P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2023.v36i02.02

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Genetic Diversity Studies for Yield and Yield attributing Characters in Colored Sorghum Genotypes

Kiran[1], Suvarna[1], B. V. Tembhurne[1], G. Girish[2], Shivaleela[1] and M. Lakshmikanth[1]

Abstract

The experiment was carried out at the College of Agriculture, Raichur, during *rabi* 2020. It was undertaken to assess the nature of genetic variability and diversity among 120 colored sorghum genotypes. The study revealed wide variation for yield and yield attributing traits, high GCV and PCV coupled with high heritability and genetic advance was observed for neck of panicle, peduncle length, 100-grain weight. The traits *viz.,* plant height, neck of panicle, peduncle length, panicle length, 100-grain weight, panicle weight and grain yield per plant showed high heritability and genetic advance as percent of mean. Wide genetic diversity was observed among the genotypes as evidenced by the formation of seven clusters for the 120 colored genotypes based on different traits studied. Out of ten characters studied, contribution of plant height towards genetic divergence was the highest followed by panicle weight.

Keywords: Colored sorghum, Diversity, Genotypic coefficient of variation, Phenotypic coefficient of variation, Yield.

[1]College of Agriculture, University of Agricultural Sciences, Raichur, Karnataka, India.

[2]Agriculture Research Station, Raichur, Karnataka, India.

***Author for correspondence:**

suvarnagpb@uasraichur.edu.in

Received: 17/03/2022 **Revised:** 04/07/2023

Accepted: 05/07/2023

How to cite this article: Kiran, Suvarna, Tembhurne, B.V., Girish, G., Shivaleela, Lakshmikanth, M. (2023). Genetic Diversity Studies for Yield and Yield attributing Characters in Colored Sorghum Genotypes. *Indian J. Plant Genetic Resources*. 36(2), 208-215. **DOI:** 10.61949/0976-1926.2023.v36i02.02

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], popularly called as jowar, is the "king of millets" or "Great Millet" and is the fifth most important cereal crop in the world after rice, wheat, maize and barely, in terms of production and utilization. The word sorghum is derived from the latin word "Sorgo" which means "raising above". It is known as a failsafe crop and camel of crops because of its drought tolerance, heat tolerance, and high photosynthetic efficiency. So, it is considered as an important staple food crop in arid and semi-arid regions of the world (Anagholi *et al*., 2000). Sorghum is originated in Africa. It is an often cross-pollinated, diploid (2n=20) and C_4 grass plant species, which belongs to the family "Graminae" and tribe "Andropogeneae". Cultivated sorghum has five basic races, *viz*., bicolor, durra, guinea, caudatum and kafir and ten intermediate races.

In India, during the period of 2017 to 2021, sorghum had an average area of 2.93 m ha with an average production of 2.55 million tones and the average productivity was 872 kg/ha. Correspondingly in Karnataka during the same period, the average area of sorghum was 0.80 m ha with an average production of 0.79 million tonnes and the productivity was 996 kg/ha (Anon., 2022).

Sorghum grain contains different pericarp colors *viz*., white, yellow, brown, purple, red, black, etc. These colored sorghum grains vary with respect to nutritional contents. White sorghum has low levels of total phenolic contents and has very low levels or zero levels of tannin and 3-deoxyanthocyanidin (Awika and Rooney, 2004). Yellow sorghum is rich in flavanones and has slightly higher total phenolic contents than white sorghum (Dykes *et al.*, 2011). Red sorghum has moderately high levels of phenolic compounds but lacks tannins. Black sorghum is genetically red and is a special type of red sorghum because the red pericarp changes into black under sunlight radiation during maturation. Black sorghum has high levels of phenolic contents that are concentrated in the pericarp, particularly the content of 3-deoxyanthocyanidins (Dykes *et al.*, 2009 and 2013). Brown sorghum, also known as tannin sorghum, has pigmented testa and high levels of condensed tannins (Awika and Rooney, 2004).

So, developing genotypes with high yield potential coupled with nutritionally superior quality grains is the prime objective of the breeding programme. Improvement in grain yield and quality depends on the nature and extent of genetic variability, heritability and genetic advance in the base population along with information on the nature of association between yield and its components helps in simultaneous selection for many characters.

