International Journal of Agriculture and Food Science 2025; 7(8): 1017-1024

ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2025): 4.97
IJAFS 2025; 7(8): 1017-1024
www.agriculturaljournals.com
Received: 08-05-2025
Accepted: 13-06-2025

Manish V Boratkar
Foragen Seeds Private
Limited, Hyderabad,
Telangana, India

Hasanali Nadaf
Foragen Seeds Private
Limited, Hyderabad,
Telangana, India

Corresponding Author:
Manish V Boratkar
Foragen Seeds Private
Limited, Hyderabad,
Telangana, India

Defining the selection criteria for forage pearl millet (*Pennisetum glaucum* (L.) R. Br.) accessions using cluster analysis, PCA, and correlation

Manish V Boratkar and Hasanali Nadaf

DOI: https://www.doi.org/10.33545/2664844X.2025.v7.i8i.672

Abstract

A comprehensive evaluation of 480 distinct accessions of forage pearl millet, employing an augmented design methodology at the Foragen Seeds Private Limited Research Farm, which is situated in Hyderabad during the kharif season of 2024. significant and positive correlation were showed for traits like plant height, panicle length, panicle girth, number of tillers, stem girth, number of leaves and leaf length. Therefore, these traits can be considered for selection of parental lines for further hybrid breeding program. The accessions taken into consideration for the study showed a broad range of genetic differentiation for forage yield component characteristics. The mean of eight traits in 480 accessions with 51.8% variances was used to extract the first three main components with eigenvalues greater than one. The first, second, and third major components yielded variances of 21.4, 16.9, and 13.4%, respectively. 480 accessions were divided into ten groups using the K-mean clustering technique, which was based on eight quantitative traits and clearly distinguished between them for each quantitative trait. Based on their parental and geographic origins, the majority of accessions were not grouped together into a single cluster. The first principal component (PC1), which explained 21.4% of the variation with the main contributing traits i.e. panicle length, panicle girth, stem girth, and leaf width was the most significant component according to PCA analysis. Based on cluster analysis, a unique accession FFPMA-110 was grouped in cluster 7 followed by accessions of cluster 9 were FFPMA-2, FFPMA-34, FFPMA-40, FFPMA-58, FFPMA-68, FFPMA-69, FFPMA-185, FFPMA-194, FFPMA-204, FFPMA-208 and FFPMA-397 therefore, breeders can use these accession directly as inbred lines and also for further hybridization with low yielding clusters like cluster 1, 3, 4, 6 and 8 for forage yield improvement in pearl millet.

Keywords: Forage pearl millet, genetic diversity, principal component, cluster mean, correlation

Introduction

Pearl Millet (*Pennisetum glaucum* (L.) R. Br.) is the champion of drought resistance. Pearl millet, also known as bajra, is one of India's most popular drought-resistant crops. Bajra is a popular crop in arid and semi-arid areas because of its capacity to survive harsh heat and drought conditions. A wide variety of high-yielding hybrids with sufficient adaptation to various agro-ecologies were produced as a result of the trait diversification technique. The successful efforts of the national program of pearl millet improvement toward genetic diversification of hybrids were demonstrated by a recent study that examined 122 commercial hybrids and found significant variation in flowering time (42–58 days), tillering (1.1–4.4 panicles/plant), individual grain size (7.6–17.3 mg), plant height (185–268 cm), and panicle length (20–33 cm) (Yadav *et al*., 2017) [1]. Correlation studies are crucial in pearl millet breeding, particularly for forage quality traits, as they help to identify relationships between different traits and facilitate the selection of superior genotypes for various breeding programs. Here are some key findings from recent correlation studies (Annamalai *et al*., 2020) [2]. PCA helps in identifying the discriminatory characters that contribute most to the overall variation observed among different pearl millet genotypes (Karunya *et al*., 2021) [3]. This is crucial for breeders to focus their selection efforts on the most impactful traits for forage improvement. To improve heterozygosity in hybrids, different parental materials can be found using genetic diversity assessment. Pearl millet breeders has made extensive use of these methods. (Pucher *et al*., 2015, Animasaun *et al*., 2017, Mithlesh *et al*., 2020, Boratkar *et al*., 2025) [4, 5, 7]. In order to assess pearl millet forage accessions, investigate the link between various genotypes using a clustering and PCA approach, and select distinct germplasm appropriate for a further hybridization program, the current study was conducted.

