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Characterization and Evaluation of Finger Millet (*Eleusine coracana* L.) Core Set Germplasm Using Principal Component Analysis

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Abstract

The present study was aimed to characterize 520 finger millet germplasm using multivariate traits. Wide variation was observed for most of the traits indicated the scope of improvement of these characters by direct selection. Phenotypic correlation between grain yield per plant was highly significant and positively associated with number of basal tillers per plant, number of fingers per ear and straw weight. Whereas, grain yield per plant is negatively associated with days to fifty per cent flowering. Principal component analysis revealed that the first four components contributed about 65.06 per cent of the total variability. The proportions of the total variance attributed to the first four principle components were 20.07, 18.72, 15.05 and 11.22 per cent, respectively. The characters Days to 50 per cent flowering, finger length and straw weight were the most important traits contributing for the overall variability. This implied that these traits should be given emphasis in finger millet improvement programme. K means clustering method based on 8 quantitative traits among 520 finger millet germplasm was able to separate and grouped them into 23 clusters. The variability present in the finger millet germplasm gives opportunity for plant breeders for effective selection of specific donor lines for genetic improvement of finger millet.

Keywords : Finger millet, quantitative traits, phenotypic correlation, principal component analysis

Finger millet is important small millet grown in India. It is a staple food in many hilly regions of the country. It is grown both for grain and forage. Grains are rich in minerals and are the richest source of calcium used in many preparations like cakes, puddings, sweet etc. it is also a rich source of iron, protein, fiber and other minerals and is a gluten free food. It has low fat content and contains mainly unsaturated fat. Due to rich fiber content finger millet is believed to be a good laxative and prevents constipation. It is a good food for People who suffering from diabetes, liver diseases, high blood pressure, heart weakness and asthma. Its green straw is suitable for making silage. The major finger millet growing states are Karnataka, Uttarakhand, Maharashtra, Tamil Nadu, Odisha, Andhra Pradesh and Gujarat.

In India it is cultivated over an area of 11.96 lakh ha with total production of about 19.2 lakh tonnes and with productivity of 1604 kg/ha during the year 2013-14 (Anon., 2014). Of the total area under finger millet Karnataka alone occupies 60 per cent followed by Uttarakhand and Maharashtra with 10 per ecnt each. Karnataka contributes nearly 70 per cent of finger millet production in the country followed by Uttarakhand and Maharashtra with about 9 per cent. Tamil Nadu has the highest productivity (2580 kg/ ha) followed by Karnataka (1801 kg/ha) and Uttarakhand (1372 kg/ha).

The value of germplasm is realized only when characterized for morpho-agronomic traits to unearth new gene combinations for use in crop improvement programmes. Principal Component Approach (PCA) and cluster analysis serve as potential tools in evaluating the phenotypic diversity. It is very helpful in deciding which traits of crop contributing most to yield. Subsequently these agronomic traits should be emphasized in the breeding programme. Cluster analysis identifies and classifies objects individuals on the basis of similarity of characteristics they possess. It seeks to minimize within group variance and maximize between group variance. It is helpful for parental selection in the breeding programme and crop modeling.

The National Active Germplasm site (NAGS) at PC Unit, Small Millets, University of Agricultural Sciences, Bangalore holds large number of finger millet germplasm accessions, these were characterized and 520 core set accessions were developed. These core set was utilized in our present study for evaluation and characterization with an objective of characterizing 520 finger millet germplasm by means of quantitative traits to understand association of various traits. PCA and clustering analysis which enable to classify them into distinct phenotypic groups based on their genetic variability.

Material and Methods

The experimental material for the present study comprised of 520 core accessions of finger millet available at National Active Germplasm site (NAGS), PC Unit, Small Millets, University of Agricultural Sciences, Bangalore. Core collection consists of a limited set of accessions derived from an existing germplasm collection chosen to represent the genetic spectrum in the whole collection.

