and cluster I was found to be largest with 30 genotypes, whereas the rest of the clusters were solitary. Highest contribution towards genetic divergence was made by panicle weight (19.96%), followed by grain yield per plant (18.56%) and 1000 grain weight (16.65%). The genotypes *viz.*, IS 15170, IS 7987, IS 12735, M35-1 and PKV Kranti were found to be distinct, diverse and also showed good per se performance. These genotypes can be selected as promising parents in crossing programmes to widen the variability and isolate transgressive segregants.

Keywords: *Rabi* sorghum, D^2 statistics, Genetic divergence, Phenotypic traits.

INTRODUCTION

Sorghum (*Sorghum bicolor* L.) is the world's fifth most important cereal crop after wheat, rice, maize and barley (Motlhaodi *et al.,* 2014). It is an often cross pollinated crop, diploid (2n=2×= 20), originated in Ethiopian region (Vavilov, 1951). It is a C_4 plant having high photosynthetic efficiency and higher abiotic stress tolerance (Reddy *et al.,* 2009; Kumar *et al.,* 2013). It is one of the most important staple foods for more than 500 million people in 30 countries, and fodder crop in the areas of the semi-arid tropics of the globe and cultivated in the areas dry and hard, for other crops. Africa and India account for the largest share (> 70%) of global sorghum area while Nigeria, India, USA, Ethiopia and Argentina are the major sorghum producers. *Rabi* sorghum greatly influences the economic well being of the population and grown in the Deccan plateau in the states of Maharashtra, Telangana and Andhra Pradesh. It is mostly grown under moisture residing conditions.

Knowing a crop's genetic diversity can aid a breeder in selecting appropriate parents for a breeding programme and introducing genes from distantly related germplasm (Bucheyeki *et al.,* 2009). It is possible to cross more diverse genotypes or accessions to develop superior hybrids that are resistant to biotic and abiotic stresses. Genetic diversity in crop species is a gift of nature and arises due to geographical separation, natural mutation, or due to genetic barriers to crossability. The use of morphological traits to study genetic diversity is a common practice. It's usually straightforward and affordable to score them. These easily observable morphological traits are excellent tools for preliminary evaluation because they provide a quick and convenient method of determining the extent of diversity (Mace, 2005). Using phenotypic traits to estimate genetic diversity in cultivated sorghum has been the subject of several researchers over the years (Bucheyeki *et al.,* 2008*;* Ringo, 2014; Govindaraj *et al.,* 2015; Rana *et al.,* 2015; Mofokeng *et al.,* 2017; Sejake *et al.,* 2020). These phenotypic traits are the most common approach utilised to estimate relationships between genotypes. The genetic variability of cultivated species and their wild relatives, when combined, provides a potential and continuing source for developing new and improved crop varieties. Crop improvement will be aided by a greater understanding of sorghum genetic variability. Therefore, there is a need to evaluate available accessions for genetic diversity. In the present study, an attempt has been made to determine the extent of diversity among 75 sorghum genotypes using twenty morphological traits.

MATERIAL AND METHODS

A total of 75 sorghum genotypes, including two checks (M35-1 and PKV Kranti) were evaluated in Randomized Complete Block Design at Botany Garden,

University of Agricultural Sciences, Dharwad. Each accession was raised in two rows with 45 × 15 spacing. All the recommended agronomic packages of practices were followed during the entire crop period. The observations were recorded on twenty quantitative traits *viz.*, days to 50% flowering, days to maturity, peduncle length (cm), whorls per panicle, panicle length (cm), 1000 grain weight (g), primaries per panicle, panicle width (cm), panicle weight (g), grain yield per plant (g), plant height (cm), nodes per plant, leaves per plant, stem girth (mm), 1000 grain volume, number of grains per panicle, grain density, grain length (mm), grain width (mm) and grain thickness (mm). The data was collected on all the twenty traits and subjected to Indostate software version 9.1, descriptive statistics and D^2 statistics were computed.

