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Genetic Divergence in Finger Millet (*Eleusine coracana* (L.) Gaertn.)

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A B S T R A C T

An experiment was undertaken by utilizing forty finger millet genotypes for eleven yield and yield contributing characters to assess genetic divergence. The analysis of variance has shown that there was significant variation among the genotypes in all the traits. The multivariate analysis carried out using Mahalanobis D2-statistics, indicated wider genetic diversity in the genotypes of finger millet. Out of six cluster formed, cluster I was largest with twenty three genotypes, followed by cluster II with eight genotypes, cluster V with four genotypes, cluster VI with three and III, IV were mono-genotypic. The clustering pattern indicated absence of relationship between genetic diversity and geographical origin of the genotypes. The maximum inter cluster distance was observed between cluster II and VI (D^2= 26.69) while, lowest divergence was noticed between cluster I and IV (D^2=9.43). Maximum intra cluster distance observed within cluster VI (D^2=9.18) while lowest intra cluster distance was observed within cluster II (D^2=6.91). The variance for cluster means were high for grain iron content (41.54),followed by grain yield per plant (27.82), main ear head length (11.41), 100 ml volume weight (9.23) and was low for number of fingers per earhead, grain calcium content, number of tillers per plant, number of productive tillers per plant. Based on inter-cluster distances, cluster mean and per se performance, and divergence class the genotypes viz., DHFM-36, DHFM-13, DHFM-18, DHFM-3, DHFM-12 were distinct and diverse and can be classified as promising genotypes. These five genotypes can be used for inter-crossing to obtain heterosis and also wider variability in moth bean. Hybridization between the genotypes of cluster VI with the genotypes of cluster III may result in exploiting more heterosis with maximum genetic divergence and are likely to produce desirable transgressive segregants in segregating generations for further crop improvement.

Introduction

Millet is a collective term referring to a number of small seeded annuals grasses that are cultivated as grain crops, primarily on marginal lands in dry areas in temperate, subtropical and tropical regions. Finger millet, (*Eleusine coracana*), is also known as African millet, ragi, nachani, nagali. It is important staple food in parts of eastern and Central Africa and India. Finger millet is very adaptable to a wide range of environmental and climatic conditions, thrives at higher elevations than most other tropical cereals and

tolerates salinity better than moist cereals. It is important cereal in Karnataka. It is intensively grown in Karnataka, Tamil Nadu, Andhra Pradesh, Orissa, Bihar, Gujarat, Maharashtra and in the hilly regions of Uttar Pradesh, Himachal Pradesh with a total area of 2.5 million hectares and 2.2 million tones of production. Finger millet (*Eleusine coracana* (L.) Gaertn.), is one among highly utilized belong to family Poaceae and it ranks 4th in the importance of world. Finger millet is originated from Ethiopia. It is allopolyploid with chromosome number 2n=4x=36 and evolved from a cross between two diploid species *Eleusine indica* (AA) and *Eleusine floccifolia* or *Eleusine tristachya* (BB) as genome contributors (Hiremat and Salimath, 1992). Finger millet is mostly self pollinating with some amount of cross pollination (1%) mediated by wind (Jansen and Ong, 1996, Purseglove, 1972). In India, the total area under finger millet was 1.9 million hectares with production of 1.9 million tonne and productivity 1661 kg/ha (2017). Out of these it is cultivated in Maharashtra is 966 ha and the production is 1008 tonne and productivity under Maharashtra state was 1043 kg/ha. (2014-2015).

Genetic diversity which is pre-requisite for any successful breeding programme is of paramount importance. Genetic divergence among the parents play a vital role in cultivar improvement because a cross involving genetically diverse parents is likely to generate more variability in segregating generations, and also which can be used for the desired improvement. Generally, plant breeders select the parents on the basis of phenotypic diversity. Hence the knowledge of genetic diversity among the parents with respect to characters which are to be improved is essential. Keeping these things in the view, an effort has been made in the present study to evaluate a set of moth bean genotypes with the objective to study the nature and magnitude of divergence among the genotypes of finger millet.

