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Genetic diversity studies in little millet (*Panicum sumatrense* Roth. Ex. Roemer and Schultes) genotypes: A multivariate PCA analysis

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Abstract
Principal component 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. It's utilized to examine variation and to estimate relative contribution of various characters for total variability. The experiment was conducted during *Kharif,* 2019-20 with 32 germplasm accessions of little 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 nine morphological traits were recorded and principal component analysis was done. Principal component analysis indicates that three principal components PC-1, PC-2, PC-3 and PC-4 explains 58.40%, 43.53%, 5.21% and 1.21%, respectively of the total variation. The first principal component had showed positive loading for PT (productive tillers per plant) and HI (harvest index). The second principal component had positive loading for days to 50% flowering (DF), days to maturity (DM), productive tillers per plant (PT), grain yield per plant (GY), straw yield (SY) and harvest index (HI). The third principal component had positive loading for DM, PT, GY, SY and HI. While, the fourth principal component had positive loading for PH, PT, GY and HI. The results of principal component analysis utilized in the study have revealed the high level of genetic variation and the characters contributing for the variation was identified. Hence, the genotypes of this population can be utilized for trait improvement in little millet breeding programs using the traits contributing for major variation.

Keywords: Principal component analysis, little millet, genetic diversity, multivariate analysis

Introduction
Little millet belongs to the family Poaceae, sub-family Panicoideae and the tribe Paniceae (Rachie, 1975) [11]. Little millet was domesticated in the Eastern Ghats of India occupying a major portion of diet amongst the tribal people and spread to Sri Lanka, Nepal, and Myanmar (De Wet *et al*., 1983) [3]. Little millet (*Panicum sumatrense* Roth. Ex. Roemer and Schultes) is grown in India under various agro ecological situations and commonly known as samai, samo, Moraio, Vari, Kutki. India is well known for its rich agro-biodiversity and prime contributor with 473 accessions (Upadhyaya *et al*., 2016) [16]. In India, little millet having 1.42 lakh tones of production. In Gujarat, little millet is cultivated in an area of 10,634 hectares with 9,526 tonnes of production having the productivity of 896 kg/ha (Anonymous, 2015) [1].

Little millet is a hardy crop which can withstand drought better than most of other cereal crops and water logging to a certain degree, also. The potentiality of little millet has not been exploited in India and the yield levels are very low there by indicating a greater scope for exploitation of this millet under Indian condition. In India, little millet growing states are Karnataka, Tamil Nadu, Odisha, Madhya Pradesh, Chhattisgarh, Jharkhand, Andhra Pradesh, Uttarakhand, Maharashtra and Gujarat. In Gujarat, generally little millet crop is grown in hilly tract of The Dangs and Valsad district and locally known as "Vari or Moraio". Due to highest in nutritive value of this crop, it is included under the "Nutricereal" crops (Patil *et al.,* 2019) [10]. The productivity of little millet is low due to poor soil fertility and age-old cultivation methods. The existence of variability is essential for resistance to biotic and abiotic factors as well as for wider adaptability in different set of environment. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they are grown (Patil and Patel, 2018) [7, 8]. Selection is also effective when there is presence of large genetic variability among the individuals in a population. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting judicious crop improvement programmes.

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Greater the variation in the material better is the chance for selecting promising and desired types. (Patil *et al.,* 2018 and Patel *et al.,* 2018) [7, 8, 5]

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 trait specific objective of a plant breeder. The main advantage of using PCA over cluster analysis is that each genotype is assigned to one group only. The objective of this study is to find out relative contribution of various traits for total variability of little 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 32 genotypes of Little millets in randomized block design with three replications during *Kharif,* 2019-20. The gross plot is divided into three blocks which were taken as replications while the blocks are further divided into equal 32 plots. Data of nine different traits *viz.* days to 50% flowering (DF), days to maturity (DM), plant height (PH), productive tillers per plant (PT), panicle length (PL), test weight (TW), grain yield per plant (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 four principal component shows 99.53 per cent of the entire variability. The first principal component shows 58.40 per cent of total variability due to PT and HI. Second principal component accounted for 43.53 per cent of total variability originated primarily due to DF, DM, PT, GY, SY and HI. Third principal component which explains 5.21 per cent of total variability because of DM, PT, GY, SY and HI. Fourth principal component account 1.21 per cent of gross variability primarily due to PH, PT, GY and HI. (Table 1 and 2). 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. 1, 2, 3). Pair Panels of 9 X 9 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 germplasms of this population can be utilized for trait improvement in breeding programs using those traits which contributing for grater variation. From the graph, it's very clear that the maximum variation was observed in PC2 and PC3 in comparison to other PCs. Hence, selection of genotypes from this PC would be rewording for further breeding programs.

