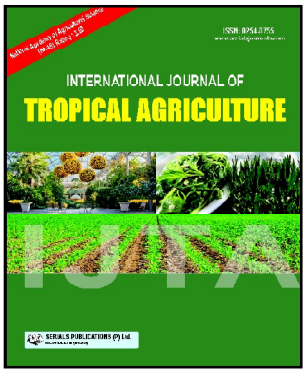

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Assessment of Genetic Diversity in Finger millet (*Eleusine coracana* L.) through Multivariate Analysis Approach

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Abstract: The experiment was conducted with 65 germplasm accessions of finger millets to study genetic diversity for yield and yield contributing traits at Hill Millet Research Station, Waghai, Dangs in randomize block design. Two Multivariate techniques, principal component analysis and cluster analysis were considered. Principal componentanalysis indicates that three principal components PC-1, PC-2 and PC-3 explains 77.46%, 13.14% and 7.71%respectively of the total variation. The first principal component had positive loading for all eight characters considered. The second principal component had positive loading for three characters viz., days to 50% flowering, days to maturity and plant height while the third principal component had positive loading values for days to 50% flowering, days to maturity, length of main ear and straw yield. 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 infinger 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 about3000 years ago (Hilu *et al.*, 1979). 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. 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 hectare (Directorate of Economics and Statistics, GOI, 2014-15). 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 (Srivastava and Sharma, 2012). Finger millet grains, particularly the seed coat, containing high amount of various phenolic compounds which have been reported to exhibit anti oxidant activity (Rao and Muralikrishna, 2002) The higher fiber content of finger millet prevents constipation, high cholesterol formation and intestinal cancer. Hence, it is recommend diabetic patients to eat finger millet and other small millets instead of rice (Pathak *et.al,* 2000). The presence of certain anti-nutritional factors in whole finger millet fractions (like phenolics, tannins, and phytates) may also help to lower the glycemic response due to decreased starch digestibility and absorption (Kumari and Sumathi 2002). It has been found that its grain contain 65-75 per cent carbohydrates, 5-8 per cent protein, 15-20 per cent dietary fiber and 2.5-3.5 per cent minerals (Chetan and Malleshi, 2007). The crop is hardy in nature and well suited to upland farming ecosystems, because of its faster growing habit and early maturity and it can perform better under adverse soil and weather conditions.

In any crop improvement program genetic variability and diversity play very import role. The higher diversity between parents shows the 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 to study morphologically complex individuals and for measuring the degree of divergence between different populations. Multivariate technique is use ful 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 has 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 assigned to one group only (Mohammadi, 2002).

The objective of this study is to find out genetic variation and to estimate relative contribution of various traits for total variability of finger millet genotypes using PCA and grouped different genotypes in to clusters by hierarchical cluster analysis.

MATERIALS 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. 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 hierarchical cluster analysis were performed using R and R-studio software.

RESULTS AND DISCUSSION

Pair panels for 8X8 matrices represents correlation, histogram and bivariate scatter plot of eight variables (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 three pairs *viz*. NPTE and GY, NPTE and SY, GY and SY. The diagonal represents histogram showing normal distribution for DM and PH, while other characters shows a skewed distribution. Moreover the units of different variables were not same so normalization of variables was carried out before analysis.

Bhanupriya *et al* in 2014 studied genetic diversity of wheat genotypes based on principle component analysis in Gangetic alluvial soil of West Bengal. They showed five principle components with lateral roots greater than one contributed 75 per cent of total variation. The result of principal component analysis showed that first Eigen vectors explained about 77.46 per cent of total variance (Table 1). Of these first three principal component with Eigen values greater than 0.78 accounted for 98.31 per cent of the entire variability. In present study first principal component has variability due to all eight characters. Second principal component accounted for 13.14 per cent of total variability originated primarily due to days to 50% flowering, days to maturity and plant height. The third principle component which explain 7.71 per cent of total variability because of days to 50% flowering, days to maturity, length of main ear and straw yield. Bi-plot represents PC1 versus PC2 which indicates that first principle component had positive loading for all eight characters considered. The second principle component had positive loading for three characters viz., flowering days, days to maturity and plant height. The glyphs in the bi-plot indicate accessions (Fig. 2). From principal component analysis it can be concluded that all the eight traits are important from breeding aspects. (Table 2).

