Biological Forum – An International Journal **16(4): 101-107(2024)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Diversity Analysis in Germplasm Lines of Pearl Millet [*Pennisetum glaucum* (L). R. Br] for Yield and Yield Related Traits

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(Received: 10 February 2024; Revised: 26 February 2024; Accepted: 15 March 2024; Published: 15 April 2024)
(Published by Research Trend)

ABSTRACT: The study aimed to assess genetic variability among 26 pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm lines by evaluating fifteen quantitative traits using Mahalanobis D2 statistic and PCA analysis. Through cluster analysis, the 26 genotypes were classified into six clusters, with the greatest inter-cluster distance observed between clusters V and VI, followed by II and V. Protein content, iron content, 1000 grain weight, days to flowering, and harvest index were identified as major contributors to total genetic divergence, collectively accounting for the majority of the divergence. Principal component analysis identified six principal components (PC1 to PC6) with eigenvalues greater than one, collectively explaining 80.53% of the total variance in the germplasm lines. PC1, PC2, and PC4, representing traits of economic importance *viz.*, number of effective tillers per plant, grain yield per plant, harvest index, panicle length, panicle harvest index, panicle weight, 1000 grain weight, and zinc content, contributed significantly to genetic divergence.

Keywords: Principal component analysis, D2 analysis, clusters, PCA and pearl millet.

INTRODUCTION

Pearl millet stands as the sixth most significant cereal globally and the third in India, following rice and wheat. Known as cattail millet or bulrush millet in English (Adam, 1996) and as 'bajra' in India, it serves as a crucial staple food, providing essential nutrients and serving as a primary calorie source for millions. This annual tillering crop is cross-pollinated and diploid (2n=2x=14), belonging to the poaceae family, panicoideae subfamily, paniceae tribe, and Pennisetum genus, with its origins traced back to western Africa. With a genome size of 1.79 Gb (Varshney *et al*., 2017). It covers 6.93 million hectares in India, yielding 8.61 million tonnes with a productivity rate of 1243 Kg/ha (Directorate of Millets Development, 2020).

The protogynous nature and high cross-pollination tendency of pearl millet, combined with the availability of various male sterility sources, facilitate the successful development of hybrid cultivars (Barathi and Reddy 2022). However, creating superior hybrids necessitates the careful selection of diverse parents, with the assessment of genetic distance between them being crucial for effective parent selection. A greater genetic distance between parents typically results in higher heterosis (Singh *et al.,* 2017). Various multivariate analyses methods measure genetic distance, among which Mahalanobis' D^2 statistic (1936), as elucidated by Rao (1952), stands out as a powerful tool for quantifying divergence among all potential pairs of genotypes within a population. Principal component analysis (PCA) and clustering represent the primary approaches for genetic distance analysis in cereals and millet crops such as rice, finger millet, and pearl millet. PCA reduces the number of variables into linear functions. Thus, the present study undertook both D^2 analysis and PCA to classify and comprehend the nature and extent of genetic diversity among 26 genotypes.

MATERIALS AND METHODS

The study was carried out at the Agronomy Instructional Farm, situated within the premises of Chimanbhai Patel College of Agriculture, affiliated with Sardarkrushinagar Dantiwada Agricultural University, located in Sardarkrushinagar, District-Banaskantha, Gujarat. Twenty-six diverse genotypes of pearl millet were sown in a Randomized Block Design (RBD) with three replications during Kharif 2021. Sardarkrushinagar is situated at 24°19′ North latitude & 72°19′ East longitude, at an altitude of 154.52 meters above mean sea level, falling within the North Gujarat agro-climatic zone characterized by a sub-tropical monsoon type climate and semi-arid conditions. The area experiences cold and dry winters, while summers are hot and dry.