Salini *et al*. (2010) [12] 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. Bhanupriya *et al.* (2014) [12] 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. Patel *et al.* (2017) [6] studied genetic diversity study in finger millet with the help of principal component analysis and found three principal components showing 98.14 per cent of total variation. Patil *et al*. (2017) [6] examined genetic diversity in finger millet using principal component analysis and found three principal components showing 98.31 per cent of total variation.

Sinha and Mishra (2015) [14] 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.* (2015) 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. Screen plot explained the percentage of variance associated with each PC obtained by drawing a graph between Eigen values and PC numbers. There is a little variance observed in each PCs after PC3.

Shobha *et al.* (2019) [13] reported the highest variability in PC1 with eigen value more than 1.0 in 67 aromatic rice genotypes. Nachimuthu *et al.* 2014 reported the highest variability in PC1 with eigen value more than 1.0 in 192 rice genotypes comprising traditional landraces and exotic genotypes. Suman *et al*. (2019) [15] studied 55 finger millet genotypes using multivariate analysis. The principal component analysis 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. Similar types of results also reported in this study in little millet multivariate analysis. From these results it can be concluded that characters like days to maturity (DM), productive tillers per plant (PT), grain yield per plant (GY), straw yield (SY) and harvest index (HI) could be used as important characters to distinguish and improve the little millet crop from the breeding point of view. This study gives to access the potential genetic diversity among little millet genotypes for selection of parents in hybridization programme to obtain better segregants in advanced generation for little millet improvement programme.

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

Principal Component	Eigen Value	Variation (%)	Cumulative variance (%)
1	114.9031	58.40	58.40
2	83.8967	34.53	92.92
3	12.6517	5.21	98.13
4	2.9392	1.21	99.34
5	0.7636	0.31	99.65
6	0.5953	0.24	99.90
7	0.2301	0.09	99.99
8	0.0195	0.01	1.00
9	0.0024	0.00	1.00

Table 2: Principal component analysis for 9 quantitative traits in 32 little millet genotypes non-rotated loadings.

