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Genetic divergence study through D^2 statistics in rabi sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

D^2 statistics was employed in the current study to evaluate the diversity among 68 genotypes originating from 28 countries and belonging to diverse races. For all of the 19 traits, a significant variation was observed among all the genotypes. The presence of 16 clusters showed that all of the genotypes had a significant diversity. Larger clusters I and II, with 27 and 24 genotypes, respectively, were the first two clusters. The largest inter cluster distance (741.61) was found between clusters VII and XV, and both clusters remained solitary, implying that the genotypes found in these clusters have heterotic responses, which might lead to the production of better segregants. The traits with the largest genetic divergence were 1000 grain weight, followed by grain length, grain breadth, and panicle weight per plant. For a future crop improvement program, these traits can be used to choose appropriate maintainer and restorer lines on different male sterile lines. Among the most diverse genotypes, DSMR-8 and DSMR-4 were discovered to be restorers, whereas IS 7987 and IS 12937 had a maintainer reaction on *maldandi*. Therefore, these lines can be a good source of restorer genes, new male sterile lines on *maldandi* to diversify the genetic base of restorers and male sterile lines.

Keywords D^2 statistics, genetic divergence, inter-cluster, sorghum

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Introduction

Over half a billion people consume sorghum as a dietary food in more than thirty nations, making it the 5th most-produced food crop across the world [1-2]. Ethiopia is the center of origin or diversity of sorghum [3]. It exhibits great tolerance to water stress [4] and is well suited to a vast range of climatic conditions, including those in arid and semiarid tropical regions around the world [5-6]. Sorghum bicolor includes both domesticated and wild-related races and offers significant genetic diversity for agronomic traits to improve the crop [7]. The goals of sorghum breeding were to increase biomass and stem sugar content for the production of biofuels, grain yield and quality for food and livestock usage, and stover yield and quality [8]. Sorghum is grown during the *rabi* season, generally referred to as *rabi* sorghum is utilized in the form of food and fodder because of its superior grain and fodder quality. Even though several hybrids have been released for the *rabi* season, the area under hybrids is incredibly small. Due to a dearth of suitable hybrids with good grain quality that are acclimated to the *rabi* season, most of the area is occupied with varieties [9]. Low heterosis in hybrids caused by

the narrow genetic base between the parental lines was among the factors limiting the production of *rabi* season hybrids. Being well-versed in a crop's genetic diversity usually helps plant breeders to select the ideal type for breeding programs and gene introgression from diverse germplasm. To create heterotic hybrids that can endure a range of environmental changes as well as abiotic and biotic stresses, it is feasible to integrate diverse genotypes. Thus, deeper comprehension of the diversity among sorghum will undoubtedly make it easier to improve the crop's genetic architecture and yield [10]. Phenotypic attributes are frequently used to assess genetic diversity since these studies typically do not need sophisticated instruments or methodologies, and they are simple to score. As a result, it is necessary to assess the genotypes for diversity and select the diverse genotypes based on their phenotypic performance. In this diversity study, 68 sorghum genotypes were evaluated and their clustering was done using Mahalanobis' D^2 statistic technique.

Methodology

A total of 68 sorghum (*Sorghum bicolor* L. Moench) genotypes belonging to 28 countries and diverse races and racial combinations were evaluated in a randomized block design with two rows of 3 m length of each genotype in two replications with a spacing of 45 × 15cm (Table 1).