Evaluation and characterization of these 520 finger millet core germplasm accessions and 3 check varieties were grown in augmented block design during kharif 2015. The characterization site, Bengaluru located at 13^0 05" N latitude and 77^0 34"E longitudes. The center is at an altitude of 924 meters above mean sea level. The annual rainfall ranges from 528 mm to 1374.4 mm with the mean of 915.8 mm. The germplasm accession were divided into 13 blocks, each consisted of 40 accessions and 3 check varieties namely GPU 45, GPU 28 and PR202. Each accession was grown in single row of 3 meter length, spaced 30cm apart, plant to plant spacing within the row was 10 cm. Crop was supplied with recommended dose of fertilizer of 50 kg N ha^{-1}, 50 kg P_2O_5 ha^{-1} and 50 kg K_2O ha^{-1} as a basal dose and 50 kg N ha^{-1} at the time of earthing up. The experiment was provided with life saving irrigation and protected from weeds, pests and diseases.

Observations were recorded from 5 randomly selected plants in each accessions for 8 quantitative characters such as Days to 50 per cent flowering, Plant height (cm), Number of basal tillers, Finger length (cm), Finger width (cm), Number of fingers per ear, Grain yield per plant (g) and Straw weight (g) as per the descriptors for *Elusine corocana* (Anonymous, 1985) except days to flowering. Flowering was recorded on single row basis.

Mean, Range, variance and standard deviation were worked out by adapting standard methods (Panse and Sukathme, 1964) using SPSS statistical package. Phenotypic correlation coefficients were calculated using the formula as suggested by Johnson *et al.* (1955). Phenotypic correlations were estimated among all traits in the entire germplasm and identified number of significant and meaningful correlation.

The data collected for all quantitative characters were subjected to analysis of variance for augmented block design according to the method suggested by Federer and Raghavarao, 1975. Principal Component Analysis (PCA) was computed using WINDOWS STAT statistical package as suggested by Johnson and Wichern (1988). PCA was computed for 8 quantitative traits to find out the relative importance of different traits in capturing the variation in entire core germplasm. Eight quantitative traits were subjected to multivariate K means cluster (Lloyd, 1982) analysis using the software WINDOWS STAT.

Results and Discussion

The mean range and variance for all the eight quantitative traits are given in Table I. Days to 50 per cent flowering was ranged from 31(GEC - 90) to 90 (GEC - 204) days, with mean value of 62.15. This shows that wide variation exists in the germplasm. GEC-90 and GEC-87 accessions early to flower, hence these accessions could be utilized for developing early duration varieties in finger millet. In the entire core set GEC 242 showed lowest plant height of 66.80 cm. Accession GEC73, GEC 1 and GEC 294 recorded more number of basal tillers of 8.20, 7.80 and 7.80 in the entire set of core accessions. With respect to the character finger length and number of fingers per ear, wide range of variation was observed from 2.60 (GEC 186) to 11.6 (GEC 516) cm for finger length, 4.60 (GEC 300) to 11.4 (GEC 169) for number of fingers. Accessions GEC 516, GEC 17, GEC 169, GEC 13 could be used to develop high yielding varieties as these accessions are having high finger length and maximum number of fingers per ear. Similarly for the

TABLE I

Pattern of genetic variability for 8 quantitative traits in 520 finger millet core germplasm

Characters	Mean	Range	Minimum	Maximum	Variance	Std. Deviation	Sem
Days to 50% flowering	62.15	59.00	31.00	90.00	42.30	6.50	0.29
Plant height (cm)	104.19	177.20	66.80	244.00	246.95	15.71	0.69
Number of basal tillers	3.91	7.00	1.20	8.20	0.94	0.97	0.04
Finger length (cm)	5.78	9.00	2.60	11.60	2.18	1.48	0.06
Finger width (cm)	0.92	2.70	0.44	3.14	0.06	0.25	0.01
Number of fingers per ear	6.94	6.80	4.60	11.40	1.07	1.03	0.05
Straw weight/plant (g)	53.06	162.85	8.50	171.35	468.26	28.25	1.23
Grain yield/plant (g)	9.59	18.95	2.2	21.15	15.404	3.92	0.17

character grain yield per plant ranged from 2.20 g to 21.15 g with mean yield of 9.59. Accessions GEC 529 (21.15 g), GEC 399 (21.13 g) and GEC 258 (21.06 g) showed maximum grain yield. Straw weight ranged from 8.50 g (GEC 380) to 171.35g (GEC 365), Maximum straw weight was recorded by accessions GEC 365 (171.35 g) and GEC 51 (170 g). Similar results for wide range of variations for plant height and grain yield per plant (Ganapathy *et al.,* 2011), finger length and number (Sarjan *et al.,* 2018) and plant height and productive tillers (Owere *et al*., 2015) were reported earlier. Top 20 accessions of finger millet identified for their superior agronomic traits are presented Table II. This wide range of variation for all the characters can be exploited to develop high yielding dwarf and early type varieties of finger millet. Similarly these accessions can be used as parent for hybridization to improve some specific traits in released varieties.