Materials and Methods

The study used 480 forage pearl millet accessions for fodder yield-related attributes in an augmented block design during Kharif 2024 at Foragen Seeds Private Limited Research Farm in Hyderabad. These accessions were separated into thirty-two blocks, each consisting of fifteen accessions. Each plot has 3.0 m-long rows spaced 30 cm apart. The plant-to-plant distance was set at 10 cm by thinning at three leaf stages. Data for eight morphological traits i.e. plant height (cm), panicle length (cm), panicle girth (cm), number of tillers, stem girth (cm), number of leaves, leaf length (cm) and leaf width (cm) were collected at harvest from five randomly selected plants in each plot. Correlation, PCA Analysis using GRAPES 1.1.0 software and cluster analysis was done using OPSTAT software using K-mean clustering algorithm. The investigation was conducted to determine the most informative and discriminating characteristics in forage pearl millet accessions.

Results and Discussion

Descriptive statistics

There is variability among the genotypes, according to the assessment of descriptive statistics, such as mean, standard deviation, and coefficient of variation (CV %) for the eight features that were assessed (Table 1). Panicle girth, stem girth, and leaf length showed variance in mean, standard deviation and coefficient of variation among all the parameters examined. A larger mean and standard deviation showed by plant height with lower CV indicates more consistent production than the mean. This is a sign of a well-optimized process. Plant height, number of leaves and leaf width showed lower CV per cent. The study's results indicated significant heterogeneity in fodder-related properties among forage pearl millet accessions. Consequently, genetic diversity analysis facilitates parent selection, preserves and employs advantageous variations, and improves understanding of evolutionary patterns in agricultural breeding programs (Bollinedi *et al*. 2020) [9].

Table 1: Summary statistics for different morphological traits of forage pearl millet accessions

Characters	Mean	SD	CV %
Plant height	194.4	40.6	0.209
Panicle length	26.5	8.9	0.336
Panicle girth	1.8	0.9	0.510
Number of tillers	6.7	2.1	0.317
Stem girth	1.3	0.6	0.452
Number of leaves	7.1	1.7	0.247
Leaf length	58.2	35.9	0.618
Leaf width	3.1	0.8	0.257

Correlation analysis

The investigation of the Pearson correlation coefficient identified multiple qualities that had a substantial positive association with related traits (Table 2 and Fig 1). Plant height had a positive and significant relationship with stem girth, panicle length, number of leaves, number of tillers and leaf length. Additionally, there is a positive but non-significant correlation with leaf width. Plant height showed non-significant and negative association with panicle girth. The present investigation unveiled that trait panicle length had a positive and significant association with leaf width, plant height, panicle girth, leaf length and stem girth. In contrast, the trait exhibited significant and negative correlation with number of tillers and number of leaves. The traits stem girth, leaf width and panicle length showed a positive and significant association with panicle girth. Additionally, a positive correlation with leaf length was noted, albeit without statistical significance. In contrast, the trait exhibit significant and negative correlation with number of tillers. Moreover, a negative correlation was observed with number of leaves and plant height, although the statistical significance was not observed. The study revealed that trait number of tillers had a positive and significant relationship with plant height and number of leaves. Additionally, there is a positive but non-significant correlation with leaf length. The trait exhibit significant and negative correlation with panicle girth, leaf width and panicle length. Meanwhile, there is a negative but non-significant correlation for stem girth. Trait stem girth had a positive and significant association with panicle girth, plant height, panicle length and leaf width. Furthermore, a positive yet statistically non-significant correlation was observed with number of leaves and leaf length. Stem girth showed non-significant and negative association with number of tillers. The traits plant height and number of tillers showed a positive and significant association with number of leaves. Additionally, a positive correlation with stem girth and leaf length was noted, albeit without statistical significance. In contrast, the trait exhibit significant and negative correlation with panicle length. Moreover, a negative correlation was observed with panicle girth and leaf width, although the statistical significance was not observed. Leaf length had a positive and significant relationship with panicle length, plant height and leaf width. Additionally, there is a positive but non-significant correlation with number of tilers, panicle girth, stem girth and number of leaves. Leaf width had a positive and significant association with panicle girth, panicle length, stem girth and leaf length. Furthermore, a positive yet statistically non-significant correlation was observed with plant height. In contrast, the trait exhibit significant and negative correlation with number of tillers. Meanwhile, there is a negative but non-significant correlation for number of leaves. Since forage yield is a complicated characteristic influenced by many different factors, correlation analysis is a useful tool for discovering traits that significantly boost yield (Aswini *et al*., 2023) [10]. Forage pearl millet green forage yield per plant could be improved by using selection criteria based on these characteristics. In numerous research, characteristics like plant height, the number of tillers, and stem girth have consistently demonstrated positive and substantial connections with the yield of green fodder (Bika and Shekhawat, 2015; Singh *et al*., 2018) [11]. The traits, i.e. panicle length, panicle girth, number of productive tillers/plant, 1000 grain weight, dry fodder yield were found to be significantly correlated with grain yield/plant (Kaushik and Dev Vart, 2022) [12].

