



# **Genetic Spectrum of Variation and Diversity for Yield and Yield Attributing Traits in Mutagenized Population of Sorghum (*Sorghum Bicolor* L. Moench)**

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

The present study was carried out in Agricultural Research Station, Hagari during *rabi* 2020, it was undertaken to assess nature of genetic variability and diversity among 200 mutant lines of M<sub>4</sub> generation. The study revealed wide variation for yield and yield attributing traits, moderate GCV and PCV coupled with high heritability and genetic advance was observed for stem girth, panicle length and panicle width. The traits *viz.*, stem girth, panicle length, panicle weight, panicle width, 100-seed weight, grain yield per plant and fodder yield showed high heritability and genetic advance as per cent of mean. A wider genetic diversity was observed for the different traits studied among the mutant lines as evidenced by the formation of thirteen clusters for the 200 mutant lines.

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Out of thirteen characters studied, fodder yield contributed majorly towards divergence with value of 37.35 per cent followed by 100-seed weight contributes (20%), grain yield contributes (15%) and other traits contribute minorly for divergence.

**Keywords:** Diversity; genetic advance; heritability; mutants; Sorghum.

## 1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench], is popularly known as “Jowar” a cultivated diploid ( $2n = 20$ ) tropical cereal  $C_4$  grass plant, is the fifth most important cereal crop grown in the world. It is a monocotyledon plant of tropical origin, belonging to Poaceae family [1]. It is called as camel of crops due to the high tolerance of water and temperature stress and also high photosynthesis efficiency; it is considered as an important crop plant in arid and semi-arid regions [2]. It is grown in India in an area about 4.09 million hectare with production of 3.48 million tonnes and productivity of 845 kg/ha. In Karnataka it is grown in 0.94 million hectare with production of 0.89 million tonnes and productivity of 945 kg/ha [3].

Mutation is considered as the ultimate source of all genetic variation. Induced mutation technology considered as a practical tool for the development of new varieties by improving the desirable character *i.e.*, early maturity, tolerance to biotic and abiotic stresses. It has been noticed that irradiation of seed with physical or chemical mutagens would lead to increase in gene frequency and promotes favourable gene modifications and creates wide genetic variability. The availability of variation in breeding material is the pre-requisite for selection and improvement of elite genotypes. Induced mutation is the possible way of restoring the genetic variation or creating new variation, also acts as a potent tool in creating novel variation and thus enhances the scope of selection.

Genetic diversity in mutant population is pre-requisite for any crop improvement programme as it helps in development of superior recombinants. The more diverse mutants can be crossed to produce superior hybrids with resistance to abiotic and biotic stresses. Understanding the wealth of genetic diversity in sorghum will facilitate further improvement of this crop for its genetic architecture [4]. The objective of this study is to determine the genetic variation and diversity present in  $M_4$  mutant population of sorghum.

## 2. MATERIALS AND METHODS

Two line seeds *viz.*, IS925 and Phule Vasudha of sorghum were sent to Bhabha Atomic Research Centre (BARC) Trombay, Mumbai. The 80 seeds of both the lines were irradiated with 300 Gy gamma rays and the irradiated seeds were also treated with 0.1 per cent Sodium azide. In  $M_3$  generation 80 irradiated and 20 irradiated + 0.1% sodium azide treated lines were selected in each genotypes at equilibrium moisture content of eight per cent. The selected  $M_3$  progenies were raised at ARS Hagari, hundred mutants from IS925 variety (80 irradiated and 20 irradiated + chemical treated) and hundred mutants from Phule Vasudha variety (80 irradiated and 20 irradiated + chemical treated) were selected from the  $M_3$  generation and used as seed material along with checks *viz.*, IS-2312, GS-23, DSV-4, E-36-1, DJ-6514, SPV-86 and M-35-1 for present investigation ( $M_4$  generation).