The germplasm comprising of twenty-six diverse varieties was sourced from the Centre for Crop Improvement, S. D. Agricultural University, Sardarkrushinagar, District: Banaskantha. The experiment followed a Randomized Complete Block Design (RCBD) with three replications. Each variety

was planted in two rows spaced at 45 cm × 15 cm, with a 1 m gap between replications. Standard agronomic practices were employed for soil preparation, sowing, and subsequent intercultural operations to facilitate optimal seedling growth. Thinning was conducted 12 days post-sowing, leaving one plant per hill. Conventional agronomic techniques were applied throughout the cultivation period.Data collection encompassed fifteen quantitative traits *viz.,* Days to flowering, days to maturity, Plant height (cm), Number of effective tillers per plant, Panicle length (cm), Panicle girth (mm), Panicle weight per plant (g), Grain yield per plant (g), Panicle harvest index (%), Dry fodder yield per plant (g), 1000 grain weight (g), Protein content (%), Harvest index (%), Iron content (%), and Zinc content (%). Measurements were taken from five randomly selected plants within each replication of every genotype. Statistical analysis was performed using WINDOSTAT ver 7.1. D2 analysis using the Tocher method and PCA analysis were conducted using NTSYSpc ver. 2.2 1t for the experimental dataset.

RESULTS AND DISCUSSION

An analysis of variance was performed on fifteen quantitative factors across 26 Pearl millet genotypes, as detailed in Table 1. The results indicate significant variations among the germplasm lines for the tested traits ($p \leq 0.01$), underscoring a notable genetic diversity and highlighting the necessity for a divergence study. Descriptive statistics, including mean values, maximum and minimum values, and coefficients of variation (CV), for the 15 morphological characters are presented in Table 3. The range of variation was most pronounced for plant height (117.60-152.90 cm), harvest index (29.42-69.67 %), iron content (41.27-151.73 %), panicle weight per plant (27.95-76.99 g), panicle harvest index (66.62-91.08 %), grain yield per plant (19.14-67.51 g), dry fodder yield per plant (21.47-68.80 g), days to flowering (47.67-71.67), days to maturity (79.34-100.00), panicle girth (16.99-28.56 mm), panicle length (16.47-27.40 cm), 1000 grain weight (5.20-10.77 g), and protein content (5.38-9.32 %). Based on the coefficient of variation, higher variability was observed for the number of effective tillers per plant, followed by panicle weight, grain yield per plant, dry fodder yield per plant, harvest index, panicle harvest index, iron content, plant height, panicle girth, zinc content, panicle length, 1000 grain weight, days to flowering, days to maturity, and protein content (Table 3). The higher range, coefficients of variation, and substantial differences in mean values for most of the characters suggest significant diversity among the genotypes and traits. These findings align with previous reports in pearl millet (Anuradha *et al*., 2018; Sharma *et al*., 2018).

Cluster analysis was conducted to elucidate the genetic relationships among various genotypes and identify suitable parents for breeding programs. The importance of genetic diversity in parental genotypes is underscored for enhancing breeding initiatives. Utilizing a hierarchical classification approach with Ward linkage clustering method based on 15 yield attributing traits, the 26 germplasm were categorized into six distinct and clearly defined clusters (Table 4). Among these, cluster 1 comprised the highest number of genotypes, thirteen, followed by cluster 2 with nine genotypes. This finding also supported by Ravindra kumar *et al.* (2022). The remaining four clusters were solitary. Monogenotypic clusters may have arisen due to geographic barriers preventing gene flow or intense natural and human selection for diverse and adaptable gene complexes (Arunachalam and Ram 1967). This suggests that many of the lines share a common origin, leading to their placement in a single cluster. This observation is supported by Athoni *et al.* (2016); Singh *et al.* (2017); Govindaraj *et al.* (2011). Maintainer lines ICMB82333 and ICMB04999, developed at ICRISAT, were grouped under two different clusters. Genotypes within the same cluster indicate a closer genetic relationship compared to those in different clusters. The distribution of genotypes across clusters revealed significant genetic variability. Average intra- and inter-cluster D2 values were estimated among the 26 germplasm (Table 5). The clustering pattern showed that varieties from different sources were grouped together, while varieties from the same source formed different clusters, indicating no relationship between geographical and genetic divergence. The maximum intra-cluster distance was observed for cluster II (D = 4.87), followed by cluster I (D=4.64), suggesting that the maximum differences occur among the genotypes within these clusters. Zero intra-cluster distance was observed for clusters III, IV, V, VI (Table 5). Similar findings were reported by Ramya *et al.* (2017); Singh *et al.* (2017).