Table 2: Correlation matrix for different morphological traits of forage pearl millet accessions

Variables	PH	PL	PG	NOT	SG	NOL	LL	LW
PH	1.0 **	0.174 **	-0.002 NS	0.122 **	0.193 **	0.155 **	0.114 *	0.024 NS
PL		1.0 **	0.157 **	-0.109 *	0.135 **	-0.099 *	0.136 **	0.181 **
PG			1.0 **	-0.238 **	0.316 **	-0.013 NS	0.072 NS	0.191 **
NOT				1.0 **	-0.04 NS	0.115 *	0.078 NS	-0.127 **
SG					1.0 **	0.04 NS	0.025 NS	0.117 *
NOL						1.0 **	0.022 NS	-0.004 NS
LL							1.0 **	0.093 *
LW								1.0 **

Plant height (cm), panicle length (cm), panicle girth (cm), number of tillers, stem girth (cm), number of leaves, leaf length (cm) and leaf width

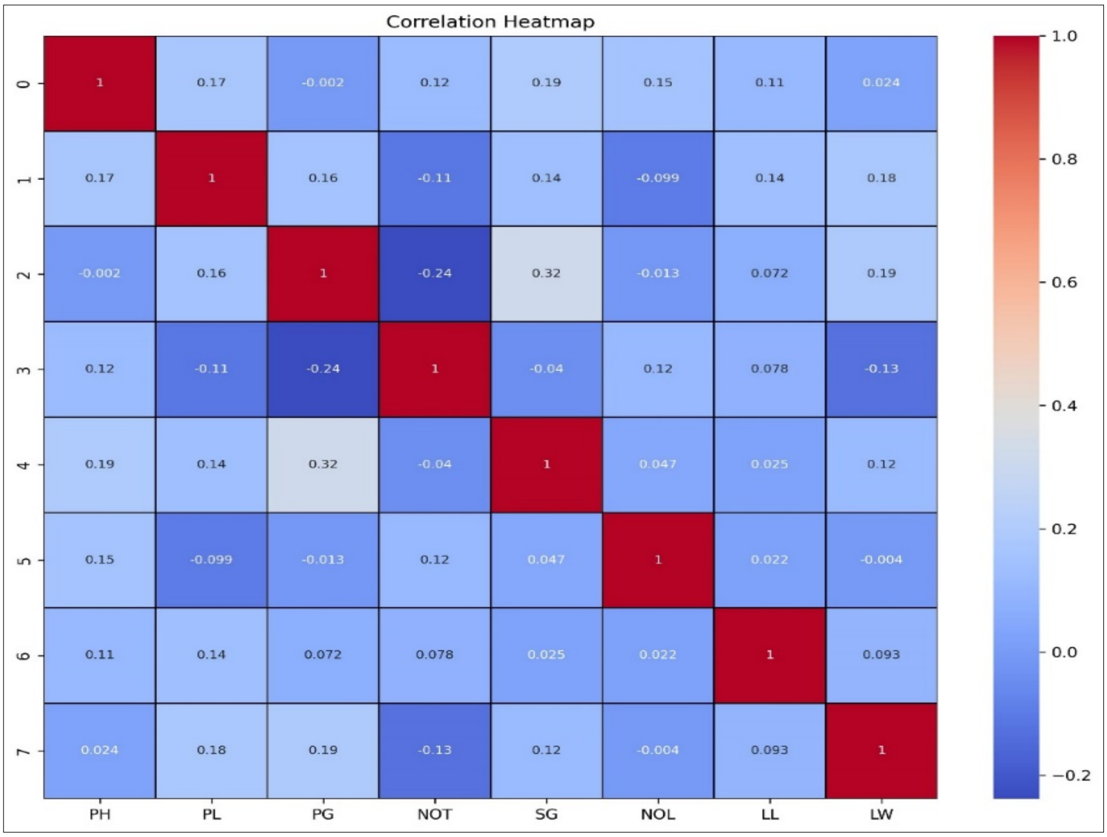

Fig 1: Correlation heatmap for different morphological traits of forage pearl millet accessions