Mutant population was grown in the field during *rabi* 2020 at Agricultural Research Station (ARS), Hagari. Geographically, the location is situated at North-Eastern Dry Zone (Zone-3) of Karnataka situated between  $15^\circ 14' N$  latitude and  $77^\circ 07' E$  longitude with an altitude of 414 meters above the mean sea level. Two hundred mutants were sown in Augmented design, [5] in 4 m length with inter row spacing of 45 cm and intra row spacing of 15 cm. Each genotype sown in one row and each block contained 50 mutants with 7 checks *viz.*, DJ-6514, IS-2312, M-35-1, DSV-4, E-36-1, SPV-86 and GS 23 replicated in 4 blocks for yield and yield attributing traits. Characters *viz.*, SPAD 45, SPAD 90, Days to 50 per cent flowering, Days to maturity, Number of leaves, Stem girth, Plant height, Panicle length, Panicle width, Panicle weight, 100-seed weight, Fodder yield and Grain yield per plant observations were recorded on five randomly selected mutant plants in each entry. The statistical analysis of the data on individual character was carried out on the mean values of each mutants using INDOSTAT package (version 8.5), the characters were subjected to statistical analysis as per Federer [5] and Mahalonobis  $D^2$  [6] to assess the variation and diversity among the mutants respectively.

### 3. RESULTS AND DISCUSSION

The M<sub>4</sub> mutant lines exhibited significant variation for 12 characters. Significant source of variation obtained for SPAD 45, SPAD 90, days to 50% flowering, days to maturity, number of leaves, stem girth, panicle length, panicle width, panicle weight, 100 seed weight, fodder yield and grain yield per plant except plant height. The analysis of variance for 200 M<sub>4</sub> mutant lines of *rabi* sorghum is represented in Table 1. The genetic variation parameters viz., Range, Mean, Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Broad Sense Heritability ( $h^2$ ) and Genetic Advance (GA) were estimated to know the extent of genetic variation for thirteen characters and presented in Table 2.

In this study higher GCV and PCV was observed in traits like panicle weight (39.53- 40.06), fodder yield (36.52- 38.34) and grain yield per plant (46.49- 46.99) these results were similar with the observations of Zinzala et al. [7]. Moderate GCV and PCV was observed in SPAD 90 (10.84-2.44), stem girth (12.56-16.02), panicle length (11.88-14.01), panicle width (14.80-15.40) and 100-seed weight (15.92-18.27) similar results are reported by Ali et al. [8], but stem girth observations is in accordance with Jain and Patel [9]. The characters which shows higher variation were chosen for further breeding program. Lowest GCV and PCV was observed in SPAD 45 (8.02-9.36), days to 50% flowering (3.89-5.08), days to maturity (4.27-5.35), number of leaves (4.52-6.02) and plant height (3.85-8.41), these results are in accordance with the Yaqoob et al. [10], but days to 50% flowering is in accordance with the results of Shivaprasad et al. [11]. The traits like SPAD 90, SPAD 45, panicle weight, panicle width, grain yield per plant, fodder yield, days to maturity, days to 50 per cent flowering showed narrow range of difference between GCV and PCV. It indicates that these traits were less influenced by the environment and showed their potential genotypic performance. But traits like number of leaves, stem girth, plant height, panicle length and 100-seed weight showed large difference between GCV and PCV and this shows that these traits were more influenced by environment, selection of these traits is not rewarding.

High heritability along with genetic advance as per cent of mean was recorded for traits viz., stem girth (61.50-20.33), panicle length (71.82-20.76), panicle width (92.31-29.33), panicle

weight (97.37-80.47), 100-seed weight (75.99-28.63), fodder yield (90.75-71.77) and grain yield per plant (97.89-94.89), which indicates that there was low environmental influence and greater role of genetic component of variation and this shows that additive gene action present in these traits. High value of additive gene effects is an indication of higher breeding value so the selection of these characters is effective for desired genetic improvement. These findings are similar with Shivaprasad et al. [11] and Mofokeng et al. [12]. Moderate heritability coupled with low genetic advance was observed for days to 50 per cent flowering (58.45-6.13) and number of leaves (56.50-7.01). It depicts that control of traits is due to both additive and non-additive gene actions. The high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding. These findings are in suitable with earlier reports of Abraha et al. [13] and Khandelwal et al. [14].

