

MULTIVARIATE DIVERSITY ANALYSIS OF YIELD AND YIELD COMPONENTS IN PEARL MILLET [*Pennisetum glaucum* (L.) R. BR].

K AMUDHA*

Agricultural Research Station, Bhavanisagar-638 451, Tamil Nadu, India

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Abstract

Genetic diversity was determined in 50 pearl millet germplasm accessions based on yield and yield components using multivariate diversity analysis. Cluster analysis categorized the 50 genotypes into nine clusters with largest number of genotypes (31) present in cluster I. Clusters III and VIII were identified as distantly related clusters with cluster VIII possessing maximum cluster mean value for various productive traits such as spike girth, single ear head weight, single plant yield and single ear head threshed weight. Characters such as single plant yield, plant height and single ear head weight contributed the maximum towards divergence. So these traits may be given importance for the selection of parents. PCA revealed the existence of three principal components with eigen value more than 1.0 which contributed for 86.28% of the total variability among the traits studied. Based on PCA and cluster analysis, genotypes viz., *Kattu cumbu1*, *Kattu cumbu2*, *Kattu cumbu3* and PT7035 were adjudged as potential genotypes for the synthesis of heterotic hybrids.

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.), often known as bulrush or bajra or cattail millet is an important grain and forage crop in Africa and South Asia as well as a forage crop in America. Unlike other cereals such as rice, wheat, maize, sorghum and barley, it can thrive under adverse climatic conditions and provide economic benefits to farmers (Sathyavathi *et al.* 2021). Besides climate resilience, nutritional composition of bajra makes it a desirable food for kids as well as adults for maintenance of healthy life style. So there is an increasing demand for pearl millet in the recent years and therefore its cultivation is gaining importance (Yadav *et al.* 2021). In India, area under pearl millet cultivation is 10.3 million tonnes. As the crop is cultivated predominantly in marginal lands with low input its productivity is very less which is 1374 kg per ha (MoA and FW 2022). So it is essential to maximize the yield potential of the crop. Therefore, evolving heterotic pearl millet hybrids is an important breeding goal to overcome the ever increase in the population, changing climatic conditions as well as food habits of the consumers. In the process of development of heterotic hybrids, identification of diversified parent with desirable traits is essential as it ensures wide adaptability and sustainability under varying climatic conditions. It could be attained through genetic diversity studies such as Mahalanobis D² statistics and principal component analysis. D² analysis will categorize the genetic material into various clusters based on the dissimilarity or similarity between genotypes and PCA which is a multivariate statistical technique condenses the variable numbers into linear functions (Das *et al.* 2017). Hence in the present study, D² and PCA were carried out to assess the genetic diversity in pearl millet genotypes based on yield and yield components.

*Author for correspondence: <amudhakpbg@tnau.ac.in>.

Materials and Methods

The research material for the present study comprised of 50 pearl millet genotypes which includes maintainer lines, restorers, hybrids and landraces. All these fifty genotypes were evaluated in Randomized Block Design (RBD) in two replications during Summer, 2023. For assessment of genetic diversity, the field was divided into homogeneous randomized blocks which represent replications in RBD. Randomized blocks were separated by 70cm wide irrigation channel. Every block comprised of 100 rows of 4m row length with each genotype raised in two rows by adopting a spacing 45x15cm. Management practices were followed as per schedule for maintaining uniform crop stand. Observations on quantitative characters such as the number of productive tillers, number of internodes, plant height, spike girth, single earhead threshed weight, 1000 seed weight, single earhead weight, spike length and single plant yield were recorded in five plants per genotype. Recorded data of the above nine traits were analyzed statistically using WINDOSTAT ver. 7.1 for the estimation of genetic diversity among the genotypes. NTsys 2.2 and XLSTAT were used for the discrimination of characters and genotypes.

Results and Discussion

D² analysis categorizes the genetic material into homogeneous clusters and assists in the selection of diverse accessions for evolution of heterotic hybrids. Accordingly in the present study, cluster analysis grouped the fifty genotypes into nine clusters based on yield and yield components with each cluster possessing varied numbers of genotypes (Fig.1). Cluster I had the largest number of 31 genotypes, while clusters IV to IX had one genotype each. This indicates that cluster I had a large number of closely related genotypes, whereas clusters IV to IX had non-related genotypes (Table 1). Majority of genotypes in cluster I were restorers while it was all maintainers in cluster II and landraces in cluster III. Inter cluster distance observed was maximum between clusters III and VIII while it was minimum between IV and V (Table 2). Utmost inter cluster distance indicates that the genotypes in these clusters were of diverse nature while least inter cluster distance indicates that the genotypes in these clusters were closely related. Cluster I had the highest within cluster distance followed by cluster II and cluster III (Table 2). Hybrids synthesized using genotypes selected from divergent clusters would exhibit high heterosis and produce many useful segregants. It also provides a chance for combining beneficial genes and recovery of desirable segregants with precise combination of traits which has got potential impact on genetic improvement. In this regard, genotypes viz., *Kattu cumbu1*, *Kattu cumbu2*, *Kattu cumbu3* and PT7035 from cluster III and VIII respectively would be selected for heterosis breeding. Similar grouping of genotypes based on morphometric traits by Govindaraj *et al.* (2011) resulted in eight clusters; Mukesh *et al.* (2014) in three clusters; Sumathi *et al.* (2016) in eleven clusters; Yadav *et al.* (2016) in seven clusters; Rasitha *et al.* (2020) in five clusters and Swamynatham *et al.* (2020) in sixteen clusters indicating that the number of clusters based on grouping will vary depending upon the genetic distance among the genotypes used in their respective study.

