

Research Paper

Assessment of genetic divergence in Finger millet [*Eleusine coracana* (L.) Gaertn.] for yield and yield contributing traits

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Abstract

Forty genotypes of finger millet (*Eleusine coracana*) were grouped into seven distinct classes based on their genetic diversity using D^2 statistic and Principal component analysis. The maximum inter-cluster distance was between cluster V and VII, followed by cluster IV and VII and cluster V and VI, suggesting thereby that there is wide genetic diversity between these clusters. PCA revealed that, the first three principal components with eigen values more than one contributed 76.411 per cent towards the total variability. The significant factors loaded in PC₁ viz., number of productive tillers per plant, ear weight per plant, days to maturity, days to 50% flowering, number of fingers per ear, plant height, 1000-seed weight, seed yield per plant and finger length contributed maximum towards divergence. The analysis showed that the genotypes GE-3434, GE-1382 and GE-4976 which are having better *per se* for yield contributing characters recorded maximum inter-cluster distance hence, can be utilized in hybridization programmes to produce desirable recombinants. Both the analysis revealed that geographical diversity and genetic diversity are not related.

Keywords: D^2 statistic, Finger millet, Genetic diversity, Principal component analysis, statistic.

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the important food crops and largely grown in southern states of India. It is the most important small millet cultivated in more than 25 countries in Africa and Asia. In India, it is cultivated on 1.3 M ha, with a production of 1.59 Mt and a productivity of 1.7 t ha⁻¹ while in Andhra Pradesh it is grown in an area of 41,000 ha with a production of 45,000 t and a productivity of 1.19 t ha⁻¹ (Ministry of Agriculture, 2013). Ragi is commonly famous as "Nutritious millet" as the grains are nutritionally superior to many cereals. It contains protein (7-10%), calcium (344 mg/100 g), iron and other minerals. It is also rich in phosphorus (283 mg/100 g) and potassium (408

mg/100 g). The carbohydrates present in finger millet have the unique property of slower digestibility.

The success of breeding programme lies on the fact that the parents involved in any particular cross should be genetically divergent. To make the hybridization programme effective and improve crops, genetic divergence among the genotypes plays an important role. The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining the F₁'s which may result in superior segregants. D² statistics is a powerful tool for quantifying the divergence between the two populations. This technique measures the divergence

at intra-cluster and inter-cluster levels and thus helps in selection of genetically divergent parents in hybridization programme. Principal component analysis (PCA) is one of the most important and powerful statistical tool for investigating and summarizing the underlying trends of variation in complex data structures (Legendre and Legendre, 1984). This analysis also reflects the importance of the largest contributor to the total variation at each axis of differentiation. Thus, this experiment was aimed at identifying genetically divergent finger millet genotypes with desirable traits for hybridization which in turn produce superior pureline varieties.

Materials and Methods

The experimental material for the present investigation consisted of forty genotypes of finger millet collected from Agricultural Research Station (ARS), Vizianagaram, Andhra Pradesh and All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore. These genotypes were evaluated during *kharif*, 2013 at Agricultural College Farm, Bapatla in a Randomized Complete Block Design with three replications. The seeds were directly sown by dibbling. Each entry was represented by four rows of 3m length. The spacing of 20 cm between rows and 10 cm within rows was followed. Observations were recorded on ten randomly chosen plants for eleven characters *viz.*, plant height, days to 50% flowering, days to maturity, number of productive tillers per plant, fingers per ear, finger length(cm), ear weight per plant(g), 1000-seed weight(g), seed protein content(%), seed calcium content(mg/100g) and seed yield per plant(g). The mean value of the recorded data was subjected to analysis of variance. Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis D^2 (Mahalanobis, 1936) and principal component analysis.

Results and Discussion

Univariate analysis of variance revealed the significant difference for all the eleven characters under study in the 40 finger millet genotypes. This

significance of difference among 40 genotypes for all characters justify further calculation of D^2 values. The 40 genotypes were grouped into seven clusters using the Tocher's method (Table 1& Fig. 1), with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values. Accordingly, cluster II was the largest cluster containing 16 genotypes. Clusters VI and VII were solitary clusters (Table 2, Fig 2).

