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Genetic Analysis of Finger Millet (*Eleusine coracana* (L.) Garetn) Germplasm through Principle component Analysis and D^2 Cluster Analysis in Himachal Pradesh

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ABSTRACT: A field experiment was conducted on 37 genotypes including 2 local checks were grown in a Randomized Block Design (RBD) with three replications during *kharif*, 2022 at Research Farm of School of Agriculture, Abhilashi University Chail chowk Mandi, Himachal Pradesh to study the nature and magnitude of divergence by using Mahalanobis D^2 statistics. The observations for 19 morphological characters was recorded. Two techniques, principal component analysis and cluster analysis were applied. Principal component analysis indicates that four principal components PC-1, PC-2, PC-3 and PC-4 explains 30.76%, 21.65%, 16.14% and 11.23% respectively of the total variation. Principal component analysis showed that first principle component had maximum of 30.76% of total variation, while the first four principle component axes together explained 82.78% of variations. On the basis of Euclidean distance, 37 genotypes were grouped into 7 different clusters using cluster analysis. Cluster 1 had highest number of genotypes followed by cluster 3 with 4 genotypes, cluster 2, 4, 5, 6 and 7 with one genotype. Therefore, there was a significant diversity among these clusters and genotypes from these clusters could be used as parents for hybridization. Grain yield contributed maximum toward the genetic divergence in 37 genotypes of finger millet. For majority of the desirable traits, including biological yield, 100 seed weight, flag leaf blade width, peduncle length and number of fingers per ear, cluster 5 exhibited the highest cluster mean. Clustering through D^2 analysis revealed maximum inter cluster distance between cluster 6 and 7 (5053.66) followed by cluster 6 and 4 (4962.99), cluster 2 and 6 (4524.50), 1 and 6 (4208.39), 5 and 7 (4073.57) cluster 2 and 7 (3715.87). The result of the present study could be exploited in planning and execution of future breeding strategy in finger millet.

Keywords: Principal component analysis, Finger millet, Cluster analysis, RBD, Euclidean distance, Genotype, Hybridization.

INTRODUCTION

Millets have always remained one of the staple food and serve as a vital crop to ensure food security in semi-arid areas. In the past, millets were associated with lower socio economic classes. *Eleusine coracana* L. Garetn, is also known as finger millet, is an Allotetraploid (2n=4X=36) minor grain millet from the genus *Eleusine* and family Poaceae. The name finger millet is originating from the panicle's finger like branching. It is also known as bird's foot millet, coracana, african millet, kurukkan andragi. In Himachal Pradesh it is commonly known as kodra. Finger millet is originated from East Africa (Ethiopian and Ugandan highlands) and came to India around 200 BCE. India is recognized as a secondary centre of diversity due to the extensive variability created by the cultivation of finger millet over a long period of time under a variety of agro climatic condition, as well as the connected effects of natural and human selection. After sorghum and pearl millet, it is the third most important cereal crop in the nation among small millets. In India, it is primarily grown as a rainfed crop because of its valuable food grain. Finger millet plant is an annual plant that grows uprightly. Its root system is made up of many adventitious fibrous roots that have the capacity to

efficiently and thoroughly absorb moisture from the soil and crop is generally self -fertilized. The seeds are typically reddish brown in colour and small in size. For most varieties, finger millet grows best with 12 hours of day light per day and hence known as short day plant. Though compared with other millets like pearl millet and sorghum, it is generally considered as a drought tolerant crop, it actually prefers moderate rainfall (>500mm annually). Finger millet is a valuable cereal due to the high nutritional content of the grains and its excellent storage properties. It is also known as 'Nutritious millet' because the grains have more nutrients than many cereals. It is a good source of calcium, iron and other minerals. Finger millet grain can be stored for years without storage pest infestation which makes it a perfect food grain commodity for famine-prone areas. Although the grains are used for human consumption, their higher fibre content helps to prevent intestinal cancer, high cholesterol and constipation. Hence, diabetics are advised to eat finger millet and other small millets instead of rice. The crop residues are great source of dry matter for livestock especially in dry season. Finger millet straw has up to 61% digestible nutrients overall, hence making it an excellent fodder source. In India, finger millet is cultivated in an area of 11.94 lakh ha with a production of 19.85 lakh tonnes and average productivity of 1662 kg per ha (Anonymous, 2019).

