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Genetic Diversity Study in Finger Millet (*Eleusine coracana* L.) Genotypes: A Multivariate Analysis Approach

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ABSTRACT

Multivariate analysis is an important statistical tool through which we can easily assesses important polygenic characters which are of great importance in a plant breeding programme. The experiment was conducted during kharif, 2016 with 65 germplasm accessions of finger millet to study genetic diversity for yield and yield contributing traits at Hill Millet Research Station, Waghai, Dangs, Gujarat in a randomize block design. The observations for eight morphological characters were recorded. Two multivariate techniques, principal component analysis and cluster analysis were applied. Principal component analysis indicates that three principal components PC-1, PC-2 and PC-3 explains 42.81%, 18.43% and 11.80% respectively of the total variation. The first principal component had showed positive loading for all eight characters considered except for number of tillers per plant. The second principal component had positive loading for two characters viz., days to number of tillers per plant and grain yield while the third principal component had positive loading values for days to 50% flowering, days to maturity, plant height, length of main ear, number of tillers per plant. In cluster analysis sixty five genotypes were grouped into five distinct clusters on basis of Euclidean distance. The result of present study could be exploited in planning and execution of future breeding strategy in finger millet.

Keywords: *Principal component analysis, Cluster analysis, Finger millet, Genetic diversity.*

INTRODUCTION

Finger millet is an important small millet grown at large scale in continent of Asia and Africa. It was domesticated around 5000 years ago in eastern Africa (possibly Ethiopia) and introduced in India about 3000 years ago[4]. It is an important staple food after rice, wheat, pearl millet and sorghum in India. It provides food for millions of people residing in arid and semi-arid tropics.

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In India, it is cultivated on 1.2 million hectares with a production of 2.06 million tones and average productivity of 1706 kilogram per hectar[1]. Finger millet as compared to the other crops is a very rich source of calcium; the calcium content is thirty times more than that of rice and wheat[12]. Finger millet grains especially the seed coat contains high amount of various phenolic compounds which exhibit anti-oxidant activity[13]. The higher fiber content of finger millet prevents constipation, high cholesterol formation and intestinal cancer. It has been found that its grain contain 65-75 per cent carbohydrate, 5-8 per cent protein, 15-20 per cent dietary fiber and 2.5-3.5 per cent minerals[3]. The crop is hardy in nature and well suited to upland farming ecosystems because of its faster growing habit, early maturity and its better performance under adverse conditions.

In any crop improvement program genetic variability and diversity play very important role. The higher diversity between parents shows higher heterosis in progeny and more chance of getting transgressive segregation. To develop improved crop variety over existing cultivated variety, breeder has to identify diverse parents having high genetic variability for combining desirable characters.

Multivariate analysis is very important tool to study morphologically complex individuals and for measuring the degree of divergence between different populations. Multivariate technique is useful for analyzing multiple measurements on each individual under study. It is widely used in analysis of genetic diversity whether it is morphological, molecular marker or biochemical. Among the multivariate techniques, principal component analysis (PCA) and cluster analysis have been very important in selecting genotypes for breeding program that meet the objective of a plant breeder. The main advantage of using PCA over cluster analysis is that each genotype is assigned to one group only[8].

The objective of this study is to find out relative contribution of various traits for total variability of finger millet genotypes using PCA and also aiming to group genotypes into distinct clusters by cluster analysis.

MATERIAL AND METHODS

The experiment was conducted at Hill Millet Research Station, Navsari Agricultural University, Waghai (Dangs) using 65 genotypes of finger millets in randomized block design with three replications during *kharif*, 2016. The gross plot is divided into three blocks which were taken as a replications while the blocks are further divided into equal 65 plots. Data of eight different characters *viz.* days to 50% flowering (DF), days to maturity (DM), plant height (PH), length of main ear (LME), number of tillers per plant (NTPE), number of fingers per ear (NFPE), grain yield (GY), straw yield (SY) were taken from ten randomly selected plants from each replication. PCA and cluster analysis were performed using R and R-studio software.

