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Multivariate Analysis in Finger Millet (*Eleusine coracana* (L.) Gaertn.)

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ABSTRACT

The experimental material comprised 55 diverse genotypes of finger millet (*Eleusine coracana* (L.) Gaertn) were evaluated to asses genetic diversity using multivariate methods including principal component analysis (PCA) and cluster analysis. Principal component analysis identified four principal components with eigen values more than one which contributed 74.06 per cent of cumulative variance with days to 50% flowering, finger length and inflorescence width being the most important characters in the first principal component. The total genotypes were grouped into eight clusters. The number of accessions per cluster varied from 14 accessions in cluster IV to two accessions in cluster VI where cluster V is unitary with single genotype. The objective of the present study was to determine the extent of diversity present in the material.

Key words: *Cluster analysis ,Finger millet, Multivariate analysis, Principal component analysis.*

Finger millet (*Eleusine coracana* (L.) Gaertn.), popularly known as "Ragi" in India ranks third in importance among millets after sorghum and pearl millet. Finger millet cultivation is more widespread compared to other millets and seen from sea level in south India to high lands of Himalayas in north and Gujarat in west to Manipur in east. This crop is ideal for dryfarming due to its low input requirement, early maturity and rejuvenation capacity after alleviation of stress.

Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population (Arun Prabhu *et al*., 2008). Genetic divergence is essential to select the parents for future breeding program. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations (Neelam *el al.,* 2014).

Principal component analysis (PCA) or Canonical (vector) analysis is a sort of multivariate analysis. It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axis of differentiation. PCA measures divergence between varieties in terms of spatial distance rather than quantifying it as D^2 does. Hence it is a potential tool in knowing diversity.

Principal component scores for genotypes were used as an input for clustering using Ward's minimum variance method. The tree like structure called dendrogram, constructed based on Euclidean^2 distance computed from PCA scores of genotypes gives the information about the clusters.

The usefulness of multivariate methods for handling morphological variation in germplasm collections have been demonstrated in many crop plants. Examples among the cereals include barley (*Hordeum vulgare* L.) (Cross, 1992); finger millet (*Eleusine coracana* (L.) Gaertn.) (Hussaini et al., 1977). Utilization of principal component analysis combined with hierarchical cluster analysis in genetic divergence studies was reported by earlier workers Hari Krishna *et al.* (2005), Jaya Lakshmi (2007) in finger millet. Multivariate analysis by means of PCA and Cluster analysis is a useful tool in quantifying the degree of divergence at genotypic level. Hence, the present study was attempted to estimate the extent and nature of genetic diversity present among 55 genotypes for 14 traits.

MATERIAL AND METHODS

The experimental material consisted 55 finger millet genotypes obtained from Agricultural Research Station, Vizianagaram (A.P.,). The material was grown in randomized block design with three replications at Agricultural college farm, Naira

Table 1. The Eigen values per cent variance, cumulative percent variance for principal components in finger millet.

Character	PC1	PC2	PC3	PC4
Eigene Value (Root)	5.995	1.972	1.449	0.953
% Var. Exp.	42.818	14.087	10.349	6.807
Cum. Var. Exp.	42.818	56.905	67.255	74.062

Table 2. Character loading four principle components in 55 finger millet genotypes.

Character	PC_1	PC_2	PC_3	PC_4
Days to 50% Flowering	0.349	0.166	0.169	0.035
Plant Height (cm)	0.228	-0.367	0.317	-0.326
No. of Basal Tillers	-0.305	-0.271	-0.199	0.012
Flag Leaf Length (mm)	-0.097	-0.509	-0.065	-0.032
Peduncle Length (mm)	-0.362	0.079	-0.130	-0.057
Inflorescence Exertion (mm)	-0.301	-0.044	0.026	-0.200
Inflorescence Length (mm)	0.281	-0.202	-0.441	0.147
Inflorescence Width (mm)	0.328	0.028	0.111	0.167
Number of Fingers/ Ear	-0.349	-0.009	-0.073	0.164
Finger Length	0.332	-0.023	-0.348	0.051
Finger Width	-0.108	0.392	0.475	0.085
Grain Yield/ Plant	-0.083	-0.454	0.425	-0.087
Seed Protien Content (%)	0.234	-0.017	0.003	-0.584
Calcium Content (mg/100g)	-0.099	0.307	-0.264	-0.643

