

Principal component analysis for yield and its attributing characters of pearl millet (*Pennisetum glaucum* [L.] R.Br.)

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ABSTRACT

An experiment was conducted at Agricultural Research Station, Navgaon (Alwar) during kharif season of 2019 to study the genetic divergence among 31 genotypes of pearl millet based on quantitative data of grain yield and its nine component traits using hierarchical cluster and principal component analysis (PCA). Principal Component Analysis (PCA) indicated that three components with eigen values more than one accounted for about 73.35% of the total variation among nine quantitative characters responsible for seed yield in pearl millet genotypes. The principal components PC1, PC2 and PC3 contributed about 37.44%, 22.63% and 13.28%, respectively to the total variation. The first principal component exhibited high positive loading for grain yield, stover yield, plant height, spike length, spike thickness and 1000-grain weight which contributed more to the diversity. The second principal component showed high loading for days to 50% flowering, days to maturity and 1000-grain weight. Cluster analysis grouped the genotypes into five clusters indicated that grain yield, stover yield, 1000-grain weight and days to maturity contributed maximum towards genetic divergence. The grouping patterns of genotypes in principal component analysis and cluster analysis were almost in agreement with each other with minor deviations. The maximum inter cluster distance between genotypes of cluster V and III with cluster II, indicate that genotypes included in these clusters have high heterotic response and produce better seggregants of used in Pearl millet hybridization programme.

Key words: Principal component, Genetic diversity, D²-value, cluster distance, cluster mean

INTRODUCTION

Pearl millet (*Pennisetum glaucum* [L.] R.Br.), a dual-purpose cereal crop, is grown extensively throughout the semi-arid regions of India. It exhibits tremendous amount of genetic diversity because of its wide distribution across the world, well adaptation under harsh environmental conditions and cross pollinated mechanism with protogynous flowering (Satyavathi *et al.* 2013 and Singh *et al.* 2013). In western part of India the environmental vagaries and varied rainfall pattern leads to the occurrence of terminal stress during grain formation phase of pearl millet. Therefore, the grain yields are greatly dependent on the ability of the varieties to mature before the exhaustion of soil moisture. Genetic diversity is pre-requisite for any crop improvement programme, as it helps in the development of superior recombinant (Kaushik *et al.* 2018). It represents the heritable variation within and between populations. Information on the genetic diversity and distance among the breeding lines and the

correlation between genetic distances are important for determining breeding strategies, classifying the parental lines, defining heterotic groups, and predicting future hybrid performance (Acquaah 2012). Genetic distance estimates for population grouping it is crucial to understand the usable variability existing in the population panel (Nachimuthu *et al.* 2014). Among different methods available one of the approaches is to apply multivariate analysis. Principal Component Analysis (PCA) is a powerful tool in modern data analysis because this is a well-known multivariate statistical technique which is used to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson 1972 and Morrison 1978) and also to rank genotypes on the basis of PC scores. Principal components are generally estimated either from correlation matrix or covariance matrix. Hence in this study, an attempt has been made to perform the diversity analysis in pearl millet hybrids for grain yield and its associating characters.

MATERIALS AND METHODS

Experiment was conducted at Agricultural Research Station, Navgaon (Alwar), Sri Karan Narendra Agriculture University, Jobner-Jaipur (Rajasthan). The Agriculture Research Station, Navgaon-Alwar is situated at extreme North East Corner between 76°07'-28°02' N latitude. The average rainfall of the zone is 500 mm. The crop was grown under normal crop season. The 31 pearl millet genotypes was grown on 18.07.2019 in randomized block design with three replications during Kharif, 2019. Each plot consisted of six rows of 5 m length and 50 cm apart. The crop was provided with fertilizers to supply 60:30 N: P kg ha⁻¹. The entire P were applied as basal and the nitrogen in two splits of equal amounts one as basal and the other as top dressing after 45 days of sowing. The crop was raised under completely rain fed conditions. Recommended cultural and agronomic measures were followed during the crop period. Quantitative characters were taken into consideration for estimating substantial variation and relationship among pearl millet genotypes. Nine quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height,

number of tillers per plant, spike length, spike thickness, 1000-grain weight, grain yield and fodder yield were taken for estimating genetic diversity. The data collected were subjected to multivariate analysis utilizing Mahalanobis D² statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software TNAU-STAT. Accessions were grouped into five clusters following Tocher's method as suggested by Rao (1952). The necessity of the principal component analysis (PCA) for measuring the degree of divergence has been established by SPSS 16.0 version.

