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Research Article

Principal component and diversity analysis for discrimination of genotypes and yield related traits in pearl millet [*Pennisetum glaucum* (L.) R.Br.]

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Abstract
A total of 25 pearl millet genotypes were evaluated for nine traits by PCA and cluster analysis to determine the genetic diversity among the individuals. Three of the nine principal components (PCs) had more than 1.0 eigen values, indicating a total variability of 68.71 per cent. From the D^2 analysis, five major groups were formed as clusters I, II, III, IV and V consisting of 18, 1, 4, 1 and 1 genotypes, respectively. Clusters I and IV had desirable mean values for plant height, number of productive tillers/plant, thousand grain weight and single plant yield. Maximum variability in the experimental material was observed to be contributed by single plant yield, followed by leaf blade length and leaf sheath length. From the PCA and cluster analysis, the genotypes CO 10, PT 6481, PT 6676, PT 6475, PT 6570 and PT 6675 could be used for selection and hybridization. Genotypes in highly diverse clusters could be exploited for harnessing heterosis and for the selection of superior segregants.

Key words: Pearl millet, D^2 analysis, Principal component analysis

INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R.Br.] is the sixth most important cereal food crop after wheat, rice, maize, barley and sorghum, with a majority of the area in Africa and the Indian sub-continent (FAO, 2020). India is the largest producer of pearl millet in the world with 10.36 million tonnes produced from 7.54 m. ha. (INDIASTAT, 2021). Being one of the oldest cultivated cereal crops (Manning *et al*., 2011), it plays a key role in the food, nutritional as well as economic security of poor farmers (Srivastava *et al*., 2020). Day by day, the demand for pearl millet production increases due to its wider adaptability to climatic conditions and nutritional characteristics (Tako *et al*., 2015).

Recent research has revealed that the yield has been static over the past many decades and in order to meet the food demand, it is imperative that the yield plateau need to be breached. The availability of higher genetic diversity among parents is a prerequisite for the development of superior cultivars.

The principal component analysis (PCA) is the most often used method for evaluating genetic variation which helps in the identification of characteristics that assist in the classification of genotypes into distinct groups based on similarities in one or more characters (Kumari *et al*., 2021) Mahalanobis (1936) recommended

a method known as "D^2 statistics" for determining genetic diversity in available genotypes. It also determines the proportional contribution of each component character to the total divergence by measuring the degree of diversification. When it comes to a complicated feature like yield, a single character does not matter as much to a plant breeder as the combined quality of a number of good characteristics *viz.* spike length, spike girth, thousand grain weight, and single plant yield, performs. So, in order to increase yield, parents must be chosen based on a number of quantitatively divergent characteristics, which may be fulfilled by Mahalanobis D^2 statistic (1936). Therefore, the present study was undertaken to screen the pearl millet genotypes for genetic diversity.

MATERIALS AND METHODS
The study was conducted at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore, during *Summer*, 2020. A total of 25 genotypes of pearl millet were used for evaluation. The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications. All the management practices were followed meticulously to maintain good crop standard. Different biometrical traits, *viz.* plant height, the number of productive tillers per plant, spike length, spike girth, leaf sheath length, leaf blade length, thousand grain weight, and single plant yield, related to grain yield was recorded on five randomly selected plants from each entry in all replications. The data were subjected to statistical analysis in WINDOSTAT ver. 7.1 to assess the diversity among the genotypes. Discrimination of traits and genotypes were assessed through NTsys 2.2and XLSTAT.

RESULTS AND DISCUSSION
The principal component analysis is a multivariate analysis used to reduce the complex data set to a lower dimension and gives us information regarding the importance and contribution of each component to the total variance

(Pujar *et al.*, 2020). In this study, PCA was performed with nine quantitative traits on pearl millet genotypes. Out of the nine, three principal components (PCs) exhibited eigen value greater than 1.0 and accounted for 68.71 per cent of total variability among the traits that were observed.