The maximum inter-cluster distance was between cluster V and VII (4451.42), followed by cluster IV and VII (3589.81), cluster V and VI (3163.07), cluster IV and VI (3015.21), cluster I and VII (2837.67), cluster II and VII (2206.00) and cluster III and Cluster V (1819.02). This suggested that there is wide genetic diversity between these clusters. The genotypes GE-3434 and GE-1382 belonging to same geographical area i.e. Africa were grouped in two different farthest clusters, hence indicating geographical divergence and genetic diversity are not correlated. These results are in accordance with those of Jain *et al.* (1981, 2002), Rao (1992), Kadam (2008) and Kumar *et al.* (2010). The minimum intra-cluster distance was found in cluster I ($D^2 = 97.57$), followed by cluster V ($D^2 = 173.42$). The maximum intra-cluster distance was observed for the genotype falling in cluster IV ($D^2 = 492.70$). This implies that these clusters have the genotypes with varied genetic architecture. The clusters VI and cluster VII showed zero intra-cluster distance due to monogenotypic nature.

Cluster means indicate average performance of all genotypes present in a particular cluster. The cluster mean values for 11 characters are presented in Table 4. The data indicated a wide range of mean values between the clusters. Plant height had a range of 85.32 cm (cluster VI) to 121.00 cm (cluster VII), days to 50% flowering had a range of 58.00 days for cluster VI to 77.22 days for cluster V, days to maturity had a range of 88.00 days (cluster VI) to 114.00 days (cluster VII), number of productive tillers ranged from 2.83 (cluster VI) to 4.40 (cluster I), number of fingers per ear varied from 3.73 (cluster VI) to 6.70 (cluster I), finger length varied from 5.86 cm (cluster VI) to 8.08 cm (cluster VII), ear weight per plant ranged

from 14.49 g (cluster VI) to 25.97 g (cluster VII), 1000-seed weight varied from 3.36 g (cluster VI) to 4.23 g (cluster I), seed protein content varied from 6.17 percent (cluster V) to 13.66 percent (cluster VII), seed calcium content varied ranged from 253.00 mg/100g (cluster VI) to 414.05 mg/100g (cluster IV) and seed yield per plant varied from 9.51g (cluster VI) to 18.73 g (cluster I).

Table 1. Clustering pattern of 40 finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes by Tocher's method

Cluster number	No. of genotypes	Name of genotype (s)
I	5	GE-3138, Kalyani, Indaf-9, Srichaitanya, GE-2723
II	16	GE-1746, GPU- 82, GPU-48, IE- 2296, VL-149, GE-2941, GPU-66, BR-10, GE-666, GE-4736, GE-2078, IE-4795, GPU-67, IE-501, GE-3266, GE-258
III	7	GE-2127, GE-4437, IE-3077, DHRS-1-1, TNAU-12-14, OEB-532, IE-2323
IV	7	GE-3090, GE-1274, GE- 3225, GE-4976, IE-2652, GE-145, GE-4707
V	3	Ratnagiri, Godavari, GE-1382
VI	1	GE-995
VII	1	GE-3434

The mean performance of the clusters of 11 characters showed that, the cluster I was recorded highest seed yield per plant (18.73g) and was characterised by more number of productive tillers per plant (4.40), fingers per ear (6.70) and 1000-seed weight (4.23g). The cluster VI was early for days to 50% flowering and days to maturity with lowest values. It include only one genotype GE-995. The cluster I showed highest seed yield per plant followed by cluster IV and cluster VI. The genotypes included in these clusters can be used as diverse sources in future breeding programmes.

Principal components (Eigen value greater than one), Eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table 3. In the present study, the first three

principal components with eigen values more than one contributed 76.411 per cent towards the total variability. The first three principal components PC_1 , PC_2 , and PC_3 with values of 46.687%, 16.081% and 13.643% respectively, contributed maximum to the total variability. The principal component with eigen values less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first three principal components.

Seed calcium content, plant height, days to maturity and days to 50% flowering in the second principal component (PC_2); plant height, seed yield per plant, days to 50% flowering, days to maturity in the third principal component (PC_3); seed protein content (0.864) and ear weight per plant in the fourth principal component (PC_4) were the major contributors to each principal components.