(A.P.,). Each entry was grown in two rows of three meter length with a spacing of 30×10 cm. The data was recorded on 10 randomly selected plants for 14 quantitative traits *viz.,* days to 50% flowering (plot basis), plant height (cm), number of basal tillers, flag leaf length (mm), peduncle length (mm), inflorescence exertion (mm), inflorescence length (mm), inflorescence width (mm), length of finger (mm), width of finger (mm), number of fingers ear^{-1}, seed protein content (%) (estimated by Microkjeldahl method), calcium content (mg/100g) (estimated by Versenate titration method) and grain yield plant^{-1} (g). The data were subjected to Principal component analysis (Jackson, 1991) and Agglomerative Hierarchical cluster analysis (Anderberg, 1993) using the software 'INDOSTAT'.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the characters under study, indicating considerable amount of variability present in the experimental material. Principal component analysis (PCA) identified four principal components with eigen values more than one which contributed 74.06 per cent of cumulative variance (Table.1). The first principal component (PC_1) contributed (42.82%). The characters *viz.,* days to 50% flowering (0.35), finger length (0.33), inflorescence width (0.32), seed protein content (0.23) and plant height (0.22) contributed maximum variance in the first principal component (PC_1) and signifying their importance in divergence.

The second principal component (PC_2) described 14.01 per cent of total variance and the characters *viz.,* finger width (0.39), calcium content (0.31) and peduncle length (0.08) showed the maximum variance in this principal component.

The third principal component (PC_3) was characterized by 10.35 per cent contribution towards the total variability. The characters *viz.,*

Table 3. Clustering pattern of 55 finger millet genotypes by Ward's minimum variance method.

Cluster No.	No. of genotypes	Name of genotype(s)
I	8	IE 4673, IE 4759, IE 2322, IE 3077, IE 3618, IE 2217, IE 2323, IE 196
II	7	IE 3391, IE 2619, IE 5817, IE 3317, VR 762, VR (w) 936
III	11	IE 3614, IE 3470, IE 4709, IE 4734, IE 4110, VR 708 IE 6337, IE 2590, IE 6082, IE 4795, IE 2884
IV	14	IE 2296, IE 6473, IE 3945, IE 6294, IE 6421, PR 202, IE 588, IE 4329, IE 6326, IE 4646, IE 4671, IE 2457, IE 4570
V	1	IE 2790
VI	2	IE 2652, IE 4816
VII	4	IE 2093, IE 3543, IE 501, IE 2293
VIII	8	IE 6154, IE 4545, IE 5537, IE 5106, IE 5367, VR 847, IE 6350, IE 4163

Table 4. Average intra (diagonal) and inter-cluster Eucledian^2 values among eight clusters in 55 finger millet genotypes.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	260.72	389.68	596.56	542.10	1406.05	1469.63	1504.04	2242.80
Cluster II		98.45	408.60	367.41	989.31	1442.44	1708.82	1767.34
Cluster III			194.57	1094.12	1883.57	2752.68	742.75	861.69
Cluster IV				210.11	860.27	626.24	2851.86	3180.19
Cluster V					0	1318.80	3983.54	3643.98
Cluster VI						180.79	5248.21	5848.86
Cluster VII							158.01	750.42
Cluster VIII								220.91

finger width (0.47), grain yield plant^{-1} (0.42), and plant height (0.32), contributed maximum variance in this principal component.

Principal factor scores for all the 55 genotypes were estimated in all 3 PC's and utilize to construct precise 2D plot. All the genotypes were plotted for PC_1, PC_2 and PC_3 which cumulatively explained 67.25 per cent of variability accounted for all the characters (Table.2).