The research observed the maximum inter-cluster distance between clusters V and VI (D = 7.43), followed by cluster II and V (D=7.11), cluster III and VI (D = 6.95), cluster I and VI (D = 6.91), cluster III and V (D=6.65), cluster IV and VI (D = 6.57), cluster II and IV (D = 6.40), and cluster II and VI (D = 5.98). The smallest inter-cluster distance was noted between cluster I and III (D = 5.16). This indicates substantial diversity among the genotypes, as inter-cluster distances exceeded intra-cluster distances, signifying genetic diversity within these clusters. This diversity suggests potential for increased heterosis in crosses, aligning with Falconer (1964). Therefore, selection of lines from these clusters with high genetic diversity could be beneficial for hybridization programs, as supported by similar findings by Ramya *et al.* (2017).

Cluster mean performance across the six clusters (Table 6) revealed a wide range of genetic diversity. Cluster III exhibited the highest mean for grain yield per plant (59.07 g) and dry fodder yield (68.80 g), attributed to component traits such as tillers per plant (2.30), plant height (131.03 cm), panicle length (20.27 cm), panicle girth (21.73 mm), panicle weight (37.19 g), and 1000-grain weight (7.88 g). Cluster VI showed the lowest mean values for days to flowering (47.67) and days to maturity (80.00), while recording the highest mean values for 1000-grain weight (8.74 g) and Fe content (151.73 %). Cluster V exhibited the highest mean values for panicle harvest index (87.73 %) and harvest

index (66.60%). Cluster IV demonstrated the highest mean for protein (9.32 %) and Zn (53.12 %). Intercrossing genotypes within these clusters could induce variability in respective traits, facilitating the rational improvement of grain yield in pearl millet. Clusters III, VI, IV, and VII displayed desirable performance based on mean values, suggesting that genotypes within these clusters could be utilized to develop new and improved inbreds, subsequently contributing to the development of high-yielding hybrids. Similar results indicating high diversity in pearl millet were reported by Kumar *et al.* (2017); Sharma *et al.* (2020); Kumar *et al.* (2022). Selection of parental combinations for hybridization should prioritize traits contributing significantly to genetic divergence.

The ranking of each character variable's contribution to the D2 was conducted, assigning I to the highest value. The sum of these ranks across all possible combinations, calculated using the formula [n(n – 1)/2] = 325 where n represents the number of characters, provided insights into the order of priority in terms of percentage contribution to total divergence. These percentages are detailed in Table 7 and depicted in Fig. 1. Among all the characters, protein content (48.31%) made the highest contribution to diversity, ranking first 157 times out of 325 combinations. This was followed by iron content (23.08%), 1000 grain weight (12.00%), and days to flowering (4.62%), while harvest index (3.08%), zinc content (2.77%), days to maturity (1.85%), and grain yield per plant, panicle girth, and length (1.23%) each contributed to total genetic divergence. Conversely, panicle harvest index (0.31%) and panicle weight (0.31%) each contributed only once, while characters such as plant height, number of effective tillers per plant, and dry fodder yield per plant did not contribute to total genetic divergence, as shown in Table 7. These findings are consistent with the studies of Swamynatham *et al*. (2020); Athoni *et al*. (2016).