Materials and Methods

The experimental material comprising forty genotypes of finger millet were grown in Randomized Block Design with three replications at the research farm of Department of Genetics and plant breeding, College of Agriculture, Dhule, during Kharif season of 2017. The seeds were sown by dibbling. Each entry was represented by single row of 22.5 m length with spacing of 10 cm between rows. Data were recorded on five randomly and competitive plants of each genotype from each replication for eleven quantitative characters viz., days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, number of productive tillers per plant, main earhead length (cm), number of fingers per earhead, 100 ml volume weight (g), grain yield per plant (g), grain iron content (mg/100 g), grain calcium content (mg/100 g). Effective method suggested by Mahalanobis (1936) known as "Mahalanobis D2 statistics" or "D^2 technique" is widely used to know genetic diversity in the germplasm. It was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters and a logical grouping of genotypes following Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance for eleven characters indicated that the genotypes used in the present studies were significantly different (Table 1). The mean performances of 40 genotypes of finger millet for eleven characters studied are presented in Table 2. The genotype DHFM-6 (77.66 days) was the earliest for flowering (78 days) and genotype DHFM-6 (115.00 days) days to maturity (115

days). The genotype DHFM-12 (137.33 cm) was found tall, genotypes DHFM-18 (8.46) exhibited significantly higher number of tillers per plant, genotype DHFM-18 (8.10) produced maximum number of productive tillers per plant, genotype DHFM-39 (13.00 cm) produced maximum length of main earhead, genotype DHFM-31 (10.33) recorded maximum number of fingers per earhead, genotype DHFM-27 (119.33 g) recorded maximum 100 ml volume weight, genotype DHFM-18 (39.33 g) recorded highest grain yield, genotype DHFM-3 (12.42 mg) recorded significantly high iron content, genotype DHFM-40 (416.33 mg) recorded significantly high calcium content.

On the basis of D^2 values, the forty genotypes evaluated for eleven characters were grouped into six clusters by using the Tocher's method as described by Rao (1952). Cluster I was largest with 23 genotypes followed by cluster II (8 genotypes), cluster V (4 genotypes) and cluster VI (3 genotypes), while clusters III and IV were monogenotypic. In the present investigation grouping of genotypes into 6 clusters suggested the presence of substantial amount of genetic diversity in the material under investigation. The clustering pattern and the ecogeographical regions of origin of each line are given in Table 1 and 3. Cluster I was the largest including 23 lines indicates that there was no association between clustering pattern and ecogeographical distribution of the cultures. Murty and Arunachalam (1966) and Somayajulu *et al.,* (1970) while working with different crops, reported that geographical distribution does not necessary reflect genetic divergence. Cluster II which include 8 lines, cluster V include 4 lines and cluster VI include 3 lines under study had varieties from different eco-geographical regions, thus supporting the view that geographic distribution and genetic divergence do not follow the same trend. Wide range of diversity was reported by many workers while evaluating finger millet genotypes Naik (1991), Rao (1992), Sheriff (1992), Bandyopadhyay (1998), Vadivoo *et al.*, (1998), Satish (2003), Sripichitt *et al.*, (2006), Bedis *et al.*, (2007), Sathish *et al.*, (2007b), Kadam (2007), Anantharaju *et al.*, (2008), Kadam (2008), Prabhu *et al.*, (2008), Kumar *et al.*, (2010), Sahu *et al.*, (2012), Karad *et al.*, (2013), Suryanarayana *et al.*, (2014), Kumari *et al.*, (2015), Negi *et al.*, (2017).

The maximum intra cluster distance was observed for cluster IV (D^2 =5.12) followed by cluster III (D^2=4.90) suggesting that genotypes present in these clusters might have different genetical architecture (Table 4). However, lowest intra cluster distance was observed in cluster I (D^2=3.85) indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from common gene pool. Cluster V, VI and VII showed no intra cluster distance due to its monogenotypic nature.