The plot of PC_1, PC_2 and PC_3 showed character differentiation of genotypes according to their cluster membership for each cluster. The mean scores of the 55 genotypes were used as input for clustering in order to group the genotypes into different clusters. Ward's minimum variance method was followed to group the genotypes into eight clusters and used in constructing dendrogram (Fig.1). The clustering pattern revealed that the genotypes originating from different geographical regions got themselves grouped into different clusters, indicated that the geographic biodiversity is not the responsible factor in determining genetic biodiversity.

The 55 finger millet accessions were grouped into eight clusters (Table.3). The number of accessions per cluster varied from 14 accessions in cluster IV to two accessions in cluster VI where cluster V is unitary with single genotype. Of the eight clusters formed, cluster II has minimum intra cluster Euclidean^2 distance value of 98.45 followed by cluster VII (158.01), cluster VI (180.78), cluster III (194.57), cluster IV (210.11), cluster VIII (220.91) and cluster I (260.71). The inter cluster Euclidean^2 distances varied from 367.41 (between cluster II and cluster IV) to 5848.86 (cluster IV

Table 5. Mean values of eight clusters estimated by Ward's minimum variance method from 55 finger millet genotypes.

Cluster	Days to 50% Flowering	Plant Height (cm)	No. of Basal Tillers	Flag Leaf Length (mm)	Peduncle Length (mm)	Inflorescence Exertion (mm)	Inflorescence Length (mm)
1 Cluster	66.74	108.02	2.99	360.42	213.67	118.12	74.91
2 Cluster	90.33	126.24	2.09	338.68	197.52	100.49	66.04
3 Cluster	81.09	111.07	2.02	334.50	210.18	112.27	62.88
4 Cluster	90.00	117.94	2.14	330.92	193.90	98.31	73.80
5 Cluster	95.00	133.93	2.13	428.20	152.67	49.78	189.67
6 Cluster	93.00	126.65	1.88	356.22	210.00	127.67	86.25
7 Cluster	55.50	77.00	3.55	312.93	219.43	120.92	56.87
8 Cluster	90.54	116.75	1.96	316.57	198.54	107.39	78.09

Cluster	Inflorescence Width (mm)	Number of Fingers Ear^{-1}	Finger Length	Finger Width	Grain Yield Plant^{-1}	Seed Protien Content (%)	Calcium Content (mg/100g)
1 Cluster	61.14	7.45	77.42	10.12	11.16	9.83	300.09
2 Cluster	52.72	6.52	67.50	10.39	8.79	10.72	309.64
3 Cluster	50.50	6.43	65.39	10.31	7.69	9.88	335.07
4 Cluster	54.79	6.59	74.83	10.85	8.63	9.53	282.38
5 Cluster	129.33	7.13	186.67	9.93	11.08	10.22	289.85
6 Cluster	63.75	6.63	86.00	11.70	8.98	7.15	245.17
7 Cluster	44.53	7.49	60.77	8.95	7.12	10.02	361.12
8 Cluster	53.91	6.51	79.71	10.71	7.79	9.42	383.23

and VIII). Cluster distances were presented in Table-4.

Cluster means were computed for the 14 characters studied on pooled basis and are presented in Table-5. Cluster V recorded high mean values for days to 50% flowering (95.00), plant height (113.93), flag leaf length (428.20), inflorescence length (189.67), inflorescence width (129.33) and finger length (186.67). Cluster I recorded high mean values for number of fingers ear^{-1} (7.45), grain yield plant^{-1} (11.16) while cluster VII showed high mean values for number of basal tillers (3.55) and peduncle length (219.43).

Based on these studies crosses may be effective between the genotypes of these clusters to obtain better and desirable segregants. Trangressive segregants for yield and yield component traits may be expected by identifying and hybridizing the best cross combination utilizing the clustering pattern of the genotypes as the present study aimed. The similar results were reported by Hari Krishna *et al.* (2005) and Jaya Lakshmi (2007).