Path analysis studies revealed that plant height and main ear length showed true relationship by establishing positive association and direct effect on grain yield per plant both at genotypic and phenotypic levels and number of productive tillers per plant, days to 50% flowering and number of fingers per ear at genotypic level and days to maturity at phenotypic level (Jyothsna *et al.,* 2016).

Major finger millet growing states in India are Karnataka followed by Uttrakhand, Maharashtra, Tamil Nadu, Andhra Pradesh, Orissa, Gujarat, Jharkhand and Bihar. A comparative study has been made to assess the nature and magnitude of genetic divergence for yield and its components in finger millet and also to identify divergent parents from distantly related clusters for suitable hybridization. In plant breeding, genetic diversity plays an important role to exploit heterosis or to generate productive recombinants. Assessment of a large number of germplasm for genetic diversity is of immense importance in selection of diverse genotypes for hybridization programme. Therefore, realising the importance of germplasm in the development of desirable varieties, breeders are now looking for more diverse forms from various sources for further augment the yield potential of the genotypes.

MATERIAL AND METHODS

The experiment was carried out at the Research Farm of School of Agriculture, Abhilashi University Mandi, Himachal Pradesh during *kharif* 2022. The experimental farm is situated at 31.5591555 latitude and 77.009466 longitude at an elevation of 2065 m. Agro-climatically, the location represent the mid hill zone of Himachal Pradesh (Zone II) and is characterized by humid sub humid- temperate climate with high mean annual rainfall (1876mm). The soil is acidic in nature with pH ranging from 5.0 to 5.6 and soil texture is silty clay loam. The experimental material for the present investigation consisted of 37 finger millet genotypes, out of which 35 finger millet genotypes was procured from IIMR, Hyderabad and 2 local checks were collected from Chachyot, Himachal Pradesh. The list of genotypes along with their source is given in Table 1. A Randomized Block Design (RBD) with three replication was used to carry out the experiment. Each genotype was raised in two rows with row length 1.2 m each and row to row and plant to plant spacing 25×8 and 30cm at a depth of 2-3cm in each replication, respectively. All the genotypes were randomized separately in each replication. The data was recorded from five randomly selected plants from each genotype in each replication.

Table 1: Accession and source of Finger Millet used in this study.

Sr. No.	Accession	Source
1.	IC-0344943	IIMR Hyderabad
2.	IC-0345088	IIMR Hyderabad
3.	IC-0392499	IIMR Hyderabad
4.	IC-0345134	IIMR Hyderabad
5.	IC-0345085	IIMR Hyderabad
6.	IC-0344951	IIMR Hyderabad
7.	IC-0257869	IIMR Hyderabad
8.	IC-0345135	IIMR Hyderabad
9.	IC-0344953	IIMR Hyderabad
10.	IC-0345148	IIMR Hyderabad
11.	IC-0382639	IIMR Hyderabad
12.	IC-0345080	IIMR Hyderabad
13.	IC-0345091	IIMR Hyderabad
14.	IC-0283828	IIMR Hyderabad
15.	IC-0344841	IIMR Hyderabad
16.	IC-0344954	IIMR Hyderabad
17.	IC-0392497	IIMR Hyderabad
18.	IC-0344955	IIMR Hyderabad
19.	IC-0392487	IIMR Hyderabad
20.	IC-0356087	IIMR Hyderabad
21.	IC-0344952	IIMR Hyderabad
22.	IC-0345138	IIMR Hyderabad
23.	IC-0344944	IIMR Hyderabad
24.	IC-0345111	IIMR Hyderabad
25.	IC-0345082	IIMR Hyderabad
26.	IC-0383629	IIMR Hyderabad
27.	IC-0345107	IIMR Hyderabad
28.	IC-0345147	IIMR Hyderabad
29.	IC-0392505	IIMR Hyderabad
30.	IC-0344956	IIMR Hyderabad
31.	IC-0283679	IIMR Hyderabad
32.	IC-0391548	IIMR Hyderabad
33.	IC-0344950	IIMR Hyderabad
34.	IC-0392493	IIMR Hyderabad
35.	IC-0392492	IIMR Hyderabad
36.	Local-1	Chachyot (H.P)
37.	Local-2	Chachyot (H.P)