Principal component analysis

The results of the principal component analysis for forage yield related traits were presented in the Tables 3, 4 and Fig. 2, Fig. 3, Fig. 4. Three main components with eigen values greater than one accounted for 51.8% of the overall variability in our investigation. 21.4% of the overall variability was explained by the first main component. According to Table 3, the second and third principal components accounted for 16.9% and 13.4% of the overall variability, respectively. High positive loadings for features including panicle length, panicle girth, stem girth, and leaf width indicated their considerable contribution to overall variance, whereas PC1 accounted for 21.4% of the total variability. Low negative loadings indicated that traits such as the number of tillers and leaves contributed inversely to this component (Table 4). With substantial positive loadings for parameters including plant height, number of tillers, number of leaves, and leaf length, PC2 explained 21% of the overall variability, demonstrating their important role. Contrarily, traits with strong negative loadings, such as plant height (first cut), number of tillers (first cut), and number of new tillers, showed an opposite role in the variation explained by this component. While traits like panicle length, number of tillers, leaf length, and leaf width had negative loadings, indicating an inverse relationship with this component's variance, PC3, which accounted for 15% of the total variability, was distinguished by strong positive loadings for stem girth and number of leaves. The relative significance of different traits in explaining the variability was shown by the PCA results. By giving priority to traits that have a large positive contribution in important principle components, these findings can direct trait-based selection tactics in breeding programs. Varimax rotation was used to further enhance trait connections with each principle component, providing information about the relationships between the traits (Kaiser, 1959) [13].

The first two principal components, PC1 (21.4%) and PC2 (16.9%), are represented by the two main axes in the PCA biplot. A considerable amount of the dataset's variability, which was derived from several initial features, may be explained by these two primary axes. The longer the arrow, the stronger the correlation. PC1 was highly positively correlated with plant height, panicle girth, and stem girth, while PC2 was more strongly correlated with the number of tillers. A small angle suggests a strong positive association, an angle near 90 degrees implies little to no correlation, and an angle near 180 degrees indicates a strong negative correlation. The angle between two arrows shows the correlation between the features. A significant positive association indicated by small angles between plant height, leaf length, stem girth, panicle length, panicle girth and leaf width; this means that when plant height was high, leaf length, stem girth, panicle length, panicle girth and leaf width were also likely to be high (Fig. 4). The arrows for the number of leaves and the number of tillers, on the other hand, were nearly 180 degrees away, suggesting a negative or non-existent correlation. Higher numbers of leaves were linked to lower numbers of tillers. Longer arrows were identified for plant height, stem girth, panicle girth, and number of tillers; these parameters account for a greater percentage of the variance in PC1 and PC2, indicating that they are important in separating the observations in your data. The most significant characteristics influencing the overall variation in the data were found using principal component analysis. Four principal components accounted for 51.8% of the overall variability, according to the analysis, which broke down associated variables into independent components. The first component benefited greatly from traits including plant height, panicle length, panicle girth, stem girth, leaf length, and leaf breadth, while the second component was largely determined by the quantity of tillers and leaves. This method assisted in elucidating the links between traits and directed breeding choices according to the most significant factors. Strong reliability with research on fodder pearl millet by Gupta (2022) [14] and Khandelwal *et al*. (2023) [15] is explained by the results of this study. Patterns seen in earlier pearl millet research were reflected in the identification of important characteristics that affect production and quality, such as plant height and productive tillers (Patil, 2020) [21].

Table 3: Total variance explained by different principal components

Principal components	Eigen values	Per cent Variance	Per cent cumulative variance
PC1	1.719	21.493	21.493
PC2	1.358	16.972	38.465
PC3	1.072	13.404	51.869
PC4	0.932	11.648	63.518
PC5	0.863	10.782	74.299
PC6	0.795	9.942	84.242
PC7	0.674	8.431	92.672
PC8	0.586	7.328	100