Genetic diversity in the crop species is one of the precious gifts of nature. Phenotypic traits are conventional tools to analyse genetic diversity. The genetic variability of cultivated crops and their wild relatives together form a potential and continued source for breeding new and better crop varieties, a better understanding of the genetic diversity in colored sorghum would greatly contribute to crop improvement with a view of grain nutritional quality and other important agronomic traits. Therefore, there is a need to evaluate the available accessions for genetic diversity in the colored sorghum genotypes and identify the best accessions according to their performance.

Understanding the wealth of genetic diversity in sorghum will facilitate further improvement of this crop for its genetic architecture. This study aims to determine the genetic variation and diversity present in the colored sorghum genotypes.

Material and Methods

The experimental material comprised of 120 colored sorghum genotypes. The indigenous and exotic collections were obtained from R.S. Paroda Gene-bank, ICRISAT, Patancheru. The five checks used in the study were M 35-1, Paiyur 2, AKJ 1, IS 2312 and DJ 6514.

M 35-1, IS 2312 and DJ 6514 were obtained from ARS, Hagari, UAS, Raichur, AKJ 1 was obtained from RARS, Vijayapur, UAS, Dharwad and Paiyur 2 was obtained from TNAU, Coimbatore. The list of genotypes used for the study is presented in Table 1.

The genotypes along with five checks were sown on 30-10-2020 (*rabi,* 2020) in an augmented design. Each entry was sown in a single line. The checks were replicated in 3 blocks. Each block was of 4 m length with uniform spacing

Table 1A: List of colored sorghum genotypes with country origin and checks used in the present study

Sl. No.	*Genotype*	*Country*
1	IS 2502	United states of America
2	IS 2582	United states of America
3	IS 2618	United states of America
4	IS 3817	Mali
5	IS 3579	Sudan
6	IS 522	Mexico
7	IS 6508	India
8	IS 7013	Sudan
9	IS 7527	Nigeria
10	IS 8222	Uganda
11	IS 8792	Zimbabwe
12	IS 9664	Sudan
13	IS 9667	Sudan
14	IS 11180	Ethiopia
15	IS 12643	Ethiopia
16	IS 14094	South Africa
17	IS 14897	Cameroon
18	IS 14904	Cameroon
19	IS 14905	Cameroon
20	IS 15098	Cameroon
21	IS 16006	Cameroon
22	IS 16169	Cameroon
23	IS 16202	Cameroon
24	IS 16310	Cameroon
25	IS 16316	Cameroon
26	IS 16398	Cameroon
27	IS 17591	Yemen
28	IS 18301	Niger
29	IS 18639	Nigeria
30	IS 18679	United States of America
31	IS 19298	Sudan
32	IS 19299	Sudan
33	IS 19498	Sudan
34	IS 20301	Niger
35	IS 20842	United states of America
36	IS 21835	Sudan
37	IS 21868	Yemen
38	IS 22436	Sudan
39	IS 22897	Sudan

40	IS 22942	Sudan	81	IS 28982	Yemen
41	IS 22949	Sudan	82	IS 29012	Yemen
42	IS 22970	Sudan	83	IS 29013	Yemen
43	IS 23864	Yemen	84	IS 29014	Yemen
44	IS 23865	Yemen	85	IS 29031	Yemen
45	IS 23890	Yemen	86	IS 29032	Yemen
46	IS 23916	Yemen	87	IS 29033	Yemen
47	IS 23950	Yemen	88	IS 29052	Yemen
48	IS 23953	Yemen	89	IS 29055	Yemen
49	IS 23954	Yemen	90	IS 30722	Cameroon
50	IS 23955	Yemen	91	IS 30736	Cameroon
51	IS 24001	Yemen	92	IS 30754	Cameroon
52	IS 25040	Sudan	93	IS 30781	Cameroon
53	IS 28000	Yemen	94	IS 30800	Cameroon
54	IS 28001	Yemen	95	IS 30802	Cameroon
55	IS 28009	Yemen	96	IS 31706	Yemen
56	IS 28014	Yemen	97	IS 31718	Yemen
57	IS 28015	Yemen	98	IS 31731	Yemen
58	IS 28017	Yemen	99	IS 31732	Yemen
59	IS 28049	Yemen	100	IS 31906	Yemen
60	IS 28050	Yemen	101	IS 32072	Yemen
61	IS 28056	Yemen	102	IS 32079	Yemen
62	IS 28065	Yemen	103	IS 32121	Yemen
63	IS 28074	Yemen	104	IS 32163	Yemen
64	IS 28172	Yemen	105	IS 32165	Yemen
65	IS 28176	Yemen	106	IS 32185	Yemen
66	IS 28198	Yemen	107	IS 33158	Cameroon
67	IS 28200	Yemen	108	IS 33159	Cameroon
68	IS 28202	Yemen	109	IS 33310	Cameroon
69	IS 28210	Yemen	110	IS 33317	Cameroon
70	IS 28217	Yemen	111	IS 33323	Cameroon
71	IS 28224	Yemen	112	IS 33336	Cameroon
72	IS 28230	Yemen	113	IS 33343	Cameroon
73	IS 28237	Yemen	114	IS 34723	Cameroon
74	IS 28243	Yemen	115	IS 35642	Chad
75	IS 28244	Yemen	116	IS 35823	Russian Federation
76	IS 28250	Yemen	117	IS 35838	Russian Federation
77	IS 28265	Yemen	118	IS 38527	Ethiopia
78	IS 28791	Yemen	119	IS 39564	Ethiopia
79	IS 28792	Yemen	120	IS 40175	Mauritania
80	IS 28966	Yemen			