The mean value of these plants was computed and used for statistical analysis. For characterization of different genotypes of finger millet following observations were recorded on visual assessment basis *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of tillers per plant, flag leaf blade length (cm),

flag leaf blade width (cm), flag leaf sheath length (cm), peduncle length (cm), number of fingers per ear, total number of ears per plant, finger length (cm), finger width (cm), length of longest finger (cm), width of longest finger (cm), production per plant (g), grain yield (g), biological yield (g), 100 seed weight (g), harvest index (%). PCA and D^2 analysis were calculated as per Hotelling (1933); Mahalanobis (1936).

RESULT AND DISCUSSION

A. Principle component analysis

In the present study, principal component analysis for 19 quantitative traits revealed six principal components out of which maximum variability was found in first four components which contributed to 82.78% variance. All characters account for 30.76 per cent of the total variability in the first principal component except for days to 50 per cent flowering, plant height, flag leaf blade length. Second principle component accounted for 21.65 per cent of total variability for all characters except for harvest index, grain yield, days to 50 per cent flowering, days to maturity, biological yield, production per plant, number of fingers per ear, peduncle length, flag leaf sheath length. Third principal component shows 16.14 per cent of total variability due to all characters except for 100 seed weight, grain yield, finger width, biological yield, production per plant, plant height, peduncle length, finger length, total number of ears per plant. Fourth principle component shows 11.21 per cent of total variability due to all characters except for flag leaf blade width, grain yield, days to 50 per cent flowering, finger width, production per plant, finger length and length of longest finger (Table 2, 3). Similar results were also reported by Patel *et al*. (2017); Suman *et al*. (2019).

Table 2: Eigen value, per cent variance and cumulative variance of principle components:

Principle component	Eigen value	Variance	Cumulative variance
PC1	5.84	30.76	30.76
PC2	4.11	21.65	52.41
PC3	3.07	16.14	68.55
PC4	2.13	11.23	79.78
PC5	1.30	6.861	86.64
PC6	1.07	5.618	92.26

Table 3: Principal component analysis for 19 quantitative traits in 37 finger millet genotypes.

Particulars	PC1	PC2	PC3	PC4
Days to 50% Flowering	-0.213	0.034	0.255	-0.318
Days to maturity	0.106	-0.015	0.465	0.193
Plant height (cm	-0.258	0.196	-0.119	0.321
No. of tillers per plant	0.162	0.193	0.010	0.365
Flag leaf blade length (cm)	-0.026	0.186	0.318	0.417
Flag leaf blade width (cm)	0.204	0.038	0.039	-0.014
Flag leaf sheath length (cm)	0.366	-0.089	0.206	0.016
Peduncle length (cm)	0.322	-0.055	-0.238	0.064
Number of fingers per ear	0.354	-0.046	0.189	0.093
Total number of ears per plant	0.301	0.152	-0.025	0.076
Finger length (cm)	0.074	0.469	-0.014	-0.130
Finger width (cm)	0.147	0.392	-0.031	-0.255
Length of longest finger (cm)	0.075	0.401	0.112	-0.277
Width of longest finger (cm)	0.203	0.383	0.064	-0.151
Production per plant (g)	0.314	-0.221	-0.119	-0.224
Grain yield (g)	0.285	-0.255	-0.128	-0.244
Biological yield (g)	0.165	-0.021	-0.369	0.300
100 seed weight (g)	0.104	0.168	-0.428	0.172
Harvest index (%)	0.250	-0.162	0.315	0.151