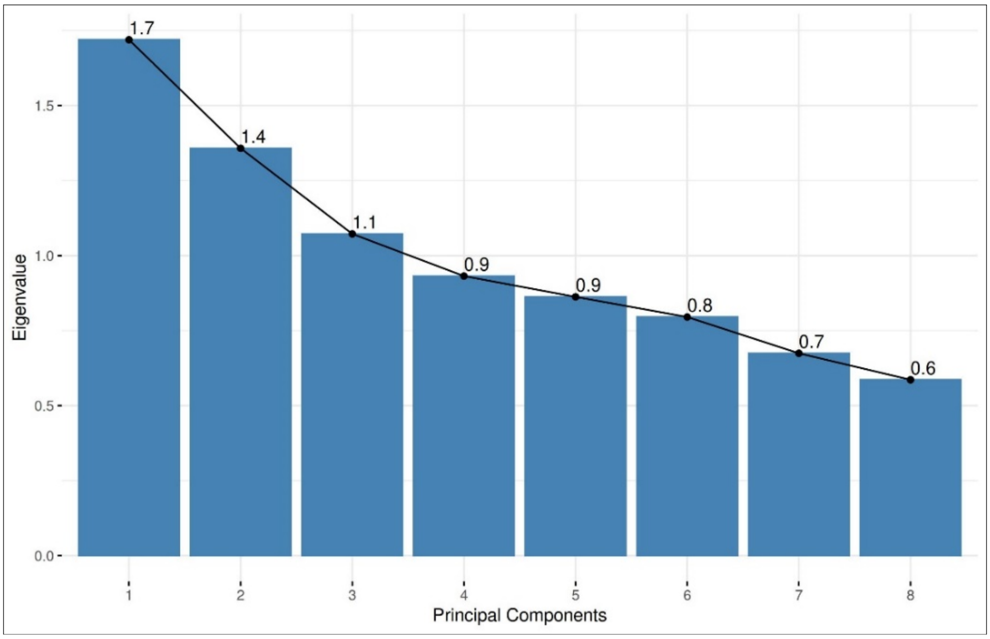

Fig 2: Eigen values corresponding to different principal components.

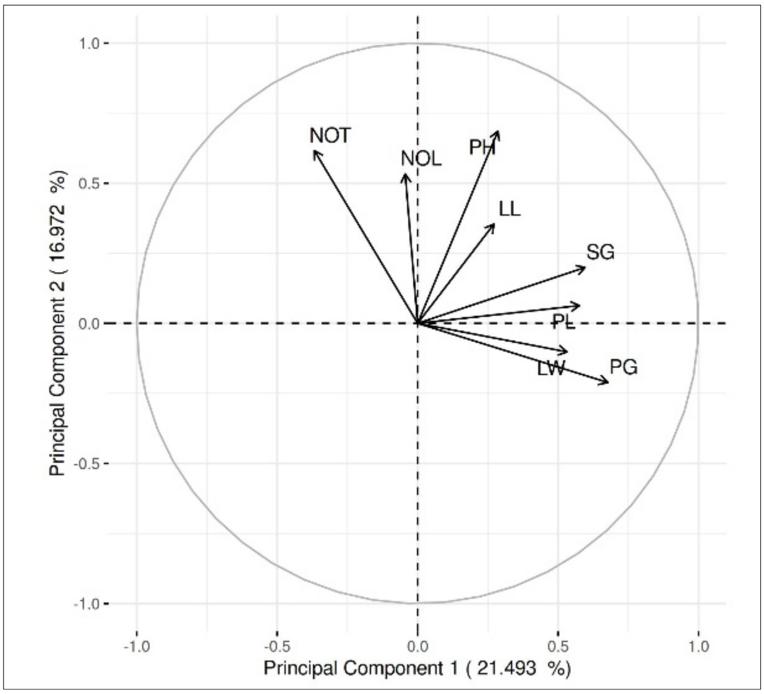

Fig 3: Principal component analysis (PCA) biplot showing trait distribution for forage pearl millet accessions

Table 4: Principal component matrix showing higher loading displaying characters

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PH	0.218	0.588	0.001	**0.355**	0.27	0.155	-0.522	0.333
PL	0.439	0.054	-0.43	0.324	0.314	0.174	0.611	-0.105
PG	0.516	-0.181	0.291	-0.118	-0.361	0.083	0.188	0.656
NOT	-0.28	0.529	-0.117	0.04	-0.226	-0.598	0.382	0.268
SG	0.454	0.171	0.422	0.273	-0.313	-0.292	-0.044	-0.572
NOL	-0.034	0.457	0.474	-0.503	0.28	0.336	0.323	-0.129
LL	0.207	0.304	-0.541	-0.426	-0.515	0.254	-0.169	-0.182
LW	0.406	-0.088	-0.144	-0.494	0.454	-0.565	-0.194	0.008