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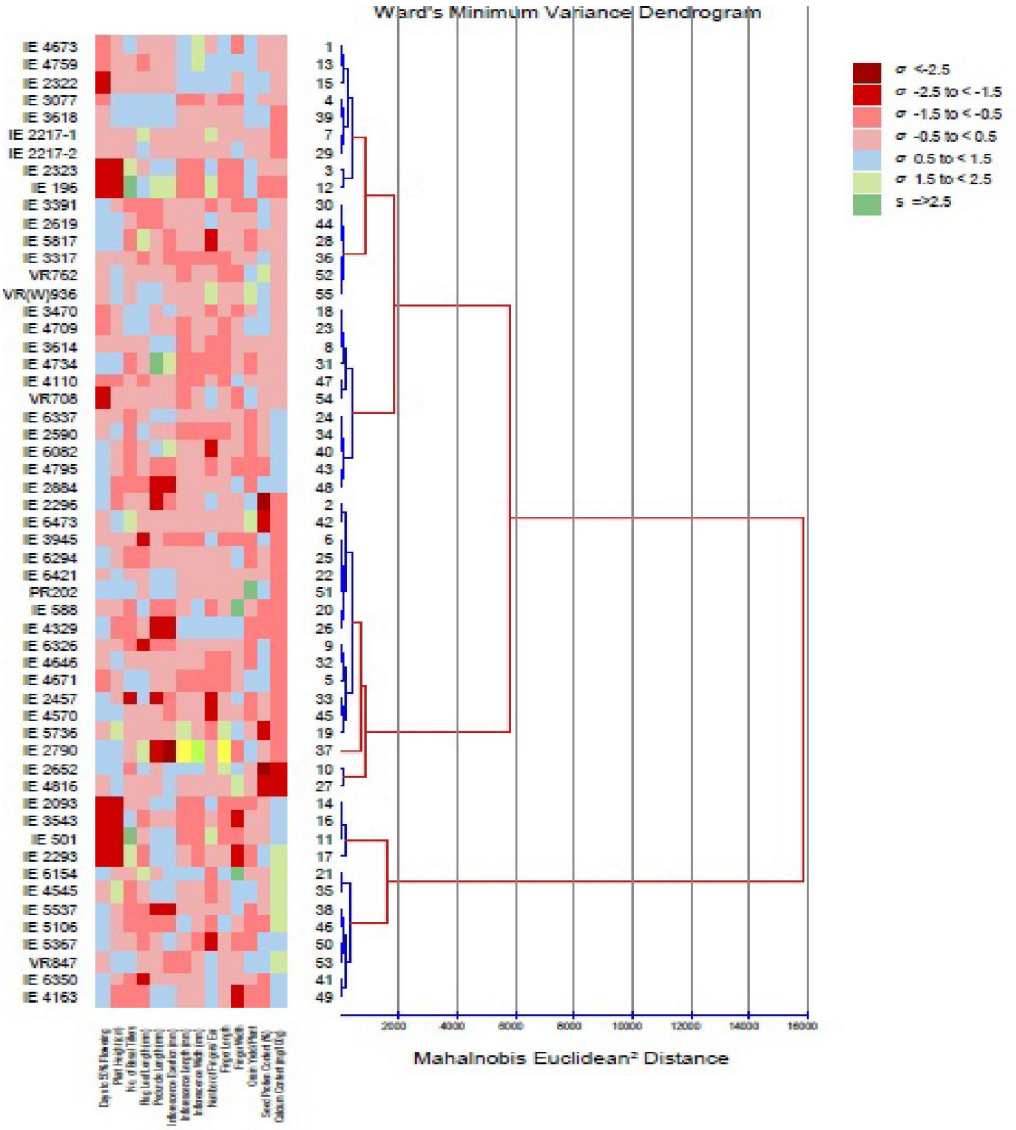
Figure 1. Dendrogram, constructed based on Euclidean² distance by Ward's minimum variance method.



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