Analysis of variance showed significant difference for all the quantitative characters in the entire core set of accessions suggesting significant variability for all the traits. Hence, there is an opportunity for plant breeder to undertake further breeding activities like hybridization programme. Substantial variation in finger millet has been reported in previous studies by Naik *et al.* (1994) and Prasad Rao *et al*. (1994).

Correlation

Grain yield is a complex character influenced by a large number of other component characters. A knowledge on the association between yield and other biometrical traits and also among component traits helps in improving the efficiency of selection. The correlation between the characters may exist due to various reasons such as pleiotropy, genetic linkage and association of loci or blocks of loci governing variability for different characters located on same chromosome.

The association of all morphological traits was estimated by correlation analysis (Table III). Among the 8 morphological traits studied Number of basal tillers per plant (0.297), Number of finger per ear (0.127) and straw weight (0.299) had significant and positive correlation with grain yield per plant at P = 0.01 level. Earlier workers Kadam *et al*, 2009 and Dagnachew *et al*, 2012 reported that number of number of fingers per ear and productive tillers per plant has significant positive association with grain yield. Similarly days to 50 per cent flowering has significant positive correlation with plant height (0.109), Finger length (0.094). Plant height has significant positive association with finger length (0.242), finger width (0.190) and straw weight (0.369). Number of productive tillers plant, finger length and finger width has significant positive association with straw weight. Maximum positive correlation observed for most of the characters with grain yield per plant, indicated that all these characters could be simultaneously improved and it also suggested that increase in any one of them would lead to improvement in other character. Hence selection

TABLE II

Top 20 accessions of finger millet identified for their superior agronomic traits

High yielding accessions		Early flowering accessions		Dwarf accessions		Accessions with more no. of basal tillers		Accessions with longer finger length		Accessions with more number of fingers		Accessions with more straw weight	
Germplasm Accession no.	Grain yield per plant (g)	Germplasm Accession no.	Days to 50% flowering	Germplasm Accession no.	Plant height (cm)	Germplasm Accession	No. of basal tillers	Germplasm Accession no.	Finger length (cm)	Germplasm Accession no.	No. of finger per ear	Germplasm Accession no.	Straw weight (g)
GEC-529	21.15	GEC-90	31.00	GEC-242	66.80	GEC-73	8.20	GEC-516	11.60	GEC-169	11.40	GEC-365	171.35
GEC-399	21.13	GEC-87	32.00	GEC-350	68.20	GEC-1	7.80	GEC-17	10.40	GEC-131	11.20	GEC-51	170.00
GEC-258	21.06	GEC-89	32.00	GEC-400	69.60	GEC-294	7.80	GEC-73	10.38	GEC-149	11.20	GEC-73	141.30
GEC-55	21.01	GEC-91	32.00	GEC-348	69.80	GEC-112	7.60	GEC-104	10.36	GEC-114	11.00	GEC-164	134.75
GEC-365	20.94	GEC-93	32.00	GEC-57	70.80	GEC-101	7.40	GEC-136	10.34	GEC-1	10.80	GEC-92	125.00
GEC-112	20.79	GEC-115	32.00	GEC-509	72.00	GEC-110	7.20	GEC-81	10.12	GEC-406	10.80	GEC-312	118.20
GEC-220	20.32	GEC-140	32.00	GEC-259	72.60	GEC-37	7.00	GEC-224	10.00	GEC-113	10.60	GEC-452	115.00
GEC-56	20.12	GEC-301	32.00	GEC-332	73.00	GEC-56	7.00	GEC-34	9.92	GEC-23	10.00	GEC-310	114.40
GEC-163	20.12	GEC-447	32.00	GEC-279	74.80	GEC-347	7.00	GEC-284	9.52	GEC-58	9.80	GEC-399	113.90
GEC-201	19.86	GEC-117	33.00	GEC-59	75.00	GEC-163	6.60	GEC-331	9.52	GEC-339	9.60	GEC-371	110.75
GEC-17	19.56	GEC-104	34.00	GEC-347	75.60	GEC-434	6.60	GEC-377	9.50	GEC-103	9.40	GEC-182	110.00
GEC-452	19.52	GEC-365	34.00	GEC-401	75.60	GEC-116	6.50	GEC-347	9.44	GEC-173	9.20	GEC-18	108.45
GEC-30	19.23	GEC-113	48.00	GEC-276	75.80	GEC-229	6.50	GEC-450	9.40	GEC-283	9.20	GEC-4	107.55
GEC-92	19.07	GEC-114	49.00	GEC-78	76.00	GEC-171	6.40	GEC-517	9.10	GEC-286	9.20	GEC-56	103.90
GEC-246	18.98	GEC-112	50.00	GEC-260	76.20	GEC-302	6.40	GEC-342	9.06	GEC-395	9.20	GEC-546	102.25
GEC-229	18.89	GEC-33	51.00	GEC-280	76.40	GEC-435	6.40	GEC-317	9.06	GEC-432	9.20	GEC-15	100.25
GEC-73	18.85	GEC-23	52.00	GEC-330	76.60	GEC-52	6.20	GEC-220	9.00	GEC-100	9.00	GEC-38	98.40
GEC-312	18.67	GEC-58	52.00	GEC-151	77.20	GEC-15	6.00	GEC-164	8.96	GEC-294	9.00	GEC-435	98.10
GEC-394	18.38	GEC-220	52.00	GEC-495	77.60	GEC-102	6.00	GEC-71	8.86	GEC-374	9.00	GEC-50	98.00
GEC-453	18.35	GEC-459	52.00	GEC-402	78.40	GEC-547	6.00	GEC-29	8.76	GEC-28	8.80	GEC-335	98.00