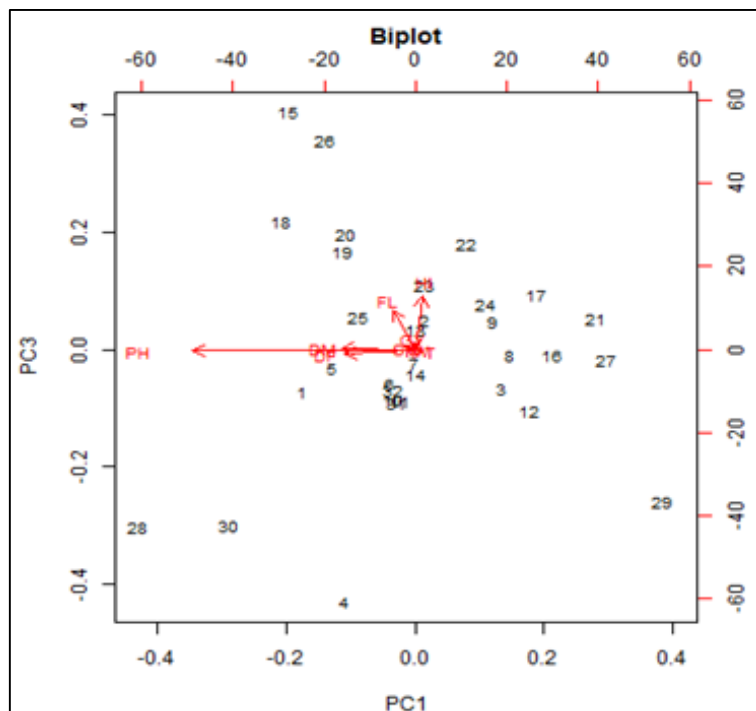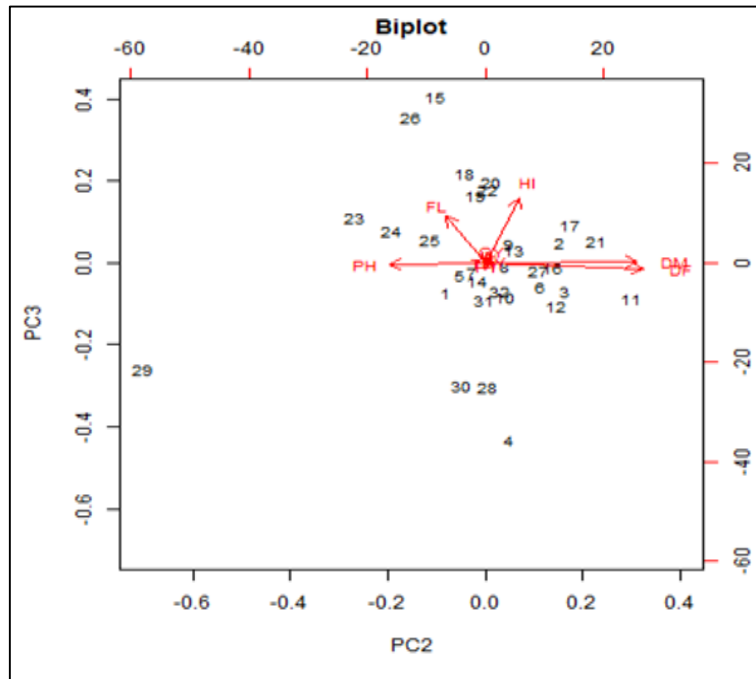| Particulars	PC1	PC2	PC3	PC4
DF	-0.2884	0.6442	-0.0678	-0.1613
DM	-0.2981	0.6210	0.0189	-0.0457
PH	-0.9038	-0.3909	-0.0201	0.1707
PT	0.0308	0.0079	-0.0321	0.1326
FL	-0.0914	-0.1584	0.5793	-0.7765
TW	-0.0000	-0.0003	-0.0030	-0.0003
GY	-0.0025	0.0259	0.1193	0.0452
SY	-0.0308	0.0324	0.0165	-0.1174
HI	0.0283	0.1402	0.8022	0.5535
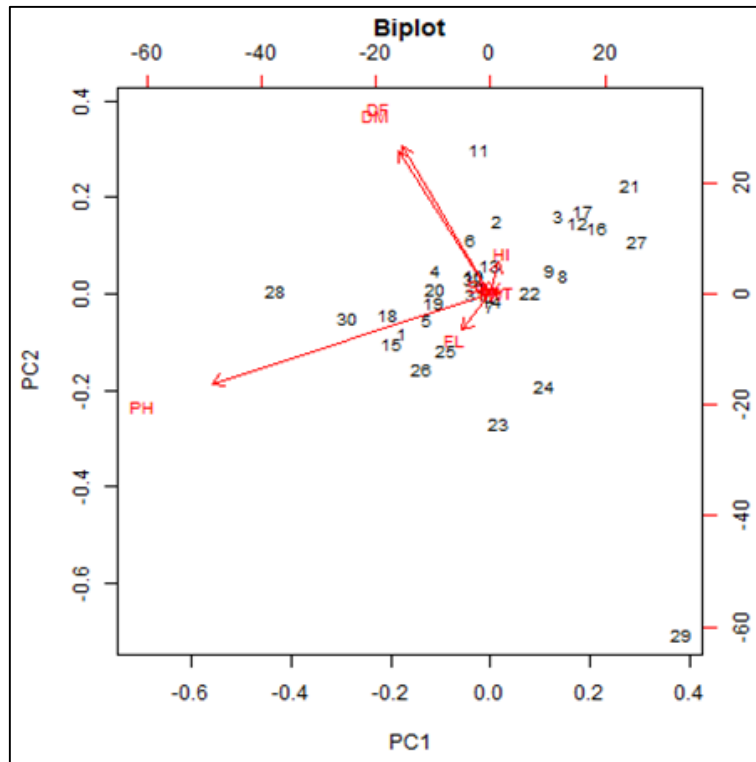