RESULTS AND DISCUSSION

In present investigation, the analysis of variation showed considerable level of variability among different genotypes of pearl millet for most of the traits (Table 1). The largest variation was observed for fodder yield (216.27%) and plant height (170.04%). The variation was found low for grain yield, days to 50% flowering and days to maturity. This variability among the pearl millet genotypes could attribute to the inherent genetic differences or adaptation to local environmental condition.

Table 1: Variations in quantitative traits of pearl millet genotypes

Characters	Mean	Standard deviation	Variance (%)
Days to 50% flowering	47.78	3.83	14.67
Days to maturity	83.24	4.66	21.71
Plant height (cm)	184.27	13.04	170.04
Tillers per plant	2.45	0.33	0.11
Spike length (cm)	22.58	1.81	3.26
Spike thickness (cm)	2.78	0.37	0.14
1000-grain weight (g)	9.18	1.46	2.12
Grain yield (q ha ⁻¹)	19.39	5.51	30.30
Stover yield (q ha ⁻¹)	45.86	14.71	216.27

Correlation coefficient for different quantitative characters (Table 2) revealed that grain yield was significantly and positively correlated with plant height, number of tillers per plant, spike length and fodder yield. However, days to 50% flowering, days to maturity, spike thickness and 1000-grain weight were non significantly correlated with grain yield. Regarding inter-correlation, days to 50 per cent flowering exhibited positive significant correlation with days to maturity while, plant height exhibited positive significant relationship with spike length, spike thickness, 1000-grain weight and stover yield. The spike length showed highly positive significant correlation with stover yield. It is

suggested that selection of these traits will be useful for future breeding programme in pearl millet. The results were in agreement with Ezeaku *et al.* (2015) and Kumar *et al.* (2014). It is suggested that selection of these traits will be useful for future breeding programme in pearl millet. Days to maturity, days to 50% flowering and 1000-grain weight were the characters contributing positively to the second principal component (PC2) accounting for 22.63 per cent of the variability explained. It showed that bolder seeds, late flowering and later maturing plants had less effective tillers, less spike length and ultimately less grain yield as well as stover yield (Choudhary *et al.* 2015).

Table 2: Correlation coefficients among 9 quantitative traits in pearl millet genotypes

	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers per plant	Spike length (cm)	Spike thickness (cm)	1000-grain weight (g)	Grain yield (q ha ⁻¹)	Stover yield (q ha ⁻¹)
Days to 50% flowering	1.000	0.786**	-0.006	0.068	-0.143	0.04	0.228	-0.171	0.034
Days to maturity		1.000	0.233	0.027	0.014	0.299	0.435*	-0.082	0.117
Plant height			1.000	0.17	0.446*	0.498**	0.452*	0.399*	0.515**
Tillers per plant				1.000	0.158	0.174	-0.128	0.395*	0.290
Spike length					1.000	0.349	0.262	0.541**	0.530**
Spike thickness						1.000	0.484**	0.312	0.292
Test weight							1.000	0.265	0.274
Grain yield								1.000	0.881**
Stover yield									1.000

PCA analysis revealed that the first three components in the PCA analysis were with Eigen values more than one and contributed to a maximum of 73.35 per cent of the variability among 31 pearl millet genotypes evaluated for

nine different quantitative traits. These three principal components were retained based on the screen plot and threshold Eigen value greater than 1 (Fig. 1 and Table 3).