Maximum inter cluster distance was observed between cluster II and VI (D^2=26.69) followed by cluster IV and VI (D^2=25.37), cluster I and IV (D^2= 22.90), cluster II and V (D^2=17.84), cluster III and VI (D^2= 17.31), cluster V and VI (D^2=16.91), cluster II and IV (D^2=15.88) cluster II and III (D^2=14.75) indicating, wide divergence among these clusters. These also suggest that genotype present in one cluster differ entirely from those presenting other clusters. The minimum inter cluster distance was found between cluster III and IV (D^2 =13.61), cluster I and V (D^2= 11.66), cluster IV and V (D^2=11.44), cluster I and II (D^2=11.26), cluster I and III (D^2 =11.08), cluster III and V (D^2=10.87) cluster I and IV (D^2= 9.43). The less inter cluster distance between these clusters revealed that genetic constitution of genotypes had close proximity.

Based on mean performance of clusters for 11 characters (Table 5). It was observed that cluster VI exhibited the highest grain calcium content and was characterized by days to maturity, 100 ml volume weight, days to 50per cent flowering, plant height, grain yield per plant, grain iron content, main earhead length, number of fingers per earhead, number of tillers per plant, number of productive tillers per plant. All these characters appeared to have played important role in determining grain yield of these cluster. Cluster I and cluster VI showed nearly comparable grain yield. Cluster II was characterized by less days to 50 per cent flowering, days to maturity, number of tillers plant, number of productive tillers per plant, main earhead length, grain yield per plant. Cluster IV was characterized by high days to 50 per cent flowering, days to maturity, number of tillers per plant, number of productive tillers per plant, number of fingers per earhead, grain yield per plant.

On the basis of mean performance of different clusters, it was observed that cluster IV, VI, and III were performing well for most of the characteristics.

The variance of cluster mean provides information on relative importance of different characters towards grain yield. The present study revealed that grain iron content (41.54 per cent) contributed more to genetic diversity as reflected from the Table 6 which was followed by grain yield per plant (27.82), main earhead length (11.41), 100 ml volume weight (9.23), grain calcium content (3.72), number of fingers per earhead (3.59), number of tillers per plant (1.03), number of productive tillers per plant (1.03), days to 50 per cent flowering (0.26), plant height (0.26), days to maturity (0.13). These results were agreement with the observations of Jayaprakash Naik (1991) and Satish (2003) for main earhead length and number of fingers per earhead, Anantharaju and Meenakshiganesan (2008) main ear length followed by total number of fingers per earhead, grain yield per plant, grain yield per plant, main earhead lenght, number of tillers per plant, number of productive tillers per plant in finger millet (*Eleusine coracana* (L.) Gaertn.) (Fig. 1–3).

Table.1 Analysis of variance for eleven characters in finger millet

Sr. No	Characters	Mean sum of square		
		Replication	Genotype	Error
1	Days to 50% flowering	33.908	279.59**	16.429
2	Days to maturity	33.033	393.21**	35.272
3	Plant height (cm)	41.308	415.080**	45.445
4	No. of tillers / plant	0.582	7.679**	0.308
5	No. of productive tillers / plant	0.410	6.308**	0.210
6	Main earhead length (cm)	0.290	11.546**	0.272
7	No. of fingers / earhead	0.614	6.986**	0.374
8	100 ml volume weight (gm)	16.808	662.402**	14.859
9	Grain yield / plant (gm)	8.258	210.99**	4.053
10	Grain iron content (mg/100 gm)	0.069	19.561**	0.069
11	Grain calcium content (mg/100 gm)	1210.40	11756.44**	554.75

*, ** Indicates significance at 5% and 1% level, respectively.