Genotypes were not grouped based on the origin or geographical location in the present study as genotypes belonging to different regions are grouped under the same cluster which is in conformity with the findings of Animesaun *et al.* (2017). Grouping of germplasm accessions of pearl millet irrespective of origin supports its evolution from a common parent and separation by geographical locations (Jauhar 1981), thereby underscoring the importance of selection of distantly related accessions for genetic improvement programmes based on existence of genetic diversity present in it rather than the geographical distances.

Average performance of all genotypes within a specific cluster for a particular trait is represented by the cluster mean. In the present investigation, all the nine clusters showcased a

broad range of mean values for the different traits expressing the large magnitude of diversity amongst the genotypes. Cluster VIII uttered maximum cluster mean value for various traits such as spike girth, single plant yield, single ear head weight and its threshed weight followed by cluster IX for number of productive tillers and spike length and cluster V for 1000 seed weight (Table 3). Therefore, the genotype PT7035 in cluster VIII, ICMB04111 in cluster IX and PT6708 in cluster V, can be used as trait specific donors in the crossing programme. Exhibition of highest cluster mean value for various productive traits by cluster VIII and existence of utmost inter cluster distance among clusters III and VIII suggest that hybridization between PT7035 in cluster VIII and genotypes viz., *Kattu cumbu1*, *Kattu cumbu2* and *Kattu cumbu3* in cluster III would produce hybrids with more heterotic potential for yield and other economic traits.

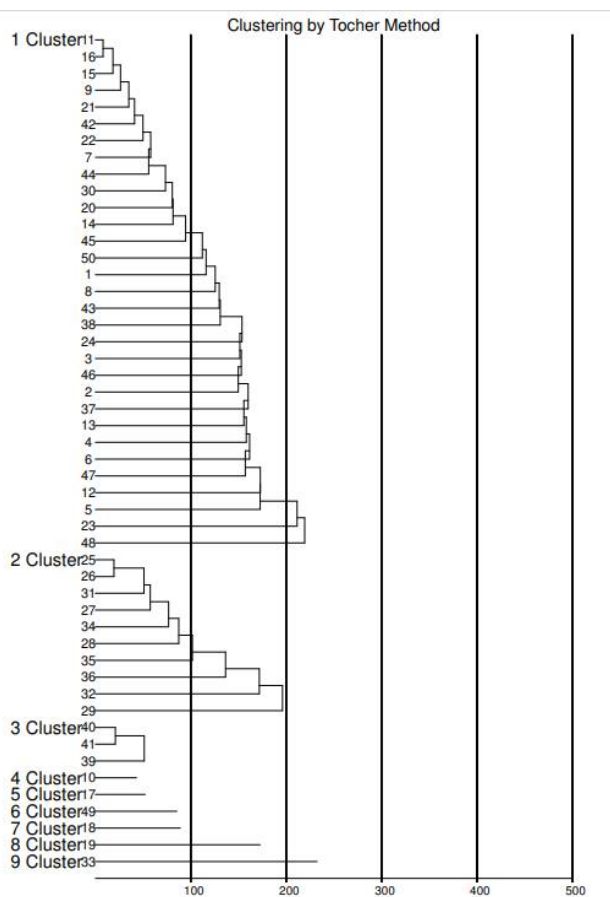


Fig. 1. Clustering pattern of 50 pearl millet germplasm accessions.

Single plant yield exhibited the highest percentage contribution towards total divergence followed by plant height, single earhead weight and its threshed weight, 1000 seed weight, spike length, spike girth, and number of internodes whereas number of tillers contributed nil to divergence due to selection of uniform lines for these characters (Table 4, Fig. 2). Thus plant height, single earhead weight, spike length, spike girth, single earhead threshed weight, number of

internodes, 1000 grain weight and single plant yield were the traits to be given importance in selecting diverse genotypes. These findings confirms the previous reports of Kumar *et al.*(2020), Rasitha *et al.* (2020) and Swamynatham *et al.*(2020).

