

Multi-Trait Analysis and Clustering of Forage Pearl Millet Genotypes in Semi-Arid Conditions

Abstract

The present study evaluated genetic variability and trait associations in 103 forage pearl millet genotypes (97 genotypes and 6 checks) across three distinct environments (e.g., the Kharif season of 2022 (E1), Summer season of 2023 (E2), and Kharif season of 2023 (E3)) during 2022-23. Sixteen morphological traits were assessed using a randomized complete block design with two replications. Significant differences were observed among genotypes, environments, and genotype \times environment interactions. Correlation analysis identified key traits positively associated with green fodder yield, such as leaf length, leaf width, and plant height at first cut. Principal component analysis revealed that four principal components explained 72% of the total variability, with the first component influenced by leaf count and width. Hierarchical cluster analysis grouped genotypes into five clusters, with Cluster IV showing superior forage traits. This study identifies promising genotypes for future breeding programs focused on improving forage productivity in arid and semi-arid regions.

Keywords: Forage improvement, Trait associations, Principal component analysis, Cluster analysis, Biomass yield

1. Introduction

Pearl millet (*Pennisetum glaucum* L. R. Br.) is an important cross-pollinated crop in arid and semi-arid regions of Asia and Africa. In India, it covered 7.57 million hectares in 2022-23, producing 11.43 million tons, though production is expected to decrease in 2023-24 (Ministry of Agriculture & Farmers Welfare, Government of India). The development of genetically diverse forage pearl millet varieties has advanced significantly, with several high-yielding genotypes and hybrids showing promise in trials (Yadav et al., 2021; Harinarayana et al., 2005).

Forage yield is a complex trait influenced by various morphological and physiological factors. To improve forage yield, breeders need to understand the relationships between these traits. Statistical tools like ANOVA allow for the assessment of genetic variability and environmental effects, while correlation analysis helps identify traits with significant impact on yield (Javed et al., 2016; Da Silva et al., 2017). However, simple correlation may overlook

complex interactions among traits, which can be addressed by Principal Component Analysis (PCA) (Sneath&Sokal, 1973). PCA has been effective in identifying key trait associations in pearl millet (Sathya et al., 2014).

Understanding genetic diversity is essential for breeding programs, and hierarchical cluster analysis helps group genotypes based on their morphological traits, enhancing the identification of superior parents (Bridges, 1966; Sharma et al., 2018; Kumar et al., 2017a, 2017b; Rani and Khandelwal, 2023; Meena et al., 2021). This approach aids in maximizing heterotic expression and achieving transgressive segregation in hybrid combinations (Govintharaj et al., 2018). The present study employs these statistical techniques to evaluate genetic variability, trait associations, and genetic diversity in forage pearl millet genotypes.

2. Materials and methods

2.1 Experimental Material and Design

The experimental material consisted of 103 forage pearl millet genotypes, including 97 breeding lines derived from indigenous landraces at the Indian Institute of Millets Research (IIMR), Hyderabad, and six check varieties. Field evaluations were conducted across three distinct temporal environments at IIMR during the 2022-2023 period: the Kharif season of 2022 (E1), Summer season of 2023 (E2), and Kharif season of 2023 (E3). The experiments were arranged in a randomized complete block design (RCBD) with two replications, where the germplasm was divided into four trial groups, each containing 25 genotypes.

The experimental sites were located at IIMR in Hyderabad (17°19'N latitude, 78°23'E longitude, 556 meters above sea level). The sites were selected to represent typical growing conditions for pearl millet in this region. The distinct seasonal environments were chosen to assess the genotype performance under varying climatic conditions, which may include different temperature, rainfall, and photoperiod conditions.

2.2 Data Collection and Statistical Analysis

Phenotypic data were collected on sixteen morphological traits, including leaf length (LL), leaf width (LW), number of leaves (NL), internodal length first cut (ILFC), stem thickness first cut (STFC), plant height first cut (PHFC), leaf-stem ratio (LSR), number of tillers first cut (NTFC), number of new tillers (NNT), number of tillers regrowth (NTR), green fodder yield first cut (GFYF), dry fodder yield first cut (DFYF), green fodder yield second cut (GFYS), dry fodder yield second cut (DFYS), total green fodder yield (TGFY), and total dry fodder yield (TDFY). Data were collected on five randomly selected competitive plants per genotype within each environment. Fodder yields were calculated based on the harvested fodder from plots during the 2022-2023 growing seasons.

