International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
www.chemijournal.com
IJCS 2021; 9(1): 1536-1540

Received: 02-11-2020
Accepted: 13-12-2020

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Principal component analysis in finger millet (*Eleusine coracana* L.) genotypes for diversity studies

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DOI: https://doi.org/10.22271/chemi.2021.v9.i1v.11442

Abstract
Using multivariate analysis we can easily assesses important polygenic characters which are of great importance in a plant breeding programme. The experiment was conducted during kharif, 2018 with 60 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 and the multivariate technique, principal component analysis estimated. Principal component analysis indicates that three principal components PC-1, PC-2, PC-3, PC-4, PC-5, PC-6 and PC-7 explains 52.15%, 33.37%, 6.51%, 4.69%, 1.48%, 1.25% and 0.52% respectively of the total variation. The first principal component had showed positive loading for days to 50% flowering (DF), days to maturity (DM), finger length (FL), fingers per earhead (FE) and negative loading for plant height (PH), productive tillers per plant (PT), test weight (TW), grain yield (GY), straw yield (SY) and harvest index (HI). The second principal component had positive loading for DF, DM, PH, FL, TW, GY and SY while negative loadings for PT, FE and HI. The third principal component had positive loading values for DF, PT, FL, FE, GY and SY. The fourth principal component had positive loading for DM, PT, TW and SY while negative loadings for DF, PH, FL, FE, GY and HI. The fifth principal component had positive loading for DF, DM, PT, GY, SY and HI while negative loadings for PH, FL, FE and TW. The sixth principal component had positive loading for DF and PH while negative loadings for DM, FL, FE, TW, PT, GY, SY, and HI. The seventh principal component had positive loading for DF, DM, PT, FL, GY and HI. While negative loadings for PH, FE and SY. The results of this study have revealed the high level of genetic variation and the traits contributing for the variation was identified. Hence the genotypes of this population can be utilized for trait improvement in breeding programs using those characters which contributing for major variation.

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 3000Year's ago (Salini *et al.*, 2010) [9]. 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. (Anonymous, 2015) [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 wheat and rice (Chaudhary *et al.*, 2015) [3]. Finger millet grains especially the seed coat contains high amount of various phenolic compounds which exhibit anti-oxidant activity (Patil *et al.*, 2019) [8]. 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 (Khan *et al.* (2015) [4]. 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 (Patel *et al.*, 2018) [6].

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, Gujarat using 60 genotypes of finger millets in randomized block design with three replications during *kharif*, 2018. The gross plot is divided into three blocks which were taken as a replications while the blocks are further divided into equal 60 plots. Data of ten different traits *viz.* days to 50% flowering (DF), days to maturity (DM), plant height (PH), productive tillers (PT), finger length (FL), fingers per earhead (FE), test weight (TW), grain yield (GY), straw yield (SY) and harvest index (HI) 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

Principal Component Analysis

Principal component analysis in this study showed that first seven principal component shows 99.97 per cent of the entire variability. The first principal component shows 52.15 per cent of total variability due to all the characters except for number of tillers per plant. Second principal component accounted for 33.37 per cent of total variability originated primarily due to days to 50 percent flowering, number of tillers per plant, grain yield and straw yield. Third principal component which explains 6.51 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 4.69 per cent of gross variability primarily due to plant height, test weight and grain yield. Fifth principal component accounts 1.48 per cent of total variability due to days to flowering, days to maturity, productive tillers, grain yield, straw yield and harvest index. Sinha and Mishra (2015) [11] studied variability for eighteen quantitative characters of 55 rice landraces and found that the first five principal components contributed 74.34 per cent of total variability.