RESULTS AND DISCUSSION

Descriptive Statistics

The mean values of the data were subjected to statistical analysis in order to study the descriptive statistics like mean, variance, maximum, minimum, skewness, kurtosis and coefficient of variation (%). (Table 1) The genotypes in the collection can flower as early as 74 days and late as 110 days with a mean of 98.64 days. Days to maturity ranged from 101 to 146 days with a mean of 129.5 days. Plant height varies from 98.6 to 147.27 cm with an average of 132.62 cm. Length of main ear varies from 5.53 to 10.4 cm with an average of 7.8 cm. Number of tillers of plant ranges between 6 and 10 with a mean of 7.24. Grain yield per plant varies from 1.18 to 4.39 g with an average of 2.98 g. Straw yield per plant ranges between 3.66 to 16.4 g with an average of 9.49 g. The traits like length of main ear, number of tillers per plant, number of finger per ear and straw yield per plant were found positively skewed while all the other traits were negatively skewed. Maximum kurtosis was observed in plant height while the minimum kurtosis was observed in grain yield

per plant. The coefficient of variation ranges between 5.74 to 33.72%.

Correlation studies

Pair panels for 8 X 8 matrices represent correlation, histogram and bivariate scatter plot of eight morphological traits. (Fig 1). Upper half represents correlation coefficients while the lower half represents bivariate scatter plot among different variables. Diagonal represent whether different variables are normally distributed or not. The highest correlations were observed between days to flowering and days to maturity. The diagonal represents the type of the distribution of various traits.

Principal component analysis

Bhanupriya *et al.*[2] studied genetic diversity of wheat genotypes based on principal component analysis in Gangetic alluvial soil of West Bengal. They showed five principal components with lateral roots greater than one contributed 75 per cent of total variation. Salini *et a.l*[9] evaluated 368 genotypes of proso millet based on principal component analysis and found that first five Eigen vectors contributed about 93.2 per cent of total variance. Sinha and Mishra[11]. studied variability for eighteen quantitative characters of 55 rice landraces and found that the first five principal component contributed 74.34 per cent of total variability. Khan *et al.*[6]. studied multivariate analysis for morphological diversity of bread wheat (*Triticum aestivum* L.) germplasm lines in Kashmir valley and the result revealed that three principal components with Eigen value grater then one contributed 83.60 percent of total variation for days to flowering, days to maturity, yield, plant height. The units of different variables were not same so normalization of variables was carried out before analysis. Principal component analysis in this study showed that first five principal component shows 90.09 per cent of the entire variability. The first principal component shows 42.81 per cent of total variability due to all the characters except for number of tillers per plant. Second principal component accounted for 18.43 per cent of total variability originated primarily due to days 50 percent flowering, number of tillers per plant, grain yield and straw yield. Third principal component which explains 11.80 per cent of total variability because of days to 50% flowering, days to maturity, length of main ear, plant height and number of tillers per plant. Fourth principal component accounts 9.36 per cent of gross variability primarly due to plant height and grain yield (Table 2 & 3). Bi-plot represents distribution of accessions on the basis of PC-1 and PC-2 scores and relationship of different traits with PC-1 and PC-2. (Fig. 2). From the results it can be concluded that days to 50% flowering, days to maturity, plant height, grain yield and straw yield are important traits from breeding aspects to distinguish between accessions.

Cluster analysis

Karad and Patil[5] studied a set of sixty five finger millet accessions for twelve morphological characteristics and grouped the accessions into five distinct clusters in which Cluster I was largest with 236 accessions followed by 36 in cluster II, 12 in cluster X, 14 each in cluster VI and XV. were found with, , 14, 14, accessions respectively. Cluster IX comprised of 10 accessions , Cluster VIII had 8 accessions, cluster XII with 6 accessions and cluster XI and V with 4 accessions each. Clusters III and IV consisted of 2 accessions and remaining clusters were found with single accessions. Salini *et al.*[9] studied 364 genotypes of proso millet and grouped these accessions into seventeen distinct clusters. Kumar *et al.*[7] studied one hundred and fourty diverse genotypes of finger millet for genetic divergence study and grouped these genotypes in ten different clusters. Hierarchal cluster analysis was carried out in this study using distinct 65 genotypes which were grouped into five distinct cluster. The clusters formed were non-overlapping in nature. Cluster V was largest with eighteen accessions and cluster III was smallest with nine accessions (Table 4). The clustering pattern was represented using the dendrogram (Figure 3). Hybridization can be exploited best when carried between accessions of distinct clusters under the diversity studies.