Karad and Patil (2010) studied a set of sixty five finger millet accessions for twelve morphological characteristics. To study nature and magnitude of genetic divergence the genotypes were grouped into five clusters. Salini and *et al.* (2010) studied 364 genotypes of proso millet and grouped in to seventeen 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

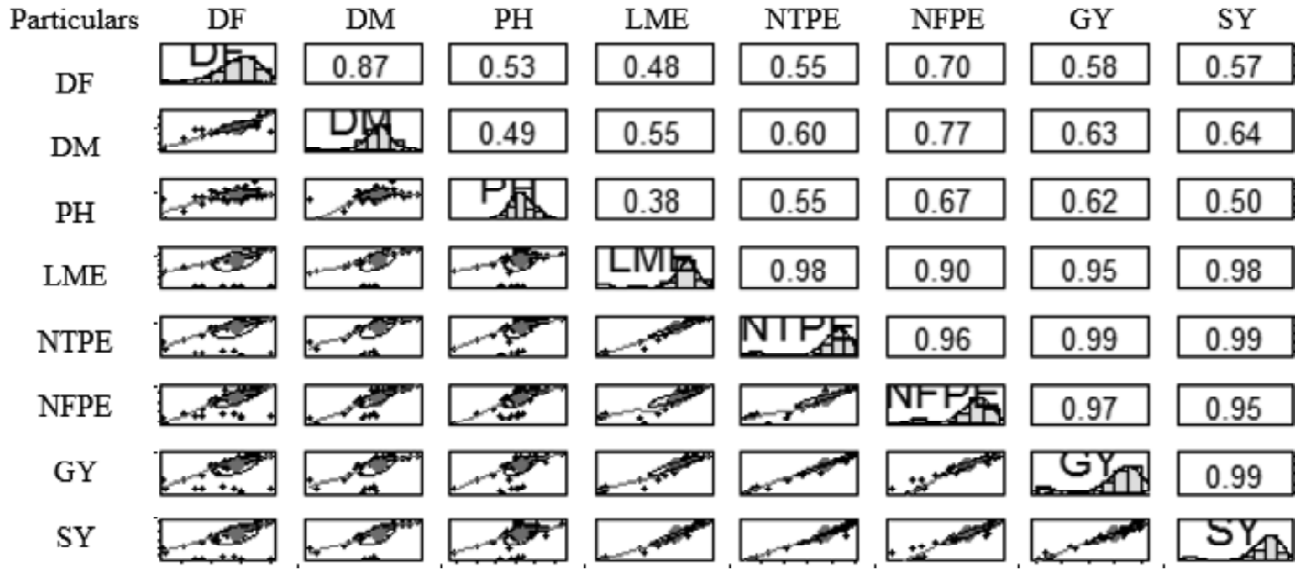

Figure 1: Pair Panels for 8X8 Matrices represents Pearson correlation, histogram and bivariate scatter plot among the morphological characters

