Research Article

Ekin
Journal of Crop Breeding and Genetics

10(1):27-35, 2024

www.ekinjournal.com

Ekin International biannual peer-reviewed journal

Genetic Diversity Analysis for Morphological Traits in Sorghum [*Sorghum bicolor* (L.) Moench]

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Citation:

Shafiqurrahaman M., Dahiya GS., Dehinwal AK., Kumar V., 2024. Genetic Diversity Analysis for Morphological Traits in Sorghum [*Sorghum bicolor* (L.) Moench]. Ekin J. 10(1):27-35.

Received: 16.09.2023 ***Accepted: 24.10.2023*** ***Published Online: 31.01.2024*** ***Printed: 31.01.2024***

ABSTRACT

In present investigation 150 sorghum germplasm lines were studied for two years. The findings exhibited high heritability in association with high genetic advance. During 2015-16,82 genotypes (maximum) were grouped in cluster I, followed by cluster IV and cluster II with 22 and 19 genotypes, respectively, and cluster III having 11 genotypes, cluster VII having nine genotypes only, cluster X consisted of three genotypes, while V, VI, VIII and IX clusters remain confined to single genotype. The cluster distances ranged from 16.98 to 84.52 (within the clusters) and 40.65 to 73.37 (between clusters). Similarly, for 2016-17 are grouped into different clusters revealed that the highest number of genotypes (96) were confined to cluster I, followed by cluster IV, cluster II, cluster V, cluster III and cluster VI with 18, 17, 10, 8 and 1 genotype(s), respectively. The cluster distances ranged from 29.30 to 76,38 (within the clusters) and 0.00 to 71.11 (between clusters). Further for pooled data sorghum genotypes are grouped in to different clusters indicated that the 82genotypes (maximum) were associated with cluster I, followed by cluster IV, cluster III, cluster II, cluster VIII and cluster V with 19, 18, 15, 8 and 4 genotypes, respectively, cluster VI, cluster VII and cluster IX had only one genotype. The cluster distances ranged from 26.85 to 117.88 (within the clusters) and 65.87 to 117.88 (between clusters). The inter-cluster distances were more than intra-cluster distances, which pointed towards wide genetic diversity among the genotypes of various clusters than those of same cluster.

Keywords*:* Sorghum, clustering, polymorphisms, genetic divergence

Introduction

Among the forage crops, forage sorghum (*Sorghum bicolor* (L.) Moench) could be a deliberate choice because of the crop's xerophilic physiognomies, quick growing habit, adaptation potential, high palatability, rationality, digestibility, and widespread range of uses as fresh green fodder, roughage, and silage fodder. Moreover, it also has adaptability over a wide range of soils and climates (Borad et al., 2007). It is a well-known *kharif* crop for animal fodder, further genetic modification in its agronomic traits for forage will certainly benefit to reduce the gap between fodder demand and supply for the maximizing livestock production. In order to start enterprising with sorghum as a fodder and remunerative crop, there is an instant need to develop new cultivars/hybrids having high forage yield and quality (Shafiqurrahaman et al., 2022). To develop such forage varieties or hybrids, information and knowledge on genetic make-up is most important for the devising of an efficient breeding strategy for genetic improvement of sorghum as a forage crop. The genetic studies of quantitative and qualitative characters is needed before to start any breeding program for improvement of forage sorghum germplasm for these traits.

Possibility of attaining required genetic improvement in a crop depends mainly on the magnitude of genetic variability (Kaushik et al., 2020). The morphological variability uttered by a plant genotype or a group of genotypes in any plant species can be

divided into genotypic and environmental parameters (Raiger et al., 2021). The genotypic parameters being the heritable portion of the total variability in study material, its magnitude for fodder yield and its attributes, influences the selection approaches to be implemented by the plant breeder (Vu et al., 2019). The realization of any hybridization generally relays upon the selection of best suited diverse parents in genetic characters (Nguyen et al., 2017). Mahalanobis D^2 statistics founded on multivariate studies of quantitative characters is a commanding tool for the measurement of genetic divergence among different populations based on statistical distances for multivariate analysis (Mahalanobis, 1936). A complete awareness of the genetic relationship with diversity among the genotypes of sorghum will be helpful to development of new cultivars that can avoid drought stress, stand with low soil fertility, and resist against pests and diseases and also increase crop productivity under low input environments (Yuvaraja et al., 2019). Diversity study can also be a helpful device for mining germplasm collections for provinces associated with adaptive or agronomic desirable characters. Therefore, keeping said points in view, present investigation on forage sorghum was done.