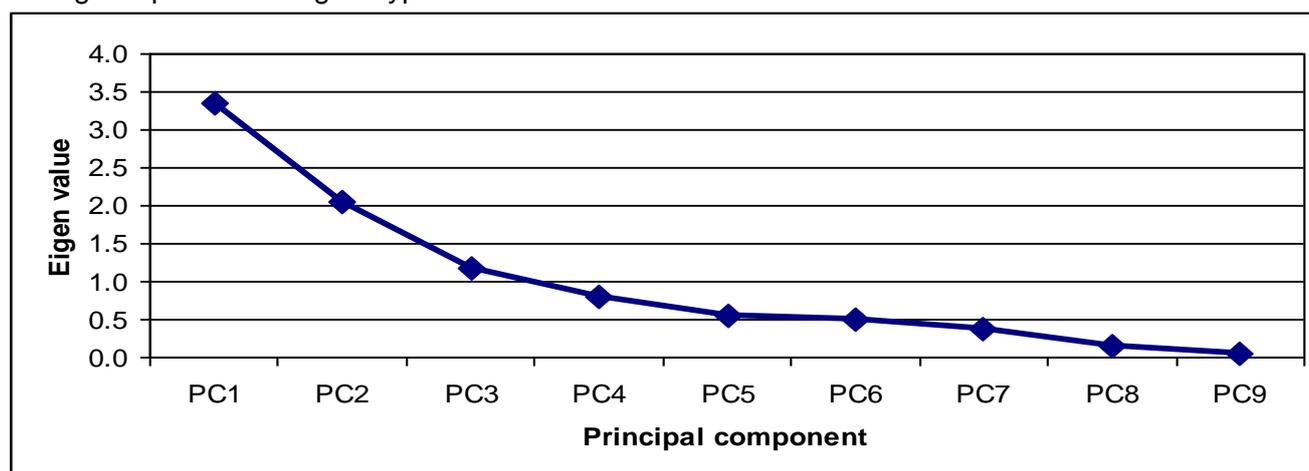


Fig1: Scree plot showing the Eigen value variation for nine quantitative traits in pearl millet

Table 3: Eigen value and percent of total variation for various principal components

Component	Eigen values	Variance explained (%)	Cumulative (%)
PC1	3.369	37.438	37.438
PC2	2.037	22.634	60.072
PC3	1.195	13.277	73.349
PC4	.794	8.826	82.175
PC5	.542	6.025	88.201
PC6	.480	5.335	93.536
PC7	.359	3.988	97.524
PC8	.160	1.777	99.301
PC9	.063	.699	100.000

A critical analysis of data reveals that all the traits analyzed in first component (PC1) contributed in a positive direction, however, with a variable magnitude (Table 4). The major yield contributing characters like stover yield, grain

yield, plant height, spike length and spike thickness contributed maximum 37.44% variability to the first principal component (PC1). Thus, this component could be the weighted average of the characters which determined the

yield level in pearl millet. The present study suggested that these traits had the largest participation in the divergence and carried the largest portion of its variability. Similar trend using PC analysis in pearl millet for the characters grain yield, stover yield, spike length and plant height has been reported elsewhere (Singh *et al.* 2018; Choudhary *et al.* 2015; Karunya *et al.* 2021). Days to maturity, days to

50% flowering and 1000-grain weight were the characters contributing positively to the second principal component (PC2) accounting for 22.63 per cent of the variability explained. It shows that bolder seeds, late flowering and later maturing plants had less effective tillers, less spike length and ultimately less grain yield as well as stover yield (Choudhary *et al.* 2015; Pujar *et al.* 2020).

Table 4: Factor loadings of nine characters with respect to different PC's (Principal components)

Characters	PC1	PC2	PC3
Days to 50 per cent flowering	0.052	0.586	0.385
Days to maturity	0.174	0.61	0.163
Plant height (cm)	0.411	0.034	-0.205
Number of tillers per plant	0.195	-0.14	0.679
Spike length (cm)	0.377	-0.19	-0.128
Spike thickness (cm)	0.358	0.135	-0.252
1000-grain weight (g)	0.321	0.309	-0.407
Grain yield (q/ha)	0.43	-0.297	0.187
Stover yield (q/ha)	0.45	-0.161	0.205

The third principal component accounting for 13.28% of the variability explained high positive component loading from number of tillers per plant and days to 50% flowering and high negative component loading from 1000-seed weight and spike thickness. The positive and negative loading show the presence of positive and negative correlation trends between the components and the variables. Therefore, the above mentioned characters which load high positively or negatively contributed more to the diversity and they were the ones responsible for that most differentiated the clusters. Assessment of workable diversity in an available set of germplasm assumes greater significance, while

initiating any breeding programme. The major objective in the present study was to select good genotypes for grain yield and, yield contributing characters with early maturity (Choudhary *et al.* 2015). In the PCA analysis, 31 genotypes grouped into three clusters showing wide diversity. The hierarchical clustering pattern of Pearl millet genotypes based on Mahalanobis squared Euclidean distance matrix obtained from quantitative data using Ward method is depicted in Figure 2. The experimental material was assigned into eight clusters at an average D^2 value of 68.62, revealing the existence of variability among genotypes for the traits characters under study.

Table 5: Grouping of pearl millet inbreds in different clusters

Clusters	No. of genotypes	Composition of cluster
I	13	HHB-272, MPMH-21, RHB-177, AHB-1269, HHB-197, AHB-1200, GHB-538, Ankur-13271, RHB-173, XMT 1497, ICMV 221, GHB 905, MPMH-17
II	2	HHB-67 (Improved), HHB-223
III	13	HHB-299, 86 M 86, PB 1705, JBV-2, GHB 558, Proagro 9444, 86 M 01, Kaveri Super Boss, Pusa Composite 383, Pusa Composite 701, MP 7792, GHB-732, KBH-108
IV	2	GHB-744, local seed
V	1	Dhanshakti

The distribution pattern of genotypes among various clusters showed considerable genetic variability existed among the genotypes. The cluster 1 and III comprised 13 genotypes each followed by cluster II and IV with 2 genotypes each and cluster V had single

genotype. The dendrogram also observed the relative magnitude of resemblance among the different clusters (Table 5). Likewise, grouping of genetic material based on quantitative data in pearl millet was reported by Chaudhary *et al.* (2015) and Kumar *et al.* (2015).