Table 1. Origin and races of the genotypes used for the diversity study

SN.	Genotypes	Origin	Race	SN.	Genotypes	Origin	Race
1	IS 27912	South Africa	Kafir-caudatum	35	IS 12735	Yemen	Caudatum-bicolor
2	IS 30536	Korea	Caudatum-bicolor	36	IS 24175	Tanzania	Guinea
3	IS 28313	Yemen	Durra-caudatum	37	IS 19975	Senegal	Guinea
4	IS 2413	Iran	Bicolor	38	IS 9108	Kenya	Caudatum
5	IS 19389	Bangladesh	Caudatum	39	IS 2872	Egypt	Caudatum-bicolor
6	IS 29335	Swaziland	Caudatum	40	IS 26025	Mali	Guinea
7	DSMR-4	India	Durra	41	IS 4581	India	Durra
8	IS 25249	Ethiopia	Durra-bicolor	42	IS 602	USA	Bicolor
9	IS 12804	Turkey	Bicolor	43	IS 21645	Malawi	Guineas
10	IS 29392	Lesotho	Kafir	44	IS 22616	Myanmar	Bicolor
11	IS 7987	Nigeria	Guinea	45	IS 24139	Tanzania	Guinea
12	IS 31043	Uganda	Caudatum	46	IS 12883	India	Durra
13	IS 30466	China	Caudatum-bicolor	47	IS 14290	Botswana	Kafir-durra
14	IS 4060	India	Durra-bicolor	48	IS 29914	Zimbabwe	Caudatum
15	IS 29568	Lesotho	Kafir-caudatum	49	IS 25989	Mali	Guinea
16	IS 15945	Cameroon	Guinea-caudatum	50	IS 24348	India	Caudatum
17	IS 15478	Cameroon	Guinea-caudatum	51	IS 20679	USA	Guinea-caudatum
18	IS 5919	India	Durra	52	IS 9745	Sudan	Caudatum
19	IS 8012	Japan	Bicolor	53	IS 24492	South Africa	Kafir
20	IS 29468	Lesotho	Guinea-caudatum	54	IS 23590	Ethiopia	Guinea-caudatum
21	IS 26617	Madagascar	Caudatum-bicolor	55	IS 995	USA	Caudatum-bicolor
22	IS 14861	Cameroon	Caudatum	56	IS 16528	Cameroon	Guinea
23	DSMR-8	India	Durra	57	IS 32439	India	Guinea
24	IS 2397	South Africa	Kafir	58	IS 10302	Thailand	Caudatum
25	IS 12302	Zimbabwe	Caudatum	59	IS 19676	Zimbabwe	Kafir
26	IS 29654	China	Kafir-bicolor	60	IS 27887	South Africa	Caudatum-bicolor
27	IS 30451	China	Caudatum-bicolor	61	IS 28614	Yemen	Durra-caudatum
28	IS 33353	Kenya	Caudatum	62	IS 12937	Ethiopia	Kafir
29	IS 26046	Mali	Guinea	63	IS 20743	USA	Bicolor
30	IS 4698	India	Durra	64	PKV Kranti	India	Durra
31	IS 19445	Botswana	Kafir	65	BJV 44	India	Durra
32	IS 24462	South Africa	Caudatum-bicolor	66	IS 4515	India	Durra
33	IS 30383	China	Caudatum-bicolor	67	IS 2312	India	
34	IS 22720	Somalia	Durra	68	M-35	India	Durra

The trial was conducted during *rabi*-2017 at the Botanical Garden, Dept. of Genetics and Plant Breeding, UAS, Dharwad, India. The data were collected on five randomly selected plants for 19 characters *viz*., days to 50% heading, peduncle length (cm), panicle length (cm), panicle breadth (mm), primaries per panicle, whorls per panicle, leaves per plant, nodes per plant, plant height (cm), stem girth (mm), panicle weight (g), grain yield per plant (g), 1000 grain weight (g), grains per

panicle, 1000 grain volume (cc), grain density, grain length (mm), grain width (mm) and grain thickness (mm). Mean values were recorded replication-wise and subjected to RBD analysis [11]. The significant differences among all the genotypes were tested by the 'F'-test. Mahalanobis'(1936) D^2 statistic was used to examine genetic diversity [12] and genotype clustering was carried out using Tocher's approach.

Results and Discussion

Analysis of variance displayed highly significant differences for all the traits (Table 2) indicating the presence of enough variance to exploit. Using Tocher's approach and D^2 statistics the 68 genotypes were distributed into 16 groups containing a variable number of entries (Table 3) revealing the existence of substantial diversity among the genotypes.

Table 2. Analysis of variance in respect of various productivity traits in sorghum

Source of variation	DF	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
Replication	1	3.09	26.36	6.45	0.91	172.19	2.77	1.74	2.08*	3824.27**	9.69*
Treatments	67	177.62**	290.77**	85.49**	130.34**	407.30**	5..38**	3.48**	3.97**	3771.18**	3.88**
Error	67	11.93	17.28	5.18	16.07	59.15	1.71	0.48	0.35	295.51	1.71
CD @ 5%		6.89	8.30	4.54	8.00	15.35	2.61	1.39	1.17	34.31	2.61
S. E.		**2.44**	**2.94**	**1.61**	**2.83**	**5.44**	**0.92**	**0.49**	**0.41**	**12.16**	**0.93**
Source of variation	**DF**	**X11**	**X12**	**X13**	**X14**	**X15**	**X16**	**X17**	**X18**	**X19**	
Replication	1	193.71	100.52	0.0003	116706.60	0.89	0.002	0.197*	0.052	0.012	
Treatments	67	116573**	1117.52**	118.73**	440363.74**	79.57**	0.040**	0.432**	0.421**	0.196**	
Error	67	56.52	38.14	3.04	61211.59	3.87	0.0134	0.030	0.018	0.016	
CD @ 5%		15.01	12.33	3.48	493.83	3.93	0.23	0.35	0.27	0.25	
S. E.		**5.32**	**4.37**	**1.23**	**174.95**	**1.39**	**0.08**	**0.12**	**0.09**	**0.09**	