Materials and Methods

Experimentation and data recording: The field trial was sown in a randomized block design (RBD) with three replications during 2015-16 and 2016-17 to examine the morphological genetic divergence among the genotypes of sorghum (*Sorghum bicolor* (L.) Moench.). All the150 sorghum genotypes (Table 1) were collected from NBPGR, New Delhi and planted at, Forage Section Research Area, Department of Genetics and Plant Breeding (CCSHAU Hisar, India). Hisar is located in the semi-arid subtropics and the experimental site in Hisar was situated at 29° 10' N latitude, and 75° 46' E longitude at an altitude of 215.2 meters above mean sea water level. Each genotype was accommodated in 3m row length with spacing 45x15 cm. The data was recorded on plant height (cm), stem diameter (cm), number of leaves/ plant, effective tillers/plant, leaf length of blade (cm), leaf width of blade (cm), panicle length without peduncle (cm), 1000 seed weight (g), green fodder yield/plant (g) and dry fodder yield/plant (g).

Statistical analysis: The analysis of variance (ANOVA)according to RBD was done on the basis of the model described in Panse and Sukhatme (1967). Phenotypic coefficient of variance (PCV) and genotypic coefficient of variability (GCV) were estimated according to Singh and Chaudhary (1982). Heritability in broad sense and Genetic advance were estimated as suggested by Burton and Devane (1953). Genetic divergence estimated as per Mahalanobis (1936). All the germplasm accessions were clustered into various groups according to Tocher's method (Rao, 1952). The intra- and inter-distances were also estimated as per the criterion used in clustering to the same cluster should at least on the average, display a lesser D^2 values, than those belonging to diverse clusters.

Results and Discussion

Heritability, PCV, GCV and Genetic Advance

For initiating any crop breeding, evidence on the nature and magnitude of genetic variability is of immense importance because occurrence of significant variability in the base germplasm confirms better probabilities of evolving desired outcome. During 2015-16, PCV, GCV, heritability and genetic advance (Table 2) are found valuable in defining the method of selection to make genetic improvement in a specific population for a definite character. It was constantly not essential for high heritability to be related with desirable genetic advance. The high heritability joined with desirable genetic advance specifies that additive genetic effects are dominant and simple will be useful for desirable improvement. High heritability was perceived for studied traits, except leaf length and leaf width. High heritability was found associated with high genetic advance for the characters viz., plant height, stem diameter, number of leaves/plant, effective tillers/ plant, panicle length excluding peduncle, 1000-seed weight, green fodder yield/plant (g) and dry fodder yield/plant (g). It may be because of the occurrence of additive gene action for above traits and selection for their genetic improvement is recommended. Moderate heritability coupled with moderate genetic advance was observed for leaf length of blade (cm) and leaf width of blade (cm). The high GCV and PCV were detected for plant height, stem diameter, number of tillers/plant, and number of leaves/plant, panicle length excluding peduncle, 1000-seed weight, green fodder yield/plant and dry fodder yield/plant. Moderate GCV and moderate PCV was observed for leaf length. Whereas, moderate GCV and high PCV for leaf width of blade (cm) was observed. The differences in GCV and PCV is low for these traits indicating less environmental effect for these traits.

Likewise, during 2016-17, PCV, GCV, heritability and genetic advance are convenient in decisive the technique of selection desired genetic improve in a particular population for a particular character. High heritability is not necessary to be found accompanying with high genetic advance for the required trait. High heritability and high genetic advance linkage specify

the presence of additive genetic effects therefore simple selection method is suggested for desirable improvement. In the present study except leaf length and leaf width high heritability was detected for the characters studied. High heritability and high genetic advance, both were associated with each other for plant height, stem diameter, number of leaves/plant, number of tillers per plant, panicle length except peduncle, 1000-seed weight, green fodder yield/plant and dry fodder yield/plant. It may be due to the presence of additive gene action for these characters and selection may be effective for their improvement. Moderate heritability coupled with moderate genetic advance was observed for leaf length of blade (cm) and leaf width of blade (cm). High GCV and high PCV were observed for traits like plant height (cm), stem diameter (cm), number of tillers per plant, number of leaves per plant, panicle length without peduncle, 1000 seed weight, green fodder yield per plant (g) and dry fodder yield per plant (g). Moderate GCV and moderate PCV was observed for leaf length of blade (cm) and leaf width of blade (cm). The differences between GCV and PCV is fewer for these traits indicating less environmental effect for these characters.