Table 1: Mean values of different yield and yield contributing traits in finger millet

Particulars	Max.	Min.	Mean	Variance	Skewness	Kurtosis	CV %
Days to 50% flowering	110	74	98.64	58.17	-1.20	4.67	7.73
Days to maturity	146	101	129.5	55.43	-1.16	6.54	5.74
Plant height (cm)	147.27	98.6	132.62	65.58	-1.22	6.90	6.10
Length of main ear (cm)	10.4	5.53	7.80	1.65	0.07	2.03	16.46
Number of tillers per plant	5	2	2.88	0.31	0.37	2.30	19.33
Number of finger per ear	10	6	7.24	0.54	0.33	2.71	10.14
Grain yield per plant (g)	4.39	1.18	2.98	1.01	-0.307	1.83	33.72
Straw yield per plant (g)	16.4	3.66	9.49	9.47	0.08	2.07	32.42

Table 2: Principal components showing the Eigen values, proportion of variance explained and cumulative variance

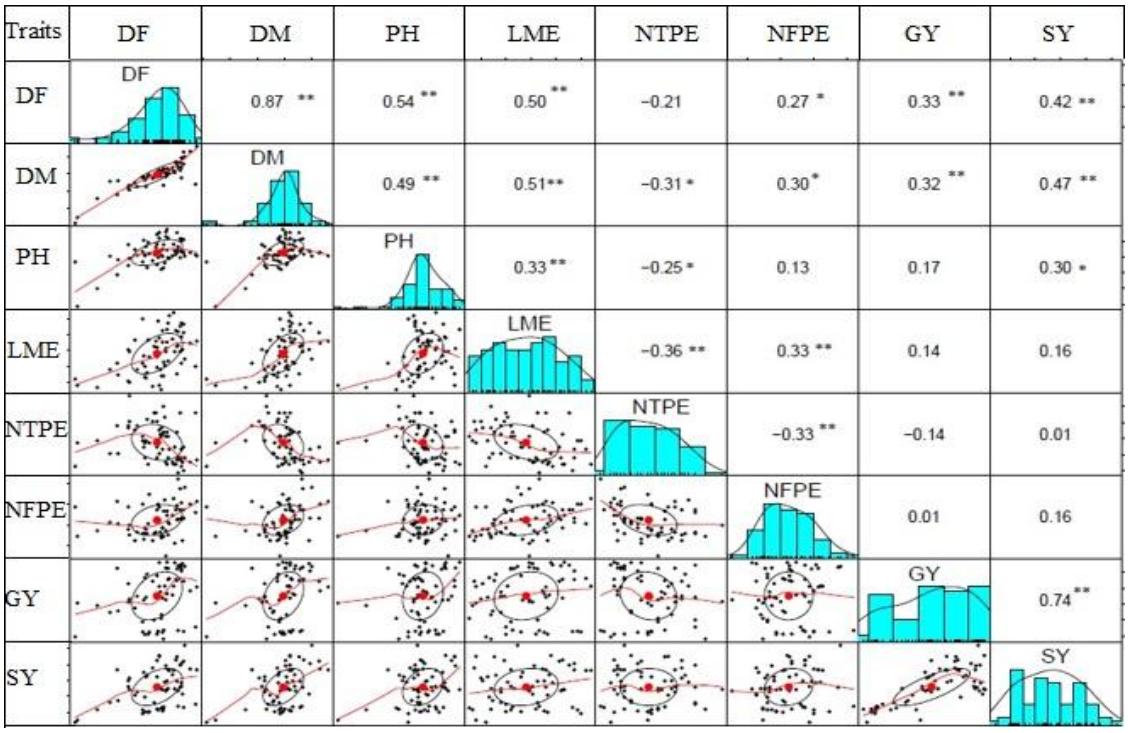
Principal Component	Eigen Value	Variation (%)	Cumulative variance (%)
1	1.850	42.81	42.81
2	1.214	18.43	61.24
3	0.971	11.80	73.05
4	0.865	9.36	82.40
5	0.784	7.68	90.09
6	0.697	6.08	96.17
7	0.457	2.61	98.79
8	0.310	1.20	100