#### 3.1 Genetic Diversity

The present investigation was made to study the divergence pattern present in the mutant lines based on D<sup>2</sup> analysis, given by Mahalanobis [6]. D<sup>2</sup> is a reliable method to understand the genetic diversity present in mutant population using torchers method. An estimation of genetic diversity within and between the groups of germplasm is vital and beneficial for proper selection of parents to determine higher heterosis and to get potential segregants.

#### 3.2 Group Constellation

In this study D<sup>2</sup> was applied to all 200 mutants and which classified the total mutants into thirteen clusters Table 3. The analysis of cluster pattern showed that, highest number of mutants were present in cluster-I (134), followed by cluster-II (37), cluster-III (15), cluster-VI (12) remaining all clusters viz., cluster-IV, cluster-V, cluster-VII, cluster-VIII, cluster-IX, cluster-X, cluster-XI, cluster-XII, cluster-XIII were solitary one. The pattern of distribution of genotypes into various clusters was at random suggesting that the genetic diversity was not related to geographic diversity. The results are in consistent with the Shinde et al. [15] and Kavya et al. [16].

#### 3.3 Intra and Inter Relation of Clusters

Average inter and intra cluster distances for thirteen characters in M<sub>4</sub> sorghum mutant lines

**Table 1. Analysis of variance for yield and yield attributing traits in M<sub>4</sub> sorghum mutant lines**

Source of Variation	df	SPAD 45	SPAD 90	DFF	DM	NL	SG	PH	PL
Block (Eliminating Check + Mutants)	3	4.46	7.79	0.32	4.32	2.3 **	0.15 *	426.10	1.86
Entries (Ignoring Blocks)	206	18.93 **	21.48 **	21.22 **	55.8 **	0.72 **	0.09 **	1314.16 **	6.93 **
Checks	6	20.89 **	39.79 **	24.48 *	68.32 **	2.46 **	0.11 *	3625.48 **	10.30 **
Mutants	199	18.47 **	20.82 **	15.82 *	40.61 **	0.54 *	0.08 *	538.68	5.98 **
Checks v/s Mutants	1	98.51 **	43.04 **	1077.55 **	3002.89 **	25.32 **	1.72 **	141767.48 **	176.47 **
Error	18	4.93	5.00	6.57	14.77	0.24	0.03	425.87	1.68

  

Source of Variation	df	PWD	PW	100SW	FY	GYPP
Block (Eliminating Check + Mutants)	3	0.02	13.95	0.1	348.67	13.94
Entries (Ignoring Blocks)	206	0.48 **	269.16 **	0.34 **	1958.21 **	192.47 **
Checks	6	1.13 **	104.67 **	1.05 **	5580.06 **	121.73 **
Mutants	199	0.46 **	272.54 **	0.30 **	1855.81 **	195.02 **
Checks v/s Mutants	1	1.79 **	583.36 **	4.00 **	605.12*	109.76 **
Error	18	0.03	7.17	0.07	171.69	4.11

df = Degrees of freedom; SPAD 45= Soil Plant Analysis Development at 45 days; SPAD 90= Soil Plant Analysis Development at 90 days; DFF = Days to 50% flowering; DM = Days to maturity; NL= Number of leaves; SG= Stem girth (cm); PH= Plant height (cm); PL= Panicle length (cm); PWD=Panicle width (cm); PW=Panicle weight (g); 100SW=100-seed weight (g); FY= Fodder Yield (g); GYPP= Grain yield per plant (g)

**Table 2. Estimation of range, mean and different genetic parameters for yield and yield attributing traits of M<sub>4</sub> sorghum mutant lines**