PC1 accounted for 34.16 per cent of the total variance and almost all studied characters showed positive loading in this principal component except the number of productive tillers and thousand grain weight. The factor loading of principal components showed that PC1 accounted for maximum variability for traits like plant height, spike length, leaf sheath length, leaf blade length and leaf blade width. PC2 accounted for 22.28 per cent of the total variance and showed maximum variability for spike girth, thousand grain weight and single plant yield. PC3 showed 12.26 per cent of variability and captured maximum variability for the number of productive tillers per plant (**Table 1**). Similar results were reported by Rasitha *et al.* (2020) in which 63.81 per cent of total variability was observed and leaf blade length, leaf sheath length, spike length and plant height contributed more in PC1. Jain *et al.* (2021) also observed that plant height influenced more in PC1.

The biplot analysis was carried out on the basis of two major principal components (PC1 and PC2). To make visualization easier, genotypes and variables were combined into a single biplot graph. The PCA biplot accounted for 56.44 per cent of total variability and revealed that plant height, spike length, thousand grain weight and single plant yield were the most discriminatory variables. The genotypes *viz.* PT 6481, CO10, GMR 15, PT 6710, and PT 6674 were found to be placed farthest from the biplot origin and accounted for more variability for traits of respective principal components than other genotypes (**Fig. 1**).

Table 1. Principal component analysis (PCA) of pearl millet genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
PH	0.879	0.047	-0.181	0.107	0.031	-0.191	-0.361	-0.111	-0.030
PT	-0.306	0.272	0.531	0.717	-0.045	0.134	-0.111	0.060	0.004
SL	0.871	-0.073	-0.147	0.277	0.112	-0.212	0.174	0.202	-0.096
SG	0.063	0.594	-0.012	-0.080	0.782	0.157	-0.006	0.009	0.026
LSL	0.857	-0.024	-0.227	0.155	-0.158	0.366	0.059	0.025	0.160
LBL	0.568	0.421	0.543	-0.067	-0.060	-0.377	0.172	-0.147	0.053
LBW	0.575	0.079	0.526	-0.447	-0.135	0.388	-0.075	0.086	-0.076
1000TGW	-0.239	0.832	-0.149	-0.214	-0.249	-0.250	-0.113	0.203	0.059
SPY	0.004	0.833	-0.350	0.135	-0.247	0.251	0.110	-0.138	-0.100
Eigenvalue	3.074	2.006	1.104	0.901	0.797	0.676	0.237	0.147	0.059
Variability (%)	34.157	22.287	12.268	10.009	8.854	7.513	2.629	1.632	0.652
Cumulative %	34.157	56.444	68.711	78.720	87.574	95.086	97.715	99.348	100.000