RESULTS AND DISCUSSION

The analysis of variance indicated significant differences among the studied genotypes, revealing the presence of enough variability for all the traits under study. Based on the D^2 statistics and Tochar method the 75 genotypes were classified into ten clusters (Table 1) indicating the existence of sufficient diversity in the material. Cluster I was found to be the largest, with 30 genotypes, followed by clusters II, IV and III with 27, 8 and 4 genotypes, respectively. whereas the rest of the cluster were found to be solitary and revealed their diverse and unique nature. Kavya *et al.* (2019); Umakanth *et al.* (2019) also documented solitary clusters. Intermating between the genotypes of these solitary and unique genotypes may produce desirable transgressive segregants.

The average intra and intercluster distances are presented in the Table 2. The cluster I showed the minimum intra cluster distance, revealing the genetic similarity of the genotypes of this cluster, whereas the cluster IV showed the maximum intra cluster distance (84.10). The inter cluster D^2 value ranged from 38.65 to 289.91. Minimum inter cluster distances were observed between clusters V and IX revealing the genetic closeness of the genotypes of these two clusters. However, maximum inter cluster D^2 values were observed between the clusters VII and X followed by V and VII, indicating that the genotypes of these clusters may give heterotic response and transgressive segregants upon crossing in the segregating generations. Similar results were also reported by Shivani and Shreelakshmi (2013).

Table 1: Distribution of 75 sorghum genotypes in different clusters.

Cluster No.	Name of genotype	No. of genotypes	Origin
1	IS 4060, IS 21083, IS 9745, IS 14861, IS 20743, IS 26737, IS 29304, IS 19975, IS 26025, IS 19676, IS 27887, IS 24348, IS 20195, IS 12883, IS 26617, IS 19389, IS 21645, IS 22616, IS 4698, IS 6351, IS 995, IS 23590, IS 22720, IS 12937, IS 28313, IS 24175, IS 15945, IS 25989, IS 24139 and DJ-6514	30	India(5), Kenya(1), Sudan(1), Cameroon(2), USA(2), South Africa(2), Swaziland(1), Senegal(1), Mali(2), Zimbabwe(1), Niger(1), Madagascar(1), Bangladesh(1), Malawi(1), Myanmar(1), Ethiopia(2), Somalia(1), Yemen(1) and Tanzania (1)
2	IS 30466, IS 10302, IS 30536, IS 59108, IS 29914, IS 2413, IS 5919, IS 29568, IS 33353, IS 29392, IS 2397, IS 27912, IS 16528, IS 25249, IS 31043, IS 8012, IS 29335, IS 2872, IS 29468, IS 29654, IS 14290, IS 30383, IS 4581, IS 26046, IS 5667, IS 11619 and IS 24462	27	China(3),Thailand(1),Korea(1), Zimbabwe(1), Iran(1), India(3), Lesotho(3), Kenya(1), South Africa(3), Cameroon(1), Ethiopia(2), Uganda(1), Japan(1), Swaziland(1), Egypt(1), Botswana(1) and Mali(1)
3	IS 30451, IS 17941, IS 28614 and IS 10969	4	China(1), India (1),Yemen(1) and USA(1)
4	IS 17980, IS 15478, IS 25910, DSMR-8, IS 11473, IS 24492, IS 12302 and IS 20679	8	India(1), Cameroon (1), Mali(1), Botswana(1), Ethiopia(1), South Africa(1) and Thailand(1) and USA(1)
5	PKV Kranti	1	India
6	M35-1	1	India
7	IS 602	1	USA
8	IS 12735	1	Yemen
9	IS 7987	1	Nigeria
10	IS 15170	1	Cameroon

Table 2: Average intra and inter cluster distances (D^2) for 75 sorghum genotypes (Bold figures indicate intra-cluster distances).