Character	Range			Co-efficient of variation		h <sup>2</sup> (bs)%	Expected Genetic advance @ 5%	Genetic advance as % of mean
	Min	Max	Average	GCV	PCV			
<b>SPAD 45</b>	33.80	58.50	45.82	8.02	9.36	73.33	6.50	14.16
<b>SPAD 90</b>	27.00	48.00	36.73	10.84	12.44	75.97	7.15	19.49
<b>DFF</b>	64.00	84.00	78.44	3.89	5.08	58.45	4.80	6.13
<b>DM</b>	101.00	129.00	119.40	4.27	5.35	63.64	8.37	7.03
<b>NL</b>	9.40	13.60	12.25	4.52	6.02	56.50	0.86	7.01
<b>SG</b>	1.16	2.51	1.77	12.56	16.02	61.50	0.36	20.33
<b>PH</b>	205.00	357.20	278.40	3.85	8.41	20.94	10.03	3.64
<b>PL</b>	10.80	23.00	17.53	11.88	14.01	71.82	3.62	20.76
<b>PWD</b>	3.00	6.30	4.38	14.80	15.40	92.31	1.28	29.33
<b>PW</b>	23.60	96.00	41.37	39.53	40.06	97.37	33.16	80.47
<b>100SW</b>	1.58	4.24	2.99	15.92	18.27	75.99	0.85	28.63
<b>FY</b>	65.00	260.00	112.53	36.52	38.34	90.75	80.65	71.77
<b>GYPP</b>	16.80	82.30	29.79	46.49	46.99	97.89	28.20	94.89

GCV = Genotypic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; h<sup>2</sup>(bs)% = Broad Sense Heritability; GA = Genetic Advance; GAM = Genetic Advance Mean; SPAD 45= Soil Plant Analysis Development at 45 days; SPAD 90= Soil Plant Analysis Development at 90 days; DFF = Days to 50% flowering; DM = Days to maturity; NL= Number of leaves; SG= Stem girth (cm); PH= Plant height (cm); PL= Panicle length (cm); PWD=Panicle width (cm); PW=Panicle weight (g); 100SW=100-seed weight (g); FY= Fodder Yield (g); GYPP= Grain yield per plant (g)

**Table 3. Clustering pattern of 200 M<sub>4</sub> sorghum mutant lines along with checks**

Cluster	No. of Entries	Mutant Lines	
		IS925 mutants	Phule Vasudha mutants
I	70+64	IS925-RD-61, IS925-64, IS925-105, IS925-RD-76, IS925-7-1, IS925-85, IS925-134, IS925-RV-6, IS925-6, IS925-19, IS925-14, IS925-9, IS925-96, IS925-RD-65, IS925-21-1, IS925-90, IS925-RV-8, IS925-RD-48, IS925-127, IS925-117, IS925-RD-50, IS925-113, IS925-58, IS925-10, IS925-132, IS925-20, IS925-144, IS925-133, IS925-7, IS925-RD-71, IS925-RD-41, IS925-130, IS925-54, IS925-RV-2, IS925-1, IS925-8, IS925-RV-13, IS925-124, IS925-RD-101, IS925-RD-46, IS925-RD-8, IS925-110, IS925-RD-74, IS925-17, IS925-83, IS925-102, IS925-2, IS925-44, IS925-23, IS925-RD-34, IS925-80, IS925-4, IS925-23, IS925-46, IS925-RD-37, IS925-115, IS925-72, IS925-87, IS925-118, IS925-123, IS925-29, IS925-RD-30, IS925-108, IS925-24, IS925-RD-25, IS925-11, IS925-RD-15, IS925-116, IS925-RV-4, IS925-16.	PV-RD-45, PV-7-1, PV-RD-34, PV-16, PV-13, PV-RD-21, PV-RD-9, PV-18, PV-50, PV-RD-29, PV-18, PV-RD-13, PV-RD-54, PV-9, PV-RD-87, PV-RD-28, PV-37, PV-33, PV-RD-43, PV-RD-68, PV-RD-19, PV-RD-20, PV-26, PV-RD-10, PV-RD-49, PV-RD-38, PV-48, PV-RD-22, PV-17, PV-11, PV-6-E, PV-RD-52, PV-6, PV-35, PV-61, PV-60, PV-12, PV-RD-25, PV-RD-33, PV-RD-14, PV-58, PV-RD-40, PV-RD-36, PV-RD-50, PV-22, PV-RD-41, PV-RD-20, PV-RD-53, PV-20, PV-RD-47, PV-47, PV-RD-5, PV-RD-18, PV-RD-48, PV-23, PV-38, PV-RD-3, PV-1, PV-RD-11, PV-17, PV-22, PV-RD-35, PV-7, PV-RD-15
II	12+25	IS925-5, IS925-7, IS925-RD-98, IS925-3, IS925-101, IS925-2-1, IS925-138, IS925-22, IS925-120, IS925-RV-3, GS-23, IS925-28.	PV-RD-32, PV-11, PV-8, PV-RD-57, PV-1, PV-44, PV-RD-4, PV-5, PV-RD-44, PV-RD-30, PV-RD-62, PV-3, PV-13, PV-14, PV-23, PV-52, PV-16, PV-2, PV-9, PV-10, PV-6, PV-RD-6, PV-RD-27, PV-RD-31, PV-17-1.
III	12+3	IS925-16, IS925-RD-53, IS925-RD-19, IS925-128, IS925-70, IS925-38, IS925-RV-16, IS-2312, IS925-34, E-36-1, IS925-39, DJ-6514.	PV-49, PV-24, PV-RD-46.
IV	1	IS925-109	-
V	1	-	PV-53
VI	5+7	IS925-41, IS925-RD-47, IS925-RV-7, IS925-RD-21, IS925-21,	PV-19, PV-RD-7, PV-41, PV-RD-51, PV-57, PV-RD-1, PV-45.
VII	1	SPV-86	-
VIII	1	IS925-37	-
IX	1	M-35-1	-
X	1	IS925-RD-44	-
XI	1	IS925-131	-
XII	1	DSV-4	-
XIII	1	IS925-RD-16	-