TABLE III

Phenotypic correlation co-efficient between 8 quantitative traits in 520 finger millet germplasm

Characters	Days to 50% flowering	Plant height (cm)	No. of basal tillers	Finger length (cm)	Finger width (cm)	No. of fingers per ear	Straw weight per plant (g)	Grain yield per plant (g)
Days to 50% flowering	1.000	0.109 *	- 0.070	0.094 *	- 0.001	- 0.230 **	0.107	- 0.263 **
Plant height (cm)		1.000	- 0.116 **	0.242 **	0.190 **	- 0.027	0.369 **	- 0.011
No. of basal		1.000	- 0.020	0.021	0.023	0.212 **	0.297 **	Tillers
Finger length (cm)				1.000	0.130 **	0.049	0.145 **	-0.018
Finger width (cm)					1.000	0.010	0.110 *	0.045
No. of fingers per ear						1.000	- 0.153 **	0.127 **
Straw weight per plant (g)							1.000	0.299 **
Grain yield per								1.000

criteria should consider all these characters for the improvement of grain yield in finger millet.

Significant negative correlation observed for days to 50 per cent flowering (-0.263) with grain yield per plant (P = 0.01). this indicates that increase in one character would lead to decrease in other character. Negative association of days to flowering with grain yield is beneficial association because early types are most preferred by farmers. Early types will escape from drought situations. Similarly days to 50 per cent flowering has negative association with grain yield has been reported by Thippeswamy and Sajjanar (2017) in foxtail millet.

Principal Component Analysis

PCA was applied as a reductionist approach of the multivariate data, to measure the importance and contribution of each component to the total variance. PCA provides information on the independent impact of a particular trait to the total variance, wherein each coefficient of Eigen Vectors indicates the degree of contribution of every original variable, with which each principal component is associated. PCA analysis revealed the importance of the first five principal components in discriminating the entire core set of finger millet germplasm. The percentage of variation explained by the first four principal components and the vector loadings for each agronomic characters and PC are given in Table IV.