The analysis thus identified the maximum contributing variables *i.e.*, number of productive tillers, ear weight per plant, days to maturity, days to 50% flowering, fingers per ear, plant height, 1000-seed weight and seed yield per plant. It is important to study the variance as the relative contribution than the signs (indicative of direction) in principal component analysis.

Table 2. Average intra and inter-cluster D2 values among seven clusters with 40 finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes

Cluster No.	I	II	III	IV	V	VI	VII
I	97.57	343.39	931.68	852.15	280.93	1940.16	2837.67
II		201.84	580.87	586.45	755.34	1518.31	2206.00
III			205.01	1479.44	1819.02	468.68	972.69
IV				492.70	1042.42	3015.21	3589.81
V					173.42	3163.07	4451.42
VI						0.00	615.19
VII							0.00

Diagonal values are intra-cluster distances. Off the diagonal values are inter-cluster distances.

Table 3. Eigen values, proportion of the total variance represented by first four Principal components, cumulative per cent variance and component loading of different characters in finger millet [*Eleusine coracana* (L.) Gaertn.]

	PCA1	PCA2	PCA3	PCA4
Eigen Value (Root)	5.135	1.768	1.500	0.920
% Var. Exp.	46.687	16.081	13.643	8.372
Cum. Var. Exp.	46.687	62.768	76.412	4.785
Plant height (cm)	0.306	0.220	0.306	0.031
Days to 50% flowering	0.374	0.138	0.201	0.195
Days to maturity	0.379	0.184	0.092	0.174
No. of productive tillers	0.411	0.098	-0.004	-0.031
Fingers per ear	0.318	-0.169	-0.289	-0.183
Finger length (cm)	0.095	-0.191	-0.642	-0.207
Ear weight per plant (g)	0.393	0.021	-0.088	0.216
1000-seed weight (g)	0.305	-0.005	-0.433	0.129
Seed protein content (%)	-0.193	-0.116	-0.208	0.864
Seed calcium content (mg/100g)	-0.084	0.689	-0.231	-0.160
Seed yield per plant (g)	0.223	-0.576	0.259	-0.127

PC = Principal component

Table 4. Mean values of seven clusters estimated by Tocher's method from 40 finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes

Cl No.	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of productive tillers	Fingers per ear	Finger length (cm)	Ear weight per plant (g)	1000-seed weight (g)	Seed protein content (%)	Seed calcium content (mg/100g)	Seed yield per plant (g)
I	111.33	75.20	108.93	4.40	6.70	7.23	21.60	4.23	7.69	274.40	18.73
II	107.68	69.71	103.58	3.61	5.45	6.41	18.84	3.74	8.24	338.69	12.57
III	90.15	63.57	92.29	3.40	5.65	6.81	18.09	3.98	10.18	313.90	13.49
IV	105.45	71.29	106.81	3.53	5.66	7.22	18.06	4.06	7.04	414.05	15.25
V	115.34	77.22	108.22	4.07	6.59	8.00	20.55	3.95	6.17	260.67	14.79
VI	85.32	58.00	88.00	2.83	3.73	5.86	14.49	3.36	11.72	253.00	9.51
VII	121.00	76.33	114.00	2.90	6.13	8.08	25.97	4.17	13.66	331.00	16.50