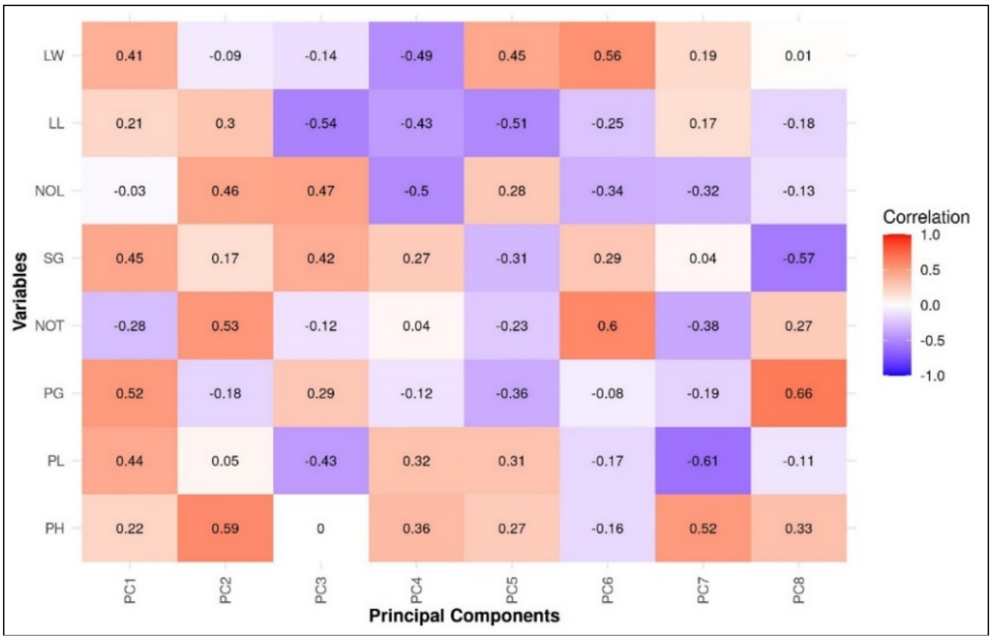

Fig 4: Correlation between variables and principal components

Cluster analysis

The k-mean clustering of forage pearl millet accessions for forage yield related traits revealed ten distinct clusters. Cluster analysis is a crucial data classification method that makes it easier to separate the genetic material into several homogeneous categories. It makes it easier to pick a variety of lines for crossing by classifying the genotypes according to morpho-genetic characteristics. Cluster analysis offers the chance to combine various gene combinations and produce desired segregants through crossing between the chosen, diversified, and desirable lines.

Mean values of five clusters for different quantitative traits are given in Table 7. It was evident that genotypes with high panicle length, panicle girth, number of tillers, leaf length, and leaf width were present in cluster 7. Plant height and panicle features are crucial selection indicators to increase pearl millet productivity. Cluster 2, 7, 9 and 10 was showed high plant height 232, 255, 232 and 265 cm respectively. These results were in agreement with the previous findings by Sharma *et al*., 2025 [18] and Triki *et al*., 2023 [19] in pearl millet. For improving the plant height accessions of clusters 2, 7, 9 and 10 would be crossed to the accessions of clusters 1, 3, 4, 5, 6 and 8. Also, used as inbred line for further forage hybrid development programme. According to the results, it was easy to select parents for various desirable qualities from clusters based on their merits, and the cluster means of various clusters determine which characters should be picked for hybridization. These results are in agreements with the findings of Nivedha *et al*., 2024 [20]. Cluster 7 was unique cluster with high values for all traits except stem girth and number of leaves. So, we can use this accession to cross with other members of the clusters for improvement of forage traits. Cluster 1 and 2 grouped 62 and 64 accessions respectively. Whereas, cluster 3 and 4 grouped 118 and 114 accessions respectively. Genetically related populations having common parentage were found grouped in same clusters (Patil *et al*., 2020) [16]

Table 7: Mean of ten clusters of forage pearl millet accessions for forage yield component traits

