EVALUATION OF VARIATIONS IN PEARL MILLET (*PENNISETUM GLAUCUM*) GENOTYPES FOR YIELD AND ITS ATTRIBUTING TRAITS UNDER SEMI-ARID CONDITIONS BY PRINCIPAL COMPONENT ANALYSIS

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SUMMARY

To estimate the extent of genetic diversity of 56 Pearl millet genotypes for eight morphological characters, an experiment was carried out at the research farm of Forage Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar in *kharif* 2020-21. In Principal component analysis (PCA) the eigenvalues were used to determine how many factors to retain. In the present study, the first four principal components (PCs) had eigen values greater than one, and they cumulatively explained 71.3% of the total variation present in the original dataset. The first principal component (PC 1) explained 20.30% of the total variability, while the PC 2, PC 3, and PC 4 explained 19.2%, 17.3%, and 14.5% of the total variability, respectively. O 54, O 34, O 25, O 15, and O 40 were found as the top-ranking genotypes upon PCA analysis with high positive PC1 scores. These genotypes, showed highest overall mean values for the traits positively related to grain yield and its attributing traits. These findings can be useful in formulating breeding strategies for future hybridization programs for yield improvement and are appropriate for classification of diversity among pearl millet germplasm.

Key words: Eigen value, Pearl millet, Principal Component and Variation

Pearl millet [*Pennisetum glaucum* (L.) R. Br., syn. *Cenchrus americanus* (L.) Morrone] is the most important *kharif* season millet crop in the semi-arid, arid regions of India and sub-Saharan Africa. It is an annual diploid (2n=2x=14) plant of the family *Poaceae* and is a C_4 monocot species with high cross pollination (Ramu *et al*., 2023). In India, it is mainly cultivated in states, Rajasthan, Uttar Pradesh, Hayrana and Gujarat (APEDA 2022-23). In Haryana, during year 2021-22, the pearl millet was grown on 483.1 thousand-hectare area, with the productivity of 23.18 q/ha and overall production of 1119.7 thousand tonnes (DAFW, Haryana 2021-22). Pearl millet is source of nutritious source of food for poorest populations of arid and semi-arid areas of tropical and sub-tropical countries. This crop has high protein efficiency ratio with balanced amino acid profile. Higher fiber content and its gluten free characteristic causes retardation in the digestion of food and release of glucose in the blood stream. Hence, food items prepared from pearl millet are suitable for diabetes patients due to their low glycemic index (Kumar *et al*., 2024).

Genetic diversity among genotypes holds significant value for breeding programs, the development of new agricultural techniques, expanding production diversity, and generating novel high-quality products (Dewangan *et al*., 2019). This diversity serves as a crucial resource for accessing genes essential for various breeding endeavors. Understanding genetic diversity patterns and levels accurately is essential for predicting potential heterotic combinations before initiating breeding crosses, thereby conserving both time and financial resources. Such insights enable the strategic introduction of desirable genes from wild germplasm into high-yielding germplasm pools, facilitating the analysis of genetic diversity within germplasm collections, and identifying alternative combinations for generating segregating progenies with maximum genetic variability (Raiger *et al*., 2021). Principal component analysis (PCA) methods can serve as valuable tools for identifying groups of genotypes with desirable traits for breeding purposes and for uncovering patterns of variation among genotype accessions, as well as for determining correlations between genotypes (Choudhary *et al*., 2015). Principal component analysis summarizes the variability inherent in the original data.

The objective of the current study was to assess the extent of genetic diversity present in 56 Pearl millet genotypes for eight morphological characters through principal component analysis. This analysis aids in the selection of potential parental genotypes for the development of transgressive segregants.

MATERIALS AND METHODS

The current study was conducted on 56 genotypes of Pearl millet (Table 1), which were sourced from various origins and cultivated during the *kharif* season of 2020-21. The experiment took place at the research farm of the Forage Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar. A randomized block design with three replications was employed for the experimental layout. Each genotype was planted in a single-row plot measuring 3 m in length, with a row-to-row spacing of 45 cm. Plant-to-plant distance was maintained at 10-12 cm. The cultivation followed all recommended practices to ensure optimal crop growth. The study area is situated in a semi-arid subtropical region, located on the outer fringes of the southwest monsoon region, characterized by a tropical monsoonal climate with an average annual rainfall of approximately 452 mm.

Eight morphological traits including plant height (cm), days to 50% flowering, panicle length (cm), panicle diameter (cm), number of productive tillers, grain yield per plant (g), dry fodder yield per plant (g), and 100-seed weight (g) were recorded from five competitive plants per paired row in each replication. Principal component analysis was performed on the dataset of 56 Pearl millet genotypes using SPSS 26. Graphs were generated using both SPSS 26 and Excel.