The differences among GCV and PCV are less for these traits indicating less environmental effect for these traits. Similar findings were described by Vinodhana et al., (2009) for PCV and GCV for plant height, and 1000- seed weight. Bello et al., (2007) reported high PCV, high GCV and high heritability for leaf length, leaf width, number of leaves per plant, plant height and 1000 seed weight. Likewise, high heritability and high genetic advance for plant height and fodder yield per plant was reported by Wadikar et al., (2018). More or less similar research findings were stated for high PCV, GCV, high heritability associated with high genetic advance for plant height, number of tillers/plant, green fodder yield/plant, dry fodder yield/plant, 1000-seed weight and panicle length excluding peduncle, and also moderate GCV, PCV, heritability associated with moderate genetic advance for leaf length and leaf width by Singh et al., (2010) and Deepak et al., (2017).

Genetic divergence

Development of high yielding varieties is documented as a definite area since population explosion with expansion and decreasing crop cultivation areas are the serious aspects causing fodder uncertainty for animals in emerging countries Most of the varieties available with us were developed by selection so new varieties have reduced genetic variability and selection in these genotypes further reduced the genotypic variability. As the genotypic variability for the desirable traits has exhausted from the genotypes there is need to identify new genes contributing to desirable traits. Diversity in germplasm offers chance for breeders to create new and genetically superior variety with required traits as germplasm has broad genetic base. That's why, deification of genotypes for crossing should be relay on genetic divergence among genotypes and not on geographic background. Therefore, genotypes grouping based on different ecogeographic areas into single group could be credited to the regular exchange of germplasm among different locations and its further selection of different geographic areas, may consequence in genetic drift.

In the present study150 genotypes of sorghum were categorized into different clusters using Tocher's method (Rao 1952) based on the D^2 values (Table 3-4). Grouping of sorghum genotypes into ten clusters showed that the 82 genotypes were grouped in cluster I, followed by the cluster IV and cluster II with 22 and 19 genotypes respectively, cluster III having 11 genotypes, cluster VII having nine genotypes, cluster X having three genotypes, while V, VI, VIII and IX clusters having single genotype. The cluster distances ranged from 16.98 to 84.52 (within the clusters) and 40.65 to 73.37 (between clusters) for year 2015-16. Similarly, for year 2016-17 genotypes were placed in different groups indicating that the 96 genotypes were involved in cluster I, followed by cluster IV, cluster II, cluster V, cluster III and cluster VI with 18, 17, 10, 8 and 1 genotype, respectively. The cluster distances ranged from 29.30 to 76.38 (within the clusters) and 0.00 to 71.11 (between clusters). Further for pooled data, genotypes were assembled in to different clusters indicating that the highest number of genotypes were involved in cluster I, followed by cluster IV, cluster III, cluster II, cluster VIII and cluster V with 19, 18, 15, 8 and 4 genotypes, respectively. However, cluster VI, cluster VII and cluster IX had single one only.

The results on intra- and inter- cluster distances are accessible in Table 5-6. The data range revealed the cluster distances from 26.85 to 117.88 (within the clusters) and 65.87 to 117.88 (between clusters). The higher inter-clusters distances than the intra-cluster, revealed the extensive diversity among the genotypes of different clusters rather than the same one. This advocated that genotypes occurring in same cluster had very less diversity and selection of parents for hybridization within the cluster is not found promising for the development of noble segregants. The greater distances among the cluster, further demonstrating substantial volume of diversity amongst the genotypes used in present studied. Based on D^2 analysis, inter-cluster distance is the chief selection criterion for genotypes for hybridization.