Table 3: Principal component analysis for 8 quantitative traits in 65 finger millet genotypes non-rotated loadings

Particulars	PC1	PC2	PC3	PC4
Days to 50% flowering	0.4660	-0.0162	0.3247	-0.1655
Days to maturity	0.4760	-0.0392	0.2247	-0.1310
Plant height (cm)	0.3477	-0.0629	0.4346	0.2899
Length of main ear (cm)	0.3500	-0.3245	0.0046	-0.0010
Number of tillers per plant	-0.2364	0.4101	0.4420	-0.6560
Number of fingers per ear	0.2317	-0.3663	-0.5153	-0.6007
Grain yield (g)	0.2913	0.5474	-0.3809	0.2455
Straw yield (g)	0.3438	0.5354	-0.2214	-0.1406

Table 4: Distribution of 65 finger millet germplasm accessions into five distinct clusters

Clusters	Number of genotypes	Constituent accessions
I	**15**	WN-569, WN-591, WN-467, WN-559, WN-561, WN-566, WN-567, WN-572, WN-577, WN-592, WN-609, WN-581, WWN-28, GNN-7, WWN-26.
II	**13**	WN-584, WN-562, GPU-67, WN-593, GN-4, PR-202, WWN-32, WWN-34, WWN-35, WWN-37, WN-602, GN-5, WN-578.
III	**9**	WN-542, WN-564,WN-509, WN-510, WN-544, WN-548, WN-550, GPU-28, GNN -6.
IV	**10**	WN-586, WN-583, WN-588, WN-589, WN-594,WN-604, WN-599, WN-603, WN-627,VL-149.
V	**18**	WN-494, WN-509, WN-560, WN-585, GPU-45, WN-574, WN-575, WN-522, WN-568, WN-573, WN-576, WN-579, WN-582, WN-587, WN-590, WN-629, WN-630, WN-580.



* indicates significance at p = 0.05, ** indicates significance at p = 0.01.

Fig. 1: Pair Panels for 8 X 8 Matrices represents Pearson correlation, histogram and bivariate scatter plot among the morphological characters