TABLE IV

Vector loadings and percentage of variation explained by the first four principal Components in 520 fingermillet germplasm

	PC1	PC2	PC3	PC4
Eigen Value	1.61	1.50	1.20	0.90
Variance explained (%)	20.07	18.72	15.05	11.22
Cumulative variance explained (%)	20.07	38.80	53.84	65.06
Eigen vectors				
Days to 50% flowering	0.51	0.15	0.35	0.16
Plant height (cm)	0.47	-0.29	-0.26	0.05
Number of basal tillers	-0.26	-0.43	0.40	0.01
Finger length (cm)	0.35	-0.25	-0.36	0.41
Finger width (cm)	0.22	-0.32	-0.29	-0.79
Number of fingers per ear	-0.31	-0.16	-0.53	0.38
Straw weight/plant (g)	0.28	-0.46	0.38	0.18
Grain yield/plant (g)	-0.34	-0.55	0.10	0.01

The percentage of total variation explained by four principal components was 65.06 per cent. The PC 1, the most important coordinate accounted for 20.07 per cent in the entire core set germplasm. PC 1 separates accessions mainly on 5 traits (Days to 50 per cent flowering, Plant height, Finger length, Finger width, and straw weight). Days to 50 per cent flowering (0.51) contributed more to the variation followed by plant height (0.47), Finger length (0.35), straw weight (0.28) and finger width (0.22) had the highest loadings in PC1 indicating their significant importance for these components. These traits had the largest participation in the divergence and carried the largest portion of its variability. All other characters contributed negative to the first component.

Second principle component (PC 2) contributed 18.72 per cent of the total variation. A day to 50 per cent flowering is the only character which contributed more to the variation while all other character characters contributed negatively. In third principal component (PC3) characters *viz.,* Number of basal tillers (0.40), straw weight (0.38) and Days to 50 per cent flowering (0.35) contributed more for variation. Likewise the fourth principal component contributed 11.2 per cent of the total variation. The major characters that contributed highly to the variation include finger length (0.41), Number of fingers per ear (0.38), straw weight (0.18) and days to 50 per cent flowering (0.16). Considering the principle component analysis in the entire core set germplasm, three traits (Days to 50 per cent flowering, finger length and straw weight) expressed more variance in the first four principle component analysis, indicating their importance for characterization of finger millet germplasm accessions and these traits could be effectively used for further breeding programmes to create more variability. Characters with high variability are expected to provide high level of transgressive segregation in breeding populations. This is important for breeder to investigate high yielding, early maturing and dwarf varieties through conventional breeding. Similar findings with regard to contribution of characters to total variance Salini *et al.* (2010) in proso millet observed grain yield per plant, plant height, days to flowering and productive tillers per plant were contributed more for variance. Likewise in maize, Azad *et al.* (2012) reported traits such as grain yield per plant and plant height contributed more for total variance.

Diversity Analysis

K means cluster analysis based on quantitative traits divided 520 core set finger millet germplasm in to 23 clusters (Table V). The clustering pattern could be utilized in choosing the diverse genotypes which were likely to generate the highest possible variability for various economic characters. Cluster 6 was the largest comprising of 42 accessions which were mostly characterized by tall plants with longer finger length and low yielding accession. Cluster 13 comprising of 41 accessions which were predominantly characterized by dwarf types with medium duration accessions. Apart from cluster 6 and 13 large number of core accessions were grouped in clusters 3, 18, 16, 23 and 14 with 35, 34, 32, 30 and 29 accessions, respectively.

TABLE V

Number of accessions constituted in 23 clusters of 520 finger millet germplasm

Cluster number	No. of Accessions in the cluster	Cluster number	No. of Accessions in the cluster
1	13	13	41
2	23	14	29
3	35	15	13
4	14	16	32
5	8	17	16
6	42	18	34
7	27	19	25
8	17	20	21
9	25	21	1
10	25	22	14
11	28	23	30
12	7		

Cluster 21, 12, and 5 has less number of accessions. These clusters had wide diversity for various characters. Hybridization using genotypes belong to cluster 21, 12, and 5 might be used for exploitation of hybrid vigour. Similar results were reported by Salini *et, al.* (2010) using Proso millet genotypes were grouped into 17 clusters. Geethanjali and Jagadeeshwar (2016) reported four clusters in foxtail millet and Ulaganathan and Nirmalakumari, 2015 reported 16 clusters in finger millet germplasm. Murugan and Nirmalakumari (2006) grouped seventy five genotypes into nine clusters, Selvarani and Gomathinayagam (2000) grouped fifty genotypes into six clusters, Maloo and Bhattachargee (1999) grouped forty genotypes into four clusters in foxtail millet germplasm.