***, ** indicates significant at 5 % and 1% level respectively**

X1. Days to 50 % flowering, **X2**. Peduncle length (cm), **X3**. Panicle length (cm), **X4**. Panicle breadth (mm), **X5**. Primaries per panicle **X6**. Whorls per panicle, **X7**. Leaves per plant, **X8**. Nodes per plant, **X9**. Plant height (cm), **X10**. Stem girth (mm), **X11**. Panicle weight per plant (g), **X12**. Grain yield per plant (g), **X13**. 1000 grain weight (g), **X14**. Grains per panicle, **X15**. 1000 grain volume (cc), **X16**. Grain density, **X17**. Grain length (mm), **X18**. Grain width (mm), **X19**. Grain thickness (mm)

Previous studies [13-14] also reported enough clusters and considerable diversity among the lines studied. As in previous studies [13-14], the data on inter-cluster distances were utilized in the current study to choose genetically diverse and agronomically better genotypes. Table 4, lists the average inter and intra-cluster distance and the nearest and farthest clusters for each other. The inter-cluster distance was recorded as highest (741.61) between clusters VII and XV and both clusters remained solitary. Whereas the lowest inter-cluster distance (59.77) was recorded between clusters IV and VI having one and four genotypes, respectively. The highest intra-cluster distance (93.59) was recorded in cluster VI. Cluster I and II were the larger clusters consisting of 27 and 24 genotypes, respectively. The degree of genetic diversity present between the parental lines is typically used to predict heterosis and the performance of hybrids [15-16]. “Intercrossing of genotypes from these divergent groups would lead to a greater opportunity for crossing over, which releases hidden potential variability by disrupting the undesirable linkages”[17]. A wide range of genetic diversity is anticipated in the offspring resulting from such diverse crosses, increasing the possibility of identifying transgressive segregants in subsequent generations. To retrieve transgressive segregants, these genotypes might be employed in a multiple-crossing procedure [18].

In the present experiment, most of the clusters were found to be solitary clusters. The presence of solitary clusters in the present investigation viz., IS 32439, IS 4581, PKV Kranti, IS 15478, IS 12937, IS 25249, IS 28614, DSMR-8, IS 7987, IS 20679, IS 602, IS 12735, and DSMR-4 display the uniqueness of these genotypes. The earlier workers also reported the presence of solitary clusters and their uniqueness [19-21]. These diverse lines can also be used as the source of yield, yield attributes, and quality traits of seeds for the improvement of existing cultivars. Even these lines can be used in conversion programs for the generation of new male sterile and restorer lines as some of

Table 3. Distribution of genotypes in sixteen different clusters and their sterile and fertile reaction on *milo* and *maldandi* source of male sterility

Cluster No.	Name of genotypes	No. of genotypes	Origin	Race
1	IS 29568(MA_1^2, A_4), IS 5919, IS 2397(MA_4), IS 8012(MA_1^1, A_4), IS 31043(MA_4), IS 2933, IS 2872(MA_4), IS 29468, IS 24139(MA_4), IS 33353(MA_11, A_1^2), IS 30536(MA_4), IS 27912(MA_4), IS 29392(MA_4), IS 29914(MA_1^2, A_4), IS 30383(MA_4), IS 30466(MA_4), IS 9108, IS 26046 (RA_1^1 and A_1^2), IS 21645(MA_1^1), IS 4515(MA_4), IS 19445 (MA_1^1, A_1^2), IS 14290(M), IS 16528, IS 12804, IS 2312, IS 12302 (MA_4)and IS 29654 (MA_1^2, A_4)	27	Botswana (2), Cameroon (1), China (3), Egypt (1), India (2), Iran (1), Japan (1), Kenya (3), Korea (1), Lesotho (3), Malawi (1), Mali (1), South Africa (2), Swaziland (1), Turkey (1), Uganda (1) and Zimbabwe (2)	Caudatum (6), Caudatum-bicolor (4), Durra (3), Kafir (2), Bicolor (3), Guinea (3), Guinea-caudatum (1) and Kafir-caudatum (3), Kafir-bicolor (1) and Kafir-durra (1)
2	IS 19975(RA_4), IS 20743(MA_4), IS 25989(MA_4), IS 14861(MA_4), IS 26025, IS 9745(M), IS 19676, IS 4060, IS 28313(MA_1^1, A_4), IS 15945(M), IS 24348(M), IS 995(MA_4) &(RA_1^1), IS 26617 (M), IS 12883, IS 27887, IS 19389(MA_4) &(RA_1^1), IS 22720(MA_1^1, A_4), IS 10302(MA_4), IS 23590, IS 24139(MA_4), IS 24175(MA_4), IS 24492(MA_1^1, A_1^2), IS 4698(M)and IS 22616(MA_4)	24	Bangladesh (1), Cameroon (2), Ethiopia (1), India (4), Madagascar (1), Mali (2), Myanmar (1), Senegal (1), Somalia (1), South Africa (2), Sudan (1), Tanzania (2), Thailand (1), USA (2), Yemen (1), Zimbabwe (1)	Guinea (5), Caudatum (5), Bicolor (2), Durra-bicolor (1), Durra-caudatum (1), Guinea-caudatum (2), Caudatum-bicolor (3), Durra (3) and Kafir (2)
3	IS 32439	1	India	Guinea
4	IS 4581(M)	1	India	Durra
5	PKV Kranti	1	India	
6	IS 30451(MA_4), IS 24462(MA_1^1, A_1^2), M-35 and BJV44	4	China, India (2), South Africa	Caudatum-bicolor (2)
7	IS 15478(MA_4)	1	Cameroon	Guinea-caudatum
8	IS 12937(MA_4)	1	Ethiopia	Kafir
9	IS 25249(MA_4)	1	Ethiopia	Durra-bicolor
10	IS 28614(MA_4)	1	Yemen	Durra-caudatum
11	DSMR-8 (RA_1^1 and A_4)	1	India	Durra
12	IS 7987(MA_4)	1	Nigeria	Guinea
13	IS 20679	1	USA	Guinea-caudatum
14	IS 602(MA_4)	1	USA	Bicolor
15	IS 12735	1	Yemen	Caudatum-bicolor
16	DSMR-4(MA_1^1) and (RA_4)	1	India	Durra