**Table 4. Average inter and intra cluster distances for thirteen characters in M<sub>4</sub> sorghum mutant lines**

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	<b>1298.06</b>	6440.99	5153.93	14726.37	14030.32	23673.52	15534.89	16505.00	6179.25	7572.09	6580.41	14194.02	39201.24
II		<b>1692.57</b>	11130.01	3204.91	3141.36	8243.82	21792.82	5046.31	4462.23	6941.78	10001.08	11058.02	19011.18
III			<b>1631.47</b>	19384.84	17512.00	27496.10	4507.60	27094.72	4023.71	20538.94	19791.64	6792.84	35893.79
IV				<b>0.00</b>	268.02	2538.86	29693.56	2532.63	7690.57	12038.44	17915.88	12796.28	9285.91
V					<b>0.00</b>	2841.23	26672.68	3730.72	6418.56	13171.20	18917.23	10516.94	8371.16
VI						<b>3249.58</b>	36777.61	5737.06	12862.80	19912.83	27554.20	16714.53	6872.15
VII							<b>0.00</b>	43339.64	7879.38	39857.36	39357.63	5236.30	37893.06
VIII								<b>0.00</b>	14800.79	6727.22	12277.96	24435.76	18794.80
IX									<b>0.00</b>	16454.44	18338.03	2342.45	18692.52
X										<b>0.00</b>	1097.57	30172.91	41569.49
XI											<b>0.00</b>	32998.98	51906.20
XII												<b>0.00</b>	15833.05
XIII													<b>0.00</b>