Figure 1B: Checks used in the present

Sl. No.	*Check*
1	M 35-1
2	AKJ 1
3	Paiyur 2
4	IS 2312
5	DJ 6514

of 45 cm between rows and 15 cm between plants. All the necessary package of practices and need-based plant protection measures were followed to raise healthy crop. Observations were recorded for the characters *viz*., days to 50% flowering, days to maturity, plant height (cm), neck of panicle (cm), peduncle length (cm), panicle length (cm), panicle width (cm), 100-grain weight (g), panicle weight (g) and grain yield per plant (g). Observations were taken on randomly selected five plants in each genotype and average of this was recorded as mean data for each character in each genotype (Plate 1 and 2).

Results and Discussion

The genetic variability parameters *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance as percent of mean (GAM) were computed to know the extent of genetic variability for ten characters and presented in Table 2.

Phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) values were high for grain yield per plant (53.37 and 45.02%) followed by neck of panicle (50.53 and 49.92%), panicle weight (45.24 and 43.45%), peduncle length (35.05 and 31.39%), panicle width (32.93 and 24.73%) and 100-grain weight (27.06 and 26.49%), respectively. This indicates that the material showed more

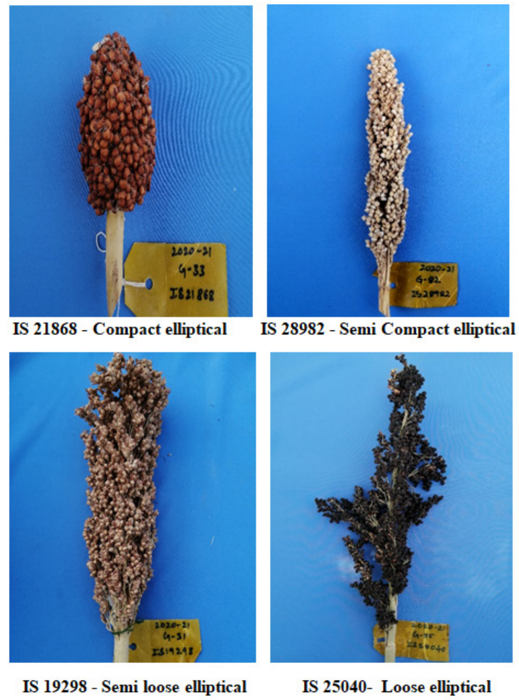

Plate 1: Variation for inflorescence compactness and shape in colored sorghum genotypes.

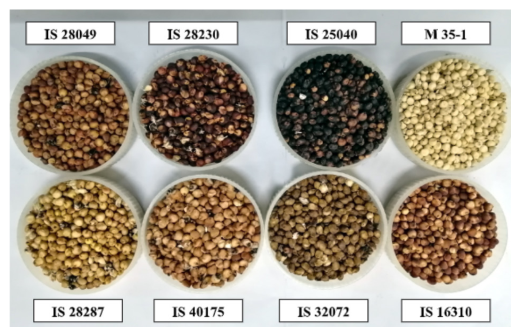

Plate 2: Variation for grain color in sorghum genotypes

Table 2: Genetic variability parameters for yield and yield attributing characters