Cluster No	No. of members	Accession Nos.	PH	PL	PG	NOT	SG	NOL	LL	LW
1	62	FFPMA-21, FFPMA-24, FFPMA-25, FFPMA-26, FFPMA-50, FFPMA-56, FFPMA-108, FFPMA-109, FFPMA-118, FFPMA-119, FFPMA-127, FFPMA-135, FFPMA-137, FFPMA-142, FFPMA-146, FFPMA-147, FFPMA-151, FFPMA-157, FFPMA-178, FFPMA-179, FFPMA-192, FFPMA-214, FFPMA-222, FFPMA-233, FFPMA-246, FFPMA-256, FFPMA-266, FFPMA-267, FFPMA-270, FFPMA-274, FFPMA-277, FFPMA-278, FFPMA-289, FFPMA-298, FFPMA-305, FFPMA-313, FFPMA-341, FFPMA-342, FFPMA-344, FFPMA-348, FFPMA-351, FFPMA-352, FFPMA-354, FFPMA-363, FFPMA-365, FFPMA-368, FFPMA-374, FFPMA-375, FFPMA-380, FFPMA-382, FFPMA-399, FFPMA-400, FFPMA-408, FFPMA-414, FFPMA-420, FFPMA-422, FFPMA-424, FFPMA-446, FFPMA-447, FFPMA-449, FFPMA-466, FFPMA-472	150	26.0	1.8	6.3	1.1	6.6	60.3	3.1
2	64	FFPMA-28, FFPMA-38, FFPMA-41, FFPMA-54, FFPMA-59, FFPMA-62, FFPMA-63, FFPMA-75, FFPMA-76, FFPMA-77, FFPMA-79, FFPMA-89, FFPMA-93, FFPMA-98, FFPMA-102, FFPMA-103, FFPMA-104, FFPMA-121, FFPMA-165, FFPMA-168, FFPMA-174, FFPMA-184, FFPMA-196, FFPMA-199, FFPMA-212, FFPMA-215, FFPMA-216, FFPMA-218, FFPMA-224, FFPMA-227, FFPMA-236, FFPMA-282, FFPMA-286, FFPMA-293, FFPMA-312, FFPMA-315, FFPMA-316, FFPMA-319, FFPMA-326, FFPMA-330, FFPMA-334, FFPMA-338, FFPMA-340, FFPMA-343, FFPMA-346, FFPMA-347, FFPMA-350, FFPMA-364, FFPMA-372, FFPMA-377, FFPMA-385, FFPMA-390, FFPMA-410, FFPMA-436, FFPMA-440, FFPMA-457, FFPMA-458, FFPMA-459, FFPMA-463, FFPMA-465, FFPMA-473, FFPMA-477, FFPMA-479, FFPMA-480	232	29.1	1.7	6.9	1.4	7.5	61.8	3.2
3	118	FFPMA-1, FFPMA-3, FFPMA-4, FFPMA-11, FFPMA-14, FFPMA-29, FFPMA-32, FFPMA-35, FFPMA-45, FFPMA-48, FFPMA-51, FFPMA-57, FFPMA-71, FFPMA-81, FFPMA-85, FFPMA-87, FFPMA-88, FFPMA-95, FFPMA-100, FFPMA-101, FFPMA-116, FFPMA-124, FFPMA-126, FFPMA-134, FFPMA-136, FFPMA-138, FFPMA-139, FFPMA-140, FFPMA-141, FFPMA-143, FFPMA-144, FFPMA-148, FFPMA-191, FFPMA-210, FFPMA-217, FFPMA-220, FFPMA-225, FFPMA-231, FFPMA-232, FFPMA-238, FFPMA-241, FFPMA-242, FFPMA-243, FFPMA-244, FFPMA-247, FFPMA-251, FFPMA-252, FFPMA-254, FFPMA-257, FFPMA-258, FFPMA-260, FFPMA-261, FFPMA-268, FFPMA-271, FFPMA-276, FFPMA-279, FFPMA-290, FFPMA-294, FFPMA-295, FFPMA-296, FFPMA-297, FFPMA-299, FFPMA-300, FFPMA-301, FFPMA-303, FFPMA-304, FFPMA-306, FFPMA-307, FFPMA-308, FFPMA-309, FFPMA-310, FFPMA-311, FFPMA-323, FFPMA-324, FFPMA-332, FFPMA-335, FFPMA-336, FFPMA-337, FFPMA-345, FFPMA-353, FFPMA-356, FFPMA-357, FFPMA-358, FFPMA-361, FFPMA-362, FFPMA-366, FFPMA-367, FFPMA-371, FFPMA-376, FFPMA-386, FFPMA-387, FFPMA-388, FFPMA-398, FFPMA-404, FFPMA-406, FFPMA-407, FFPMA-412, FFPMA-415, FFPMA-417, FFPMA-418, FFPMA-421, FFPMA-423, FFPMA-425, FFPMA-428, FFPMA-431, FFPMA-432, FFPMA-434, FFPMA-439, FFPMA-443, FFPMA-444, FFPMA-445, FFPMA-448, FFPMA-450, FFPMA-452, FFPMA-453, FFPMA-454, FFPMA-455, FFPMA-470	177	25.1	1.8	6.6	1.2	6.9	57.9	3.0
4	114	FFPMA-15, FFPMA-16, FFPMA-22, FFPMA-36, FFPMA-37, FFPMA-39, FFPMA-42, FFPMA-49, FFPMA-52, FFPMA-53, FFPMA-55, FFPMA-64, FFPMA-72, FFPMA-74, FFPMA-80, FFPMA-82, FFPMA-86, FFPMA-90,	204	26.7	1.8	6.7	1.3	7.2	60.8	3.1