The data on cluster means are presented in Table 7 for 2015-16, Table 8 for 2016-17 in compasses the presence of huge genetic diversity in sorghum study material. Genetic diversity available in the germplasm was also advocated by the considerable volume of difference among cluster means for diverse traits. Similar findings were noticed by Prasad and Biradar (2017) in which the different genotypes were classified into 22 groups, whereas cluster-I had maximum of 115 genotypes, followed by cluster-II having 45 genotypes only. Highest inter-cluster distance was found among clusters-III and XXI, followed by among cluster-XIII and XXI. Damor et al., (2017) reported five clusters of sorghum genotypes. According them, Cluster I had maximum of 40 genotypes but, cluster II had 16 genotypes, cluster IV only two genotypes, while cluster III & V with single genotype. Meena et al., (2016) also observed the genotypes were grouped into ten clusters. Maximum distance among clusters was observed in clusters II & IX, whereas minimum was in VI & VIII. Maximum distance within the cluster was found in cluster-IX followed by cluster-VII. Likewise, Kumar et al., (2010) also grouped accessions into eight clusters. The cluster-I comprised of 15 genotypes and cluster-V of 10 genotypes, cluster IV of 9 ones. The inter cluster distances were higher among cluster-VII & VIII followed by cluster-III and VII and cluster V and VIII. In sorghum, such findings were also observed by Yuvaraja et al., 2019.

Character contribution in genetic divergence

The data of present study depicted that each trait had performed at number one rank and its respective contribution (%) towards genetic divergence (Table 9). For 2015-16, relative contribution of characters such as panicle length without peduncle was highest towards genetic divergence (31%), followed by 1000 seed weight (29.03%), green fodder yield (20.48%), followed by total tillers/plant, plant height, leaves per plant, dry fodder yield/plant, stem diameter and leaf length of blade, respectively, to the genetic divergence in decreasing order. Similarly, for 2016-17 share of panicle length without peduncle was highest in total genetic divergence (33.44%), followed by 1000 seed weight (27.45%), green fodder yield (17.66%), followed by total tillers per plant, plant height, leaves per plant, dry fodder yield and stem diameter respectively to the genetic divergence in decreasing order. Similar results were reported by Singh et al., (2008) for number of leaves/plant found greatest involvement towards plant divergence followed by green fodder yield and leaf breadth. Khadakabhavi et al., (2014) for yield/plant reported maximum contribution in genetic divergence followed by 1000-seed weight, length of panicle, height and days to 50% flowering, these characters can be exploited for further genetic enhancement.

To develop new varieties or hybrids of forage sorghum, information and knowledge on genetic make-up is most important for the devising of an efficient breeding strategy for genetic improvement of forage sorghum. In present study, information on genetic variability, divergence, inheritance and genetic advance of important quantitative and qualitative characters seems to very important to draft a new breeding program for genetic improvement of forage sorghum germplasm for these traits.

Table 1. List of forage sorghum germplasm lines.

S. No	Accession No	S. No	Accession No	S. No	Accession No	S. No	Accession No	S. No	Accession No
1	IC-485180	31	IC-240855	61	IC-485003	91	IC-485233	121	IC-585202
2	EC-486333	32	IC-240856	62	IC-485009	92	EC-464430	122	IC-585203
3	IC-484860	33	IC-240859	63	IC-485011	93	IC-298598	123	IC-585204
4	IC-546929	34	IC-240860	64	IC-485244	94	IC-298601	124	IC-585205
5	IC-121559	35	IC-240861	65	IC-484515	95	IC-298605	125	IC-585209
6	IC-484320	36	IC-240862	66	IC-484583	96	IC-309905	126	IC-585218
7	IC-484895	37	IC-240864	67	IC-484628	97	IC-309906	127	IC-585219
8	IC-484962	38	IC-240865	68	IC-484696	98	IC-309907	128	IC-585225
9	IC-484968	39	IC-240866	69	IC-484714	99	IC-309914	129	IC-585233
10	IC-485002	40	IC-240871	70	IC-485145	100	IC-309944	130	IC-585234
11	IC-485024	41	IC-240872	71	IC-485177	101	IC-353607	131	IC-585239
12	IC-240831	42	IC-240876	72	IC-484591	102	IC-585143	132	IC-585240
13	IC-240832	43	IC-240877	73	IC-484729	103	IC-585174	133	IC-296496
14	IC-240833	44	IC-240879	74	IC-484750	104	IC-585176	134	IC-395722
15	IC-240835	45	IC-240880	75	IC-484767	105	IC-585177	135	IC-395816
16	IC-240837	46	IC-240881	76	IC-484826	106	IC-585180	136	IC-436867
17	IC-240838	47	IC-436857	77	IC-484855	107	IC-585184	137	IC-413297
18	IC-240839	48	IC-240883	78	IC-484351	108	IC-585185	138	IC-413299
19	IC-240840	49	IC-240884	79	IC-484418	109	IC-585189	139	IC-436523
20	IC-240841	50	IC-484974	80	IC-484430	110	IC-585190	140	IC-436527
21	IC-240842	51	IC-485023	81	IC-484444	111	IC-585191	141	IC-436572
22	IC-240843	52	IC-485028	82	IC-484445	112	IC-585192	142	IC-436577
23	IC-240845	53	IC-485030	83	IC-484489	113	IC-585193	143	IC-527019
24	IC-240846	54	IC-485039	84	IC-484491	114	IC-585194	144	IC-527022
25	IC-240848	55	IC-484819	85	IC-484510	115	IC-585195	145	IC-397246
26	IC-240849	56	IC-484869	86	IC-484637	116	IC-585196	146	IC-436682
27	IC-240850	57	IC-484870	87	IC-484658	117	IC-585197	147	IC-436752
28	IC-240851	58	IC-484911	88	IC-485143	118	IC-585198	148	IC-436791
29	IC-240852	59	IC-484989	89	IC-485188	119	IC-585200	149	IC-436916
30	IC-240853	60	IC-484997	90	IC-485202	120	IC-585201	150	IC-436796