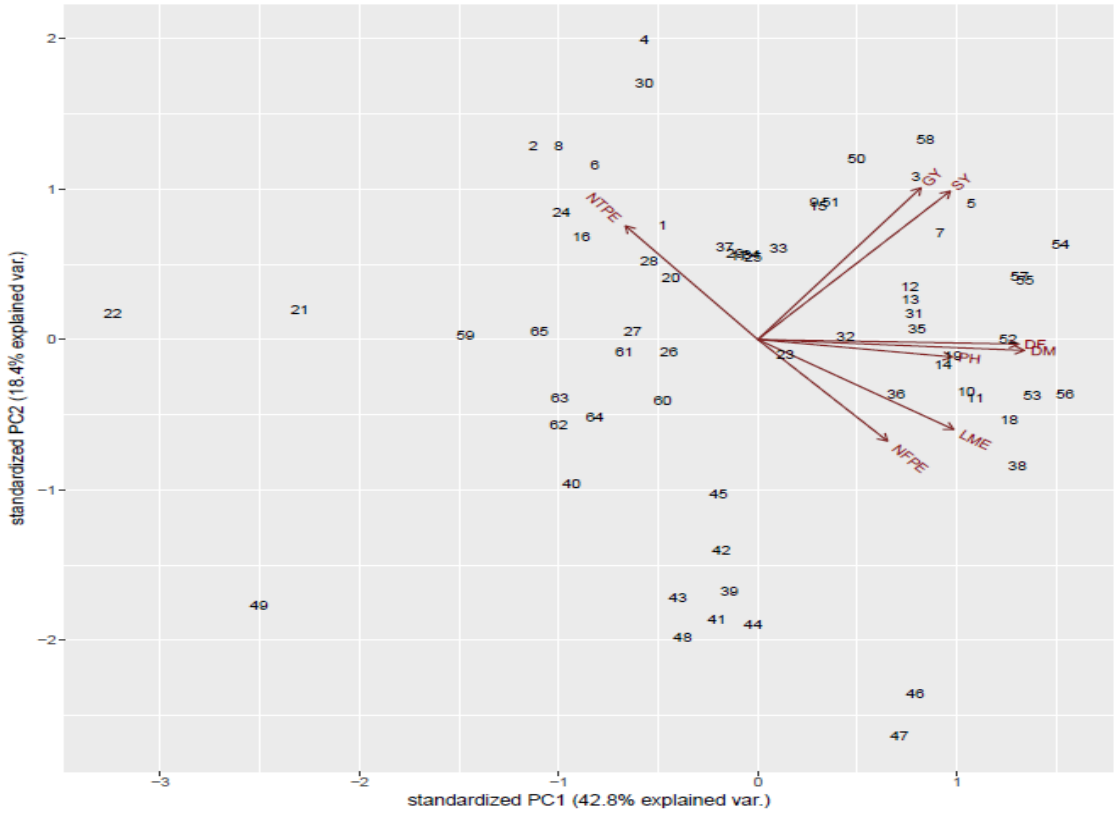


Fig. 2: Bi plot formation on basis of PC1 and PC2 values

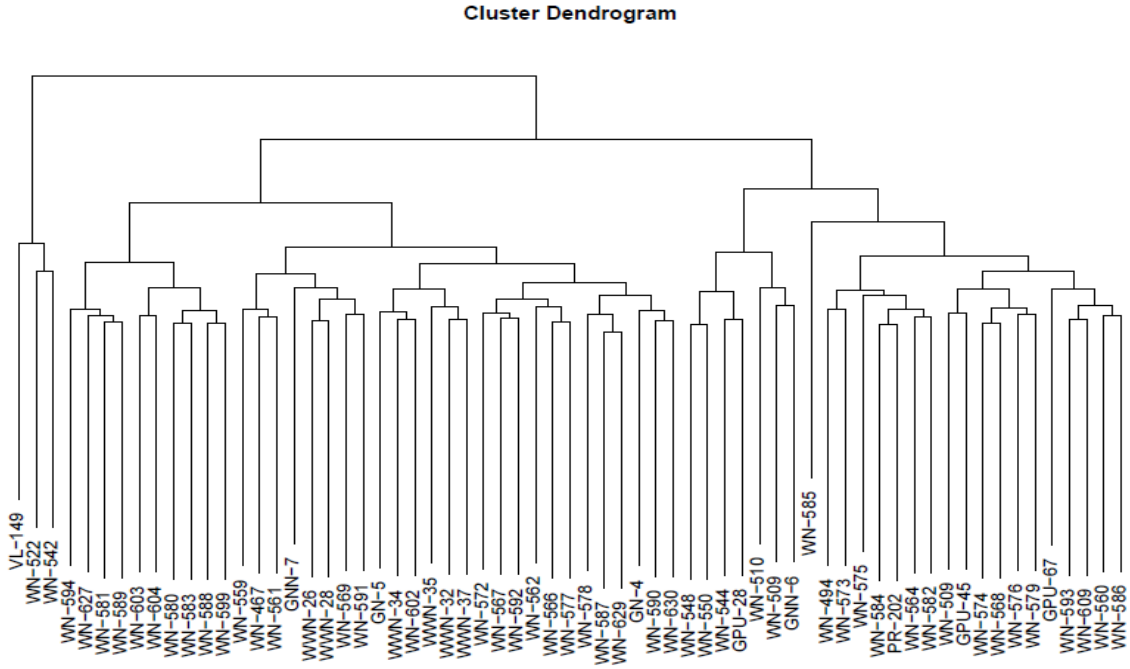


Fig. 3: Dendogram depicting clustering pattern of 65 germplasm accessions obtained by cluster analysis

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