'R' refers to restorer on A_1^1, A_1^2 and A_4 'A_1^1' refers to *Milo* (104A) cytoplasm, 'A_1^2' refers to *Milo* (401A) cytoplasm, 'A_4' refers to *Maldandi* cytoplasm, 'M' refers to maintainer on A_1^1, A_1^2 and A_4 'MA_1^1'refers to maintainer on 104_A, 'MA_1^2'refers to maintainer on 401A, and 'MA_4' on refers to maintainer on *Maldandi*.

Table 4. Average intra and inter cluster distances (D^2) for sixteen clusters of sorghum

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**66.40**	176.29	131.56	88.97	139.89	112.65	305.79	87.23	93.30	226.19	118.17	158.83	243.72	371.80	223.86	142.86
II		**83.24**	111.44	230.17	376.26	213.50	117.47	120.33	248.25	124.01	146.48	411.63	111.53	178.38	502.48	334.22
III			**0.00**	230.82	323.66	224.86	161.58	67.64	205.88	218.21	197.70	386.35	189.46	163.19	370.86	226.31
IV				**0.00**	82.18	59.77	390.06	190.94	137.34	160.70	139.71	104.06	301.76	431.64	202.19	159.29
V					**0.00**	193.61	543.48	258.08	144.10	379.98	235.64	81.52	499.83	598.01	193.69	243.78
VI						**93.59**	374.79	183.76	155.65	166.88	151.81	185.90	248.21	442.10	279.61	158.81
VII							**0.00**	215.45	399.78	192.24	206.19	613.35	148.76	176.84	741.61	563.80
VIII								**0.00**	115.80	225.74	122.15	264.29	189.41	272.73	335.67	184.14
IX									**0.00**	333.35	183.31	200.64	262.74	493.78	281.21	117.97
X										**0.00**	183.71	395.53	132.33	239.29	516.07	394.37
XI											**0.00**	195.77	188.95	358.51	371.29	284.11
XII												**0.00**	483.62	692.17	142.40	270.44
XIII													**0.00**	262.44	600.73	386.79
XIV														**0.00**	655.44	505.04
XV															**0.00**	283.12
XVI																**0.00**

these lines behaved as maintainers and some as restorers on milo and maldandi male sterility sources (Table 3). The traits exhibiting high contribution towards genetic divergence can help in the selection of genotypes for improvement of that trait. Among the 19 traits, the highest contribution towards total divergence was displayed by 1000 grain weight followed by grain length, grain width, and panicle weight per plant (Table 5). Although the 1000-grain weight contributed the highest to the overall divergence, importance should be given to other diverging traits viz., grain length, grain

Table 5. Per cent contribution of different characters towards genetic divergence in sorghum