Data processing and statistical analyses were performed using R version 4.4.0 (2024-04-24 ucrt) in RStudio. Genotype-by-environment interaction effects were assessed using the `anova_joint` function from the `Metan` package (Olivoto and Lúcio, 2020). Correlation analysis of trait associations was conducted using the `corr_coef` function. Genetic diversity was explored through hierarchical cluster analysis using the `hclust` function in the `stats` package, which allowed for visualization of genetic relationships among genotypes.

To identify key patterns of variation among the genotypes, principal component analysis (PCA) was conducted using the `MASS` package. PCA reduced dimensionality and highlighted the primary drivers of variation in the dataset. The `factoextra` package was used for generating visualizations, including eigenvalue plots and trait-genotype association biplots, to interpret complex relationships within the data.

3.Results and discussion

3.1 Analysis of variance for green fodder yield and related traits

The pooled analysis of variance (ANOVA) for total green fodder yield and related traits across three environments is presented in Table 1. The results indicated significant variability among genotypes, as reflected by the significant mean sum of squares for genotypes across pooled environments. This suggests the presence of genetic variation for the traits under study. Similarly, the mean sum of squares for environments was significant, highlighting the differences among the environments used to evaluate the genotypes. Moreover, the genotype \times environment interaction was highly significant, suggesting that the genotypes responded differently to the varying environmental conditions, further emphasizing the role of environmental factors in shaping the performance of the genotypes.

The observed variation in green fodder yield and related traits among the genotypes aligns with previous studies, such as those by Harinarayan et al. (2005), Thomas et al. (2019), Kapoor (2020), Shalini et al. (2020), and Parmar et al. (2022), which also reported significant variability among genotypes for these traits. The significant genotype \times environment interaction suggests the need for selecting genotypes that can perform well across diverse environmental conditions.

Table 1. Mean squares from pooled analysis of variance for forage yield and attributing traits of forage pearl millet genotypes in 3 seasons

Source of variation	Df	LL	LW	NL	ILFC	STFC	PHFC	LSR	NTFC
ENV	2	9781.3***	28.3***	70***	12.9***	12.7***	158937.8***	0.7***	424.3***
REP(ENV)	3	20.5	0.03	0.7	2.65	3.4*	167.39	0	0.26
GEN	102	110***	0.3***	1.6***	8.1***	3.7***	747.52***	0.1***	2.11***
GEN: ENV	204	10992.4***	0.2***	0.6***	4.1***	1.5***	689.75***	0.02***	2.12***
Residual	306	7912.9	0.1	0.2	1.1	1	148.1	0	0.6
CV (%)		8.3	8.3	5.5	5.5	8.9	7.7	21.4	11.5
OV mean		61.5	3.4	7.4	19	11.3	157.2	0.5	6.8
Source of variation	Df	NNT	NTR	GFYFC	DFYFC	GFYSC	DFYSC	TGFY	TDFY
ENV	2	1090.4***	14.05***	7098.3***	1965***	21140.07***	4835.4***	38699.5***	10061.2***
REP(ENV)	3	0.6	0.12	134.68	26.6	11.66	0.008	163.64	26.12
GEN	102	1.3***	1.76***	434.3***	100.5***	103.17***	28.6***	396.2***	86.1***
GEN: ENV	204	2***	0.70***	194.2***	47.3***	124.68***	27.8***	149.8***	35.5***
Residual	306	0.6	0.4	52.6	15.7	13.8	3.1	68.9	20
CV (%)		13.8	19.1	20.9	24.2	20.2	19.8	15.6	17.7
OV mean		5.7	3.1	34.6	16.4	18.4	8.9	53.1	25.3

Where, (LL=Leaf length, LW=Leaf width, NL=Number of leaves, ILFC=Internodal length first cut, STFC=Stem thickness first cut, PHFC=Plant height first cut, LSR=Leaf stem ratio, NTFC=Number of tillers first cut, NNT=Number of new tillers, NTR=Number of tillers regrowth, GFYFC=Green fodder yield first cut, DFYFC=Dry fodder yield first cut, GFYSC=Green fodder yield first cut, DFYSC=Dry fodder yield second cut, TGFY=Total green fodder yield, TDFY=Total dry fodder yield)

3.2 Correlation for Fodder Yield and Related Traits in Pooled Environments

The Pearson correlation coefficient analysis revealed several traits that showed a significant positive correlation with total green fodder yield across pooled environments. These traits include leaf length, leaf width, number of leaves, green fodder yield (second cut), dry fodder yield (second cut), plant height (first cut), number of tillers (first cut), number of new tillers, green fodder yield (first cut), dry fodder yield (first cut), and internodal length (first cut) (Figure 1).