PH: Plant height, PT: Number productive tillers per plant, SL: Spike length, SG: Spike girth, LSL: Leaf sheath length, LBL: Leaf blade length, TGW: Thousand grain weight, SPY: Single plant yield
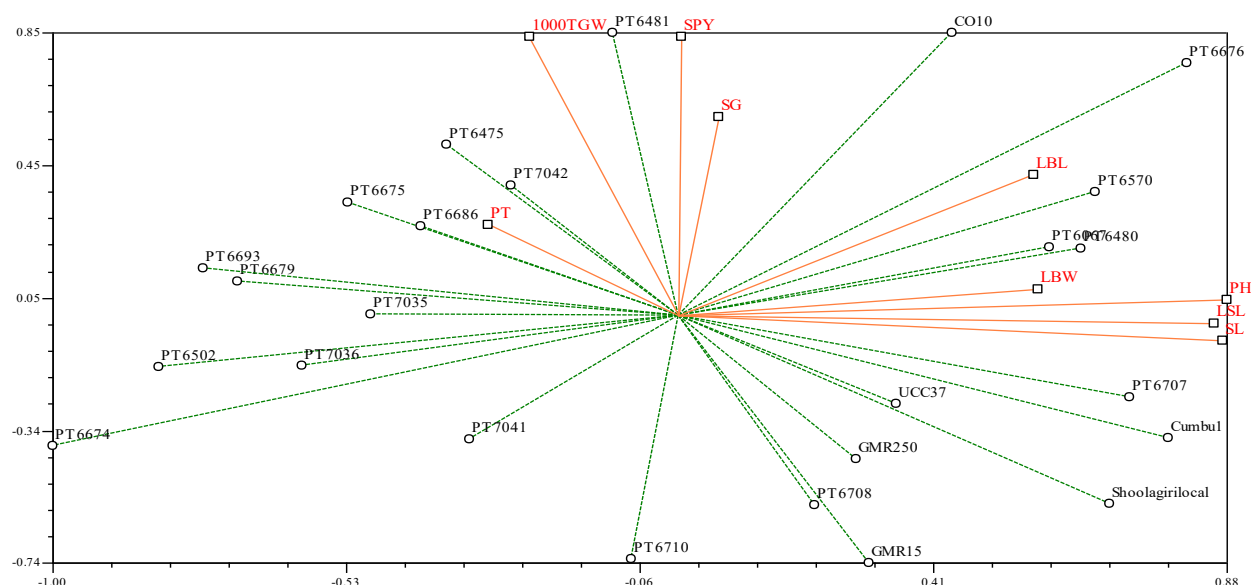
Fig. 1. Biplot representing the distribution of 25 genotypes and nine traits of pearl millet among PC1 and PC2

In the present study, the genotypes were selected on the basis of more than one PC score in the three PCs (**Table 2**). In PC1, the positive scores ranged from 1.06 (UCC 37) to 2.48 (PT 6676). In PC2, the positive values of the component ranged from 1.03 (PT 6675) to 2.59 (CO 10). In PC3, the positive scores ranged from 1.57 (PT 6707) to 2.12 (PT 7042). PT 6676, PT 6570, CO 10 was common in both PC1 and PC2. In both PC1 and PC3, PT 6707 was found to be common. PT 7045 was found to be common in PC2 and PC3 (**Table 2**).

Based on PCA, which highlights the characters with maximum variability, it can be concluded that PC2 showed maximum variability for single plant yield, thousand grain weight and spike girth and top ranked genotypes on this PC2 were CO 10, PT 6481, PT 6676, PT 6475, PT 7042,

PT 6570 and PT 6675. Hence, the above genotypes would be useful for yield enhancement in future breeding programmes.

The possibility to choose genetically diverse parents has been made feasible by the quantification of genetic diversity using biometrical techniques such as the Mahalanobis D^2 statistics (Sumathi *et al.,* 2016; Sharma *et al.,* 2020; Swamynatham *et al.,* 2020). Analysis of genetic diversity among 25 genotypes for nine quantitative by D^2 analysis for nine quantitative traits resulted in grouping of the genotypes into five clusters. These five primary clusters were then divided into sub-clusters. Cluster I was highly populated, with 18 lines, followed by cluster III, which had four genotypes and clusters II, IV, and V and each had only one genotype (**Fig. 2**).

Table 2. Selected genotypes based on PC score (value more than one)