Table.2 Mean performance of finger millet genotype

Sr. No	Genotypes	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No. of tillers / plant	No of productive tillers /plant	Main earhead length (cm)	No of fingers / earhead	100 ml volume weight	Grain yield / plant	Grain iron content (mg / 100 gm)	Grain calcium content (mg / 100gm)
1	DHFM-1	88.33	125.00	89.00	5.44	5.40	7.66	6.33	66.00	21.66	3.00	284.00
2	DHFM-2	94.66	125.33	95.33	6.66	6.00	7.33	7.33	113.66	17.90	11.86	390.00
3	DHFM-3	85.00	125.33	88.00	6.00	5.33	12.33	7.00	76.00	28.70	12.42	383.33
4	DHFM-4	94.33	129.66	101.00	5.66	5.33	8.00	6.33	95.66	19.80	5.52	354.33
5	DHRM-5	86.66	126.00	95.00	6.66	5.33	10.00	6.66	61.00	18.50	4.65	233.33
6	DHFM-6	77.66	115.00	117.33	2.67	2.33	6.00	5.00	107.66	7.00	3.75	322.00
7	DHFM-7	82.33	123.66	116.33	3.66	3.67	8.33	4.66	71.33	9.00	5.24	343.33
8	DHFM-8	93.00	127.66	120.00	6.66	5.33	10.00	6.66	72.00	20.66	4.31	308.00
9	DHFM-9	83.00	127.33	112.66	3.66	3.00	6.00	6.33	57.00	8.33	3.41	326.00
10	DHFM-10	87.66	127.66	83.66	4.66	4.66	9.00	9.33	79.00	15.20	3.66	254.66
11	DHFM-11	91.66	132.00	85.66	4.00	3.66	7.00	6.66	73.33	21.80	4.32	205.00
12	DHFM-12	92.33	130.00	137.33	5.66	5.66	8.33	6.00	61.00	20.00	12.35	402.66
13	DHFM-13	96.33	125.66	96.00	6.66	6.33	9.66	8.33	72.00	26.00	6.85	277.00
14	DHFM-14	82.33	122.66	111.66	5.66	5.00	8.33	5.00	82.00	12.00	5.12	180.00
15	DHFM-15	83.00	125.66	111.66	4.00	4.00	9.00	4.00	82.00	11.00	2.84	397.00
16	DHFM-16	83.00	123.33	106.00	4.00	3.66	6.00	5.33	63.00	6.33	3.45	402.00
17	DHFM-17	94.00	142.33	110.33	7.00	5.66	7.33	6.33	65.00	19.33	4.20	415.66
18	DHFM-18	93.00	140.66	104.66	8.46	8.10	10.00	9.06	67.33	39.33	4.71	408.00
19	DHFM-19	80.00	117.33	94.33	3.00	2.67	7.00	8.00	69.66	7.00	3.83	322.00
20	DHFM-20	79.33	116.66	92.66	2.00	2.00	8.00	6.00	106.00	7.00	3.68	326.00
21	DHFM-21	92.00	140.66	101.33	6.46	6.13	7.66	7.66	72.00	21.00	4.87	247.00
22	DHFM-22	91.00	134.66	92.00	5.46	5.13	7.33	9.00	72.00	18.00	3.39	331.00
23	DHFM-23	87.00	127.66	75.33	6.00	5.33	6.33	6.66	74.66	14.00	2.22	277.00
24	DHFM-24	92.33	132.00	104.00	6.00	5.00	9.00	6.33	63.33	18.00	3.61	292.00
25	DHFM-25	92.33	131.00	104.33	4.00	3.67	6.66	8.66	66.00	18.66	3.40	305.00