RESULTS AND DISCUSSION

The principal component analysis is a multivariate analysis technique which is used to reduce the complexity of the data set to a lower dimension and provides information regarding the importance and contribution of each component towards the total variance (Pujar *et al.*, 2020). In the present study first four principal components had eigen value greater than one and they cumulatively explained 71.3 per cent of the total variation present in original data set (Table 2). The first principal component explained 20.30 per cent of the total variability. The PC 2, PC 3, and PC 4

explained 19.2, 17.3 and 14.5 per cent of the total variability, respectively. Above results revealed that the maximum variability was spread within first four principal components where PC1 showed the highest variability among four. It was also recommended by previous workers to consider the characters or genotypes lying near and showing more PC1 score for catching the variability of particular character (Ramya *et al.*, 2017; Jain and Diwan, 2021).

Further principal component analysis was carried out using varimax rotation to check character association with respective principal components (Table 3). Correlation value of greater than ±0.5 was considered to select relevant characters in different principal factors (Kaiser, 1998). From Table 3 is evident that PC 1 showed high positive loading for dry fodder yield (0.834), number of productive tillers (0.812), whereas it showed negative loading for days to flowering (-0.111), panicle length (-0.174) and 1000-seed weight (-0.067). PC 2 enabled high positive loading for grain yield per plant (0.812), 1000-seed weight (0.845), whereas it showed negative loading for days to 50% flowering (-0.124), plant height (-0.020), and dry fodder yield per plant (-0.128). Since, PC 2 captured maximum variability for grain yield and 1000 seed weight, the genotypes captured under this component can be utilized in improvement of crop for above mentioned traits. PC 3 showed high positive loading for plant height (0.810) and panicle length (0.810). PC 4 shows high loading for days to 50% flowering (0.757) and panicle diameter (0.742), whereas it shows negative loading for plant height (-0.032), number of productive tillers (-0.176) and 1000-seed weight (-0.112). The characters which showed high positive or high negative values of factor loadings contributed more to the diversity. The sign of factor loadings here indicates the relationship between variable and principal components (Kalagare *et al.*, 2022). The pattern of variation explained by different PCs for various traits was fairly in agreement with the reports of previous works in Pearl millet by Gupta *et al.*, (2022) and other crops like maize where Al-Naggar *et al.*, (2014) also reported that first two PCs accounted for about 46 per cent of variation with weight of grains, the number of spikelets spike, spike length.

The list of top ten pearl millet genotypes based on their PC scores are arranged in Table 4. In PC 1, the genotypes O 2, O 1, O 37, O 23, O 46, O 47, O 5, O 53, O 7, and O 25 showed maximum score. The genotypes O 54, O 34, O 25, O 15, O 40, O 17, O 47, O 26, O 53, and O 4 scored maximum in PC 2. The

TABLE 1

Details of pearl millet germplasm lines evaluated in the present investigation

Code	Name/Pedigree of Genotype	Code	Name/Pedigree of Genotype
O 1	HBL-11	O 14	SRC II bulk/11-S1/78-1-2-3-2-1-B
O 2	H13/0001	O 15	82
O 3	AC 04/13	O 16	(EERC-HS-8)-5-3-1-B-B
O 4	HTP 94/54	O 17	DM/Blast R-composite-HS(Early)-S1-1-1-4-2-2-4
O 5	G-73/107	O 18	(ICMB 02333 x ICMB 92777)-10-3-1-B
O 6	H 77/833-2-202	O 19	HTP09/63 (S1-ICMV 94474)
O 7	(ICMB 92333 x EEBC C1-1)-5-B-B)	O 20	EIHFEL/13
O 8	IP 18292-1	O 21	GP 1123 K-16
O 9	21-204	O 22	PDBL/16102
O 10	A4 R-composite-HS-18 -1	O 23	TPL/16/108
O 11	A5RT-110	O 24	(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-23-4-4-2
O 12	TPT-A2-117	O 25	HPT-10-144
O 13	[((MC 94 S1-34-1-B x HHVBC)-16-2-1) × (IP 19626-4-2-3)]-B-1-1-2-3-2-B-1	O 26	ICMV 91059 S1-4-2-3-2-1-1-4-B-1-3-B-1
O 27	HHVBC tall (C1) S1-33-3-1-1-1-2-B-B-3-3-1-7	O 42	TPL/16/132
O 28	([(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-8-3-1] x ICMV 91059 S1-14-2-4-1-1-1-2-1-2-3-2-B-B-1-1 -10x(MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-23-3-1-29-1x R-lines bulk (20216-20249/K09)])-B-2-4	O 43	Thorny composite-HS-S2-B-10-2-1
O 29	NE CPBL 11-107	O 44	1660 (MT)
O 30	HTP 0819	O 45	TPL/16/114
O 31	(EERC-HS-29)-19-3	O 46	(MC 94 C2-S1-3-1-3-3-1-2-1 x SDMV 90031 S1-3-3-2-2-2-2-2)-B-8-2-1
O 32	GP 1123 K-16	O 47	TPL/16/124
O 33	GP 1177 K-16	O 48	SRC II bulk/11-S1/74-2-2-3-1-2-B
O 34	CPBL/16/102	O 49	((EERC-HS-22)-7-2-2-B x {((MC 94 S1-34-1-B × HHVBC)-16-2-1) × (IP 19626-4-2-3)]-B-28-3-1-2-2}×{JBV 3 S1-197-2-4-1}-B-3-P1-3-3-B-B)-10-2-3
O 35	EMRL/12-108	O 50	([(IP 12370-1-3 × B-Lines)-B-9-1-2-1-2-2 x MRC S1-191-2-1-5-B]-B-6-1xR-lines bulk (22680-22692/S11))-4-1-1-4-B
O 36	HFI/13	O 51	75
O 37	HMS 59 B	O 52	([(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-8-3-1] x ICMV 91059 S1-14-2-4-1-1-1-2-1-2-3-2-B-B-1-1 -10x{[((MC 94 S1-34-1-B x HHVBC)-16-2-1) × (IP 19626-4-2-3)]-B-18-2-3-2-2-BxICMR 312 S1-3-2-3-2-1-1-B-B-B-B}-B-3-4-1-1)-B-4-1
O 38	(MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-34-4-2-B-Bx(R-lines bulk (22669-22675/S11)-5-1-4-1	O 53	PDBL/16125
O 39	A4 R-composite-HS-75-1-1	O 54	TPRL-11-109
O 40	[((MC 94 S1-34-1-B x HHVBC)-16-2-1) × (IP 19626-4-2-3)]-B-34-1-3-3-1-1-B-2	O 55	MRC HS-109-1-1-1-B-2-B-1-B
O 41	(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-23-4-4-2	O 56	High Fe JBT/12-139-3