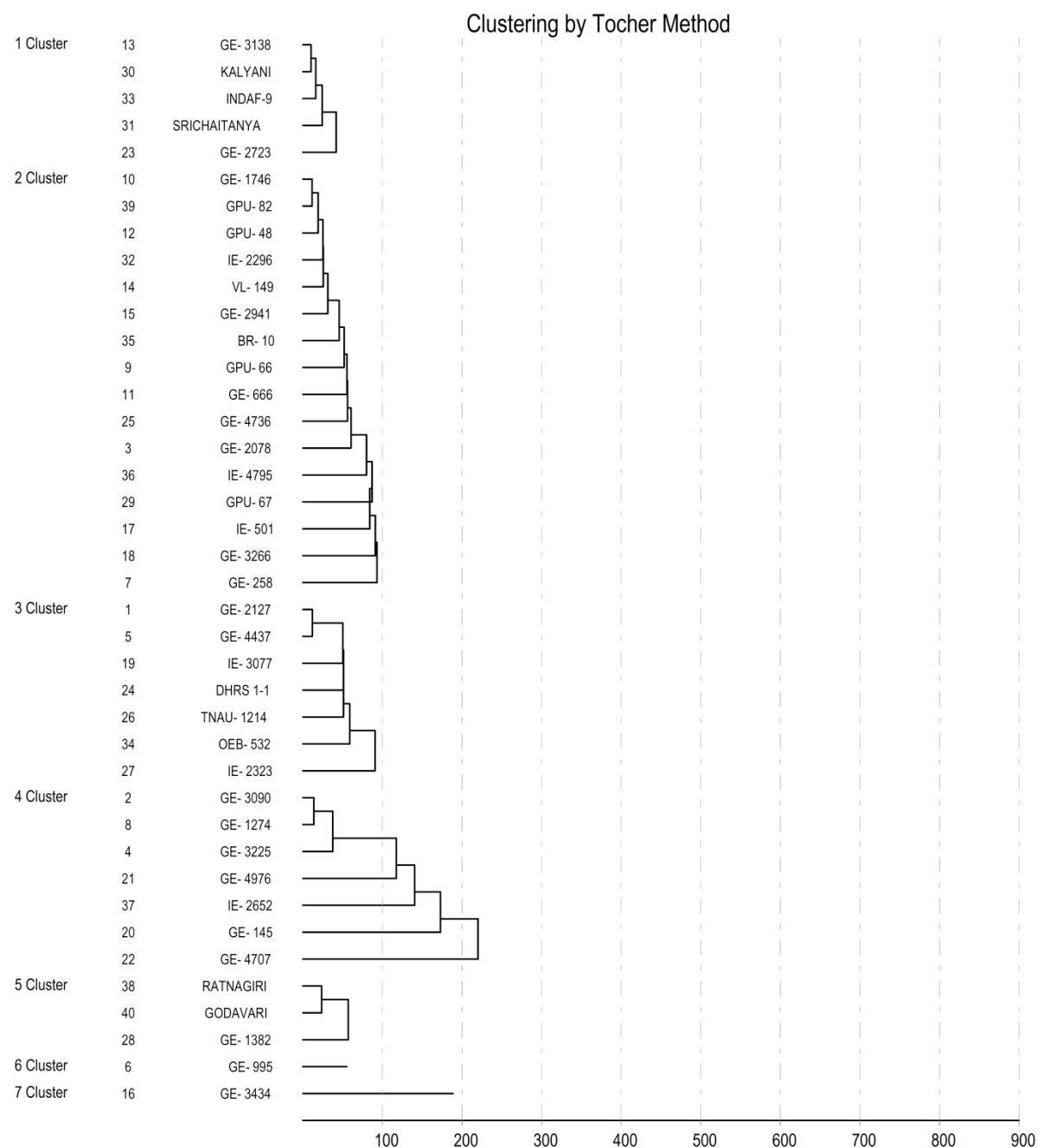


Figure 1. Dendrogram showing relationship among 40 finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes in seven clusters based on Mahalanobis' D^2 values

