

## 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 component analysis indicates that three principal components PC-1, PC-2 and PC-3 explain 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 in finger millet.

**Keywords:** Principal component analysis, cluster analysis, Finger millet, genetic diversity

### 1. Introduction

Finger Millet is 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 (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 mha with a production of 2.06 mt and average productivity of 1706 kilogram per hectare (Directorate of Economics and Statistics, 2015). 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. 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.

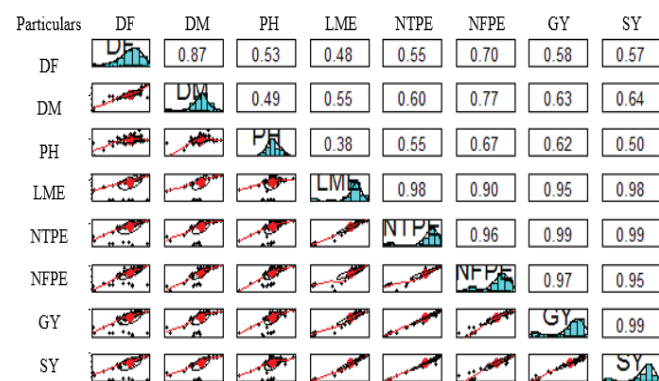
## 2. Materials and Methods

The experiment was conducted at Hill Millet Research Station, Navsari Agricultural University, Waghai (Dangs), Gujarat 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 (cm) (PH), length of main ear (cm) (LME), number of tillers per plant (NTPE), number of fingers per ear (NFPE), grain yield (g) (GY), straw yield (g) (SY) were taken from ten randomly selected plants from each replication. The principal component analysis was carried out by using Jolliffe, 2002 and Le et al. 2008) and hierarchical cluster analysis were performed using R and R-studio software. (Hill and Smith, 1976).

## 3. Results and Discussion

### 3.1. Genetic diversity using Pair panels and Bi plot formation

Pair panels for 8 × 8 matrices represents correlation, histogram and bivariate scatter plot of eight variables (Figure 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 show a skewed distribution. Moreover the units of different variables were not same so normalization of variables was carried out



All the correlation values were found significant at  $p=0.01$   
 Figure 1: Pair Panels for 8 X 8 Matrices represents Pearson correlation, histogram and bivariate scatter plot among the morphological characters

before analysis.

### 3.2. Principle component analysis

Bhanupriya et al. (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% of total variance (Table 1). of these first three principal components with Eigen values greater than 0.78 accounted

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                       |

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% 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 (Figure 2). From principal component analysis it can be concluded that all the eight traits are important from breeding aspects. (Table 2)

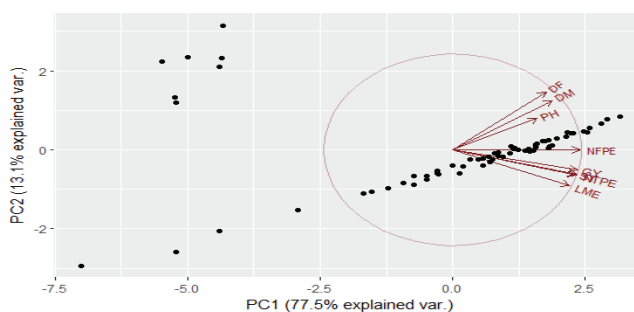


Figure 2: Bi plot formation on basis of PC<sub>1</sub> and PC<sub>2</sub> values

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   |

3.3. Hierarchical cluster analysis

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 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 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. 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. Hierarchical 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 exploited best when carried between accessions of distinct clusters.

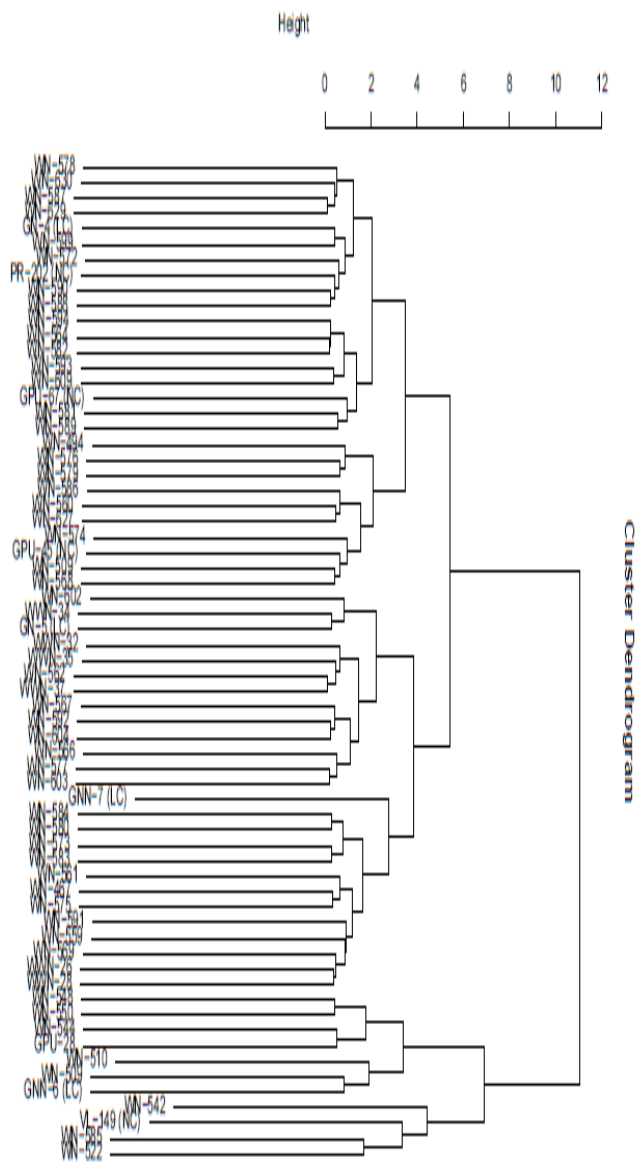


Figure 3: Dendrogram depicting clustering pattern of 65 germplasm accessions obtained by cluster analysis

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

| Clusters | No. 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) |

#### 4. Conclusion

Sixty five genotypes were grouped into five distinct clusters on basis of Euclidean distance. The first principal component had positive loading for all eight characters considered. Second principal component had positive loading for three characters viz., days to 50% flowering, days to maturity and plant height, while third principal component had positive loading values for days to 50% flowering, days to maturity, length of main ear and straw yield.

#### 5. Further Research

The result of present study could be exploited in planning and execution of future breeding strategy in finger millet and selection of parents for further crossing programme. Further this research will helpful in initiation for crossing programme on the basis of exploitation of genotypes and its execution of future breeding strategy in finger millet improvement.

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