B. Genetic Diversity

By using Mahalanobis D^2 statistics diversity of 37 finger millet genotypes was studied on the basis of 19 quantitative characters. It carried out the quantitative assessment of genetic divergence for yield and its contributing characters among the thirty seven finger millet genotypes presented in Table 4 to 7. Based on the closeness of the genotypes with respect to their D^2 values is given in Table 4, the genotypes were grouped into 7 distinct clusters. Average intra and inter cluster distance were calculated and presented in Table5.The intra-cluster distance showed the divergences among the genotypes within inter and intra cluster distance expressed relation divergence between the cluster. The study also reveals the percentage of contribution of these characters towards total divergence, clustering pattern and intra-cluster distance. By using Tocher's method and Mahalanobis Euclidean distance method, the dendrogram and cluster diagram were created. The detailed descriptions of different clusters are given here as under:

(a) Group constellation. Cluster 1 had maximum number of genotypes followed by cluster 3 with 4 genotypes, cluster 2, 4, 5, 6 and 7 with one genotype each, all genotypes showed significant diversity from whole set as well as from each other. Karad and Patil

(2013) categorized 65 genotypes into 5 clusters. Suryanaryana *et al*. (2014) grouped 35 genotypes in 6 clusters.

(b) Intra and inter cluster distances. The average D^2 values were used to assess the intra and inter cluster relationship. The intra cluster average D^2 value ranged from 246.35 to 445.31. The highest intra cluster genetic distances in cluster was because of its heterogeneous composition. Table 5 showed the average D^2 values for intra and inter cluster distances. Collaborative results have also been given by Bedis *et al*. (2007); Das *et al*. (2013); Wolie and Belete (2013). Cluster 6 and 7 had the highest inter-cluster D^2 values (5053.66) which were followed by cluster 6 and 4 (4962.99), cluster 2 and 6 (4524.50), 1 and 6 (4208.39), 5 and 7 (4073.57) cluster 2 and 7 (3715.87). The genotypes included in the clusters with highest inter-cluster distance exhibited a high degree of genetic variation and hybridization between genotypes of these clusters may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny.

Cluster 1 and 2 had the lowest inter-cluster distance (535.29), which were followed by cluster 4 and 2 (713.35), cluster 1 and 3 (816.53), cluster 7 and 5 (922.79), cluster 1 and 4 (953.10). Promising recombinants were likely to be produced in the segregating generations by crossing between genotypes belonging to clusters that were separated by small inter-cluster distance. Similar results include Kumar *et al*. (2010); Sahu and Pradhan (2012); Harti *et al.* (2013); Shinde *et al.* (2013).

(c) Cluster mean analysis for different characters. The cluster group mean across the 7 cluster mean for 19 quantitative characters is represented in Table 6. For majority of the characters under study, significant variations were found between clusters.

Cluster 5 showed highest cluster mean for biological yield, 100 seed weight and flag leaf blade width, peduncle length and number of fingers per ear. Cluster 6 comprising of genotype displayed highest cluster mean for no. of tillers per plant, grain yield, production per plant, total no. of ears per plant. Cluster 7 showed highest cluster mean for harvest index, finger width, plant height, flag leaf blade length, flag leaf sheath length. Cluster 4 showed highest cluster mean for finger length, length of longest finger and width of longest finger.

Based on the of above results, it is clear that cluster 7 had the maximum cluster mean for majority of the desired characters. Therefore, genotypes including in this cluster can be used for improvement of a large number of seed and yield contributing characters simultaneously. Earlier workers Bedis *et al.* (2007); Sahu and Pradhan (2012) also reported wide variability among clusters for yield and most of the yield contributing characters.

(d) Relative contribution of different characters towards divergence. The proportion of contribution of each character to the overall divergence is shown in (Table 7 & Fig. 2). Based on their percentage contribution, each character were ranked.

The study revealed that thirty seven finger millet genotypes under study contributed a total of 15.41% of their total divergence to grain yield, which was followed by production per plant (12.46%), length of longest finger (cm) (8.33%), harvest index (%) (7.51%), finger length (6.52%), biological yield (6.46%), plant height (5.56%), 100 seed weight (5.21%), days to 50 per cent flowering (5.00%), finger width (4.54%), days to maturity (3.65%), number of finger per ear (3.15%), number of tillers per plant (3.00%), peduncle length (2.55%), flag leaf sheath length (2.52%), flag leaf blade width (2.33%), width of longest finger (2.15%), flag leaf blade length (2.00%), total no. of ears per plant (1.65%). According to the present study characters such as grain yield, production per plant, length of longest finger, harvest index, finger length, biological yield are significant contributors to the genetic divergence according to the current study. Similar findings were reported by Suryanarayana *et al.* (2014); Devaliya *et al.* (2017); Sapkal *et al.* (2019).