The grouping of pearl millet genotypes in different clusters gives an opportunity to developing pearl millet with high grain and fodder yield. The average intra cluster distance (Table 6) ranged from 0.00 (cluster V) to 51.37 (cluster II). The maximum intra cluster distance was noted in cluster II (382.29) followed by cluster III (41.84), cluster I (39.89), cluster IV (26.32) and cluster V (0.00). Therefore, it is suggested that selection within these clusters might be carried out on the basis of highest mean for desirable traits. Such intra cluster genetic diversity among the parental lines within the same group could be due to heterogeneity, pedigree and degree of general combining ability. The relative divergence of each cluster from other clusters (inter cluster distance) indicated high order of divergence between

cluster II and cluster V (139.13) followed by between cluster II and cluster III (112.90). The genotype grouping in different clusters inspite of their place of development and geographical distribution showed that geographical isolation was not directly related to genetic diversity. These findings were supported by reports of Vidhyadhar and Devi (2007) and Chaudhary *et al.* (2015) also supported our results. The minimum inter cluster distance was observed between cluster III and cluster IV (57.24) indicating narrow genetic diversity. It shows that geographic diversity does not essentially lead to genetic diversity. The factors of original domestication and environmental conditions at the time of development also play an important role in perpetuation, adaptation and stabilization of similar genotypes.

Table 6: Average intra (diagonal and bold) and inter cluster D^2 values for five clusters in Pearl millet

Clusters	I	II	III	IV	V
I	39.89	60.60	73.31	67.38	92.03
II		51.37	112.90	104.80	139.13
III			41.84	57.24	73.42
IV				26.32	89.13
V					0.00

Our results further indicate that the mean performance of different clusters calculated for different characters revealed wide range of variation among the clusters with respect to these characters (Table 7). Cluster II including HHB-67 (Improved), HHB-223 exhibited superior performance for grain yield (23.07 q ha⁻¹), stover yield (59.17 q ha⁻¹) and also recorded least number of days to 50% flowering (41 days) and days to maturing (76.33 days). Cluster V exhibited shown highest mean values for plant height (194.33), spike thickness (3.33) and 1000-grain weight, cluster IV for number of productive tillers

per plant (2.50) and cluster III for spike length (22.95 cm). Thus, the characters contributing to most of the divergence should be given priority for the purpose of effective selection and the choice of parents for hybridization. Grain yield contributed maximum (31.18%) towards genetic divergence followed by stover yield (21.72%), 1000 grain weight (20.86%) and days to maturity (11.82%). The remaining characters contributed less genetic divergence indicating narrow genetic diversity for those characters. Kumar *et al.* (2015) reported similar results in Pearl millet.

Table 7: Mean values for yield and its components in various clusters

Character	Clusters					Contribution (%)
	I	II	III	IV	V	
Days to 50% flowering	45.79	41.00	50.49	52.17	43.00	9.24
Days to maturity	80.62	76.33	86.97	84.67	80.00	11.82
Plant height (cm)	178.56	193.50	187.74	184.67	194.33	0
No. of tillers per plant	2.53	2.40	2.44	2.50	1.67	1.08
Spike length (cm)	22.71	22.00	22.95	20.50	21.67	0.43
Spike thick-ness (cm)	2.80	2.43	2.85	2.33	3.33	3.65
1000-seed weight (g)	8.52	7.45	10.01	8.33	12.00	20.88
Seed yield (q/ha)	19.88	23.07	19.98	10.87	14.88	31.18
Stover yield (q/ha)	42.33	59.17	50.90	27.00	35.67	21.72