All the correlation values were found significant at p=0.01

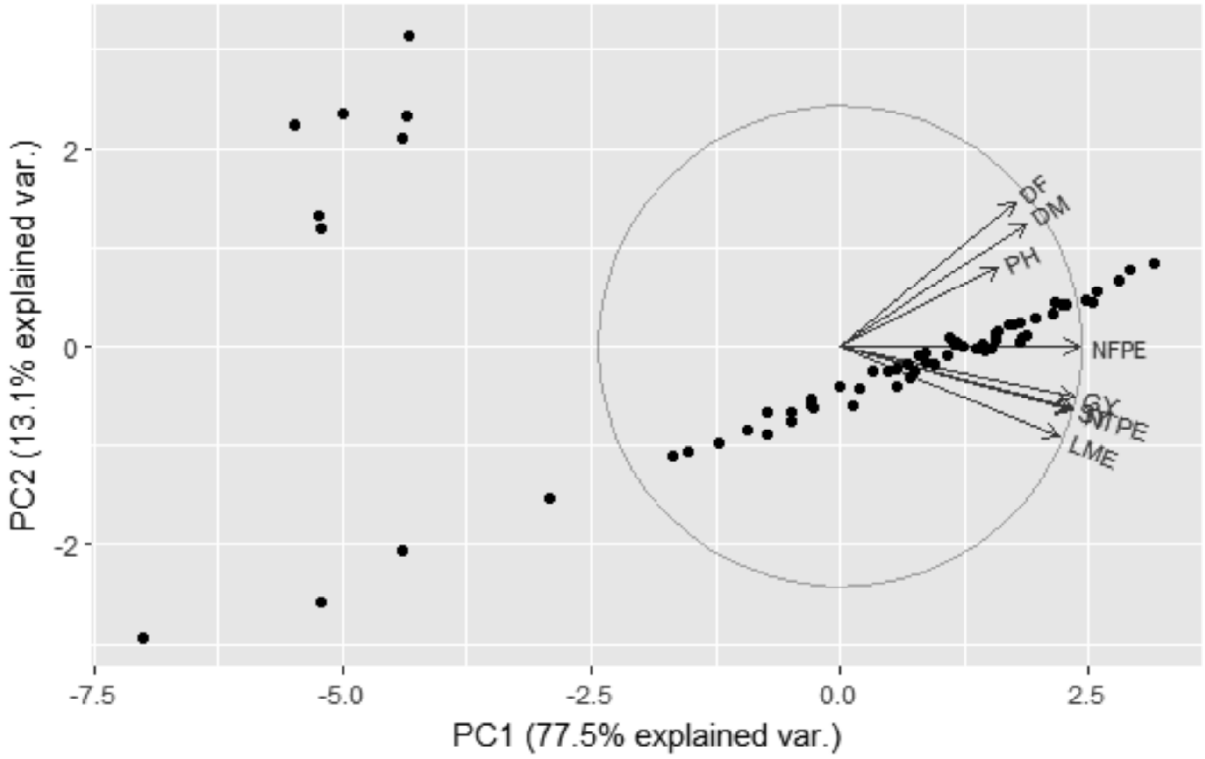

Figure 2: Bi plot formation on basis of PC1 and PC2 values

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. Kumar *et al.* (2010) studied one hundred and forty diverse genotypes of finger millet for genetic divergence study and grouped these genotype in ten different clusters. Hierarchal cluster analysis was carried out in this study using distinct 65 genotypes which were grouped in to five distinct cluster. The clusters formed were non-overlapping in nature. Fifth cluster was largest with nineteen accessions and cluster fourth was smallest with nine accessions (Table 3). The clustering pattern was represented using the dendrogram (Figure 3). Hybridization can be

Table 1
Principle components showing the Eigen values, proportion of variance explained and cumulative variance.

Principle Component	*Eigen Value*	*Variation (%)*	*Cumulative variance (%)*
1	2.489	77.46	77.46
2	1.025	13.14	90.6
3	0.785	7.71	98.31
4	0.350	1.53	99.85
5	0.103	0.13	99.98
6	0.031	0.01	99.99
7	0.002	0	1
8	0.002	0	1

Table 2
Principal component analysis for 8 quantitative traits in 65 finger millet genotypes non-rotated loadings

Particulars	*PC1*	*PC2*	*PC3*
Days to 50% flowering	0.293	0.586	0.262
Days to maturity	0.310	0.501	0.362
Plant height (cm)	0.265	0.316	-0.862
Length of main ear (cm)	0.367	-0.365	0.192
Number of tillers per plant	0.386	-0.260	-0.009
Number of finger per ear	0.399	-0.002	-0.034
Grain yield (g)	0.391	-0.204	-0.110
Straw yield (g)	0.387	-0.248	0.07

Table 3
Distribution of 65 finger millet germplasm accessions into five distinct clusters

Clusters	*Number of genotypes*	*Constituent accessions*
1	**12**	WN-494, WN-509, WN-560, WN-585, GPU-45 (NC), WN-574, WN-568, WN-576, WN-579, WN-586, WN-581, WN-627.
2	**15**	WN-569, WN-559, WN-592, WN-591, WN-599, WWN-26, WWN-28, WWN-32, WN-604, WN-467, WN-561, GN-4 (LC), WN-567, WN-566, WN-575.
3	**10**	WN-509, WN-510, WN-544, WN-548, WN-550, GPU-28, GNN -6 (LC), WN-522, WN-542, VL-149 (LC).
4	**9**	WWN-34, WWN-35, WWN-37, WN-602, GN-5 (LC), GNN-7(LC), WN-603, WN-562, WN-577.
5	**19**	WN-584, WN-587, WN-590, WN-593, WN-609, WN-629, WN-630, WN-580, WN-583, WN-588, WN-589, WN-594, WN-578, WN-572, WN-564, WN-573, WN-582, PR-202(NC), GPU-67(NC)