PCA analysis. PCA stands out as a crucial method for simplifying data analysis, effectively reducing the dimensionality of datasets while retaining the essence of the original information. It allocates balanced significance to various characteristics, thereby enhancing their collective contribution to overall diversity based on respective variances (Mohammadi and Prasanna 2003). Through PCA, total variance is decomposed and organized into distinct principal components, with the initial component explaining the majority of variability within the original dataset.

The scree plot, a straightforward graphical representation, illustrates the fraction of total genetic variance by plotting eigenvalues of the correlation matrix in descending order of magnitude. Jain and Patel (2016) suggest that eigenvalues surpassing 1 are deemed significant and meaningful indicators. In this study, the first six principal components exhibit eigenvalues exceeding 1, collectively representing the entire variance percentage in the material (Table 8 and Fig. 2).

This investigation employs principal component analysis on mean data of fifteen quantitative traits, employing a reductionist strategy that combines observed variables into optimally-weighted linear combinations, facilitating the identification of predominant plant traits contributing to overall variation. The first six principal components, with eigenvalues greater than one, elucidate 80.53% of the variance in pearl millet germplasm lines (Fig. 2). Notably, PC1, constituting 23.06% of the variation, prominently features traits such as 1000 grain weight, panicle length, panicle weight, zinc content, grain yield per plant, protein content, dry fodder yield per plant, and iron content (refer to Table 9). Subsequent principal components account for variances of 17.09%, 12.02%, 11.40%, 9.11%, and 7.83%, respectively (Tables 8 & 9).

The variations in PC2 were primarily influenced by harvest index, plant height, panicle girth, panicle weight, days to maturity, dry fodder yield per plant, number of effective tillers per plant, iron content, panicle harvest index, days to flowering, and 1000 grain weight. Similarly, PC3 accounted for 12.02% of the variance, primarily driven by panicle harvest index, iron content, dry fodder yield per plant, grain yield per plant, zinc content, and number of effective tillers per plant, among others. Meanwhile, PC4 was mainly shaped by the number of effective tillers per plant, days to maturity, zinc content, grain yield per plant, days to flowering, panicle harvest index, iron content, panicle weight, panicle length, and 1000 grain weight. The presence of positive and negative loadings in the principal components suggested both positive and negative correlation trends among the variables. Thus, traits exhibiting high positive or negative contributions played a significant role in the observed diversity, consistent with findings by Singh *et al.* (2017). The study underscored the importance of specific traits associated with each principal component in discriminating pearl millet genotypes. This aligns with previous research by Animasaun *et al.* (2017); Sangwan *et al.* (2019) in pearl millet.

PCA facilitates the consideration of multiple traits simultaneously in selecting materials, with the advantage of selectively rejecting duplicated traits. However, considering a large number of characters together can lead to increased labour and loss of precision in the selection process. Given that principal components are based on correlation matrices, only a few characters are necessary to provide sufficient information and precision. In this study, PC1, PC2, and PC4, which encompassed economically significant traits such as number of effective tillers per plant, grain yield per plant, harvest index, panicle length, panicle harvest index, panicle weight, and 1000-grain weight, explained 51.55% of the variance and were used to analyze the divergence pattern among the 26 evaluated genotypes. These traits serve as promising selection indices for enhancing pearl millet yield, consistent with findings by Ramya *et al.* (2017); Verma *et al.* (2015); Kumari *et al.* (2016). Overall, the PCA analysis demonstrated the utility of phenotypic markers in identifying key traits responsible for the largest variability among pearl millet genotypes.

Diverse patterns were evident in the D2 statistical analysis as depicted in Table 4, indicating promising outcomes from utilizing these parental lines in hybridization programs. Understanding the general combining ability of selected parents is crucial for the success of such programs. Hence, it is imperative to evaluate both parents and hybrids across various locations or seasons to facilitate the launch of successful hybridization initiatives. Additionally, assessing the correlation between genetic distance and hybrid performance, particularly concerning grain yield in pearl millet, is essential for informed decision-making in breeding programs.

Table 1: Experimental materials to be used.