Table 2. Heritability, GCV, PCV and Genetic advance value % of sorghum genotypes in 2015-16 and 2016-17.

S. No	Year	Heritability (%)	GCV (%)	PCV (%)	Genetic Advance Value % of Mean
Plant height	2015-16	78.28	23.15	26.17	42.20
	2016-17	79.18	21.80	24.50	39.96
Stem diameter (cm)	2015-16	64.05	21.49	26.86	35.44
	2016-17	68.27	22.20	26.87	37.79
Number of tillers per plant	2015-16	85.39	29.62	32.06	56.39
	2016-17	86.51	29.54	31.76	56.60
Number of leaves per plant	2015-16	63.33	23.20	29.16	38.04
	2016-17	69.75	23.71	28.38	40.78
Leaf Length of blade (cm)	2015-16	45.29	11.88	17.65	27.98
	2016-17	49.15	12.19	17.39	17.60
Leaf width of blade (cm)	2015-16	40.56	13.87	21.78	18.20
	2016-17	41.07	12.74	19.87	16.81
Panicle length without peduncle (cm)	2015-16	92.17	32.26	33.60	63.80
	2016-17	92.38	32.55	33.87	64.45
1000 seed weight (g)	2015-16	93.41	38.89	40.24	77.44
	2016-17	93.11	38.31	39.70	76.15
Green fodder yield (g)	2015-16	86.16	42.58	45.87	81.42
	2016-17	84.91	42.31	45.91	80.31
Dry fodder yield (g)	2015-16	81.94	42.53	46.99	79.31
	2016-17	81.65	42.27	46.78	78.69

Table 3. Number of genotypes in each cluster for 2015-16.

Cluster	Genotypes
Cluster1	80, 87, 126, 43, 2, 81, 88, 150, 105, 37, 149, 94, 147, 97, 29, 92, 63, 70, 106, 74, 89, 95, 28, 144, 112, 107, 114, 102, 64, 134, 135, 123, 26, 122, 6, 121, 13, 130, 60, 27, 104, 73, 133, 90, 3, 31, 52, 139, 48, 91, 8, 131, 100, 68, 38, 88, 115, 47, 128, 148, 33, 103, 111, 14, 101, 145, 54, 146, 7, 50, 59, 120, 160, 124, 98, 96, 99, 136, 49, 110,1 25, 108
Cluster 2	84,85,83,143,66,32,44,24,86,41,77,61,45,127,9,53,75,76,71
Cluster 3	132,138,129,118,141,140,117,119,12,72,10
Cluster 4	57,109,55,56,142,51,137,67,20,62,36,25,93,46,21,11,22,58,34,40,69,16
Cluster 5	15
Cluster 6	35
Cluster 7	4,5,18,42,17,19,1,113,30
Cluster 8	78
Cluster 9	79
Cluster 10	23,39,65

Table 4. Number of genotypes in each cluster for 2016-17.