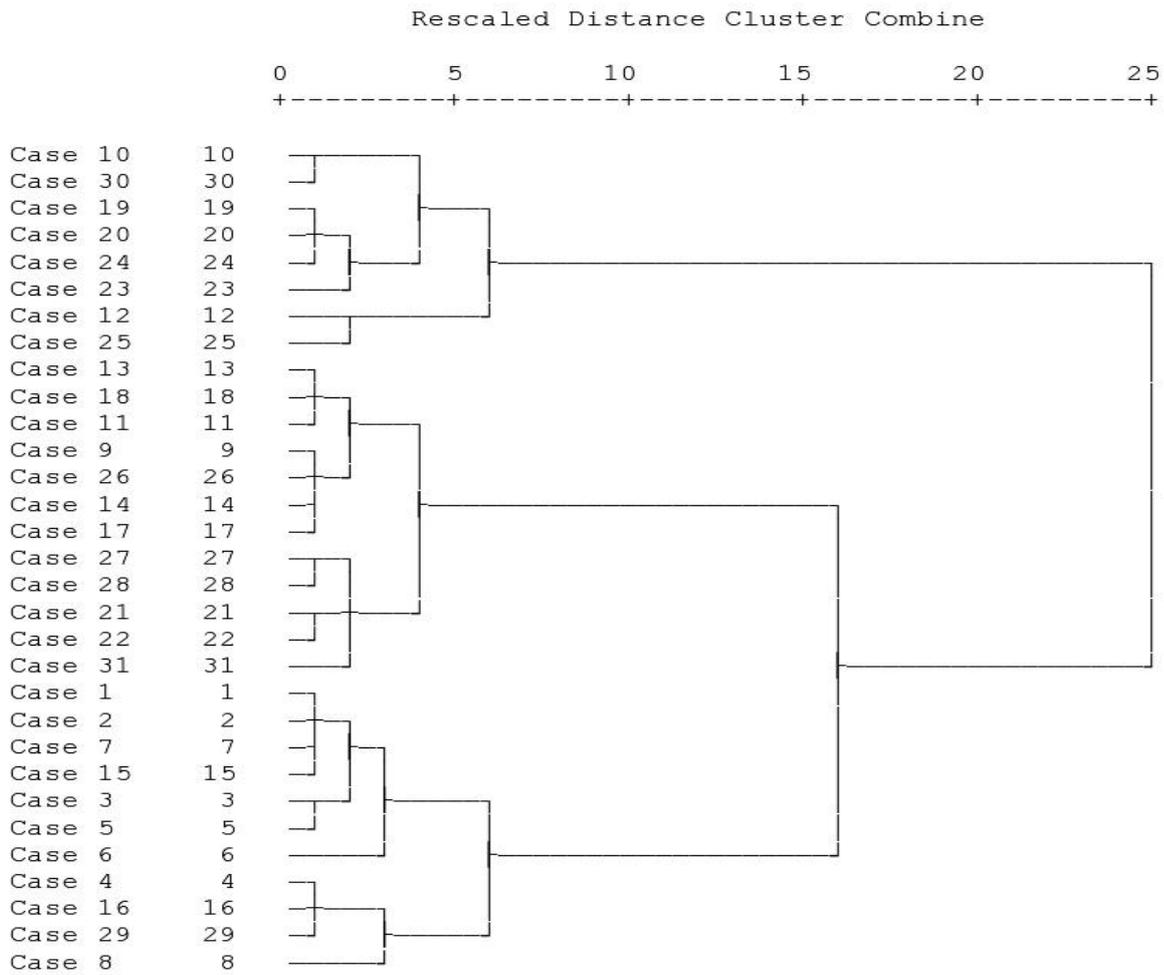


Fig 2: Ward dendrogram of 31 genotypes of pearl millet based on nine quantitative traits

The results of hierarchical cluster analysis and PCA confirmed the finding of each other. Principal factor scores (PF scores) for all the 31 genotypes were estimated for all the three PCs using Anderson-Rubin method as given in SPSS. These scores may be utilized to construct precise selection indices based on variability explained by each of the principal factor. The genotypes were plotted for PC1 and PC2 which together explained 60.10 per cent variability and included the major grain yield characters. Positive side of PC1 indicated the genotypes giving high yield (grain and stover), 1000-grain weight, plant height and spike thickness and were 12 (86M01), 25 (Dhanshakti), 11 (XMT-1497) and 21 (Kaveri Super). Similarly, positive values of PC 2 were 7(AHB-1269), 15(RHB-

173), 5(RHB-177), 3(GHB-538) and 4(HHB-197) and these genotypes combining late days to 50% flowering and late maturity. The genotypes 19 (KBH-108), 20 (86M86), 30 (Ankur-13271), 29 (JBV-2), 10 (PB 1705) and 24 (GHB-558), scored high and positively both for PC1 and PC2 i. e. the genotypes giving high yield and yield contributing characters. The groupings obtained in 3-D plot of principal components, illustrates the accession distribution in the first three principal components clearly showed the separation of 31 genotypes evaluated (Fig. 5). The pattern of clustering obtained with PCA is comparable to the UPGMA based analysis and distinguished the groups clearly and effectively. Also the results of PCA were closely in consonance with those of the cluster analysis.

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