Forage yield, being a complex trait influenced by numerous factors, benefits greatly from correlation analysis in identifying traits that significantly contribute to yield improvement (Aswini et al., 2023). Traits such as plant height, number of tillers, and culm girth have consistently shown positive and significant correlations with green fodder yield in multiple studies (Bika and Shekhawat, 2015; Singh et al., 2018). Additionally, internodal length has been reported as a key contributor to fodder yield in *Cenchrus ciliaris* by Gopalan and Ramaswamy (1981).

These findings align with previous research on pearl millet, where positive associations between key traits and fodder yield were highlighted by Dhedi et al. (2016), Aswini et al. (2023), and Andhale et al. (2024). Such consistent results underline the importance of focusing on these traits in breeding programs to enhance forage yield.

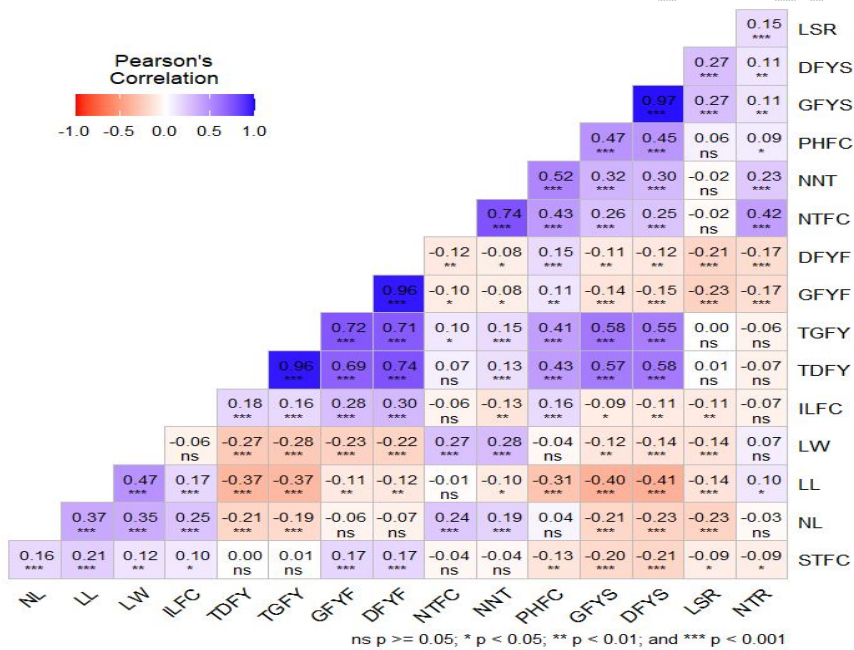


Figure 1. Genetic correlation for fodder yield and related traits among forage pearl millet genotypes across three environments

3.3 Principal component analysis

The results of the principal component analysis across pooled environments for total green fodder yield and related traits were presented in the Tables 2 and 3 and Figure 2. In our study four principal components had eigen values greater than one and they cumulatively explained 72% of the total variability. The first principal component explained 29% of the total variability. The second, third and fourth principal components explained 21%, 15% and 7% of total variability, respectively (Table 2).

Table 2. Principal component analysis summary for green fodder yield and related traits in forage pearl millet

Principal Component	Standard Deviation	Proportion of Variance	Cumulative Proportion	Eigen Value
PC1	2.14	0.29	0.29	4.57
PC2	1.84	0.21	0.50	3.37
PC3	1.57	0.15	0.65	2.48
PC4	1.03	0.07	0.72	1.05
PC5	1.00	0.06	0.78	0.99
PC6	0.96	0.06	0.84	0.92
PC7	0.86	0.05	0.88	0.73
PC8	0.75	0.04	0.92	0.57
PC9	0.67	0.03	0.95	0.44
PC10	0.58	0.02	0.97	0.33
PC11	0.54	0.02	0.98	0.29
PC12	0.43	0.01	1.00	0.19
PC13	0.21	0.00	1.00	0.04
PC14	0.13	0.00	1.00	0.02
PC15	0.00	0.00	1.00	0.00
PC16	0.00	0.00	1.00	0.00

3.3 Principal Component Analysis

The results of the principal component analysis (PCA) across pooled environments for total green fodder yield and related traits are summarized in **Tables 2 and 3** and **Figure 2**. Four principal components (PCs) with eigenvalues greater than one were identified, cumulatively explaining **72% of the total variability**.