Cluster	Genotypes
Cluster1	111,121,122,27,6,8,106,134,135,28,147,13,64,14,115,130,123,94,105,29,92,126,26,139,60,73,80,112,114,89,95,74,63,70,87,43,81,2,107,150,104,3,97,91,37,88,133,48,52,31,90,131,82,38,68,47,144,146,128,100,103,148,149,7,50,145,102,75,9,54,33,59,62,110,124,101,49,119,72,142,116,98,67,12,120,96,99,136,141,108,32,44,10,20,85,84
Cluster 2	57,109,55,56,137,51,25,36,93,46,11,22,21,58,45,61,127
Cluster 3	132,138,129,125,118,140,117,65
Cluster 4	71,76,77,78,79,41,83,143,66,53,24,86,69,1,23,40,34,39
Cluster 5	15,16,113,19,17,4,5,42,18,30
Cluster 6	35

Table 5. Intra and inter-cluster distances for 2015-16.

0	1	2	3	4	5	6	7	8	9	10
1	25.73	38.62	34.64	40.11	52.02	38.01	68.21	50.43	50.03	49.61
2		30.22	52.18	48.01	57.73	46.81	72.64	35.02	35.70	54.45
3			28.56	49.88	47.56	45.54	64.73	69.68	69.39	43.01
4				35.13	47.30	45.31	58.30	52.66	47.21	58.81
5					0.00	56.39	29.35	73.47	66.97	40.65
6						0.00	69.66	57.39	51.91	52.21
7							35.74	84.52	77.29	57.24
8								0.00	16.98	73.37
9									0.00	71.23
10										45.20

Table 6. Intra and inter-cluster distances for 2016-17.

Group	1	2	3	4	5	6
1	29.30	43.92	41.32	44.98	69.52	44.33
2		35.20	64.11	49.01	59.58	51.86
3			29.55	62.16	76.38	56.63
4				41.69	69.98	50.54
5					36.92	71.11
6						0.00

Table 7. Cluster means for 2015-16.

	Char.1	Char.2	Char.3	Char.4	Char.5	Char.6	Char.7	Char.8	Char.9	Char.10
Group.1	132.40	8.69	1.08	9.80	47.04	4.75	14.67	20.04	83.09	38.21
Group.2	117.46	9.48	1.21	9.59	49.14	4.89	24.17	17.64	84.05	38.49
Group.3	151.85	9.75	1.15	11.43	49.45	5.00	9.76	13.11	111.42	51.64
Group.4	120.06	10.64	1.40	10.20	49.17	5.00	16.07	32.80	113.12	52.28
Group.5	164.00	10.47	2.00	10.10	53.00	5.47	15.53	21.42	197.00	84.67
Group.6	50.33	10.13	2.00	12.07	46.33	4.37	12.70	20.88	53.67	25.03
Group.7	145.74	10.89	2.14	12.70	48.70	5.63	15.91	27.07	216.00	99.30
Group.8	105.33	9.53	1.00	13.60	57.00	4.20	29.80	28.32	65.33	27.33
Group.9	92.67	8.63	1.43	9.93	35.00	3.70	28.47	31.54	73.67	30.00
Group.10	133.11	10.94	1.70	11.99	50.00	5.01	15.48	6.78	143.89	67.54

Table 8. Cluster means for 2016-17.

	Char.1	Char.2	Char.3	Char.4	Char.5	Char.6	Char.7	Char.8	Char.9	Char.10
Group.1	132.47	8.95	1.10	9.66	47.28	4.96	15.14	20.50	87.00	40.26
Group.2	118.21	11.35	1.33	9.23	51.25	5.37	17.71	34.14	114.12	53.57
Group.3	164.37	9.50	1.06	11.82	49.25	5.11	8.70	9.26	108.75	50.88
Group.4	106.20	9.89	1.44	10.76	46.94	4.89	23.59	18.18	92.07	43.22
Group.5	148.57	10.99	2.16	12.61	51.03	5.53	15.24	26.75	215.53	98.30
Group.6	53.67	10.13	2.00	12.53	45.67	4.10	12.63	21.20	56.67	27.00

Table 9. Contribution (%) of different traits to diversity of fodder sorghum.