Sr. No.	Genotype	Sr. No.	Genotype
1.	15035R	14.	18587R
2.	15298R	15.	18805R
3.	15611R	16.	ICMB04999
4.	15636R	17.	1152-53B
5.	15738R	18.	2802B
6.	15990R	19.	2820B
7.	16110R	20.	2889B
8.	16127R	21.	2901B
9.	16228R	22.	5902B
10.	16834R	23.	6120B
11.	17179R	24.	7148B
12.	17369R	25.	ICMB82333
13.	18488R	26.	ICMB97111

Material received from: Centre for Crop Improvement, S. D. Agricultural

Table 2: Analysis of variance (ANOVA) for different characters of pearl millet genotypes.

Sr. No.	Character	Mean sum of square		
		Replications	Treatments	Error
	Degree of freedom	2	25	77
1.	Days to flowering	0.628	80.59**	1.14
2.	Days to maturity	1.705	79.83**	1.89
3.	Plant height (cm)	16.05	229.21**	44.36
4.	Number of effective tiller per plant	0.043	0.39**	0.039
5.	Panicle length (cm)	1.50	23.05**	0.67
6.	Panicle girth (mm)	0.191	28.01**	0.827
7.	Panicle weight per plant (g)	14.56	551.19**	22.44
8.	Grain yield per plant (g)	7.56	522.98**	12.87
9.	Panicle harvest index (%)	77.29	141.40**	29.23
10.	Dry fodder yield per plant(g)	12.58	786.74**	8.84
11.	1000 grain weight (g)	0.179	4.49**	0.071
12.	Harvest index (%)	4.58	405.77**	6.62
13.	Protein content (%)	0.003	3.05**	0.008
14.	Iron content (%)	15.82	2812.12**	19.67
15.	Zinc content (%)	2.66	64.27**	2.99

*, ** significant at 5% and 1% level of significance, respectively.

Table 3: Descriptive statistics for yield and other quantitative characters in pearl millet.

Characters	Maximum	Minimum	Mean	Std. Deviation	Coefficient of Variation
DF	71.67	47.67	60.47	1.07	1.77
DM	100.00	79.34	90.95	1.38	1.51
PH	152.90	117.60	131.32	6.66	5.07
TILLER	2.70	1.40	2.07	0.20	9.60
PL	27.40	16.47	22.25	0.82	3.68
PG	28.56	16.99	21.59	0.92	4.21
PW	76.99	27.95	50.61	4.64	9.17
GYP	67.51	19.14	40.24	3.59	8.76
PHI	91.08	66.62	79.93	5.17	6.46
DFY	68.80	21.47	36.33	2.97	8.19
TGW	10.77	5.20	8.05	0.27	3.32
HI	69.67	29.42	56.36	5.20	6.64
PRO	9.32	5.38	7.17	0.09	1.27
Fe	151.73	41.27	83.60	4.44	5.36
Zn	55.38	37.32	46.85	1.73	3.69

DF = Days to flowering, **DM** = Days to maturity, **PH** = Plant height (cm), **TILLER** = Number of effective tiller per plant, **PL** = Panicle length (cm), **PG** = Panicle girth (mm), **PW** = Panicle weight per plant (g), **GYP** = Grain Yield per plant (g), **PHI** = Panicle harvest index (%), **DFY** = Dry fodder yield per plant (g), **TGW** = 1000 grain weight (g), **HI** = Harvest index (%), **PRO** = Protein content (%), **Fe** = Iron content (%),

Table 4: Distribution of genotypes evaluated for grain yield into different clusters of pearl millet.

Cluster	No. of Genotypes	Name of genotypes
I	**13**	15611R, 2820B, 16834R, 18587R, 2889B, 16110R, 18488R, 2802B, 15035R, 2901B, 6120B, ICMB04999, 15636R
II	**9**	15298R, 15738R, 16127R, 16228R, 18805R, 115253B, 5902B, ICMB82333, ICMB97111
III	**1**	17179R
IV	**1**	7148B
V	**1**	17369R
VI	**1**	15990R

Table 5: Average intra and inter cluster D^2 value of 26 genotypes of pearl millet.