- **PC1** accounted for **29% of the total variability** and showed high positive loadings for traits such as **number of leaves** and **leaf width**, indicating their strong contribution to overall variation. Traits like **total green fodder yield**, **total dry fodder yield**, **green fodder yield (second cut)**, and **dry fodder yield (second cut)** had high negative loadings, suggesting their inverse contribution to this component.
- **PC2** explained **21% of the total variability**, with high positive loadings for traits like **green fodder yield (first cut)** and **dry fodder yield (first cut)**, highlighting their significant contribution. In contrast, traits such as **plant height (first cut)**, **number of tillers (first cut)**, and **number of new tillers** exhibited high negative loadings, indicating their opposing role in the variance explained by this component.
- **PC3**, which explained **15% of the total variability**, was characterized by strong positive loadings for **number of tillers (first cut)** and **number of leaves**, whereas traits such as **total green fodder yield** and **total dry fodder yield** had negative loadings, suggesting an inverse relationship with this component's variance.
- **PC4**, accounting for **7% of the total variability**, highlighted **internodal length (first cut)** and **green fodder yield (second cut)** with high positive loadings. Conversely, traits like **number of tillers (first cut)** and **number of new tillers** showed high negative loadings, indicating their limited or inverse contribution to this component.

The PCA results demonstrate the relative importance of various traits in explaining the variability in green fodder yield across different environments. These findings can guide **trait-based selection strategies** in breeding programs, particularly by prioritizing traits with

high positive contributions in key principal components. Further analysis with **varimax rotation** helped refine trait associations with each principal component, offering insights into the relationships among traits.

Table 3. Factor loadings of principal components with eigen values greater than one for green fodder yield and related traits

Trait	PC1	PC2	PC3	PC4
Leaf length	0.3	0.06	0.23	0.22
Leaf width	0.2	-0.1	0.35	0.11
Number of leaves	0.15	0.03	0.43	0.35
Internodal length first cut	-0.03	0.24	0.18	0.53
Stem thickness first cut	0.06	0.23	0.19	0.04
Plant height first cut	-0.29	-0.2	0.26	0.07
Leaf stem ratio	-0.06	-0.2	-0.3	0.1
Number of tillers first cut	-0.1	-0.3	0.43	-0.23
Number of tillers regrowth	0.01	-0.3	0.1	-0.37
Number of new tillers	-0.13	-0.3	0.41	-0.23
Green fodder yield first cut	-0.22	0.43	0.14	-0.23
Dry fodder yield first cut	-0.23	0.43	0.14	-0.2
Green fodder yield second cut	-0.35	-0.3	-0.1	0.3
Dry fodder yield second cut	-0.35	-0.3	-0.1	0.29
Total green fodder yield	-0.43	0.15	0.06	0.03
Total dry fodder yield	-0.44	0.15	0.05	0.05

The PCA biplot illustrates the two main axes Dim1 (28.5%) and Dim2 (21.1%) represent the first two principal components. These two main axes explain a significant portion of the variability in the dataset, which captured from multiple original traits. The colored ellipses surrounding the data points represent confidence ellipses for each group (E_1 , E_2 and E_3). The ellipses suggest that traits within each group share some similarity but are distinct from the other groups. The E_3 is more distinct from E_1 and E_2 . The ellipses E_1 and E_2 were more overlapped and the observations within each group share some similarity but are distinct from the other groups (Figure 2). The arrows represent the contribution of the traits to the principal components. The longer the arrow, the stronger the correlation. Leaf width has a strong positive correlation with Dim 1 and plant height first cut is more strongly associated with Dim2. Leaf width is positively correlated with Dim1 and slightly with Dim2, meaning it contributes heavily to the variation captured by Dim1. The angle between two arrows indicates the correlation between the traits, small angle suggest a strong positive correlation, angle close to 90 degrees indicate little to no correlation and angle close to 180 degrees indicate a strong negative correlation. In E_1 the traits like total dry fodder yield and total

green fodder yield were similar followed by green fodder yield first cut dry fodder yield first cut were similar. In E_2 green fodder yield second cut and dry fodder yield second cut were more similar. In E_3 the number of leaves and leaf length were similar. Small angles between plant height first cut and leaf stem ratio suggest a strong positive correlation, meaning that when plant height first cut is high, leaf stem ratio is also likely to be high. Conversely, arrows for plant height first cut and number of new tillers are close to 180 degrees apart, it indicates a negative correlation higher values of plant height first cut are associated with lower values of number of new tillers. Total green fodder yield and total dry fodder yield have longer arrows which explain a larger portion of the variance in Dim1 and Dim2, meaning they are key factors in differentiating the observations in your data.