Clusters	1	2	3	4	5	6	7	8	9	10
1	**42.17**	83.63	77.63	74.21	158.31	119.23	63.09	162.82	160.29	178.34
2		**44.24**	89.45	101.61	78.00	74.12	152.53	81.43	71.90	85.32
3			**59.21**	132.42	122.07	100.51	122.53	121.44	133.15	199.14
4				**84.10**	178.10	120.53	104.39	204.50	154.70	165.87
5					**00**	101.62	251.35	79.35	38.65	78.15
6						**00**	208.72	120.43	65.83	115.23
7							**00**	240.96	262.13	289.91
8								**00**	75.22	90.26
9									**00**	61.14
10										**00**

The two clusters *viz.*, I and II together possessed 57 genotypes, showing genetic similarity among them with respect to the traits under study. The narrow genetic base is attributed to sharing the same parental material in the ancestry or introgression of alleles. The genotypes with the same origin did not share the same cluster, suggesting lack of any relationship between genetic and geographic diversity. Rao *et al.* (1989) also reported similar types of findings in bajra. This indicates that the geographical origin can not be considered as criteria to estimate the diverse nature of the genotypes. Therefore, hybridization between lines of different geographical origin may or may not give desired outcomes. These results were in agreement with the earlier reports of Narkhed *et al.* (2000); Sameer Kumar *et al.* (2010); Doijad *et al.* (2016).

The cluster mean (Table 3) data revealed considerable differences among the clusters for all the traits studied. The genotypes of cluster VII followed by cluster III were the earliest to flower. Clusters VI and V comprised the genotypes which were earliest to mature. Cluster III comprised the genotypes with longer peduncle.

The genotypes of the cluster V produced more number of whorls per panicle. Cluster VII had the genotypes with larger panicle. The genotype of the cluster VIII recorded with highest 1000 grain weight. The genotypes of the cluster V had highest number of primaries per panicle. The cluster IX had the genotype with highest panicle width. The cluster X comprised the genotype with highest panicle weight. The yield per plant was observed highest by the genotypes of cluster X. Cluster III had the tallest plants and the shortest pants were recorded from cluster X. The cluster IX had the genotypes with highest number of nodes per plant as well as leaves per plant. Genotypes of the cluster VII had the thickest stem. The genotypes of the cluster VIII showed the highest 1000 grain volume. The genotype of the cluster X recorded for the highest number of grains per panicle. Highest grain density was observed by the genotypes of the cluster VI. The cluster VIII had the genotypes with longer grains. The genotype of the cluster X had highest grain width and thickness.

The contribution towards the genetic divergence was varying from trait to trait and detail is furnished in Table 4. Among the twenty characters, the panicle weight contributed the most (19.96%) towards the divergence, followed by grain yield (18.56%), 1000 grain weight (16.65%), days to 50 per cent flowering (10.63%) and peduncle length (8.14%). The present study reveals that these traits are more important for diversity and should be considered while handling the breeding material.

Table 3: Cluster means for twenty one characters in *rabi* sorghum.