Sr. No.	**Source**	**Times Ranked 1st**		**Contribution %**	
		2015-16	**2016-17**	**2015-16**	**2016-17**
1.	Plant height(cm)	655	555	5.86%	4.97%
2.	Stem diameter (cm)	31	14	0.28%	0.13%
3.	Number of tillers/plants	796	1366	7.12%	12.22%
4.	Number of leaves/plants	222	262	1.99%	2.34%
5.	Leaf Length of blade (cm)	2	0	0.02%	0.00%
6.	Leaf width of blade (cm)	0	0	0.00%	0.00%
7.	Panicle length without peduncle (cm)	3722	3737	31.00%	33.44%
8.	1000 seed weight (g)	3244	3067	29.03%	27.45%
9.	Green fodder yield (g)	2289	1967	20.48%	17.66%
10.	Dry fodder yield (g)	214	207	1.91%	1.85%

References

Borad VP, Gangani MK, Parmar HP, (2007). Character association in forage [*Sorghum bicolor* (L.) Moench]. Forage Research. 2007;32(4):213-215.

Burton GW, and Devane EM, (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal-material. Agronomy J. 45:478-481.

Damor HI, Parmar HP and Parmar DJ, (2017). D^2 analysis in forage Sorghum (*Sorghum bicolor* (L) Moench). International Journal of Chemical Studies, 5(4):337-341.

Kaushik D, Jindal Y, Kumari P and Gaur A, (2020). Qualitative characterization of sorghum genotypes for morphological traits. Forage Res., 45:269-276. http://forageresearch.in

Khadakabhavi S, Girih G, Dharmaraj PS and Lokesh R, (2014). Genetic diversity analysis in the germplasm lines of *rabi*-sorghum [*Sorghum bicolor* (L) Moench] based on quantitative trait, Int. Journal Plant Science 9:129-132.

Kumar CVS, Shreelakshmi C and Shivani D, (2010). Genetic-diversity analysis in rabi sorghum (*Sorghum bicolor* L. Moench.) local genotypes. Electronic Journal of Plant Breeding 1:527-529.

Mahalanobis PC, (1936). On the generalized distance in statistics. Proceedings of National Institute of Sciences India 2:49-55.

Meena V, Mehta AK and Khujur MJ, (2016). Genetic-divergence in fodder-sorghum [*Sorghum bicolor* (L.) Moench], Forage Res. 42:176-179.

Nguyen Ngoc Vu, Arya RK, Panchta R and Tokas J, (2017). Studies on genetic divergence in cowpea (*Vigna unguiculata*) by using D^2 statistics under semi arid condition. Forage Res. 43:197-201.

Panse VG and Sukhatme PV, (1954). Statistical methods for agriculture workers. ICAR, New Delhi, 2:381.

Prasad BHV and Biradar BD, (2017). Genetic Diversity studies in minicore collection of rabi sorghum [*Sorghum bicolor*. (L)] using D^2 statistics. International Journal of Current Microbiology and Applied Science 6(7):850-856.

Raiger HL, Yadav SK, Arya RK and Phogat BS, (2021) Studies on variability and character association for yield and yield related traits in faba bean (*Vicia faba*). Ekin J. 7:125-130

Rao CR, (1952). Advanced statistical methods in biometrical research. John Wiley and Sons, New York, USA.

Shafiqurrahaman M, Dahiya GS, Pahuja SK, Dehinwal AK and Arya RK, (2022). DUS characterization in sorghum [*Sorghum bicolor* (L) Moench.]. Forage Res. 47(4):423-431.

Singh BB and Chaudhary VS, (1982). Heterosis and genetic-variability in relation to genetic-diversity in soybean. Indian Journal of Genetics 42:324-328.

Singh SK, Anil S, Singh B, Singh A, Singh A and Kumar V, (2008). Genetic divergence in forage sorghum. Progressive Agriculture, 8:169-172.

Singh S, Dwivedi VK, Sherotria PK and Pandey S, (2010). Genetic divergence in sorghum (*Sorghum bicolor* (L.) Moench). Forage Res. 36(1):48-51.

Vu NN, Arya RK and Ravish Panchta, (2019). Studies on genetic parameters, correlation and path coefficient analysis in cowpea. Range Management & Agro-forestry 40(1):49-58.

Wadikar PB, Kuptekar SV and Deshmukh AS, (2018). Character association and component analysis for juice yield in sweet sorghum [*Sorghum bicolor* (L.) Moench]. International Journal of Current Microbiology and Applied Sciences 6:803-807.

Yuvaraja A, Chinthiya A, Sangeetha R, Viswa Bharathy S and Rajarajan K, (2019). Diversity analyses of forage traits in sorghum (*Sorghum bicolor* L.) germplasm. Forage Res. 44(4):242-246.