Cluster	I	II	III	IV	V	VI
I	**21.56 (4.64)**	32.73 (5.72)	26.69 (5.16)	31.19 (5.58)	34.63 (5.88)	47.75 (6.91)
II		**23.77 (4.87)**	32.88 (5.73)	41.00 (6.40)	50.65 (7.11)	35.87 (5.98)
III			**0.00 (0.00)**	34.71 (5.89)	44.27 (6.65)	48.42 (6.95)
IV				**0.00 (0.00)**	27.97 (5.28)	43.24 (6.57)
V					**0.00 (0.00)**	55.33 (7.43)
VI						**0.00 (0.00)**

(Note: Parent thesis indicates value of D in bracket and D^2in above mention table)

Table 6: Cluster mean for 15 different characters in 26 genotypes of pearl millet.

Cluster	DF	DM	PH	TILLER	PL	PG	PW	GYP	PHI	DFY	TGW	HI	PRO	Fe	Zn
I	59.97	90.47	134.25	2.25	23.04	22.60	55.74	44.95	81.46	26.81	8.30	62.05	7.64	62.55	46.86
II	61.64	91.67	127.69	1.98	21.62	19.67	47.68	35.53	79.63	29.98	7.79	55.45	6.44	86.52	46.18
III	60.00	94.67	131.03	2.30	20.27	21.73	37.19	59.07	77.35	68.80	7.88	29.42	7.80	50.86	49.32
IV	66.67	93.00	133.00	2.00	17.23	28.56	32.59	55.37	66.62	31.27	8.21	40.61	9.32	139.03	53.12
V	58.67	92.33	152.90	1.73	27.40	26.85	76.99	30.15	87.73	33.87	8.16	66.60	9.09	144.27	46.59
VI	47.67	80.00	122.70	1.60	23.77	22.28	39.53	44.62	79.05	20.50	8.74	60.25	6.47	151.73	47.65

DF = Days to flowering, **DM** = Days to maturity, **PH** = Plant height (cm), **TILLER** = Number of effective tiller per plant, **PL** = Panicle length (cm), **PG** = Panicle girth (mm), **PW** = Panicle weight per plant (g), **GYP** = Grain Yield per plant (g), **PHI** = Panicle harvest index (%), **DFY** = Dry fodder yield per plant (g), **TGW** = 1000 grain weight (g), **HI** = Harvest index (%), **PRO** = Protein content (%), **Fe** = Iron content (%), **Zn** = Zinc content (%)

Table 7: Contribution of various traits towards total genetic divergence.

Sr. No.	Characters	Time ranked first	Contribution (%)
1.	Days to flowering	15	4.62
2.	Days to maturity	6	1.85
3.	Plant height (cm)	0	0.00
4.	Number of effective tiller per plant	0	0.00
5.	Panicle length (cm)	4	1.23
6.	Panicle girth (mm)	4	1.23
7.	Panicle weight per plant (g)	1	0.31
8.	Grain yield per plant (g)	4	1.23
9.	Panicle harvest index (%)	1	0.31
10.	Dry fodder yield per plant(g)	0	0.00
11.	1000 grain weight (g)	39	12.00
12.	Protein content (%)	157	48.31
13.	Harvest index (%)	10	3.08
14.	Iron content (%)	75	23.08
15.	Zinc content (%)	9	2.77

Table 8: Eigenvalues and per cent variance Explained in different PCs for 15 quantitative traits in pearl millet.