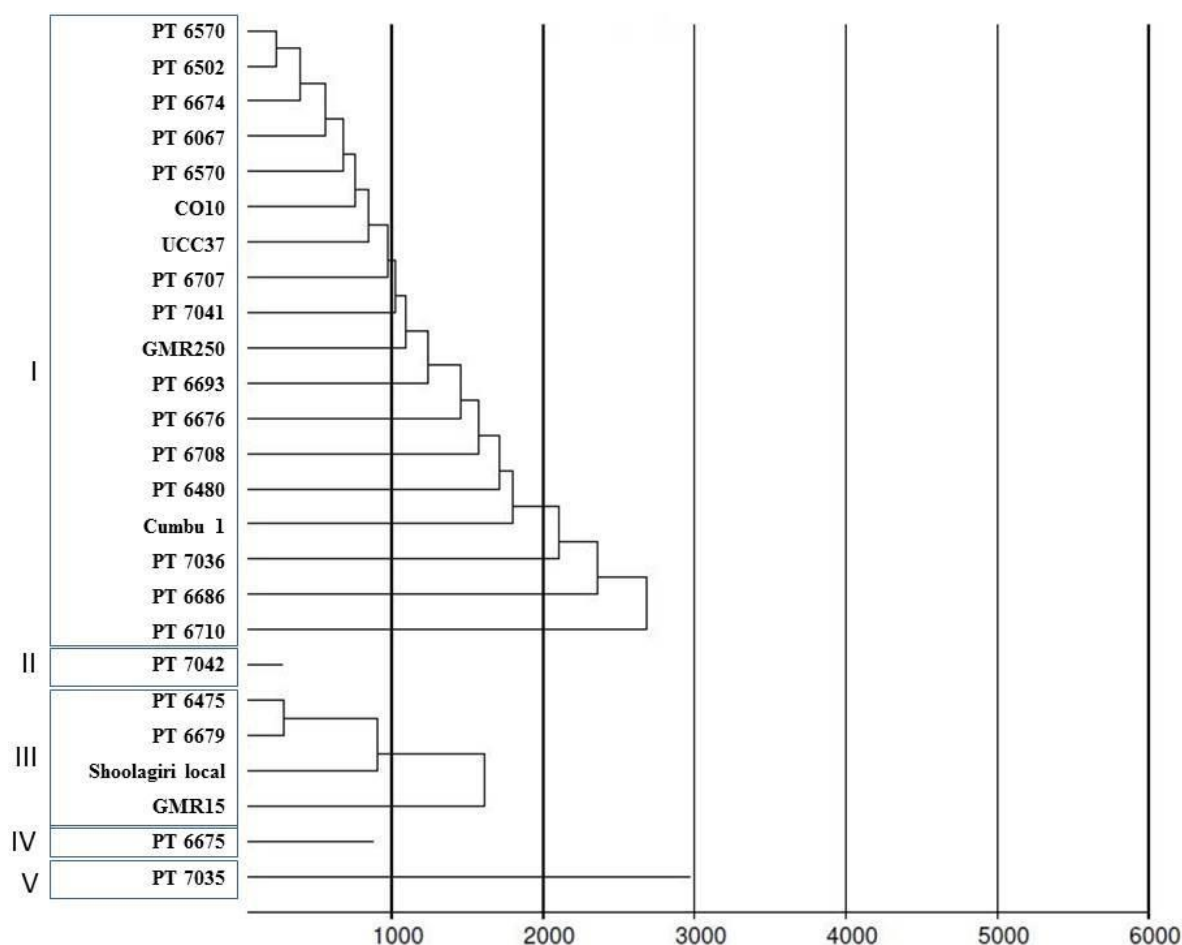| PC1		PC2		PC3	
Genotypes	PC score	Genotypes	PC score	Genotypes	PC score
PT 6676	2.49	CO 10	2.59	PT 7042	2.12
Cumbu 1	2.40	PT 6481	2.59	PT 6710	2.04
PT 6707	2.21	PT 6676	2.31	PT 7035	1.73
Shoolagiri local	2.11	PT 6475	1.56	PT 6707	1.57
PT 6570	2.04	PT 7042	1.19		
PT 6480	1.97	PT 6570	1.13		
PT 6067	1.81	PT 6675	1.03		
CO 10	1.34				
UCC 37	1.07				

Fig. 2. Dendrogram showing clustering pattern of 25 pearl millet genotypes

D^2 values of respective genotypes within and between clusters were used to compute the average inter and intra cluster distance. The intra cluster distance ranged from 0.00 to 42.05 and cluster I had the largest intra cluster distance (42.05). Clusters II, IV and V all had a minimum value of zero, as they were solitary clusters. The average distance between clusters varied from 33.54 to 151.2. Cluster III and cluster V had the greatest inter cluster distance (151.20) and cluster II and cluster IV had the least inter cluster distance of 33.54 (**Table 3**).