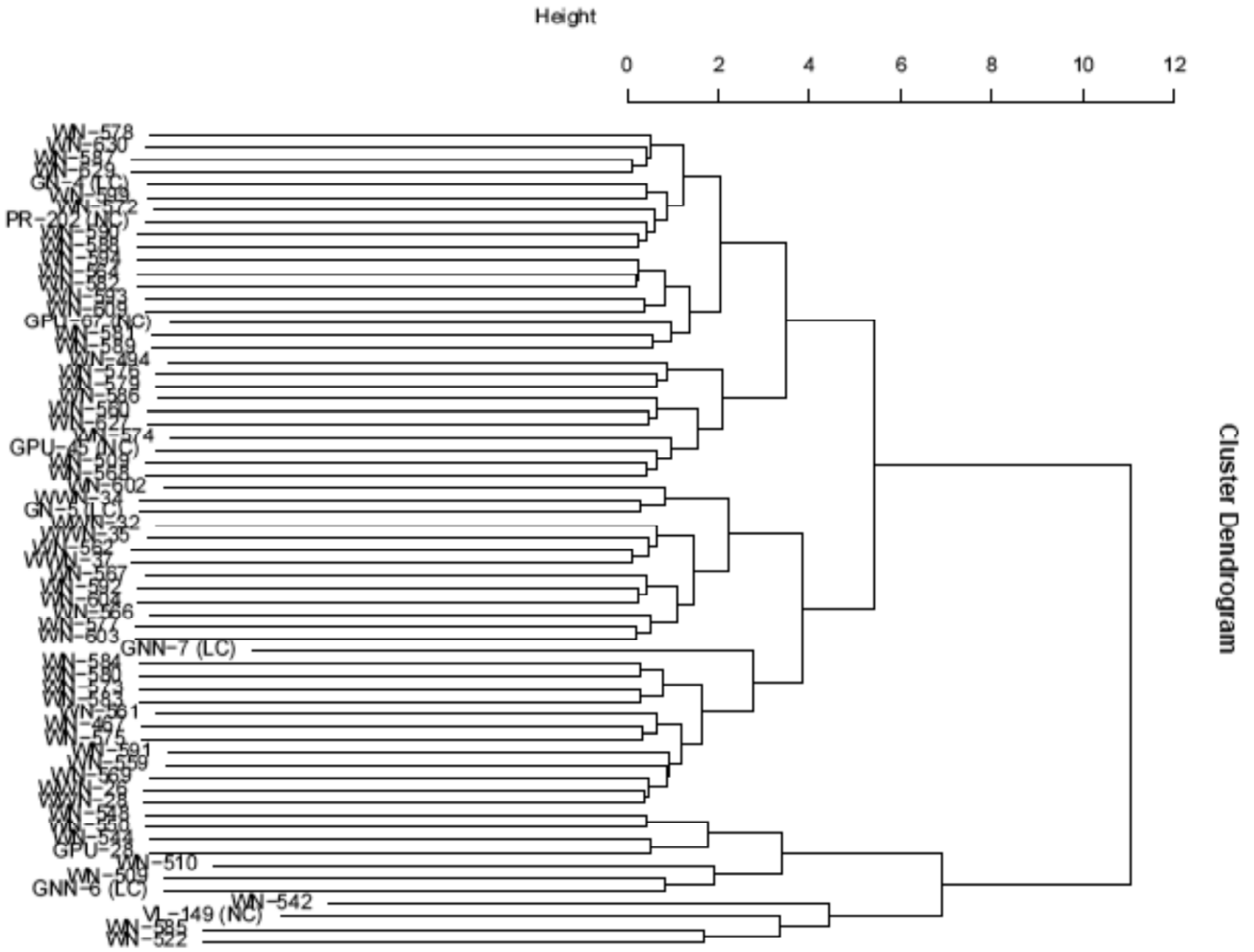

Figure 3: Dendogram depicting clustering pattern of 65 germplasm accessions obtained by cluster analysis

exploited best when carried between accessions of distinct clusters.

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