\* Diagonal values indicate intra cluster distances

\* Above diagonal values indicate inter cluster distances

**Table 5. Cluster means for thirteen characters in M<sub>4</sub> sorghum mutant lines**

Clusters	SPAD 45	SPAD 90	DFF	DM	NL	SG	PH	PL	PWD	PW	100SW	FY	GYPP	Overall score	Rank
1	45.85 (7)	37.45 (3)	78.97 (7)	120.18 (10)	12.25 (6)	1.73 (9)	280.95 (5)	16.86 (8)	4.14 (10)	32.92 (11)	2.96 (9)	90.93 (11)	22.76 (12)	108	5
2	46.46 (6)	34.95 (8)	77.73 (6)	118.24 (6)	12.34 (5)	1.91 (4)	283.55 (4)	19.21 (6)	4.94 (7)	57.29 (6)	3.13 (8)	154.05 (7)	41.97 (6)	79	8
3	45.83 (8)	37.26 (4)	75.47 (4)	114.87 (4)	11.81 (11)	1.55 (11)	220.20 (10)	16.05 (11)	4.03 (11)	31.83 (12)	2.62 (11)	87.00 (13)	23.15 (11)	121	1
4	49.70 (1)	28.10 (12)	80.00 (8)	120.00 (7)	12.20 (7)	2.19 (2)	280.00 (6)	20.20 (4)	5.70 (2)	78.00 (3)	3.74 (1)	196.00 (3)	52.60 (4)	60	13
5	45.10 (10)	27.70 (13)	81.00 (11)	126.00 (11)	13.00 (1)	1.73 (8)	270.00 (8)	12.40 (13)	3.80 (13)	72.00 (5)	2.46 (12)	195.00 (4)	50.20 (5)	114	2
6	45.19 (9)	35.68 (6)	75.58 (5)	115.92 (5)	12.00 (8)	1.90 (5)	272.10 (7)	20.13 (5)	5.34 (3)	82.41 (2)	3.17 (6)	221.25 (2)	67.28 (2)	65	12
7	46.80 (4)	38.80 (2)	71.00 (2)	108.00 (2)	12.00 (9)	1.26 (13)	160.00 (13)	17.20 (7)	4.30 (9)	28.00 (13)	2.94 (10)	90.00 (12)	18.00 (13)	109	4
8	41.90 (13)	35.40 (7)	80.00 (9)	120.00 (8)	12.80 (3)	1.89 (6)	329.00 (3)	20.80 (3)	6.20 (1)	78.00 (4)	3.35 (5)	193.00 (5)	55.30 (3)	70	11
9	47.20 (3)	32.20 (9)	70.00 (1)	105.00 (1)	11.97 (10)	1.53 (12)	230.00 (9)	15.20 (12)	4.80 (8)	42.00 (8)	3.52 (4)	140.00 (8)	33.00 (8)	93	7
10	42.90 (12)	40.90 (1)	81.00 (12)	126.00 (12)	13.00 (2)	2.51 (1)	353.00 (2)	21.80 (2)	5.00 (5)	54.50 (7)	3.14 (7)	120.00 (9)	41.20 (7)	79	9
11	47.90 (2)	37.20 (5)	80.00 (10)	120.00 (9)	12.80 (4)	2.10 (3)	357.20 (1)	22.00 (1)	5.00 (6)	35.80 (10)	3.52 (3)	99.00 (10)	26.60 (10)	74	10
12	46.60 (5)	30.60 (10)	73.00 (3)	113.00 (3)	11.70 (13)	1.80 (7)	185.00 (12)	16.20 (10)	4.00 (12)	40.00 (9)	2.20 (13)	155.00 (6)	30.00 (9)	112	3
13	43.60 (11)	29.00 (11)	81.00 (13)	126.00 (13)	11.80 (12)	1.64 (10)	210.00 (11)	16.60 (9)	5.04 (4)	92.00 (1)	3.60 (2)	255.00 (1)	77.50 (1)	99	6

SPAD 45= Soil Plant Analysis Development at 45 days; SPAD 90= Soil Plant Analysis Development at 90 days; DFF = Days to 50% flowering; DM = Days to maturity; NL = Number of leaves; SG= Stem girth (cm); PH = Plant height (cm); PL=Panicle length (cm); PW= Panicle weight (g); 100SW= 100-seed weight (g); PWD- Panicle width (cm); FY= Fodder Yield (g); GYPP= Grain yield per plant (g)