Clusters	No. of entries	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}	X_{18}	X_{19}	X_{20}
I	38	70.3	128.7	50.72	8.56	25.26	24.10	55.38	3.44	56.22	47.16	225.03	8.56	8.12	1.29	18.81	1969.88	1.30	3.95	3.48	2.37
II	24	82.6	144.3	37.34	9.60	21.69	34.92	59.39	4.16	89.82	80.09	208.57	9.08	8.43	1.40	27.16	2342.72	1.30	4.27	4.02	2.76
III	4	67.8	128.8	64.59	8.28	23.49	35.23	57.88	3.79	65.87	59.66	278.33	9.62	8.87	1.35	26.75	1696.96	1.32	3.92	3.93	2.79
IV	5	81.0	137.0	45.08	9.03	23.14	23.02	60.85	4.28	63.10	47.98	223.02	9.22	8.67	1.41	16.79	2098.57	1.40	3.84	3.63	2.42
V	1	93.7	126.3	28.50	11.27	21.59	40.05	82.73	5.26	112.47	106.35	257.99	12.00	11.20	1.59	32.67	2656.48	1.23	4.11	4.09	3.36
VI	1	78.3	122.3	35.56	8.80	16.79	42.93	62.20	4.64	80.23	62.27	224.96	10.33	9.80	1.33	31.00	1450.31	1.38	3.99	4.53	3.15
VII	1	65.3	128.3	56.67	5.20	51.67	18.16	49.73	2.45	41.70	31.60	275.55	8.47	8.00	2.07	15.33	1752.65	1.19	4.59	2.76	2.12
VIII	1	76.3	131.3	46.81	8.47	28.82	45.46	40.47	3.95	139.83	133.88	204.17	7.60	7.00	1.37	36.00	2942.10	1.26	4.97	4.34	2.98
IX	1	94.7	145.7	28.59	7.07	10.16	41.34	56.67	5.67	125.43	110.76	274.29	12.33	11.73	1.64	33.00	2682.18	1.26	4.31	4.85	3.18
X	1	92.0	145.0	25.17	8.20	15.54	32.23	46.40	4.92	146.93	134.70	175.06	8.93	8.07	1.12	26.67	4180.61	1.22	4.60	5.02	3.59

X_1- Days to 50% flowering
X_2 - Days to maturity
X_3 - Peduncle length (cm)
X_4 - Whorls per panicle
X_5 - Panicle length (cm)
X_6 - Test weight (g)
X_7 - Primaries per panicle
X_8 - Panicle breadth (cm)
X_9 - Panicle weight (g)
X_{10} - Grain yield per plant (g)
X_{11} - Plant height (cm)
X_{12} - Nodes per plant
X_{13} - Leaves per plant
X_{14} - Stem girth (mm)
X_{15} - Seed volume (cc)
X_{16} - Grain per panicle
X_{17} - Grain density
X_{18} - Grain length (mm)
X_{19} - Grain width (mm)
X_{20} - Grain thickness (mm)

Table 4: Percent contribution of characters towards divergence.

Sr. No.	Source	Contribution
1.	Panicle weight per plant	19.96%
2.	Grain yield per plant	18.56%
3.	Test weight	16.65%
4.	Days to 50 percent flowering	10.63%
5.	Plant height	10.02%
6.	Peduncle length	8.14%
7.	Days to maturity	3.96%
8.	Nodes per plant	2.05%
9.	Primaries per panicle	1.91%
10.	1000 grain volume	1.91%
11.	Panicle length	1.62%
12.	Grain length	1.48%
13.	Grain height	1.41%
14.	Grain density	0.94%
15.	Grains per panicle	0.32%
16.	Panicle width	0.29%
17.	Grain width	0.11%
18.	Whorls per plant	0.04%
19.	Leaves per plant	0.0%
20.	Stem girth	0.0%

CONCLUSION

The data on inter cluster distances and per se performances of genotypes were used to select genetically diverse and agronomically superior genotypes. The genotypes, exceptionally good with respect to one or more traits seemed to be desirable. Inter crossing of divergent groups would lead to greater opportunity for crossing over which releases hidden potential variability by disrupting the undesirable linkage (Thoday, 1960). In the present study, the genotypes *viz.*, IS 15170, IS 7987, and IS 12735, M35-1 and PKV Kranti were found to be distinct, diverse and showed good per se performance. The progeny derived from such diverse crosses are expected to have wide spectrum of genetic variability, which provides a greater scope for isolating transgressive segregants in advanced generations. In addition, these genotypes can be potential sources for the diverse alleles of yield, yield component traits and could be further evaluated for their breeding value as parents and could be utilized in sorghum crop improvement.

Acknowledgements. The author thanks ICRISAT for providing the minicore germplasm lines of sorghum.
Conflict of Interest. None.

REFERENCES

Bucheyeki, T. L., Gwanama, C., Mgonja, M., Chisi, M., and Folkertsma, R. (2008). Morphological characterization of Tanzanian sorghum. *The Kasetsart Journal*, *42*(4): 579–588.