Characters	Percent contribution	Rank
1000 grain weight (g)	25.2	1
Grain length (mm)	13.61	2
Grain width (mm)	12.03	3
Panicle weight per plant (g)	10.45	4
Plant height (cm)	5.71	5
Peduncle length (cm)	5.62	6
1000 grains volume (cc)	5.62	7
Grain thickness (mm)	4.78	8
Panicle length (cm)	4.26	9
Days to 50 % heading	3.73	10
Grains per panicle	2.72	11
Grain yield per plant (g)	1.58	12
Grain density	1.32	13
Leaves per plant	1.01	14
Panicle breadth (mm)	0.75	15
Primaries per panicle	0.61	16
Whorls per panicle	0.18	17
Stem girth (mm)	0.44	18
Nodes per plant	0.31	19

Table 6. Classification of genotypes with good per se values represented in different clusters

SN.	Characters	Clusters	Genotypes (per se values)
1	Days to 50 per cent flowering	I, II, VI, X, XIII	IS 30451 (56.50), IS 20743 (59.00), IS 14861(60.00), IS 20679 (60.00), IS 19676 (61.50), IS 24348 (62.00), IS 28614 (62.00) IS 26025 (62.50) and IS 19975 (63.00) and IS 2312 (63.78)
2	Peduncle length (cm)	I, V, IX, XI, XII	DSMR-8 (23.10), IS 31043 (23.21), IS 27912 (24.34), IS 2397 (25.80), IS 29468 (26.30), PKV Kranti (28.01), IS 30383 (28.15), IS 7987 (28.97), IS 25249 (29.42) and IS 29654 (29.66)
3	Panicle length (cm)	I, II, III, XIV, XV, XVI	IS 602 (51.67),DSMR-4 (37.82), IS 29914 (33.54), IS 19676 (33.42), IS 22616 (33.15),IS 19975 (32.22), IS 20743 (31.51), IS 32439 (31.00), IS 14861 (30.17) and IS 12735 (29.61)
4	Panicle breadth (mm)	I, II, V, VI, XI, XII, XVI	DSMR-8 (59.20), IS 7987 (57.70), IS 12302 (57.04), BJV 44 (55.47), IS 19445 (51.01), PKV Kranti (50.85), IS 31043 (50.80), DSMR-4 (47.65), M-35 (47.50) and IS 22720 (47.10)
5	Primaries per panicle	I, II, V, VI, XVI	DSMR-4 (90.50), BJV-44 (89.00), IS 2312 (87.61), IS 4515 (87.50), PKV Kranti (84.40), IS 12308 (84.25), IS 24492 (80.10), IS 29654 (79.00), IS 24139 (77.30) and IS 29568 (77.30)
6	Whorls per panicle	I, II, V, VI, XVI	IS 12308 (11.70), DSMR-4 (11.50), IS 12804 (11.50), IS 19445 (11.50), PKV Kranti (11.50), IS 29914 (11.30), IS 9108 (11.10), IS 23590 (11.00), BJV 44 (10.80) and IS 33353 (10.80)
7	Leaves per plant	I, II, IV, V, VI, XII	BJV 44 (12.00), IS 7987 (11.80), PKV Kranti (11.10), IS 24492 (10.50), IS 4581 (10.50), IS 19445 (10.20), M-35 (10.10), IS 29654 (9.90), IS 14290 (9.90) and IS 28313 (9.80)
8	Nodes per plant	I, II, IV, V, VI, XII	BJV 44 (12.60), IS 7987 (12.50), PKV Kranti (11.90), IS 4581 (11.20), IS 24492 (11.10), IS 29654 (10.70), IS 31043 (10.60), IS 24139 (10.60), IS 19445 (10.50), IS 29468 (10.40) and IS 14290 (10.40)
9	Plant height (cm)	I, II, IX	IS 30536 (130.26), IS 30383 (130.95), IS 12883 (134.04), IS 25249, (138.84), IS 30466 (144.24), IS 27912 (144.51), IS 9108 (158.37), IS 10302 (159.60), IS 29914 (160.79) and IS 16528 (165.17)
10	Stem girth (mm)	I, II, V, VI, IX, XII	PKV Kranti (16.20), IS 19389 (16.10), IS 22616 (16.10), BJV 44 (16.04), IS 25249 (15.80), IS 7987 (15.60), IS 27912 (15.40), IS 24175 (15.30), IS 30383 (15.20) and IS 29914 (15.00)
11	Panicle weight per plant (g)	I, IV, V, VI, XII, XV	IS 12735 (145.57), IS 7987 (129.30), BJV 44 (118.70), IS 9108 (115.37), PKV Kranti (112.00), IS 30466 (110.87), IS 2872 (110.70), IS 30383 (99.38), IS 5919 (99.00) and IS 4581 (95.50)
12	Grain yield per plant (g)	I, IV, V, VI, XII, XV	IS 12735 (139.66), IS 7987 (114.70), IS 9108 (107.69), PKV Kranti (106.03), IS 2872 (104.06), IS 31043 (96.66), BJV 44 (95.10), IS 30383 (91.05), IS 5919 (85.50) and IS 4581 (84.20)
13	1000 grain weight (g)	I,IV, V, VI, XII, XVI	IS 12735 (45.92), DSMR-4 (43.67), IS 4581 (43.14), IS 4515 (42.80), IS 30451 (41.82), IS 7987 (41.03), IS 27912 (40.86), IS 8012 (40.31), PKV Kranti (40.12) and BJV 44 (39.99)
14	Grains per panicle	I, II, V, XI, XII, XV	IS 30466 (3041.75), IS 12735 (3040.31), IS 9108 (2895.18), IS 7987 (2797.76), IS 2872 (2706.95), DSMR-8 (2706.46), PKV Kranti (2644.34), IS 24175 (2629.29), IS 15945 (2597.88) and IS 5919 (2568.22)
15	1000 grains volume (cc)	I, IV, V, VI, XII, XV, XVI	IS 12735 (36.00), DSMR-4 (35.25), BJV 44 (34.25), IS 7987 (34.00), IS 19445 (34.00), PKV Kranti (32.50), IS 29468 (32.50), IS 4581 (31.50), IS 26046 (31.00), M-35 (31.00) and IS 2872 (31.00)
16	Grain density	I, II, IX, XIII	IS 25249 (1.82), IS 20679 (1.75), IS 24139 (1.44), IS 15945 (1.44), IS 28313 (1.42), IS 8012 (1.42), IS 31043 (1.40), IS 23590 (1.40) and IS 14861 (1.40)
17	Grain length (mm)	I, II, III, VI, XV, XVI	DSMR-4 (5.21), IS 12735 (4.94), IS 32439 (4.90), IS 12804 (4.86), IS 19445 (4.82), IS 4515 (4.81), IS 30383 (4.78), BJV 44 (4.77), IS 30466 (4.76) and IS 19975 (4.74)
18	Grain width (mm)	I, II, VI, XII, XV, XVI	IS 7987 (4.97), DSMR-4 (4.59), IS 29392 (4.58), M-35 (4.53), IS 33353 (4.44), IS 12735 (4.32), IS 4698 (4.29), BJV 44 (4.25), IS 16528 (4.22) and IS 24462 (4.20)
19	Grain thickness (mm)	I, II, IV, VI, XII, XV	IS 7987 (3.22), IS 4581 (3.16), M-35 (3.14), IS 30451 (3.11), IS 2872 (3.05), IS 26046 (3.03), IS 29468 (3.02), IS 8012 (3.00), IS 12735 (2.98), IS 12883 (2.97) and IS 19445 (2.97)