Table 1. Grouping of genotypes by D² analysis.

Clusters	Size	Genotypes	% of total genotypes
I	31	PT5456,PT5721,PT5748,PT6029,PT6067,PT6303,PT6317,PT6475,PT6476,PT6674,PT6679,PT6680,PT6686,PT6687,PT6693,PT7036,PT7037,PT7041,PT7042,PT7043,ICMB99555, <i>Cumbu1</i> , <i>Cumbu2</i> , <i>Kizhikuppam Local</i> , <i>Nattucumbu</i> , <i>Shoolagiri Local</i> , <i>Uthangarai Local</i> ,86M38, <i>HybridC09</i> ,CO10, <i>Dhanasakthi</i>	62%
II	10	ICMB931111,ICMB93222, ICMB98222, ICMB99111, ICMB99222, ICMB00555, ICMB02777,ICMB06111, ICMB10444, ICMB1508	20%
III	3	<i>Kattucumbu1</i> , <i>Kattucumbu2</i> , <i>Kattucumbu3</i>	6%
IV	1	PT6481	2%
V	1	PT6708	2%
VI	1	COH10	2%
VII	1	PT6752	2%
VIII	1	PT7035	2%
IX	1	ICMB04111	2%

Table 2. Mean inter and intra-cluster (diagonal) distances for yield and yield related traits in 50 pearl millet accessions.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	12.35	22.59	26.94	15.31	16.06	18.18	19.75	25.35	24.50
II		12.13	23.93	28.02	28.17	32.81	32.81	35.35	21.75
III			7.63	35.84	37.80	39.64	40.56	43.86	35.25
IV				0	7.23	11.14	16.53	13.15	27.14
V					0	11.13	14.94	17.67	26.31
VI						0	11.04	21.65	29.91
VII							0	25.52	31.59
VIII								0	35.24
IX									0

PCA which is a multivariate tool for genetic diversity assessment examines the relation between large number of variables and reduces it in to a relatively smaller set without losing any important particulars of the basic data set (Das *et al.* 2017). In the present study, principal components one to three had eigen value more than 1 and contributed 86.28 % variability among the traits studied (Table 5). PC1 displayed 54.55% of total variance and showed positive loading by all features except the number of productive tillers. PC2 accounted for 19.12% of total variance with positive loading for the number of productive tillers, internodes, plant height and spike length. PC3

accounted for 12.62% of total variance with positive loading for productive tiller number, spike length, 1000 seed weight, single earhead weight, single earhead threshed weight and single plant yield (Table 6). Spike length showed positive loading in all the three principal components. Hence, it may be considered as key trait for selection to improve the crop yield. Kumari *et al.* (2018) reported that the traits plant height, leaf length, leaf width and tiller number contributed maximum towards diversity. Radhika *et al.* (2017) obtained positive contribution in four principal components by grain yield and harvest index. Rasitha *et al.* (2020) recorded positive loading towards diversity for the traits *viz.*, days to 50 percent flowering, leaf blade width and girth of the spike. Karunya *et al.* (2021) observed maximum variability for single plant yield and leaf length.

Table 3. Cluster mean value for nine quantitative characters.

Clusters	NPT	NI	PH (cm)	SL(cm)	SG(cm)	1000SW(g)	SEW(g)	SETW(g)	SPY(g)
I	4.06	7.45	179.39	26.43	9.93	12.32	32.97	25.32	89.21
II	4.21	5.21	111.82	20.77	9.86	10.56	26.33	18.55	67.93
III	4.58	7.57	167.95	16.84	6.86	6.64	13.21	6.72	32.12
IV	4.25	7.5	181.37	28.77	12.78	12.69	52.8	39.05	122.68
V	3.65	7.1	175.84	28.33	12.73	14.44	50.12	42.63	126.68
VI	4.55	7.85	194.24	33.69	13.52	12.01	43.78	35.03	125.46
VII	4.50	7.75	174.86	27.16	9.35	13.52	32.52	28.15	121.25
VIII	3.90	7.20	177.95	27.44	13.82	13.22	70.67	44.90	142.79
IX	4.90	5.25	136.02	39.57	7.86	11.96	32.71	26.80	79.88

NPT: Number of productive tillers; NI: Number of internodes; PH: Plant height; SL: Spike length; SG: Spike girth; 1000SW:1000 seed weight; SEW: Single earhead weight; SETW: Single earhead threshed weight; SPY : Single plant yield.

Table 4. Contribution of individual traits towards genetic divergence.