The cluster mean values for nine characters in 25 pearl millet lines have been presented in **Table 4**. Among the five major clusters, cluster II had the highest mean value for the number of productive tillers/plant (4.00), leaf blade length (70.85), leaf blade width (5.40) and thousand grain weight (15.25). Cluster I showed the highest mean value for spike girth (9.56), leaf sheath length (15.25). Cluster III with four genotypes had the highest mean value for plant height (191.38) and spike length (26.25). Cluster IV with single genotypes showed the highest mean value for single plant yield (99.30) (**Table 4**).

Contribution of individual character towards total divergence indicated that single plant yield (36.67%) had the highest contribution towards genetic diversity followed by leaf blade length (34.00%) and leaf sheath length (18.00%). The characters thousand grain weight (6.00%) and spike length (5.33%) contributed less towards genetic divergence. Thus, single plant yield, leaf blade length, leaf sheath length are important characters to be considered while selecting genetically diverse genotypes (**Table 4**).

Based on the cluster mean values, it can be interpreted that clusters I and IV had desirable mean values for plant height, the number of productive tillers/plant, thousand grain weight and single plant yield. Cluster III had low mean values for single plant yield. Hence, the genotypes in clusters I and IV can be crossed with low yield genotypes in cluster III to develop superior hybrids. Similarly, Verma *et al.* (2016) have also concluded that plant height and single plant yield were the greatest discriminating characteristics for the selection of different genotypes in pearl millet, while Kumar *et al.* (2015) stresses the importance of grain yield.

Table 3. Average inter and intra cluster distance

Clusters	I	II	III	IV	V
I	42.05	57.86	65.61	56.90	101.83
II		0.00	100.40	33.54	54.49
III			39.76	103.88	151.20
IV				0.00	57.71
V					0.00

Table 4. Cluster mean value and percentage of contribution for nine characters

Clusters	PH	NPT	SL	SG	LSL	LBL	LBW	TGW	SPY
I	172.62	3.22	26.17	9.56	15.25	61.02	4.34	11.42	69.40
II	154.85	4.00	19.00	9.00	10.20	70.85	5.40	15.25	61.40
III	191.38	3.00	26.25	9.14	13.36	54.80	3.94	12.02	60.83
IV	124.90	3.00	18.00	9.00	14.00	53.95	4.50	13.75	99.30
V	106.30	3.00	18.50	8.00	8.10	68.85	5.35	12.75	65.25
Percentage of contribution	0.00	0.00	0.00	5.33	18.00	34.00	0.00	6.00	36.67

PH: Plant height (cm), PT: Number productive tillers per plant, SL: Spike length (cm), SG: Spike girth (cm), LSL: Leaf sheath length (cm), LBL: Leaf blade length (cm), TGW: Thousand grain weight (g), SPY: Single plant yield (g).

From the diversity analysis, it can be concluded that the genotypes CO 10, PT 6481, PT 6676, PT 6475, PT 6570 and PT 6675 are top ranked in PCA and also grouped under cluster IV (PT6675) and cluster I with high cluster mean, indicating the importance of the clustering pattern of multivariate analysis. Per cent contribution of individual traits showed that maximum variability in the experimental material was contributed by single plant yield, followed by leaf blade length and leaf sheath length. Cluster III and cluster V showed the highest inter cluster distance indicating that crossing and hybridization among these clusters help in harnessing heterosis for hybridization and selection.

The overall results of the present study revealed that selecting suitable parents based on genetic divergence analysis would be more rewarding than selecting parents based on geographical distances in any population improvement programme. In the case of the hybrid development programme, the selection of diverse parents from different clusters is preferable. But in the case of synthetics or composites, since there is the urge to reach population homogeneity, selection of parents within clusters can be practised.

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