width, and panicle weight for the selection of genotypes. It is reported in rice that single trait-based selection is not ideal to get transgressive segregants [22]. Hence, selection should be based on multiple traits rather than a single trait. The genotypes with high per se performance for panicle weight were distributed in the groups I, IV, V, VI, XII, and XV while the genotypes for 1000 grain weight were distributed in the clusters of I, IV, V, VI, XII, XVI. The genotypes which were early for days to 50% heading were distributed in clusters of I, II, VI, X, and XIII (Table 6). The crosses between the genotypes of two opposite clusters of panicle weight viz., IS 12735 (145.57 g), IS 7987 (129.30 g) and BJV 44 (118.70 g) and earliness such as IS 30451 (56.50 days), IS 20743 (59.00 days) and IS 14861(60.00 days) or the cross between the opposite clusters of 1000 grain weight *viz*., IS 12735 (45.92 g), DSMR-4 (43.67 g) and IS 4581 (43.14 g) and earliness could lead to high yielding and early flowering recombinants/hybrids. The genotypes in these clusters may give a high magnitude of heterosis upon crossing with other genotypes and may yield transgressive segregants in segregating generations. In rice, it is reported that hybrids between the genotypes of two opposite clusters of yield traits and earliness resulted in high-yielding hybrids with earliness [22].

Relation between genetic diversity, geographical diversity, and racial diversity

The genotypes recorded into different clusters were correlated with their geographical origin (countries) and their races. It can be seen from Table 3 that the genotypes recorded in a single cluster originated across the world and belong to all races and inter-races. No relationship between genetic and geographic diversity and genetic and racial diversity was found in the current investigation. The genotypes from different countries/geographic regions clustered together and vice versa i.e. genotypes from the same countries are segregated into different clusters (Table 3). Similarly, the genotypes belong to different races and inter-races clustered together. Previous literature [23] has also found that there is no relationship between genetic and regional diversity. It seems that the genotypes share a common pedigree and common allelic constitution and geographical boundaries do not contribute to genetic divergence. The present study suggests that geographical diversity and racial diversity does not associate with genetic diversity. Thus, the selection of genotypes of different geographical origins and from different races and involving them in the crossing program may or may not yield defined results.