Principal component analysis was used to identify the most influential traits contributing to overall variation in the data. By reducing correlated variables into independent components, the analysis revealed that four principal components explained 72% of the total variability. Traits such as leaf width and number of leaves contributed strongly to the first component, while fodder yields were key to the second component. This approach helped clarify trait relationships and guide breeding decisions based on the most impactful variables.

The findings of this study explain strong reliability with the studies on forage pearl millet, by Gupta (2022); Khandelwal *et al.* (2023). The identification of key traits contributing to yield and quality, such as plant height, dry fodder yield, and productive tillers, reflects patterns observed in previous studies of pearl millet.

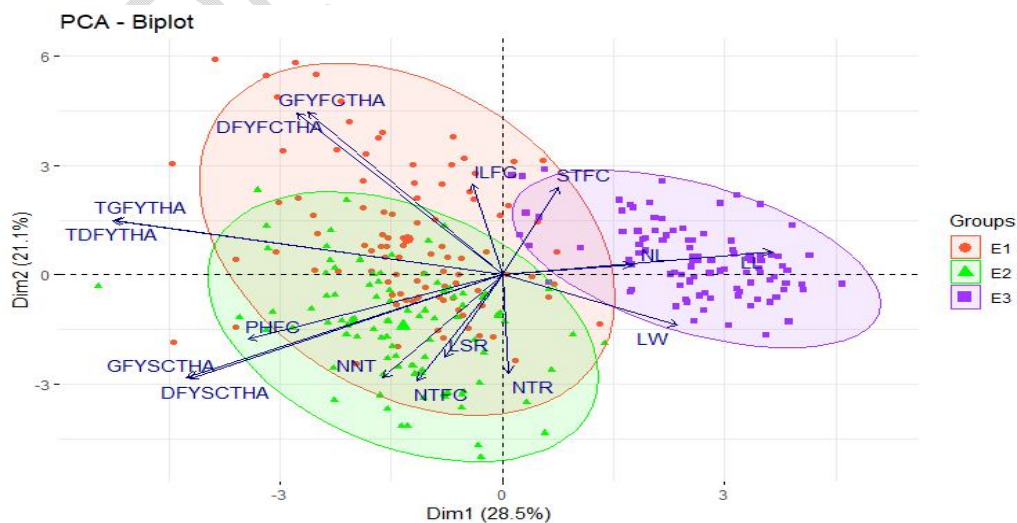


Figure 2: Principal component analysis (PCA) biplot showing trait distribution for forage pearl millet genotypes across three environments

The hierarchical clustering of forage pearl millet genotypes for forage yield and its attributes across three seasons revealed five distinct clusters. Cluster I consisted of 8 genotypes, indicating a relatively smaller group (Figure 3).

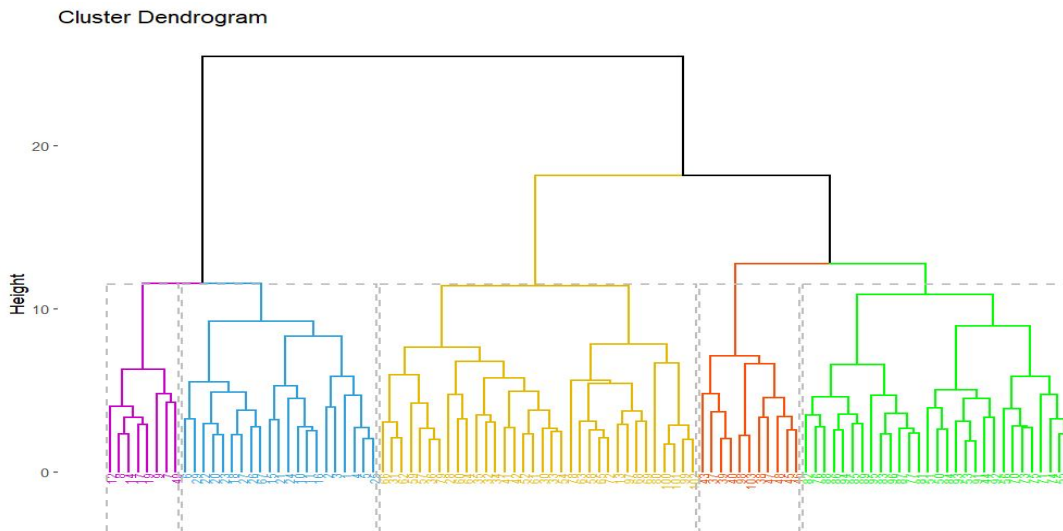


Figure 3. Hierarchical clustering plot for pooled data of 97 genotypes and 6 checks for green fodder yield and related traits in forage pearl millet pooled seasonal data