TABLE 2

Total variance explained by different principal components in pearl millet genotypes

Principal components (PC)	Eigen value	Variation explained (%)	Cumulative variation explained (%)
1	1.626	20.3	20.3
2	1.539	19.2	39.6
3	1.384	17.3	56.9
4	1.158	14.5	71.3
5	0.947	11.8	83.2
6	0.596	7.5	90.6
7	0.470	5.9	96.5
8	0.281	3.5	100

TABLE 3

Loadings (Eigenvectors) of Correlation Matrix

	PC1	PC2	PC3	PC4
DF	-0.111	-0.124	0.184	0.757
PH	0.312	-0.020	0.801	-0.032
PL	-0.174	0.086	0.810	0.034
PD	0.155	0.287	-0.277	0.742
PT	0.810	0.057	-0.015	-0.176
GY	0.003	0.801	0.198	0.190
DFY	0.834	-0.128	0.077	0.192
TW	-0.067	0.845	-0.103	-0.112

DF=Days to flowering, PH=Plant height, PL=Panicle length, PD=Panicle diameter, PT= Productive tillers, GY= Grain yield, DFY= Dry fodder yield, TW= Test weight.

genotypes showing maximum PC score in PC 2 showed highest overall mean values for the traits positively related to grain yield and its attributing traits. In PC 3, the genotypes O 1, O 40, O 17, O 27, O 30, O 36, O 52, O 7, O 53 and O 54 showed maximum PC score. In PC 4, the genotypes, O 7, O 55, O 37, O 40, O 17, O 5, O 14, O 30, O 56, and O 29 scored maximum PC score. In figure1 the pearl millet genotypes are distributed on the bases of their performance with respect to PC 1 and PC 2. PC 1 was showing high positive loading for number of productive tillers and dry fodder yield per plant while, PC 2 was showing high positive loading for grain yield per plant and 1000-seed weight. The genotypes viz. O 44, O 18 and O 2 were found to be placed farthest from the bi-plot origin. Therefore, these genotypes accounted for more variability for traits of respective principal components than other genotypes (Fig. 1). Genotypes number O 25, O 15, O 54, O 17, O 55, O 40, O 34, O 4 and O 51 clustered towards positive side of Dimension 1 (PC-1), therefore, these were better in terms of number of productive tillers and dry fodder yield per plant. Genotype number O 1, O 5, O 37, O 23, O 43, O 33, O 28, O 53, O 8 and O 47 clustered towards positive sign of Dimension 2 (PC-2), therefore, these genotypes were better in terms of grain yield per plant and 1000-seed weight. The genotypes number O 18 and O 39 were positioned on the positive side of both the factors, so they were better in both aspects i.e. number of productive tillers, fodder yield, grain yield and 1000-seed weight. Hence, these genotypes can be considered for recombination for yield enhancement in future breeding programmes.