Fertility restoration behavior

If the diverse genotypes have the maintenance and restoring ability on diverse male sterile lines *viz*., 104A, 401A, and M31-2A, it would be added advantage in the rapid development of parental lines. The restoration and maintenance behavior of the genotypes on different male sterile lines is presented along with the genotypes in different clusters (Table 3). On both of the male sterile sources (*milo* and *maldandi*), only a few lines were able to restore fertility (Table 7) while the majority of the genotypes exhibited zero percent seed set and turned out to be perfect maintainers (Table 8). The rest of the lines exhibited partial restoration (>0 to <90 % seed set on selfing). The highest number of maintainers were recorded on *maldandi* (M31-2A) male sterile source and displayed the complexity

of restoration. Among the restorers presented in Table 7, DSMR-8 and DSMR-4 were unique, diverse, restorers on *maldandi* (M31-2A) and exhibited good per se performance. Additionally, the DSMR-8 was able to restore on 104A also. These lines are the potential source for heterosis exploitation and also can be a good source for the restorer genes for the conversion program. A common maintainer IS 4581 was found to be solitary, diverse, and also exhibited good per se performance. It can be a new version of *milo* and *maldnadi* based male sterile line. Similarly, the maintainers *viz*., IS 7987, IS 12937, IS 15478, IS 25249, IS 28614 on *maldandi* were found to belong to solitary clusters and being diverse can be potent sources for the diversification of male sterile lines.

Table 7. List of identified restorers on different male sterile sources (>90 percent seed set on selfing)

SN.	Genotypes	On CMS lines
1.	IS 26046	104A & 401A
2.	IS 19389 and IS 995	104A
3.	IS 29335	401A
4.	IS 19975	M31-2A
5.	DSMR-8	104A & M31-2A
6.	DSMR-4	M31-2A

* Milo (104A and 401A), Maldandi (M31-2A)

Table 8. List of identified minicore based on fertility restoration of zero percent seed set

SN.	Genotypes	On CMS lines
1.	IS 26617, IS 15945, IS 24348, IS 4581, IS 4698, IS 9745, and IS 14290	104A, 401A & M31-2A
2.	IS 33353, IS 19445, IS 24462, and IS 24492	104A & 401A
3.	IS 28313, IS 8012, and IS 22720	104A & M31-2A
4.	IS 29568, IS 29654, and IS 29914	401A & M31-2A
5.	IS 25249, IS 29335, IS 29392, IS 30466, IS 27912, IS 2397, IS 14861, IS 15478, IS 15945, IS 19389, IS 7987, IS 22616, IS 24175, IS 25989, IS 30383, IS 30451, IS 30536, IS 31043, IS 24139, IS 4515, IS 12937, IS 28614, IS 995, IS 2872, IS 602, IS 10302, IS 12302, IS 12735 and IS 20743	M31-2A
6.	IS 21645, DSMR-4	104A
7.	None	401A

Conclusion

The heterosis and performance of the hybrids depend on the extent of genetic diversity in the parental lines. The genotypes IS 15478 and IS 12735 were discovered to belong to solitary clusters thereby unique and most diverse in the current study. Therefore, these genotypes may give good heterosis upon crossing. The maintainers, IS 7987 and IS 12937, and restorers, DSMR-8 and DSMR-4, on Maldandi, were discovered to be solitary, diverse, and to also demonstrate good per se performance. These lines can be used as a good source of yield and quality. The restorers can give restorer genes and the maintainers can be converted into new diverse male sterile lines, for the exploitation of the diversity through heterosis breeding by employing a male sterile system.

Conflict of interest

The authors declare no conflicts of interest.

References

[1] H. Doggett **(1988)**. Sorghum. 2nd edition Longman, Burnt Mill, Harlow, Essex, England.
[2] D. D. Rohrbach, H. M. Saadan, E. S. Monyo, J. A. B. Kiriwaggulu, K. Mtenga and F. Mwaisela **(2002)**. Comparative study of three community seed supply strategies in Tanzania. *Project Report*. In International Crops Research Institute for the Semi-Arid Tropics. Bulawayo.
[3] J. R. Harlan **(1971)**. Agricultural origins: Centres and non centres. Science, **174:** 468-474.
[4] Y. Kebede **(1991)**. The role of Ethiopian sorghum germplasm resources in the national breeding programme. In: J. M. M. Engels, J. G. Hawkes, M. Worede (eds.), Plant Genetic Resources of Ethiopia. Cambridge University Press, Cambridge, pp315-322.