26	DHFM-26	97.66	137.33	101.66	6.66	6.13	12.26	7.33	80.00	23.40	3.32	259.00
27	DHFM-27	91.00	140.00	95.00	6.06	5.40	9.00	5.00	119.33	19.20	5.58	364.00
28	DHFM-28	85.00	125.00	99.00	3.66	3.66	6.00	8.40	80.00	10.00	1.68	331.00
29	DHFM-29	92.66	131.33	102.00	6.00	5.20	8.33	5.00	80.66	19.66	3.79	268.33
30	DHFM-30	92.66	129.33	101.33	5.00	4.33	6.67	10.00	90.00	15.00	5.61	261.00
31	DHFM-31 (Phule Nachani)	109.33	150.66	104.33	6.00	5.33	8.67	10.33	82.00	32.40	5.70	337.00
32	DHFM-32	113.00	153.33	88.00	5.00	5.00	10.33	7.00	96.00	31.10	1.52	277.00
33	DHFM-33	103.33	150.00	118.00	7.00	6.50	12.00	7.00	74.00	28.80	3.48	241.00
34	DHFM-34	106.00	148.00	111.66	6.66	6.33	11.33	6.33	70.00	28.20	4.62	243.00
35	DHFM-35	104.33	144.33	91.66	6.66	6.67	9.33	7.33	80.00	30.80	2.61	207.00
36	DHFM-36	112.33	152.33	106.00	8.00	7.40	8.40	10.00	73.33	33.90	2.46	295.00
37	DHFM-37	107.33	154.66	103.00	7.40	7.00	10.80	7.30	64.00	26.20	4.39	250.00
38	DHFM-38	110.00	156.66	100.33	7.50	7.20	11.00	7.66	63.33	27.00	3.40	290.00
39	DHFM-39	105.00	151.33	115.00	6.80	6.40	13.00	7.66	66.00	30.00	2.94	295.00
40	DHFM-40	105.00	142.33	106.66	8.00	7.50	12.00	6.33	64.00	24.80	8.48	416.33
	G. Mean	93.43	134.04	102.23	5.60	5.17	8.78	7.03	76.78	20.16	4.65	308.05
	S.E. ±	2.34	3.42	3.89	0.32	0.26	0.30	0.35	2.22	1.16	0.15	13.59
	C.D. at 5 %	6.58	9.65	10.95	0.90	0.74	0.84	0.99	6.26	3.27	0.42	38.28
	C.V. (%)	4.33	4.43	6.59	9.91	8.87	5.94	8.69	5.02	9.98	5.64	7.64

Table.3 Grouping of forty finger millet genotypes into different clusters

Sr. No.	Cluster	No. of genotypes	Name of genotypes
1	I	23	DHFM-34, DHFM-37, DHFM-33, DHFM-38, DHFM-26, DHFM-39, DHFM-35, DHFM-8, DHFM-5, DHFM-29, DHFM-21, DHFM-24, DHFM-10, DHFM-22, DHFM-17, DHFM-11, DHFM-4, DHFM-25, DHFM-1, DHFM-23, DHFM-14, DHFM-30, DHFM-32.
2	II	8	DHFM-9, DHFM-16, DHFM-19, DHFM-28, DHFM-15, DHFM-7, DHFM-20, DHFM-6
3	III	1	DHFM-27
4	IV	1	DHFM-36
5	V	4	DHFM-13, DHFM-31, DHFM-40, DHFM-18,
6	VI	3	DHFM-3, DHFM-12, DHFM-2

Table.4 Average intra and inter cluster distance (D^2 values) for eleven characters in finger millet

Clusters	I	II	III	IV	V	VI
I	7.68	11.26	11.08	9.43	11.66	22.90
II		6.91	14.75	15.88	17.84	26.69
III			0.00	13.61	10.87	17.31
IV				0.00	11.44	25.37
V					8.71	16.91
VI						9.18

(Underlined figures indicate intra-cluster D^2 values.)

Table.5 Cluster means for eleven characters in seven clusters of forty finger millet genotypes

Sr. No	Characters	Cluster average						Cluster mean
		I	II	III	IV	V	VI	
1	Days to 50 per cent flowering	95.86	81.71	91.00	112.33	100.92	90.67	95.41
2	Days to maturity	137.19	121.75	140.00	152.33	139.83	126.89	136.33
3	Plant height (cm)	100.26	106.25	95.00	106.00	102.92	106.89	102.88
4	No. of tillers/plant	5.93	3.29	6.07	8.00	7.28	6.11	6.11
5	No. of productive tillers/plant	5.41	3.17	5.40	7.40	6.82	5.67	5.64
6	Main earhead length (cm)	9.10	7.04	9.00	8.40	10.08	9.33	8.82
7	No. of fingers/ earhead	7.14	5.97	5.00	10.00	8.52	6.78	7.23
8	100 ml volume weight	74.17	79.58	119.33	73.33	71.33	83.56	83.55
9	Grain yield/plant (gm)	21.69	8.21	19.20	33.90	30.63	22.20	22.63
10	Grain iron content (mg/100 gm)	3.83	3.49	5.59	2.46	6.44	12.21	5.67
11	Grain calcium content (mg/100 gm)	273.03	346.17	364.00	295.00	359.58	392.00	338.29