were shown in Table 4. The table implies that inter cluster values were higher than the intra cluster values. The highest intra cluster value recognized for cluster-VI (3249.58) than cluster-II (1692.57), cluster-III (1631.47), cluster-I (1298.06). Whereas, cluster-IV, cluster-V and cluster-VII to cluster-XIII were showing zero values. Maximum differences among the mutant lines within the same cluster was recorded for cluster-VI, lowest intra cluster distance displayed for cluster-I. It indicates homogenous populations and not desirable for hybridization programme. It is desirable to select mutants from clusters showing high inter cluster distance for further crossing programme. The maximum inter cluster distance was recorded between cluster-XI and cluster-XIII (51906.20), followed by cluster-VII and cluster-VIII (43339.64). The least inter cluster distance was recorded between cluster-IV and cluster-V (268.02) then between cluster-X and cluster-XI (1097.57). The crossing between cluster-XI and cluster-XIII breeds the most transgressive segregants when selected for hybridisation programme. The results are in equivalent with Prasad and Biradar [17] and Ahalawat et al. [18].

### 3.4 Cluster Means

The cluster mean values and Overall score values of thirteen characters in  $M_4$  sorghum mutants were presented in Table 5. It revealed that Cluster-IV showed maximum SPAD 45 value, Cluster-IX showed early flowering and maturing character, it is preferable to select mutants from this cluster because crop escapes from biotic and abiotic stress. Cluster-VIII showed maximum panicle width. Cluster-XI

showed maximum plant height and panicle length, which was reported by the Shinde et al. [15], and Karadi and Kajjidoni [19]. Meanwhile the cluster-V recorded highest number of leaves and low SPAD 90 values, these similar results are reported by Navinkumar, [20] and Prasad and Biradar [17]. Similarly maximum 100-seed weight was recorded in cluster-IV, it is agreement with the results of Santosh et al. [4], Prasad and Biradar [17]. Cluster-XIII showed higher panicle weight, fodder yield and grain yield. These findings are reported by the Usha and Rekha [21]. It could be suggested that mutant line present in respective cluster with high mean performance for particular quantitative traits can be utilized in breeding programme to improve these traits.

Intercrossing of divergent groups would lead to wide genetic base in the base population and greater opportunities for crossing over to occur, which in turn may release hidden variability by breaking close linkage. The progenies derived from such crosses are expected to show wide variability, providing greater scope for isolating transgressive segregants in the advanced generations [22].

### 3.5 Contribution of Different Characters towards Divergence

Table 6. represents the per cent contribution of different characters towards divergence. The analysis showed that fodder yield trait contributes highest (37.35%) towards divergence, followed by 100-seed weight contributes (20%), grain yield contributes (15%), panicle weight contributes (10%), number of leaves contributes (5%), plant height contributes (4%), stem girth

**Table 6. Per cent contribution of each character towards divergence in  $M_4$  sorghum mutant lines**

	Character	Contribution %	Times ranked first	Cumulative contribution
1	Fodder yield	37.35	9340	37.35
2	100-seed weight	20.00	5000	57.35
3	Grain yield	15.00	3750	72.35
4	Panicle weight	10.00	2500	82.35
5	Number of leaves	5.00	1250	87.35
6	Plant height	4.00	1000	91.35
7	Stem girth	3.00	750	94.35
8	Days to maturity	2.56	640	96.91
9	SPAD 90	1.49	372.5	98.40
10	SPAD 45	1.12	280	99.52
11	Panicle width	0.40	100	99.92
12	Days to 50% flowering	0.06	15	99.98
13	Panicle length	0.02	5	100

contributes (3%), days to maturity contributes (2.56%). In the same way the traits like SPAD 90 (1.49%), SPAD 45 (1.12%), panicle width (0.40%), days to 50% flowering (0.06%), panicle length (0.02%) traits contributed very less percentage towards divergence. These results are comparable with the results of Rekha et al. [23], and Prasad and Biradar [17].

#### 4. CONCLUSION

This study reports the significant difference among all the traits and also found that large variability for agronomic traits in the M<sub>4</sub> sorghum mutant population. The mutant lines were showing higher GCV, PCV, Heritability and genetic advance so, those mutants can be selected and used to develop elite genotypes. Significant diversity was present among the mutant lines; efficient exploitation of this diversity will be helpful to develop transgressive segregants in sorghum mutant population. Inter-crossing between diverse clusters will provide segregating population for yield and leads to the selection of high yielding mutants.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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