[5] A. Teshome, B. R. Baum, L. Fahrig, J. K. Torrance, T. J. Arnason and J. D. Lambert **(1997)**. Sorghum [*Sorghum bicolor* (L.) Moench] landrace variation and classification in North Shewa and South Welo, Ethiopia. Euphytica, **97:** 255-263.
[6] J. F. Rami, P. Dufour, G. Trouche, G. Fliedel, C. Mestres, F. Davries and P. Blanchard et al., **(1998)**. Quantitative trait loci for grain quality, productivity, morphological and agronomical traits in sorghum (*Sorghum bicolar* L. Moench). Theor. Appl. Genet., **97:** 605-616.
[7] G. Hart, K. F. Schertz, Y. Peng and N. H. Syed **(2001)**. Genetic mapping of *Sorghum bicolor* (L.) Moench QTLs that control variation in tillering and other morphological character. Theor. Appl. Genet., **103:** 1232-1242.
[8] B. V. S. Reddy, A. A. Kumar, P. S. Reddy and M. Elangovan **(2008)**. Sorghum germplasm: Diversity and utilization. In Sorghum Genetic Enhancement: Research Process, Dissemination and Impacts; International Crops Research Institute for the Semi-Arid Tropics: Patancheru, Andhra Pradesh, India, pp153-169.
[9] Prabhakar, J. V. Patil and P. Sanjana Reddy **(2014)**. Rabi sorghum improvement: past, present and future. Karnataka J. Agric. Sci., **27:** 433-444.
[10] M. Jayaramachandran, N. Kumaravadivel, G. Kandasamy and S. Eapen **(2011)**. Comparison of genetic variability induced by radiation and tissue culture in sorghum. Int. J. Bio-Res. Stress Manag., **2:** 329-311.
[11] G. W. Snedecor and W. G. Cochran **(1967)**. One-way classifications: Analysis of variance. In: Statistical Methods (Cochran WG ed.), Iowa State University Press. Ames,
[12] P. C. Mahalanobis **(1936)**. On the generalizes distance in statistics. Proc. Nat. Inst. Acad. Sci., India, **2:** 49-55.
[13] B. H. V. Prasad, B. D. Biradar and L. K. Verma **(2018)**. Genetic diversity studies among maintainers and restorers on milo and maldandi cytoplasm from minicore collection of sorghum using D2 statistics. Elect. J. Plant Breed., **9:** 233-243.
[14] C. V. S. Kumar, C. Sreelakshmi and D. Shivani **(2010)**. Genetic diversity analysis in rabi sorghum (*Sorghum bicolor* L. Moench) local genotypes. Elect. J. Plant Breed., **1:** 527-529.
[15] Q. Zhang, Y. J. Gao, S. H. Yang, R. A. Ragab, M. A. S. Maroof and Z. B. Li **(1994)**. A diallel analysis of heterosis in elite hybrid rice based on RFLPs and microsatellites. Theor. Appl. Genet., **89:** 185-192.
[16]W. G. Hill and T. F. C. Mackay **(2004)**. D. S. Falconer and Introduction to Quantitative Genetics. Genetics, **167:** 1529-1536.
[17] J. M. Thoday **(1960)**. Effects of disruptive selection: III Coupling and repulsion. Heredity, **14:** 35-49.
[18] D. Shivani and Ch. Sreelakshmi **(2015)**. Germplasm evaluation of rabi sorghum, *Sorghum bicolor* (L.) Moench. J. Global Biosci., **4:** 3150-3153.
[19] S. Sinha and N. Kumaravadivel **(2016)**. Understanding genetic diversity of sorghum using quantitative traits. Scientifica, **2016:** 3075023. doi: 10.1155/2016/3075023.
[20] S. B. Doijad, A. B. Bagade and A. W. More **(2016)**. Evaluation of sorghum germplasm for genetic diversity using D2 statistics. Elect. J. Plant Breed., **7:** 934-938.
[21] K. Tesfaye **(2017)**. Genetic diversity study of sorghum (*Sorghum bicolor* (L.) Moench) genotypes, Ethiopia .Acta Univ. Sapientiae, Agric. Environ., **9:** 44-54.
[22] U. Kulsum, M. D. J. Hasan, H. Begum, M. M. Billah and H. Rahman **(1970)**. Genetic diversity of some restorer lines for hybrid rice development. Bangladesh J. Agric. Res., **36:** 21-28.
[23] S. A. Rao, M. H. Mengesha and C. R. Reddy **(1989)**. Identification, characterization and geographic distribution of male-sterility restorer and maintainer lines from diverse pearl millet germplasm. Euphytica, **40:** 155-159.