Sl. No.	*Character*	*Co-efficient of variation*		*Heritability (%) broad sense*	*Genetic advance as per cent over mean (GAM)*
		Genotypic Coefficient of Variation GCV (%)	*Phenotypic Coefficient of Variation PCV (%)*		
1	Plant height (cm)	14.58	16.27	80.31	26.91
2	Days to 50 % flowering	04.42	04.72	87.96	08.54
3	Days to maturity	03.20	03.66	76.60	05.76
4	Neck of panicle (cm)	49.92	50.53	97.61	101.60
5	Peduncle length (cm)	31.39	35.05	80.18	57.89
6	Panicle width (cm)	24.73	32.93	56.38	38.24
7	Panicle length (cm)	15.56	19.13	66.17	26.07
8	100-Grain weight (g)	26.49	27.06	95.81	53.41
9	Panicle weight(g)	43.45	45.24	92.25	85.96
10	Grain yield per plant (g)	45.02	53.37	71.14	78.21

variation for these characters. The PCV and GCV values were moderate for plant height (16.27 and 14.58%) and panicle length (19.13 and 15.56%).

Similar results of high PCV and GCV for grain yield per plant, panicle length and panicle weight were reported by Khandelwal *et al.* (2015) and Swamy *et al.* (2018), for plant height and panicle length by Sushil (2014), for plant height and grain yield per plant by Arunkumar (2013) and moderate PCV and GCV for 100-grain weight, days to maturity and days to 50% flowering by Yaqoob *et al.* (2015), moderate to high PCV and GCV for days to 50% flowering, grain yield, 100-grain weight and plant height by Yohannes *et al.* (2015).

The lowest PCV and GCV values were exhibited for days to maturity (3.66 and 3.20%) and for days to 50% flowering (4.72 and 4.42%). This indicates that the studied genotypes showed less variation for these two characters. The genotypes were selected for the study based on the different seed colors and exotic. Majority of the accessions were from Cameroon and Yemen. This may be the reason for less variation in these two characters studied.

The PCV values were higher than their respective GCV values for the characters like peduncle length, panicle width, panicle weight, panicle length, plant height and grain yield per plant. It means that the apparent variation is not only due to genotypes but also due to the influence of the environment. The characters neck of panicle, 100-grain weight, days to 50% flowering and days to maturity had little difference between PCV and GCV, indicating that their variation has a genetic origin that could be exploited for further breeding programmes.

Heritability value in broad sense is presented in Table 2. The highest heritability was recorded for the characters *viz.,* neck of panicle (97.61%) followed by 100-grain weight (95.81%), panicle weight (92.25%), grain yield per row (91.01%), days to 50% flowering (87.96%), plant height (80.31%), peduncle length (80.18%), days to maturity (76.60%), grain yield per plant (71.14%) and panicle length (66.17%). This indicates that these characters showed high heritability and selection for these characters could be effective. Moderate heritability was exhibited for the character panicle width (56.38%). High heritability for the characters like grain yield per row, days to 50% flowering and plant height was reported by Khandelwal *et al.* (2015), Yaqoob *et al.* (2015) and Yohannes *et al.* (2015), for characters days to maturity, panicle length and panicle weight was reported by Bello *et al.* (2007) and Khandelwal *et al.* (2015).

The maximum genetic gain percent over a mean (GAM) was recorded for neck of the panicle (101.60%) followed by grain yield per row (98.31%), panicle weight (85.96%), grain yield per plant (78.21%), peduncle length (57.89%), 100 grain weight (53.41%), panicle width (38.24%), plant height (26.91%) and panicle length (26.07%). It indicates that additive genes govern the character and selection will be rewarding for the improvement of such trait. Whereas minimum GAM was recorded for days to 50% flowering (8.54%) and days to maturity (5.76%), which indicates that the character is governed by non-additive genes and heterosis breeding may be useful. Similar results of high GAM for the character panicle length and grain yield per plant were reported by Santosh *et al*. (2013), for grain yield per plant and plant height by Yaqoob *et al.* (2015) and for days to 50% flowering and plant height by Yohannes *et al.* (2015).