Table 4: 37 Grouping of 37 genotypes into 7 clusters on the basis of D^2 analysis.

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	28	IC-0392505, IC-0283679, IC-0382639, IC-0283828, IC-0345111, IC-0345091, IC-0345080, IC-0391548, IC-0345135, IC-0344944, IC-0344841, IC-0356087, IC-0392487, IC-0345085, IC-0345107, IC-0344955, IC-0345082, IC-0344950, IC0345138, IC-0392493, IC-0344952, IC-0392497, Landrace-1, Landrace-2, IC-0257869, IC-0344956, IC-0383629 & IC-0345148
2 Cluster	1	IC-0345147
3 Cluster	4	IC-0345088, IC-0345134, IC-0344954 & IC-0392499
4 Cluster	1	IC-0344953
5 Cluster	1	IC-0344943
6 Cluster	1	IC-0344951
7 Cluster	1	IC-0392492

Table 5: Finger millet genotypes grouped into seven clusters based on intra and inter cluster distances (D^2).

	Cluster Distances						
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**
Cluster 1	246.35	535.29	816.53	953.10	1352.59	4208.39	3105.29
Cluster 2	535.29	0.00	1386.02	713.35	922.79	4524.50	3715.87
Cluster 3	816.53	1386.02	445.31	1642.68	1301.58	2139.66	2429.00
Cluster 4	953.10	713.35	1642.68	0.00	2256.27	4962.99	3720.57
Cluster 5	1352.59	922.79	1301.58	2256.27	0.00	2388.86	4073.57
Cluster 6	4208.39	4524.50	2139.66	4962.99	2388.86	0.00	5053.66
Cluster 7	3105.29	3715.87	2429.00	3720.57	4073.57	5053.66	0.00

Table 6: Cluster mean for 19 characters of 37 genotypes in finger millet across seven clusters.

Cluster Means: Tocher Method																		
	Days to 50% flowering	**Days to maturity**	**Plant height (cm)**	**No. of tillers per plant**	**Flag leaf blade length (cm)**	**Flag leaf blade width (cm)**	**Flag leaf sheath length (cm)**	**Peduncle length (cm)**	**Number of fingers per ear**	**Total no. of ears per plant**	**Finger length (cm)**	**Finger width (cm)**	**Length of longest finger (cm)**	**Width of longest finger (cm)**	**Production per plant (g)**	**Grain yield (g)**	**Biological yield (g)**	**100 seed weight (g)**	**Harvest index (%)**
Cluster 1	68.36	101.54	82.21	2.79	29.05	0.76	34.42	8.59	8.17	2.93	3.84	0.58	5.26	0.78	12.92	15.14	128.02	0.38	12.60
Cluster 2	67.02	101.18	97.54	2.60	34.09	0.61	38.23	9.36	7.31	2.80	4.57	0.66	7.33	1.07	15.00	15.80	134.46	0.97	11.77
Cluster 3	64.40	94.23	80.63	2.26	29.97	0.91	31.26	7.74	7.96	2.43	4.14	0.61	5.83	0.81	31.76	35.79	129.50	0.25	29.20
Cluster 4	67.73	102.31	76.73	3.43	34.32	0.83	37.50	7.99	7.51	3.53	8.59	1.10	12.00	1.47	11.86	15.14	142.69	0.47	10.70
Cluster 5	59.99	89.82	94.35	2.60	33.61	0.95	33.27	10.90	8.97	2.73	2.59	0.46	3.33	0.57	36.77	47.19	302.70	1.06	15.41
Cluster 6	61.36	90.29	76.25	3.59	25.17	0.80	30.57	8.31	8.24	3.83	4.01	0.57	5.33	0.73	75.13	77.45	221.54	0.50	35.25
Cluster 7	62.64	95.35	141.66	3.39	36.85	0.79	40.43	9.86	9.13	3.73	4.86	0.68	6.00	0.97	14.01	16.62	119.34	0.27	86.76

Table 7: Contribution of each character to the genetic divergence of finger millet.