		FFPMA-91, FFPMA-92, FFPMA-94, FFPMA-99, FFPMA-105, FFPMA-106, FFPMA-112, FFPMA-114, FFPMA-117, FFPMA-120, FFPMA-122, FFPMA-123, FFPMA-125, FFPMA-129, FFPMA-131, FFPMA-133, FFPMA-145, FFPMA-149, FFPMA-150, FFPMA-152, FFPMA-153, FFPMA-154, FFPMA-155, FFPMA-156, FFPMA-158, FFPMA-162, FFPMA-164, FFPMA-166, FFPMA-169, FFPMA-172, FFPMA-175, FFPMA-176, FFPMA-182, FFPMA-183, FFPMA-195, FFPMA-197, FFPMA-200, FFPMA-207, FFPMA-209, FFPMA-211, FFPMA-221, FFPMA-226, FFPMA-230, FFPMA-235, FFPMA-249, FFPMA-255, FFPMA-262, FFPMA-263, FFPMA-264, FFPMA-265, FFPMA-283, FFPMA-284, FFPMA-285, FFPMA-288, FFPMA-291, FFPMA-302, FFPMA-314, FFPMA-317, FFPMA-318, FFPMA-320, FFPMA-321, FFPMA-325, FFPMA-327, FFPMA-328, FFPMA-331, FFPMA-333, FFPMA-339, FFPMA-349, FFPMA-355, FFPMA-359, FFPMA-360, FFPMA-369, FFPMA-370, FFPMA-373, FFPMA-378, FFPMA-379, FFPMA-383, FFPMA-389, FFPMA-393, FFPMA-409, FFPMA-419, FFPMA-429, FFPMA-430, FFPMA-435, FFPMA-438, FFPMA-441, FFPMA-442, FFPMA-451, FFPMA-456, FFPMA-462, FFPMA-467, FFPMA-469, FFPMA-471, FFPMA-475, FFPMA-476, FFPMA-478								
5	16	FFPMA-5, FFPMA-7, FFPMA-8, FFPMA-9, FFPMA-13, FFPMA-17, FFPMA-18, FFPMA-20, FFPMA-46, FFPMA-47, FFPMA-65, FFPMA-83, FFPMA-213, FFPMA-240, FFPMA-384, FFPMA-403	179	23.2	1.6	6.3	1.4	6.9	23.6	2.9
6	22	FFPMA-30, FFPMA-31, FFPMA-60, FFPMA-96, FFPMA-128, FFPMA-223, FFPMA-234, FFPMA-237, FFPMA-245, FFPMA-248, FFPMA-250, FFPMA-253, FFPMA-259, FFPMA-272, FFPMA-275, FFPMA-280, FFPMA-287, FFPMA-329, FFPMA-411, FFPMA-416, FFPMA-427, FFPMA-433	113	24.6	1.8	5.8	1.1	6.6	54.6	3.1
7	1	FFPMA-110	255	48.0	2.3	10.0	1.5	7.0	801.0	4.0
8	18	FFPMA-6, FFPMA-12, FFPMA-19, FFPMA-27, FFPMA-33, FFPMA-44, FFPMA-107, FFPMA-130, FFPMA-132, FFPMA-269, FFPMA-273, FFPMA-292, FFPMA-381, FFPMA-401, FFPMA-402, FFPMA-405, FFPMA-413, FFPMA-437	141	20.5	1.5	7.0	1.0	6.7	32.6	3.0
9	11	FFPMA-2, FFPMA-34, FFPMA-40, FFPMA-58, FFPMA-68, FFPMA-69, FFPMA-185, FFPMA-194, FFPMA-204, FFPMA-208, FFPMA-397	232	36.2	2.0	6.6	1.6	8.2	30.9	3.5
10	54	FFPMA-10, FFPMA-23, FFPMA-43, FFPMA-61, FFPMA-66, FFPMA-67, FFPMA-70, FFPMA-73, FFPMA-78, FFPMA-84, FFPMA-97, FFPMA-111, FFPMA-113, FFPMA-115, FFPMA-159, FFPMA-160, FFPMA-161, FFPMA-163, FFPMA-167, FFPMA-170, FFPMA-171, FFPMA-173, FFPMA-177, FFPMA-180, FFPMA-181, FFPMA-186, FFPMA-187, FFPMA-188, FFPMA-189, FFPMA-190, FFPMA-193, FFPMA-198, FFPMA-201, FFPMA-202, FFPMA-203, FFPMA-205, FFPMA-206, FFPMA-219, FFPMA-228, FFPMA-229, FFPMA-239, FFPMA-281, FFPMA-322, FFPMA-391, FFPMA-392, FFPMA-394, FFPMA-395, FFPMA-396, FFPMA-426, FFPMA-460, FFPMA-461, FFPMA-464, FFPMA-468, FFPMA-474	265	27.8	1.7	6.9	1.4	7.1	58.3	3.0

Acknowledgement

The authors would like to thank the Director, CEO, HR and R&D director, Foragen Seeds Private Limited, hyderabad for their great support of funding during course of this research investigation.

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