PCA results were generally are displayed as a

TABLE 4

List of top ten Peal millet accessions based on their PC scores

Rank	PC 1 DFY and PT		PC 2 GY and TW		PC 3 PH and PL		PC 4 DF and PD	
	Genotype	Score	Genotype	Score	Genotype	Score	Genotype	Score
1	O 2	2.189	O 54	1.980	O 1	2.375	O 7	2.346
2	O 1	1.718	O 34	1.972	O 40	1.755	O 55	1.518
3	O 37	1.450	O 25	1.911	O 17	1.331	O 37	1.498
4	O 23	1.162	O 15	1.678	O 27	1.327	O 40	1.209
5	O 46	1.144	O 40	1.382	O 30	1.168	O 17	1.142
6	O 47	1.064	O 17	1.333	O 36	1.150	O 5	1.078
7	O 5	1.023	O 47	1.265	O 52	1.124	O 14	1.069
8	O 53	0.935	O 26	1.210	O 7	1.112	O 30	1.064
9	O 7	0.858	O 53	1.195	O 53	0.990	O 56	1.061
10	O 25	0.844	O 4	1.137	O 54	0.878	O 29	1.030

DF=Days to flowering, PH=Plant height, PL=Panicle length, PD=Panicle diameter, PT= Productive tillers, GY= Grain yield, DFY= Dry fodder yield, TW= Test weight.
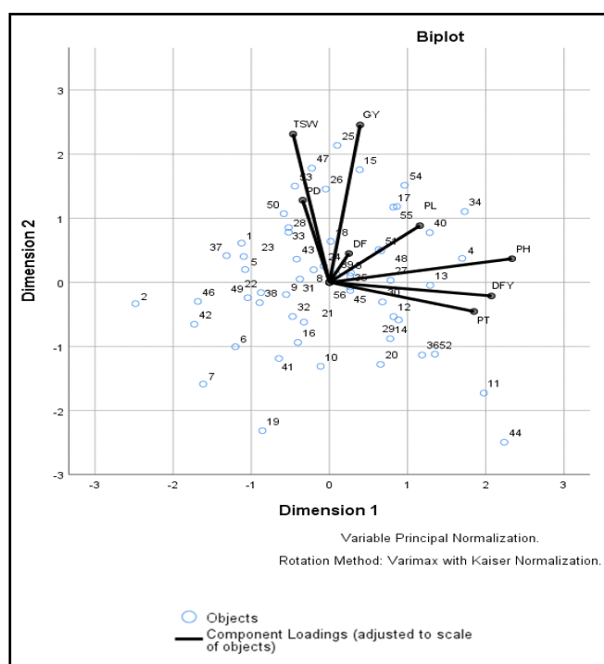
Fig. 1. Distribution of pearl millet genotypes based on principle factor 1 and 2.

bi-plot to make visualization of the correlations between the traits easier (Fig. 1). The direction of arrow denotes the maximum change in great quantity and the length could be related with the rate of change occur. The vector length *i.e.*, the distance to the bi-plot origin of a trait indicates how well the trait is represented in the bi-plot. A relatively shorter vector indicates that the variation of the trait across genotypes is either small or not well presented in the bi-plot. This can be due to its weak or lack of correlation with other traits (Yan and Fregeau-Reid, 2018). The acute coordinate angle (<90º) between the traits or principal component axis and trait shows positive whereas, obtuse angle (>90º) shows negative and right angle (=90º) indicates no correlation between the traits (Govindaraj *et al.*, 2020). The PCA bi-plot (Fig. 1) accounted for 39.6 per cent of total variability and revealed that grain yield, spike length, 1000 seed weight and dry fodder yield were the most discriminatory variables.

The genotypes *viz.*, 44, 19 and 2 were found to be scattered farthest from the bi-plot origin and other genotypes. Therefore, these genotypes accounted for more variability for traits of respective principal components than other genotypes. The vectors of 1000 seed weight, panicle diameter, panicle length and plant height are main contributors of grain yield in pearl millet (acute angle). Similarly, grain yield has no relation with dry fodder yield and number of productive

tillers (almost right angle). The vector of days to 50% flowering is the shorter than rest of the traits indicating that the variation of this trait across genotypes is either small or not well presented in the bi-plot.

CONCLUSION

Principal component analysis reduced the original 8 variables into four major principal components those explaining 71.3 per cent of total variation in the data. First principal component contributed 20.3 per cent of variation. The second, third and fourth principal component contributed 19.2, 17.3 and 14.5 per cent of total variation in the data, respectively.

According to factor loading after varimax rotation it can be concluded that PC-1 and PC-2 can be designated as yield factors as it showed high loadings for grain yield, fodder yield and 1000- seed weight. These findings can be used in breeding strategies for future hybridization programs for yield improvement and are appropriate for classification of diversity among Pearl millet germplasm.

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