Sr. No.	**Source**	**Contribution %**
1.	Days to 50% flowering	5.00
2.	Days to maturity	3.65
3.	Plant height (cm)	5.56
4.	No. of tillers per plant	3.00
5.	Flag leaf blade length (cm)	2.00
6.	Flag leaf blade width (cm)	2.33
7.	Flag leaf sheath length (cm)	2.52
8.	Peduncle length (cm)	2.55
9.	Number of fingers per ear	3.15
10.	Total no. of ears per plant	1.65
11.	Finger length (cm)	6.52
12.	Finger width (cm)	4.54
13.	Length of longest finger (cm)	8.33
14.	Width of longest finger (cm)	2.15
15.	Production per plant (g)	12.46
16.	Grain yield (g)	15.41
17.	Biological yield (g)	6.46
18.	100 seed weight (g)	5.21
19.	Harvest index (%)	7.51

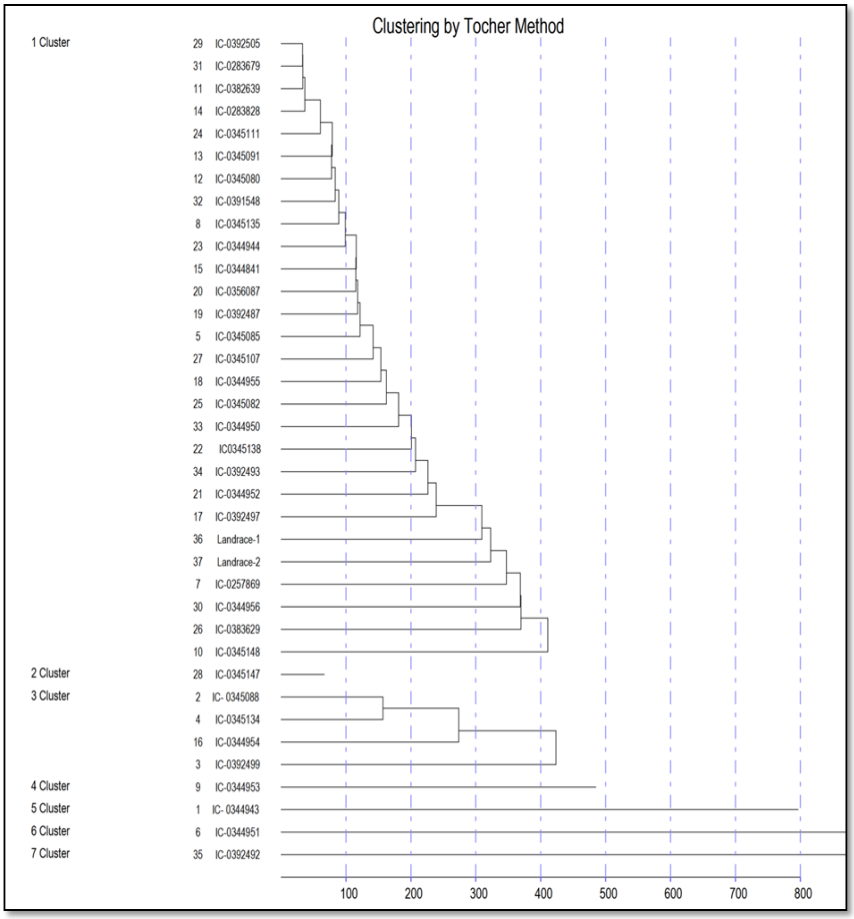

Fig. 1. Dendrogram or cluster diagram showing the relationship among 37 finger millet genotypes developed by Tocher method based on 19 quantitative characters.