Sixth principal component which explain 1.25 per cent gross variability due to days to flowering and plant height. Seventh principal component accounts 0.52 per cent total variability due to days to flowering, days to maturity, productive tillers, flag leaf length, grain yield and harvest index (Table 1 & 2). Suman *et al.* (2019) [12] studied 55 finger millet genotypes using multivariate analysis and revealed that the first 4 components with Eigen value of greater than 1.33 contributed about 66.54% of total variability. The proportions of the total variance attributable to the first 4 principal components were 33.61, 12.91, 12.14 and 7.87% respectively. Chaudhary *et al.* (2015) [3] studied 66 lines of pearl millet was analyzed for principal component analysis (PCA) and identified six principal components which explained 77.7 per cent of total variability among the 66 genotypes. Khan *et al.* (2015) [4] 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. Patil *et al.* (2017) [5] examined genetic diversity in finger millet using principal component analysis and found three principal components showing 98.31 per cent of total variation. Similar results have also noted by Patel *et al.* (2017) [5] in finger millet. Patel *et al.* (2018) [6] studied genetic diversity study in brinjal with the help of principal component analysis and found three principal components 45.5 per cent of total variation. Bhanupriya *et al.* (2014) [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.

Bi-plot represents distribution of accessions on the basis of different PC scores (PC1, PC2, PC3) and relationship of different traits with PC scores (Fig. 2). Shobha *et al.* 2019 [10] reported the highest variability in PC1 with eigen value more than 1.0 in 67 aromatic rice genotypes. Patel *et al.* studied genetic diversity study in finger millet with the help of principal component analysis and found three principal components 73.40 per cent of total variation.

Panels of 10 X 10 matrices represents bivariate scatter plot among the morphological characters in which upper half and lower half showing the distribution of different genotypes and the diagonal showing different morphological characters. The results of this study have revealed the high level of genetic variation and the traits contributing for the variation was identified. Hence, the genotypes of this population can be utilized for trait improvement in breeding programs using those characters which contributing for major variation. Salini *et al.* (2010) [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. Similar results have also noted by Shoba *et al.* (2017) [7] in rice using PCA and cluster analysis.

The units of different variables were not same so normalization of variables was carried out before analysis. Scree plot explained the percentage of variance associated with each PC obtained by drawing a graph between eigen values and PC numbers. In the present study, PC1 showed 52.15 per cent variability with eigen value 114.35 which then declined gradually (Fig.5). There is a little variance observed in each PCs after PC3. From the graph, it's very clear that the maximum variation was observed in PC1 in comparison to other PCs. Hence, selection of parent genotypes from this PC would be rewording for further breeding programs.

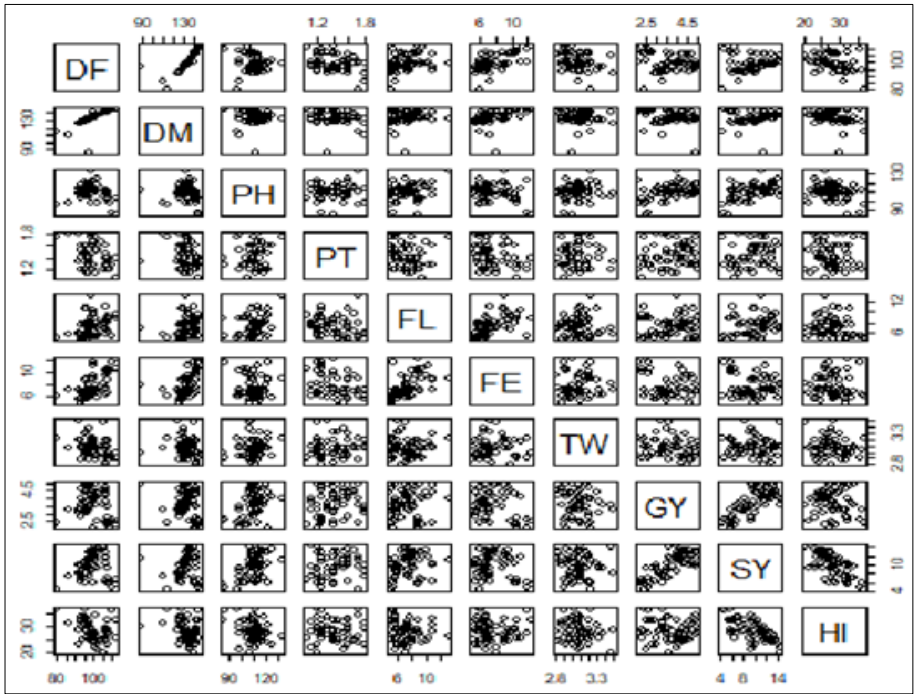

Fig 1: Pair Panels for 10 X 10 Matrices represents bivariate scatter plot among the morphological characters