Table.6 Relative percent contribution of different characters towards total genetic divergence in finger millet

Sr. No.	Characters	No. of times ranked 1St	Percent contribution
1	Days to 50 per cent flowering	2	0.26
2	Days to maturity	1	0.13
3	Plant height (cm)	2	0.26
4	No. of tillers/plant	8	1.03
5	No. of productive tillers/plant	8	1.03
6	Main earhead length (cm)	89	11.41
7	No. of fingers/ earhead	28	3.59
8	100 ml volume weight	72	9.23
9	Grain yield/plant (gm)	217	27.82
10	Grain iron content (mg/100 gm)	324	41.54
11	Grain calcium content (mg/100 gm)	29	3.72

Fig.1 Clustering by Tocher method

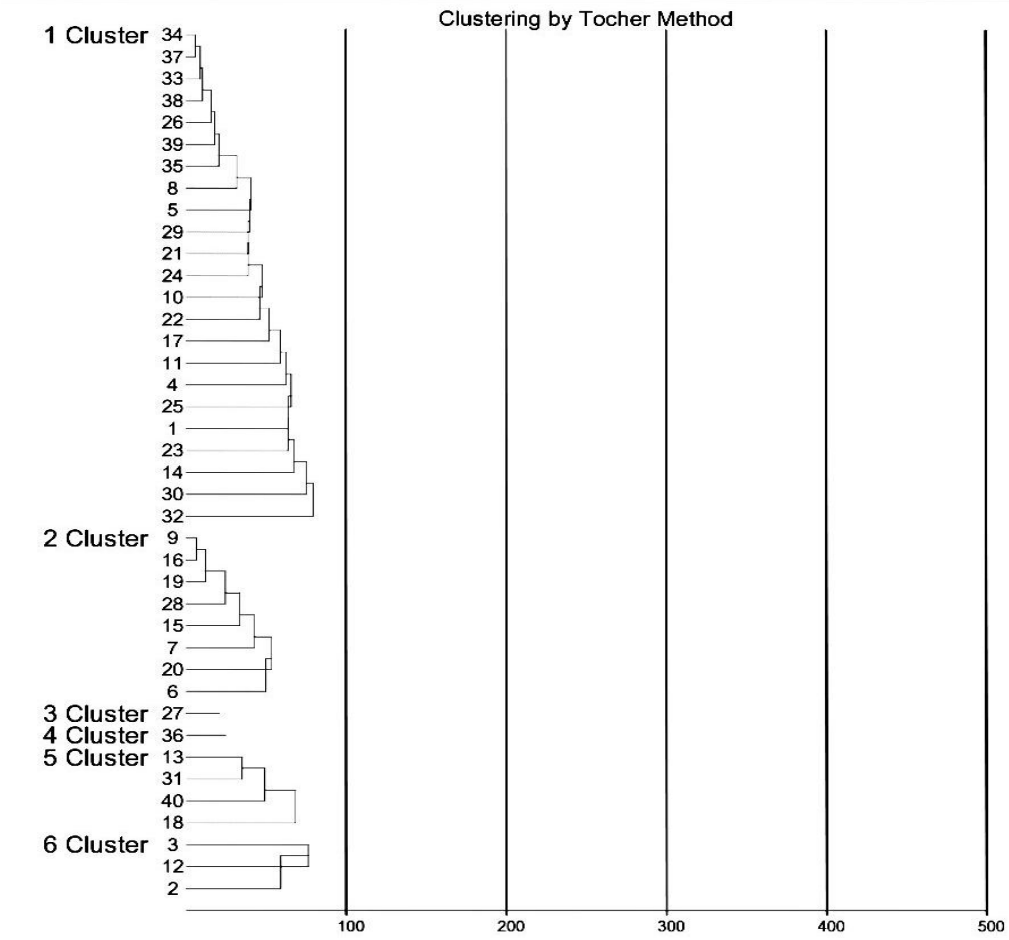
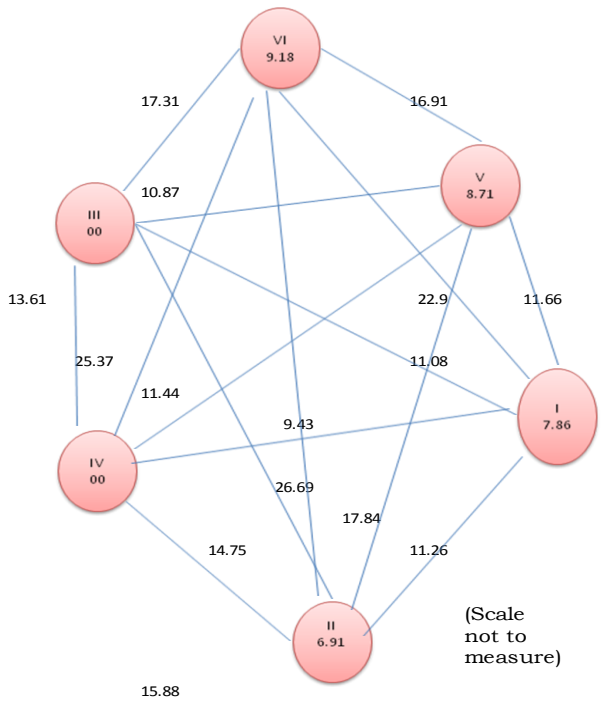