TABLE VI

The average of 8 quantitative traits for each cluster in 520 finger millet Germplasm

Cluster number	Days to 50% flowering	Plant height (cm)	No. of basal Tillers	Finger length (cm)	Finger width (cm)	No. of fingers per ear	Straw weight per plant (g)	Grain yield per plant (g)
1	44.69	92.32	4.42	5.13	0.90	8.29	7.15	12.67
2	67.00	108.27	3.42	6.28	0.98	6.37	55.00	5.20
3	62.14	101.97	3.99	5.52	0.88	7.04	46.30	9.08
4	57.93	113.26	5.20	6.44	1.07	6.74	96.95	17.45
5	37.88	112.00	4.64	6.62	1.13	7.28	66.30	13.52
6	67.36	120.86	3.32	5.89	0.99	6.43	62.05	6.59
7	58.48	100.08	4.56	5.54	0.86	7.44	55.05	15.73
8	67.18	98.76	3.64	5.91	0.83	6.49	48.60	5.14
9	59.28	84.58	3.80	4.73	0.89	7.36	34.95	9.73
10	63.20	107.08	3.92	6.10	0.86	6.88	54.30	8.00
11	58.36	93.67	4.09	5.38	0.84	7.31	46.60	12.04
12	69.86	77.00	4.01	6.10	0.83	5.97	37.00	4.14
13	61.90	89.72	3.72	5.01	0.86	6.79	29.15	8.25
14	65.28	126.27	3.93	6.41	1.09	6.84	70.95	10.69
15	60.54	73.22	3.98	4.52	0.77	6.52	33.55	8.52
16	60.69	107.97	4.14	5.87	0.92	7.21	56.85	12.46
17	68.19	137.91	3.74	7.12	0.90	7.01	65.05	6.32
18	61.32	96.04	3.88	5.58	0.92	6.99	42.15	10.77
19	61.20	117.11	3.98	6.52	0.97	7.09	65.50	12.74
20	63.67	95.51	3.61	5.53	0.89	6.85	46.25	6.80
21	62.00	244.00	2.20	4.54	0.94	6.80	32.50	13.89
22	70.21	90.16	3.93	5.48	0.91	6.44	47.70	5.35
23	64.07	112.35	3.73	6.43	0.95	7.06	58.05	8.70

Cluster means for all eight quantitative characters traits were presented in Table VI. Accession in the cluster four had shown more grain yield followed by cluster 7, cluster 21 and cluster 5. Whereas genotypes in cluster 12 has less mean grain yield. Other cluster which showed less mean grain yield are cluster 22, cluster 2 and cluster 8.

Accessions which are present in these diverse clusters can be utilized for hybridization to get transgressive segregants for the trait, which could be used for developing superior high yielding varieties. Accessions which are present in the clusters 9, 13, 22 and 1 comprised of dwarf types, these accessions could be utilized in developing dwarf types in finger millet. Cluster 4, 5 and 7 comprised of accessions with more number of tillers. Accessions which are present in clusters 1, 5, 7, 9 and 11 have more number of fingers. These accessions could be utilized in developing high yielding types as number of productive tillers is positively correlated with grain yield. Likewise genotypes in diverse clusters could be utilized in hybridization programme to develop high yielding, dwarf and early duration types in finger millet.

Germplasm evaluation and characterization is important for plant breeders and multivariate statistical analysis provides a means for estimating morphological diversity between germplasm accessions these tools are useful for the evaluation of potential breeding value of germplasm. In the present study wide variation was observed for quantitative traits. In PCA traits Days to fifty percent flowering, finger length, straw weight and finger width were found as more important for characterizing finger millet germplasm, as these traits explained more variation. For selection of yield number of basal tillers and number of fingers per ear could be indirectly used for selection as these traits are positively correlated. Intercrossing between genotypes of diverse clusters would generate broad spectrum of variability for effective selection in segregating generations for development of high yielding cultivars. Accession GEC 254 formed solitary cluster and found to be more variable thus crosses among the genotypes would exhibit high heterosis and may produce new recombinants with desired characters.

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