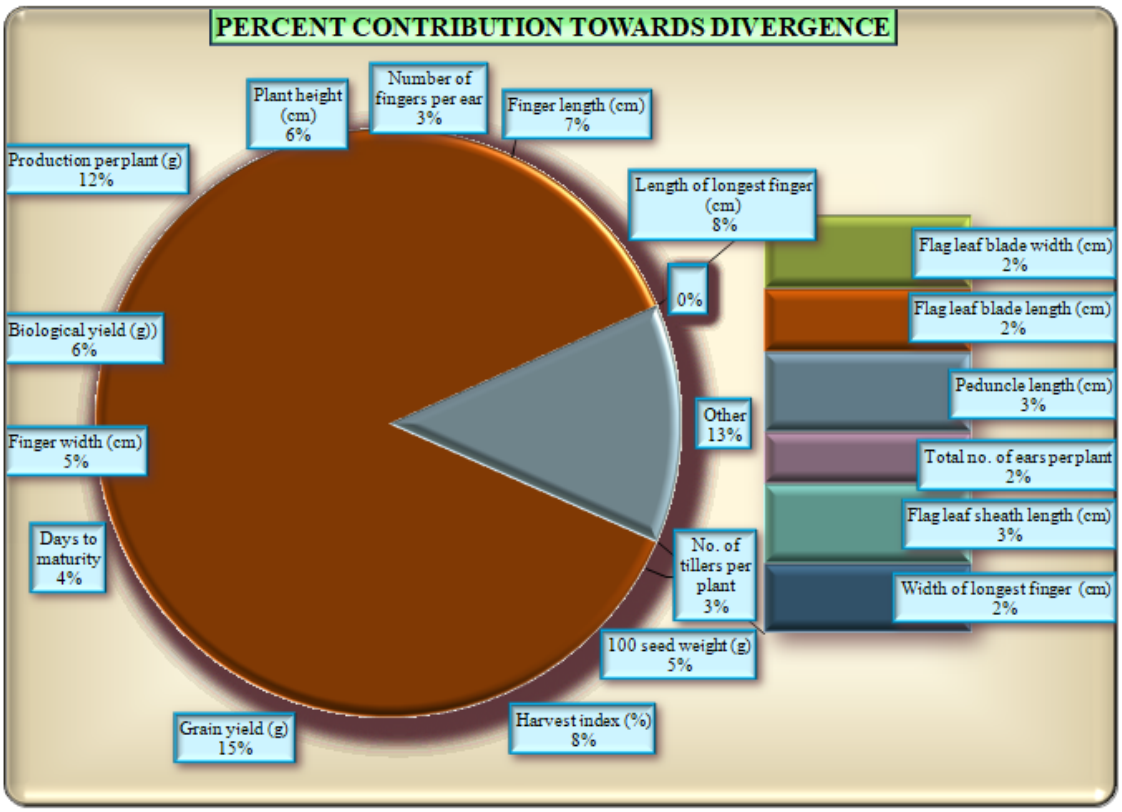

Fig. 2. Pie chart showing the contribution of each character to the genetic divergence of finger millet.

CONCLUSIONS

In conclusion, Principal component analysis for 19 quantitative traits revealed six principal components out of which maximum variability was found in first four components which contributed 82.78% to variance. Cluster analysis for yield and yield contributing traits classified all 37 genotypes of finger millet into seven clusters by using Tocher's method. Cluster 1 included maximum number of genotypes followed by cluster 3 with four genotypes, cluster 2,4,5,6 and 7 with one genotype each indicating wide diversity from whole set as well as from each other. Grain yield contributed maximum toward the total genetic divergence. Clustering through D^2 analysis revealed maximum inter cluster distance between cluster 6 and 7 (5053.66) followed by cluster 6 and 4 (4962.99), cluster 2 and 6 (4524.50), 1 and 6 (4208.39), 5 and 7 (4073.57) cluster 2 and 7 (3715.87). Therefore, there was a significant diversity among these clusters and genotypes from these clusters could be used as parents for hybridization.

FUTURE SCOPE

According to the cluster analysis there was a significant diversity among the cluster and genotypes from these clusters could be used as parents for hybridization and further breeding programme.

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Conflict of Interest. None.

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