Sl.No.	Traits	Times ranked first	Percentage of contribution
1.	Number of productive tillers	7	0.57
2.	Number of Internodes	15	1.22
3.	Plant height	265	21.63
4.	Spike length	58	4.73
5.	Spike girth	38	3.10
6.	1000 seed weight	79	6.45
7.	Single earhead weight	237	19.35
8.	Single earhead threshed weight	26	2.12
9.	Single plant yield	500	40.82

PCA biplot of 50 pearl millet accessions revealed the clustering of maintainers on left side and most of the restorers on the right side of the graph (Fig.2) which is concurrent to the reports of Radhika *et al.* (2017) and Sangwan *et al.* (2019). Presence of pearl millet accessions *viz.*, *Kattucumbu1*, *Kattucumbu2*, *Kattucumbu3* and PT7035 in diverse quadrants at extreme corners of the plot implied that these genotypes were genetically diverse with respect to each other and highly

variable from the other genotypes for all the characters. Therefore these genotypes were regarded as distantly related accessions for utilization as potential parents in genetic improvement programme towards harnessing heterosis.

Table 5. Eigen value and percentage of total variance of various principal components.

Components	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	4.909	54.550	54.550
PC2	1.720	19.115	73.665
PC3	1.135	12.615	86.280
PC4	0.543	6.029	92.309
PC5	0.341	3.787	96.096
PC6	0.167	1.859	97.955
PC7	0.101	1.120	99.075
PC8	0.052	0.573	99.648
PC9	0.032	0.352	100.00

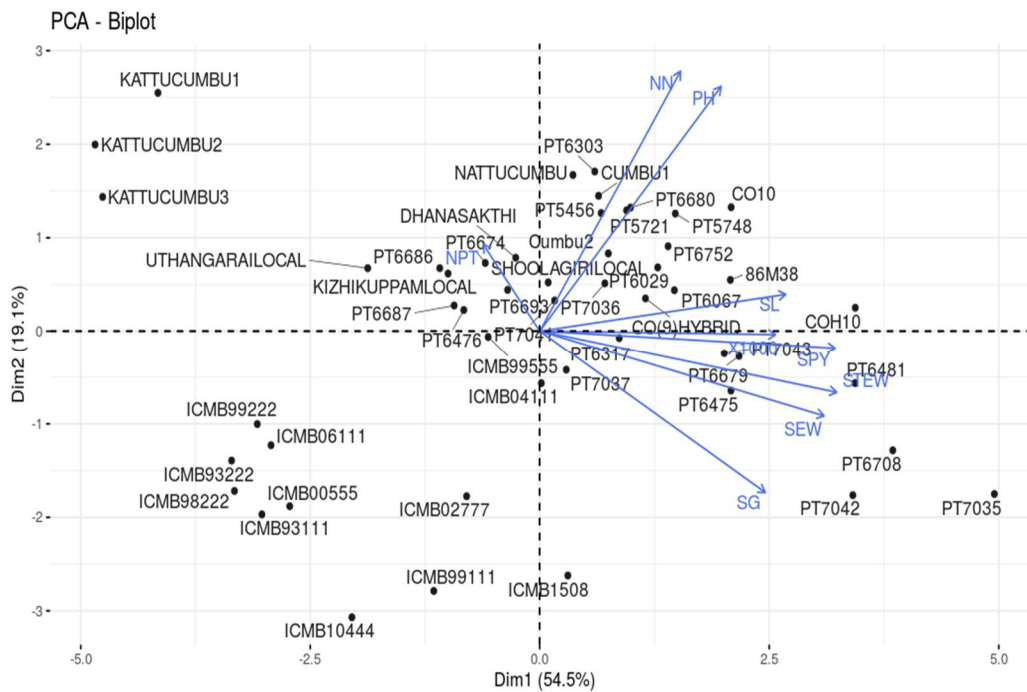


Fig. 2. PCA plot showing distribution of various traits and 50 lines of pearl millet among PC1 and PC2.

Table 6. Factor loading of various traits to different principal components.

Variables	PC1	PC2	PC3
Number of productive tillers	-0.082	0.209	0.83
Number of Internodes	0.203	0.623	-0.276
Plant height	0.262	0.586	-0.179
Spike length	0.355	0.088	0.302
Spike girth	0.326	-0.389	-0.234
1000 seed weight	0.341	-0.008	0.198
Single earhead weight	0.411	-0.205	0.012
Single earhead threshed weight	0.429	-0.148	0.03
Single plant yield	0.427	-0.041	0.128

Thus based on D^2 and principal component analysis, it can be concluded that the genetic material such as *Kattu cumbu1*, *Kattu cumbu2*, *Kattucumbu3* and PT7035 were identified as divergent genotypes for utilization as parents in the hybridization programme. Characters such as single plant yield, plant height and single ear head weight contributed the maximum towards divergence. So these traits may be given importance for the selection of parents. Present study also insists upon selection of appropriate parents for any population improvement programme based on genetic divergence analysis rather than geographical distances.

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