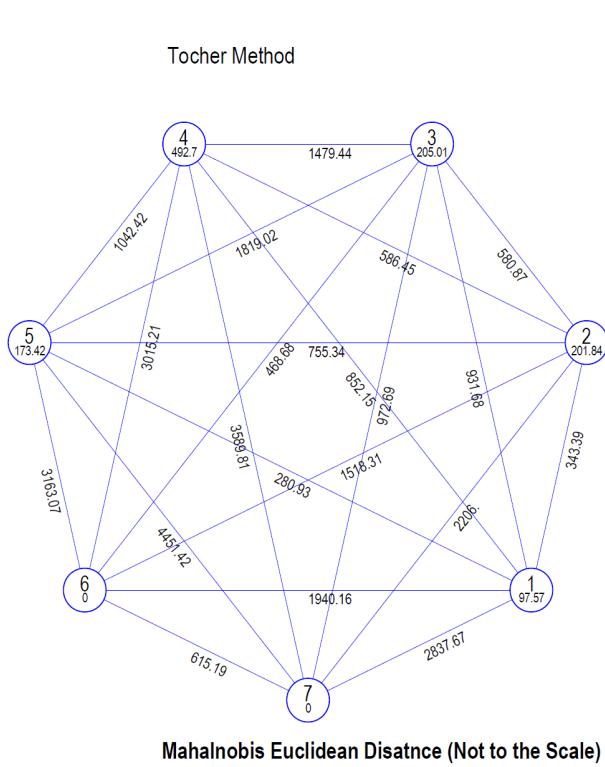


Figure 2. Intra and inter-cluster distance of 40 finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes in seven clusters based on Euclidean2 distance

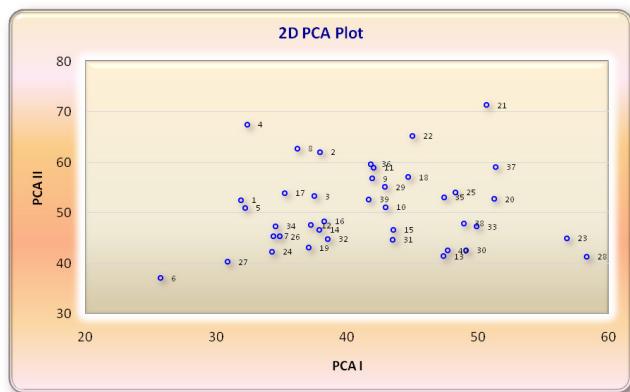


Figure 3. Two dimensional graph showing relative position of 40 finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes based on PCA scores

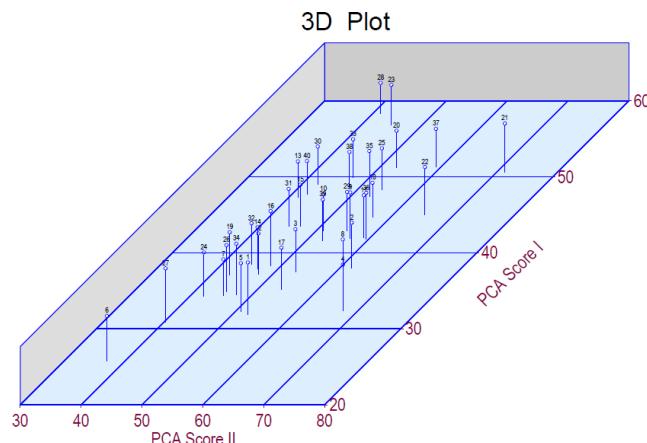


Figure 4. Three dimensional graph showing relative position of 40 finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes based on PCA scores

Using Mahalanobis' D^2 statistic it could be inferred that seed protein content, seed calcium content, days to maturity and days to 50% flowering contributed maximum towards divergence. Based on inter-cluster distance among the groups, crosses may be between genotypes belonging to cluster V (Ratnagiri, Godavari, GE-1382) and cluster VII (GE-3434), cluster IV (GE-3090, GE-1274, GE-3225, GE-4976, IE-2652, GE-145, GE-4707) and cluster VII (GE-3434), cluster V (Ratnagiri, Godavari, GE-1382) and cluster VI (GE-995) and cluster IV (GE-3090, GE-1274, GE-3225, GE-4976, IE-2652, GE-145, GE-4707) and cluster VI (GE-995).

In principal component analysis, first three principal components altogether explained 76.411% of the total variability. The significant factors loaded in PC_1 viz., number of productive tillers per plant, ear weight per plant, days to maturity, days to 50% flowering, number of fingers per ear, plant height, 1000-seed weight, seed yield per plant and finger length contributed maximum towards divergence. 2D and 3D graphs (Fig. 3 and 4) showed wide divergence between GE-3434, GE-1382 and GE-4976 signifying their usefulness in finger millet breeding. Hence, these genotypes can be utilized in hybridization programmes to produce superior recombinants.

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