Fig.2 Divergence classes

DC 4	DC 3	DC 2	DC 1	
↓	↓	↓	↓	↓
X	m-s	M	m+s	Y
(6.91)	(8.53)	(14.18)	(19.83)	(26.69)

M= The mean of seven clusters and four intra-clusters (as monogenotypic cluster III and IV had no intra-cluster distance) was 14.18.
X= Minimum value of distance 6.91.
Y=Maximum value of distance 26.69.
S=Standard deviation 5.65.
m-s= Mean - Standard deviation.
m+s= Mean + Standard deviation.

Fig.3 Cluster diagram of forty germplasm in Finger millet



The magnitude of contribution by days to 50 per cent flowering, days to maturity, plant height was low.

The mean of six clusters and four intra-clusters (as monogenotypic cluster III and VI had no intra-cluster distance) was 14.18 and standard deviation 5.65. The minimum (X) and maximum (Y) values among these distances were 6.91 and 26.69, respectively.

Grouping of cluster pairs into the divergence class (DC) is presented in Figure 2. On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC2 and DC3. While crossing among the genotypes of a cluster, the per se performance of the genotypes for different traits such as earliness (days to 50% flowering and days to maturity), plant height, number of tillers per plant, number of productive tillers per plant, main earhead length, number of fingers per earhead, 100 ml volume weight, grain yield per plant, grain iron content, grain calcium content etc. should be taken into account so, that desirable transgressive segregants would be obtained following after hybridization.

The present study revealed no parallelism between genetic divergence and geographical distribution of genotypes which was demonstrated by grouping of genotypes from same origin into different clusters separated by high genetic distance. This suggested, that genetic drift and selection in different environments may cause geographical distances.

Considering inter-cluster distances, cluster mean and per se performance, and divergence class the genotypes viz., DHMB-36, DHFM-13, DHFM-18, DHFM-3, DHFM-12 were distinct and diverse and can be classified as promising genotypes. These genotypes can be used for intercrossing to obtain heterosis and also wider variability in moth bean. Hybridization between the genotypes of cluster II with the genotypes of cluster IV may result in exploiting more heterosis with maximum genetic divergence and are likely to produce desirable transgressive segregants in segregating generations for further crop improvement.

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