Bucheyeki, T. L., Gwanama, C., Mgonja, M., Chisi, M., Folkertsma, R., and Mutegi, R. (2009). Genetic variability characterisation of Tanzania sorghum landraces based on simple sequence repeats (SSRs) molecular and morphological markers. *Afr. Crop Sci. J.*, *17*: 54201.

Govindaraj, M. Vetriventhan, M., and Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Genetics Research International*, 1–14.

Kavya, P., Satyanarayana Rao, V., Vijayalakshmi, B., Sreekanth, B., Radha Krishna, Y. and Nafeez Umar. (2019). Genetic divergence study in sorghum (*Sorghum bicolor* L.) using D^2 Analysis. *Int. J. Curr. Microbiol. App. Sci*., *8*(06): 24-31.

Kumar, A., Sharma, H., Sharma, R., Blummel, M., Reddy, P. and Reddy, B. (2013). Phenotyping in sorghum (*Sorghum bicolor* (L.) Moench). *In: Panguluri S, Kumar A. (eds), Phenotyping for Plant Breeding. New York: Springer Science and Business Media. Pp* 73–109.

Mace, G. M. (2005). An index of intactness. *Nature*, *434*: 32–33.

Mahalanobis, P. C. (1936). On the generalizes distance in statistics. *Proceedings of National Academy of Sci., 12*: 49-55.

Mofokeng, A. M., Shimelis, H. A., Laing, M. D. (2017). Agro-morphological diversity of South African sorghum genotypes assessed through quantitative and qualitative phenotypic traits. *South African J. Plant and Soil*, *34*(5): 361–370.

Motlhaodi, T., Geleta, M., Bryngelsson, T., Faith, M., Chite, S. and Ortiz, R. (2014). Genetic diversity in ex situ conserved sorghum accessions of Botswana's estimated by; microsatellite markers, *Australian J. Crop Sci., 8*(1): 35-43.

Narkhede, B. N., Akade, J. H. and Awari, V. R. (2000). Genetic diversity in *rabi* sorghum local genotypes [*Sorghum bicolor* (L.) Monech]. *J. Mah. Agri. Uni., 25*(3): 245-248.

Rana, J. C., Sharma, T. R., Tyagi, R. K., Chahota, R. K., Gautam, N. K., Singh, M., Sharma, P. N. and Ojha, S. N. (2015). Characterization of 4274 accessions of common bean (*Phaseolus vulgaris* L.) germplasm conserved in the Indian gene bank for phenological, morphological and agricultural traits. *Euphytica*, *205*: 441–457.

Rao, C. R. (1952). Advanced statistical methods in biometrical research, *John Wiley and Sons Inc, New York pp 363.*

Reddy, B. V. S., Ramesh, S., Reddy. P. S. and Kumar, A. A. (2009). Genetic enhancement for drought tolerance in sorghum. *Plant Breed. Rev., 31*: 189-222.

Sejake, T., Shargie, N., Christian, R. and Tsilo, T. (2020). Assessment of genetic diversity in sorghum germplasm using agro-morphological traits. *South African J. Plant and Soil*, *37*(5): 376-388.

Thoday, J. M. (1960). Effects of disruptive selection-III coupling and repulsion, *Heridity, 14*: 35-39.

Umakanth, A. V., Nikhil, B. S. K. and Tonapi, V. A. (2019). Genetic diversity studies in sweet sorghum [*Sorghum bicolor* (L.) Monech], a candidate crop for biofuel production. *Forage Res*., *45*(1): 28-32.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated palnts. *Chron. Bot.*, *13*: 1-366.

How to cite this article: Lokesh Kumar Verma, B.D. Biradar and A.K. Meena (2022). Assessment of Genetic Diversity in *rabi* Sorghum [*Sorghum bicolor* (L.) Monech] using D^2 Statistics. *Biological Forum – An International Journal*, *14*(1): 800-803.