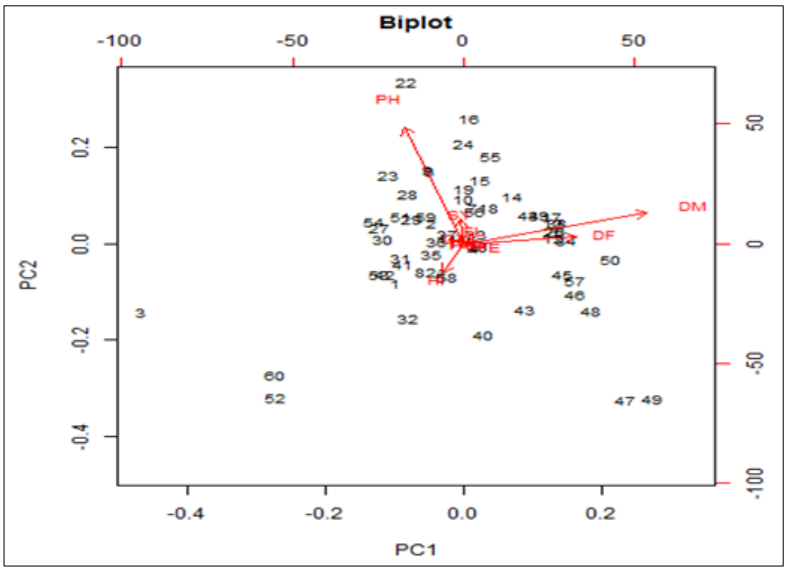

Fig 2: Bi plot formation on basis of PC1 and PC2 values

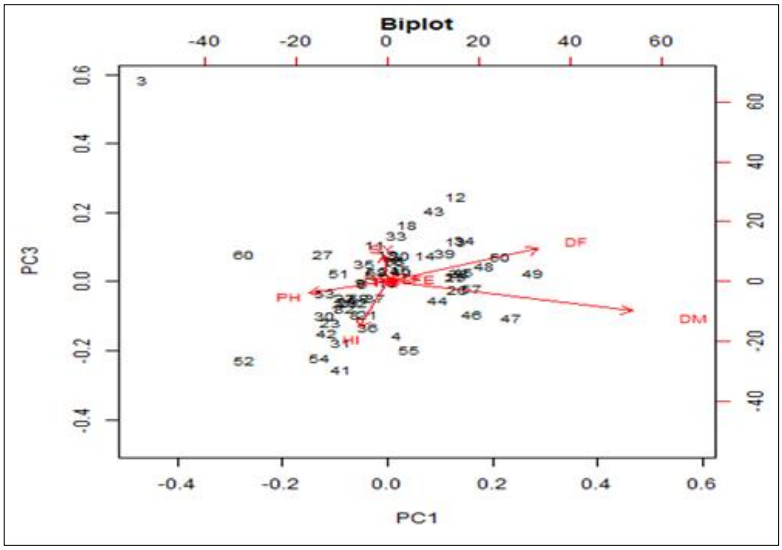

Fig 3: Bi plot formation on basis of PC1 and PC3 values

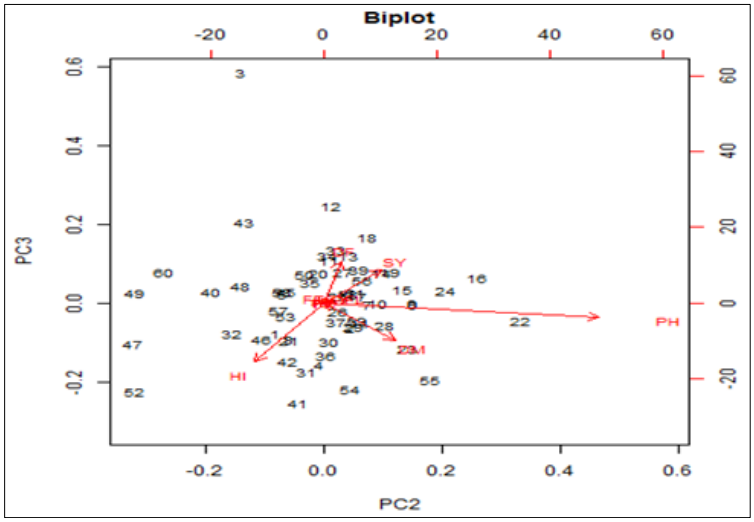

Fig 4: Bi plot formation on basis of PC2 and PC3 values

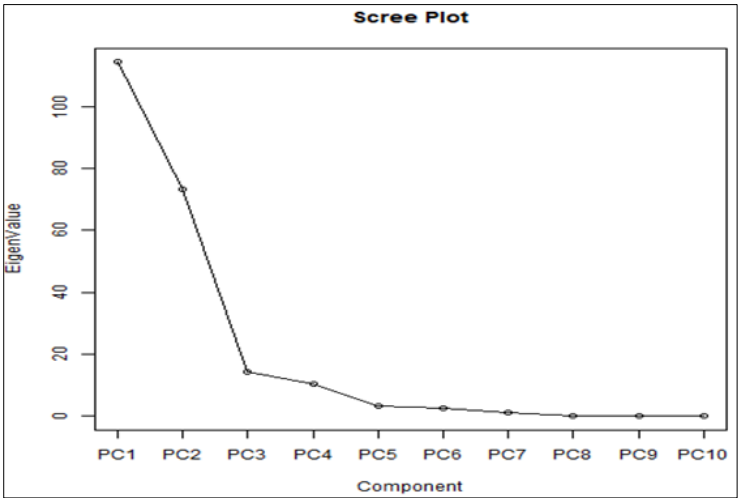

Fig 5: Scree plot

Table 1: Principal components showing the Eigen values, proportion of variance explained and cumulative variance

Principal Component	Eigen Value	Variation (%)	Cumulative variance (%)
1	114.35	52.15	52.15
2	37.17	33.37	85.52
3	14.27	6.51	92.03
4	10.28	4.69	96.72
5	3.24	1.48	98.20
6	2.74	1.25	99.44
7	1.14	0.52	99.97
8	0.03	0.01	99.98
9	0.02	0.01	99.99
10	0.01	0.01	100

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

Particulars	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DF	0.5005	0.0565	0.4675	-0.6460	0.1406	0.2934	0.0614
DM	0.8120	0.2387	-0.4180	0.3206	0.0277	-0.0723	0.0019
PH	-0.2633	0.9181	-0.1656	-0.2028	-0.0316	0.1177	-0.0650
PT	-0.0047	-0.0014	0.0022	0.0193	0.0143	-0.0235	0.0147
FL	0.0394	0.0835	0.0384	-0.2295	-0.3291	-0.6294	0.6578
FE	0.0976	-0.0210	0.0375	-0.2716	-0.2913	-0.5226	-0.7454
TW	-0.0030	0.0015	-0.0015	0.0111	-0.0300	-0.0094	-0.0202
GY	-0.0227	0.0373	0.3557	-0.0085	0.3403	-0.1684	0.0143
SY	-0.0123	0.1902	0.3784	0.2340	0.6748	-0.4321	-0.0455
HI	-0.0947	-0.2278	-0.6572	-0.5069	0.4616	-0.0995	0.0294

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