High heritability along with genetic advance as percent of mean was recorded for traits *viz.*, neck of panicle (97.61 and 101.60%) followed by 100-grain weight (95.81 and 53.41%), panicle weight (92.25 and 85.96%), grain yield per plot (91.01

Table 3: Grouping of colored sorghum genotypes based on D2 analysis

Cluster	*No. of Entries*	*Genotype*
I	113	IS 16398, IS 28000, IS 23865, IS 19498 IS 3310, IS 28243, IS 22970, IS 28074, IS 28210, IS 33343, IS 23950, IS 28014, IS 28049, IS 28001, IS 28009, IS 29014, IS 32072, IS 32121, IS 28200, IS 40175, IS 28050, IS 2312, Paiyur-2, IS 23916, IS 7527, IS 33159, IS 28202, IS 30781, IS 14904, IS 28237, IS 28230, IS 28172, IS 38527, IS 20301, IS 28791, IS 6508, IS 32163, IS 22949, IS 39564, IS 18679, IS 30736, IS 16202, IS 28966, IS 32079, M-35-1, IS 28056, IS 29055, IS 3579, IS 19298, IS 28792, IS 9667, IS 20842, IS 30800, IS 31731, IS 35823, IS 28224, IS 23953, IS 2582, IS 14897, IS 16316, IS 32165, IS 29031, DJ 6514, IS 522, IS 30754, IS 29012, IS 28017, IS 29052, IS14905, IS 7013, IS 16169, IS 28015, IS 2502, IS 32185, IS 30722, IS 31906, IS 25040, IS 2618, IS 14094, IS 31706, IS 35838, IS 29033, IS 23864, IS 8792, IS 18301, IS 3817, IS 28176, AKJ-1, IS 9664, IS 35642, IS 8222, IS 28244, IS 28198, IS 29013, IS 34723, IS 33336, IS 21835, IS 22897, IS 19299, IS 28065, IS 15098, IS 28982, IS 28265, IS 30802, IS 33317, IS 23955, IS 23890, IS 22436, IS 22942, IS 28250, IS 33323, IS 28217, IS 21868
II	3	IS 23954, IS 33158, IS 29032
III	4	IS 31718, IS 31732, IS 18639, IS 17591
IV	1	IS 16310
V	1	IS 12643
VI	1	IS 11180
VII	2	IS 16006, IS 24001

Table 4: Average Intra and inter cluster distances for eleven characters in colored sorghum genotypes

Cluster	*Cluster I*	*Cluster II*	*Cluster III*	*Cluster IV*	*Cluster V*	*Cluster VI*	*Cluster VII*
Cluster I	3889.87	20816.49	12964.75	12631.64	13079.64	10429.78	17525.44
Cluster II		2806.34	31705.34	18894.47	18046.66	37026.45	13424.02
Cluster III			3963.56	40117.58	40795.39	32700.21	22103.53
Cluster IV				0.00	1609.40	6784.53	26521.46
Cluster V					0.00	10037.09	22865.98
Cluster VI						0.00	35024.05
Cluster VII							3865.86

Diagonal values indicate intra cluster distances
Above diagonal values indicate inter cluster distances

Table 5: Cluster means for eleven characters in colored sorghum genotypes

Cluster	*PH*	*DFF*	*DM*	*NP*	*PEDL*	*PWD*	*PL*	*100GW*	*PW*	*GYPP*	*Overall score*	*Rank*
Cluster I	207.58 (5)	76.32 (4)	110.76 (3)	23.41 (3)	49.60 (5)	5.12 (4)	22.69 (4)	4.26 (3)	55.40 (5)	37.85 (4)	40	3
Cluster II	225.27 (4)	76.67 (3)	109.33 (4)	21.40 (5)	47.20 (6)	5.74 (2)	20.87 (6)	5.60 (1)	157.67 (2)	122.50 (1)	34	5
Cluster III	110.60 (7)	75.50 (5)	109.25 (5)	21.60 (4)	50.45 (4)	3.23 (7)	16.50 (7)	3.00 (6)	65.00 (6)	35.88 (5)	56	1
Cluster IV	303.20 (2)	70.00 **(7)**	108.00 **(7)**	38.20 (2)	70.04 (2)	5.50 (3)	26.80 (3)	4.60 (2)	72.00 (4)	62.00 (2)	34	6
Cluster V	306.00 (1)	78.00 (2)	111.00 (2)	5.10 **(7)**	55.20 (3)	4.10 (6)	28.80 (2)	3.80 (5)	83.75 (3)	53.75 (3)	34	7
Cluster VI	272.00 (3)	74.00 (6)	109.00 (6)	46.50 (1)	92.20 (1)	5.00 (5)	32.00 (1)	2.40 (7)	21.00 (7)	11.00 (7)	44	2
Cluster VII	196.00 (6)	78.50 (1)	116.50 (1)	16.35 (6)	28.20 (7)	6.75 (1)	21.50 (5)	3.90 (4)	172.50 (1)	22.50 (6)	38	4