Components	Eigenvalues	% of variance	Cumulative %
1	3.46	23.06	23.06
2	2.56	17.09	40.15
3	1.80	12.02	52.18
4	1.71	11.40	63.58
5	1.36	9.11	72.70
6	1.17	7.83	80.53
7	0.91	6.07	86.61
8	0.57	3.83	90.44
9	0.44	2.93	93.37
10	0.34	2.31	95.68
11	0.28	1.87	97.56
12	0.18	1.25	98.81
13	0.11	0.75	99.57
14	0.06	0.38	99.95
15	0.01	0.04	100.00

Table 9: The estimated compound matrix in first six PCs of pearl millet genotypes.

Character	PC1	PC2	PC3	PC4	PC5	PC6
DF	-0.320	0.209	-0.678	0.282	0.294	0.324
DM	-0.223	0.412	-0.421	0.405	0.228	0.439
PH	-0.148	0.674	-0.344	-0.275	-0.295	-0.273
TILLER	-0.256	0.353	0.087	0.604	-0.313	-0.355
PL	0.886	0.241	-0.092	0.065	-0.044	0.051
PG	-0.156	0.597	-0.136	-0.454	0.103	-0.366
PW	0.827	0.431	-0.036	0.137	-0.090	0.105
GYP	0.790	-0.048	0.155	0.328	0.235	-0.171
PHI	-0.412	0.214	0.473	0.229	0.084	0.136
DFY	0.080	0.356	0.419	-0.281	-0.466	0.430
TGW	0.929	0.081	-0.225	0.056	-0.074	-0.009
HI	-0.101	0.814	-0.001	-0.178	0.171	-0.065
PRO	0.231	-0.039	0.051	-0.680	0.501	0.235
Fe	0.012	0.264	0.434	0.207	0.676	-0.330
Zn	0.790	-0.048	0.155	0.328	0.235	-0.171

DF = Days to flowering, **DM** = Days to maturity, **PH** = Plant height (cm), **TILLER** = Number of effective tiller per plant, **PL** = Panicle length (cm), **PG** = Panicle girth (mm), **PW** = Panicle weight per plant (g), **GYP** = Grain Yield per plant (g), **PHI** = Panicle harvest index (%), **DFY** = Dry fodder yield per plant (g), **TGW** = 1000 grain weight (g), **HI** = Harvest index (%), **PRO** = Protein content (%),**Fe** = Iron content (%), **Zn** = Zinc content (%)

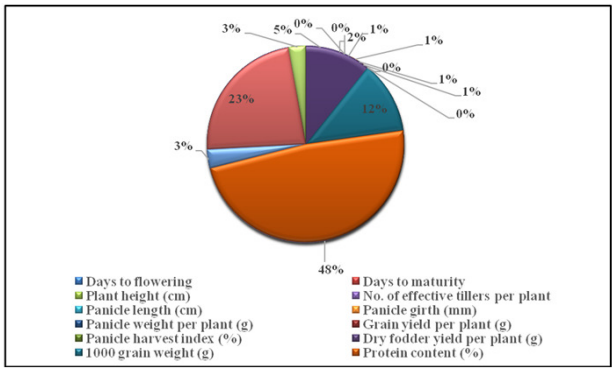

Fig. 1. Contribution of various traits towards total genetic divergence.

Fig. 2. Graph showing eigenvalues in response to number of components for the estimated variables in pearl millet.

CONCLUSIONS

The pearl millet lines that have been evaluated have a lot of variation that may be used in breeding programmes. The genotypes of Pearl millet were divided into 6 clusters in this study. The lines of cluster V and VI followed by II and V while PC1, PC2 and PC4 involving characters of major economic importance *viz.,* number of effective tiller per plant, grain yield per plant, harvest index, panicle length, panicle harvest index, panicle weight, 1000 grain weight and zinc content might be employed in the crop enhancement programme to generate potential hybrids based on genetic distances.

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How to cite this article: P.A. Goswami and P.R. Patel (2024). Genetic Diversity Analysis in Germplasm Lines of Pearl Millet [*Pennisetum glaucum* (L). R. Br] for Yield and Yield Related Traits. *Biological Forum – An International Journal, 16*(4): 101-107.