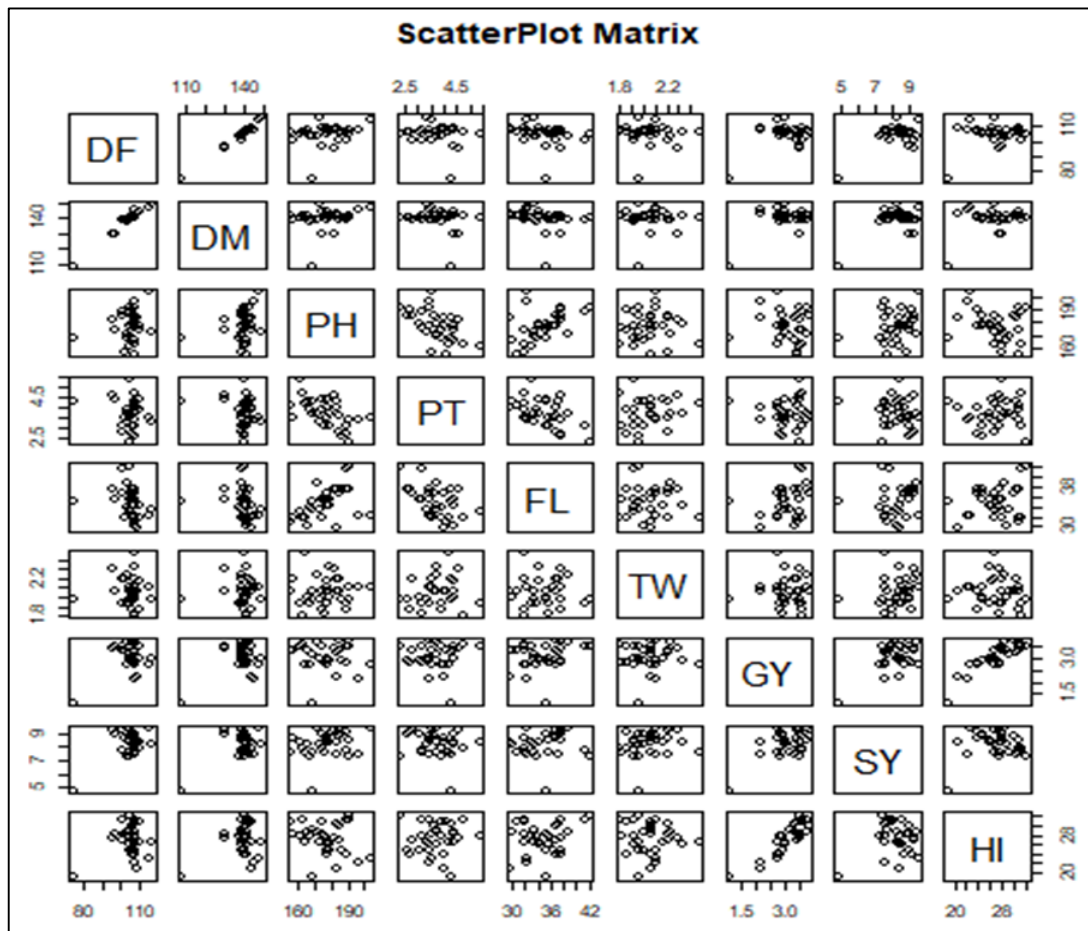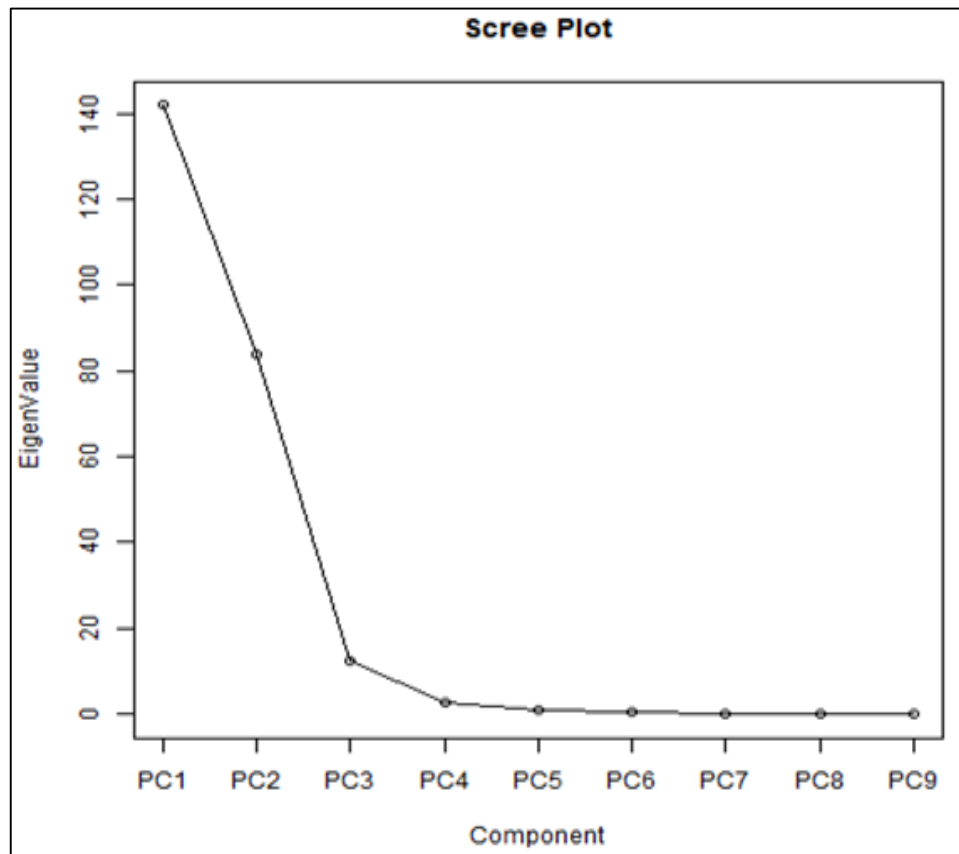
Fig 1

Fig 2

Fig 1, 2, 3: Figure Shows in PC scores (PC1, PC2, PC3) and relationship of different traits with PC scores

Graph 1: Graph shows Third principal component which explains 5.21 per cent of total variability because of DM, PT, GY, SY and HI

Graph 2: Graph shows in PC-1, PC-2, PC-3 and PC-4 explains 58.40%, 43.53%, 5.21% and 1.21%, respectively of the total variation

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