PH= Plant height (cm) DFF = Days to 50 % flowering DM = Days to maturity NP= Neck of panicle (cm)
PEDL= Peduncle length (cm) PWD=Panicle width (cm) PL= Panicle length (cm) 100GW=100 Grain weight (g) PW=Panicle weight (g) GYPP= Grain yield per plant (g)
Value in parenthesis indicates the ranking of genotypes for each character separately

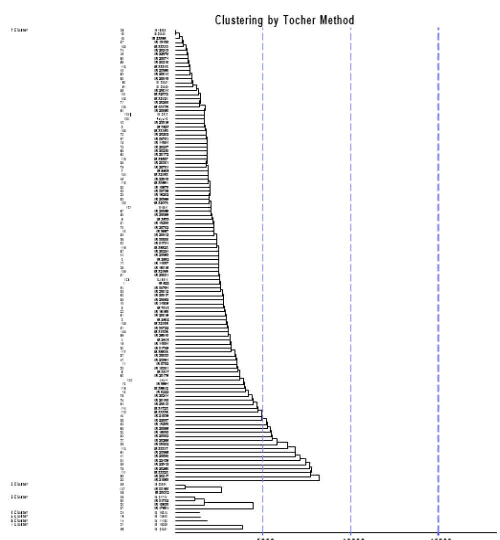

Fig. 1: Cluster diagram of colored sorghum genotypes

and 98.31%), plant height (80.31 and 26.91%), peduncle length (80.18 and 57.89%), grain yield per plant (71.14 and 78.21%) and panicle length (66.17 and 26.07%). This indicates that there was low environmental influence and greater role of genetic component of variation, which shows that additive gene action present in these traits. The high value of additive gene effects indicates higher breeding value, so the selection of these characters is effective for desired genetic improvement. Similar findings were also observed by Deepalakshmi and Ganesamurthy (2007), Nyadanu and Dikera (2014), Santosh *et al*. (2013) and Sushil (2014).

Genetic Diversity

The present investigation was undertaken to study the genetic divergence in the color sorghum genotypes using the D^2 analysis given by Mahalanobis (1936). D^2 is one of the reliable methods to understand the genetic diversity present

Table 6: Percent contribution of each character towards divergence in colored sorghum genotypes

Sl. No.	*Character*	*Per cent contribution*	*Times ranked 1st*	*Cumulative contribution*
1	Plant height	43.81	3395	43.81
2	Panicle weight	25.47	1974	69.28
3	Peduncle length	15.63	1211	84.91
4	Grain yield per plant	10.31	799	95.22
5	Neck of panicle	4.41	342	99.63
6	Panicle length	0.14	11	99.77
7	Days to 50% flowering	0.13	10	99.90
8	Days to maturity	0.10	8	100.00
9	Panicle width	0.00	000	000
10	100 grain weight	0.00	000	000

in the genotypes using Tocher's method. Estimating genetic diversity within and between germplasm groups is vital and useful for properly selecting parents to perceive higher heterosis and get potential segregants. Genetic diversity analysis has been used to quantify (a) the genetic distance between the genotypes (b) to identify divergent genotype to initiate the crossing programme (c) to know clustering pattern of genotypes.

Group Constellation

In the present investigation, D^2 was applied to all the genotypes studied, which classified the total genotypes into seven clusters (Table 3 and Figure 1). The analysis of cluster pattern revealed that, the highest number of genotypes are present in cluster I (113), followed by cluster III (4), cluster II (3) and cluster VII (2). The cluster IV, V, and VI had a solitary one. The distribution pattern of genotypes into various clusters was at random, suggesting that genetic diversity was unrelated to geographic diversity. The results are in accordance with Rohman *et al*. (2004), Sameer *et al.* (2010), Shinde *et al*. (2013) and Kavya *et al*. (2019).

Intra and Interrelation of Clusters

The average intra and inter-cluster distances for the ten characters in colored sorghum genotypes are presented in Table 4. Inter-cluster distances were higher than the intra-cluster distances. Suggesting that, wide genetic diversity existed among the genotypes of different groups. The intra-cluster average D^2 values were ranged from 0 (cluster IV, V and VI) to 3963.56 (Cluster III). The highest intra-cluster distance (3963.56) was observed in cluster III, followed by cluster I (3889.87) and cluster VII (3865.86), indicating that wide genetic variation was present among the genotypes within these clusters. So, more emphasis will be given for the genotypes belonging to these clusters during selection of parents for hybridization programme.

Cluster II (2806.34) had moderate intra-cluster distance. The lowest intra-cluster distance (0) was observed in clusters IV, V, VI which are monogenotypic (IS 16310), (IS 12343), (IS11180), respectively and were divergent from genotypes belonging to other clusters.

The inter-cluster D^2 values was ranged from 1609.40 (between cluster IV and cluster V) to 40795 (between cluster III and cluster V). The maximum inter-cluster distance was observed between cluster IV and cluster V (40795), followed by between cluster III and cluster IV (40117.58), between cluster II and cluster VI (37026.45) and between cluster VI and cluster VII (35024.05), revealing that genotypes included in these clusters are genetically diverge and may give rise to desirable genotypes in the segregating generation. The lowest inter-cluster distance was observed between cluster IV and cluster V (1609.40) followed by cluster IV and cluster VI (6784.53), indicating that these clusters' genotypes were genetically least diverse and almost of the same genetic architecture. The results are in accordance with Prasad and Biradar (2017), Ahalawat *et al*. (2018) and Kavya *et al*. (2019).

Cluster means

The cluster means and overall score value for ten characters in colored sorghum genotypes was presented in Table 5. The character days to 50 % flowering showed cluster mean value ranged from 70 (cluster IV) to 78.50 days (cluster VII). Cluster IV genotypes showed characteristic early flowering habit with mean number of days to flowering was 74 days. These clusters comprised of early flowering genotypes. While genotypes of cluster VII showed late flowering habit with mean number of days to flowering was 78.50 days. The genotypes with early flowering (Cluster IV) are preferred over late flowering because they mature early and the crop duration will be less.

Cluster VI had highest mean value for panicle length (32.00 cm), cluster VII for panicle width (6.75 cm) and panicle weight (172.50 g), cluster II for 100-grain weight (5.20 g) and grain yield per plant (122.50 g). The promising genotypes from these clusters with high mean values for different characters may be used directly for adaption or as parents in hybridization programme to achieve high yield levels.

In cluster IV, the lowest cluster mean values were observed for the characters days to 50% flowering and days to maturity. So, selecting genotypes belonging to these clusters helps develop short-duration varieties. The lowest cluster mean values for plant height (110.60 cm), neck

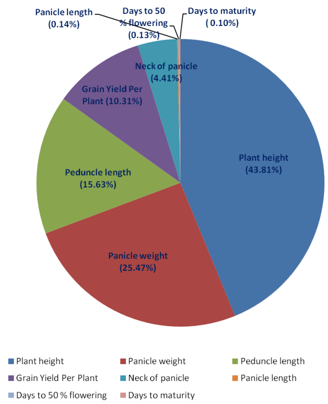

Figure 2: Contribution of major characters towards genetic diversity in colored sorghum genotypes

of panicle (5.10 cm) and peduncle length (28.20 cm) was exhibited by cluster III, V, and cluster VII, respectively, so the selection of genotypes from this cluster, helps in developing varieties with short plant height.

Contribution of Different Characters towards Divergence

Percent contribution of characters towards genetic divergence was analyzed and presented in Table 6 and Figure 2. The analysis revealed that, plant height alone contributed 43.81% to the divergence. Among yield attributing characters, panicle weight contributed 25.47% to total divergence, followed by peduncle length (15.63%), grain yield per plant (10.31%), neck of panicle (4.41%). Panicle length, days to 50% flowering, and days to maturity showed less percent of contribution towards total divergence. Whereas the characters, panicle width and 100-grain weight were not contributed to the total genetic divergence. Similar results were also reported by Rani and Rao (2012), Rekha *et al*. (2013) and Prasad and Biradar (2017).

Out of ten characters studied, four characters *viz*., plant height, panicle weight, peduncle length and grain yield per plant contributed 95.22% to the total genetic divergence. These characters should be given more importance in further breeding programmes.

References

Ahalawat NK, Arya VK, Kumar P, & Singh SK. (2018). Genetic divergence in forage sorghum [*Sorghum bicolor* (L.) Moench]. *J. Nat. Appl. Sci.,* **10(1):** 439-444.

Anagholi A, Kashiri A, & Mokhtarpoor H. (2000). The study of comparison between forage sorghum cultivars and speed feed hybrids. *J. Agric. Nat. Resour. Sci.,* **7(4):** 73-83.

Anonymous, (2022). India sorghum production and utilization. New Delhi. *http://www.indiastat.com/agriculture/2/foodgrains/17180/jowargreatmillet.*

Awika, J. M., & Rooney, L.W. (2004). Sorghum phytochemicals and their potential impact on human health. *Phytochemistry,* **65(9):** 1199–1221.

Dykes, L., Peterson, G. C., Rooney, W. L., & Rooney, L. W. (2011). Flavonoid composition of lemon-yellow sorghum genotypes. *Food Chem.,* **128(1):** 173–179.

Dykes, L., Rooney, W. L., & Rooney, L. W. (2013). Evaluation of phenolics and antioxidant activity of black sorghum hybrids. *J. Cereal Sci.,* **58(2):** 278–283.

Dykes, L., Seitz, L. M., Rooney, W. L., & Rooney, L. W. (2009). Flavonoid composition of red sorghum genotypes. *Food Chem.* **116(1):** 313–317.

Deepalakshmi, A. J., & Ganesamurthy, K. (2007). Studies on genetic variability and character association in *kharif* sorghum [*Sorghum bicolor* (L.) Moench]. *Indian J. Agric. Res.,* **41(3):** 177-182.

Kavya, P., Rao, V. S., Vijayalakshmi, B., Sreekanth, B., Radhakrishna, Y., & Umar, S. N. (2019). Genetic divergence study in sorghum (*Sorghum bicolor* L.) using D^2 analysis. *Intl. J. Curr. Microbiol. App. Sci.,* **8(6):** 24-31.

Nyadanu, D., & Dikera, E. (2014). Exploring variation, relationships and heritability of traits among selected accessions of sorghum [*Sorghum bicolor* (L.) Moench] in the upper east region of Ghana. *J. Pl. Breed. Genet.,* **2(3):** 101-107.

Prasad, B., & Biradar, B. D. (2017). Genetic diversity studies in minicore collection of *rabi* sorghum using D^2 statistics. *Intl. J. Curr. Microbiol. App. Sci.* **6(7):** 850-856.

Rani, J. K., & Rao, S. S. (2012). Genetic diversity in sorghum (*Sorghum bicolor*) for panicle components and morpho-physiological traits important for *rabi* adaptation. *Crop Res., **44*(1 & 2):** 156-160.

Rekha, C., Biradar, B.D., Salimath, P. M., & Sajjanar, G. M. (2013). Genetic divergence for grain quality and productivity traits in *rabi* sorghum. *Intl. J. Agric. Innov. Res.,* **1(5):** 132-135.

Rohman, M.M., Hakim, M.A., Sultana, N. A., Kabir, M. E., Hasanuzzan, M., & Ali, M. (2004). Genetic divergence analysis in sorghum. *Asian J. Pl. Sci.* **3(2):** 211-214.

Sameer, K. C. V., Shreelakshmi, & Shivani, D. (2010). Genetic diversity analysis in *rabi* sorghum [*Sorghum bicolor* (L.) Moench] local genotypes. *Electron. J. Pl.,* **1(4):** 527-529.

Santosh, K., Girish, G., Dharmaraj, P.S., Lokesha, R., & Jayalakshmi, S. K. (2013). Evaluation of sorghum landraces for charcoal rot resistance and yield traits in *rabi* sorghum. *M. Sc. (Agri) Thesis submitted to the Electron. J. Pl., Raichur,* Karnataka, India.

Shinde, D., Smita, C., & Jadhav, B. D. (2013). Study of genetic divergence in sweet sorghum [*Sorghum bicolor* (L.) Moench]. *BioScan.* **8(1):** 135-138.

Sushil, K. (2014). Genetic variability in land races of forage sorghum [*Sorghum bicolor* (L.) Moench] collected from different geographical origin of India. *Prime Res. on Med.,* **3(2):** 146-153.

Swami, S.S., Chaudhary, S. B., & Kute, N. S. (2015). Genetic diversity studies in *rabi* sorghum [*Sorghum bicolor* (L.) Moench]. *J. Agric. Res. Technol.* **40(2):** 203-207.

Yohannes, T., M., Weldetsion, N., Abraha, Manyasa, E., & Abraha, T. (2015). Combine selection for earliness and yield in pedigree developed sorghum [*Sorghum bicolor* (L.) Moench] progenies in Eritrea. *J. Pl. Breed. Genet.,* **3(1):** 01-08.