Moderately sized cluster was observed in Cluster II with 21 genotypes. Cluster III was the largest, with 34 genotypes, indicating a significant portion of the diversity within the genotypes. Cluster IV had 11 genotypes, while Cluster V was quite extensive, containing 29 genotypes. These clusters highlight the variability and grouping of genotypes based on their performance across multiple seasons (Figure 3 and Table 4)

Table 4. Pooled cluster composition of forage pearl millet genotypes for forage yield and its attributes in three seasons

Cluster	Number of Genotypes	Name of the Genotypes
I	8	IIMR FB12, IIMR FB8, IIMR FB14, IIMR FB17, IIMR FB19, IIMR FB9, IIMR FB7, IIMR FB49
II	21	IIMR FB6, IIMR FB29, IIMR FB22, IIMR FB20, IIMR FB23, IIMR FB18, IIMR FB 27, IIMR FB26, IIMR FB67, IIMR FB15, IIMR FB21, IIMR FB24, IIMR FB10, IIMR FB11, IIMR FB16, IIMR FB2, IIMR FB3, IIMR FB1, IIMR FB4, IIMR FB5, IIMR FB25
III	34	IIMR FB66, IIMR FB31, IIMR FB62, IIMR FB59, IIMR FB57, IIMR FB36, IIMR FB82, IIMR FB28, IIMR FB60, IIMR FB64, IIMR FB35, IIMR FB32, IIMR FB34, IIMR FB41, IIMR FB42, IIMR FB52, IIMR FB61, IIMR FB30, IIMR FB33, IIMR FB54, IIMR FB81, IIMR FB63, IIMR FB58, IIMR FB65, IIMR FB73, IIMR FB13, IIMR FB102, IIMR FB69, IIMR FB70, IIMR FB83,

IV	11	IIMR FB43, IIMR FB37, IIMR FB39, IIMR FB40, Wonder Leaf, ForagenRaftaar, IIMR FB38, IIMR FB47, IIMR FB48, IIMR FB45, IIMR FB46
V	29	IIMR FB86, IIMR FB79, IIMR FB93, IIMR FB91, IIMR FB99, IIMR FB90, IIMR FB94, IIMR FB100, IIMR FB87, IIMR FB101, IIMR FB92, IIMR FB80, IIMR FB85, IIMR FB51, IIMR FB50, IIMR FB88, IIMR FB98, IIMR FB53, IIMR FB96, IIMR FB44, IIMR FB97, IIMR FB56, IIMR FB71, IIMR FB74, IIMR FB77, IIMR FB72, IIMR FB75, IIMR FB55, IIMR FB95

Table 5. Pooled cluster mean estimates of forage yield and related traits in forage pearl millet genotypes in three seasons

Trait	Cluster	Hierarchical Clustering				
		CI	CII	CIII	CIV	CV
Leaf length		0.46	-0.28	-0.29	1.31	-0.42
Leaf width		0.39	0.18	-0.31	0.45	-0.13
Number of leaves		-1.09	-0.92	0.31	0.82	0.37
Internodal length first cut		-0.76	-1.24	0.46	1.01	-0.03
Stem thickness first cut		-0.80	-0.16	-0.25	0.98	0.54
Plant height first cut		-0.22	-0.94	0.24	-0.96	0.51
Leaf stem ratio		0.73	-0.04	0.00	0.10	-0.56
Number of tillers first cut		-0.02	0.40	-0.28	0.80	-0.07
Number of tillers regrowth		1.16	0.26	-0.18	-0.10	-0.66
Number of new tillers		-0.47	0.65	-0.27	-0.19	0.55
Green fodder yield first cut		-1.14	-0.62	-0.28	0.68	1.07
Dry fodder yield first cut		-1.14	-0.59	-0.30	0.57	1.13
Green fodder yield second cut		0.55	1.71	-0.41	0.17	-0.45
Dry fodder yield second cut		0.58	1.94	-0.38	0.05	-0.52
Total dry fodder yield		-0.90	0.48	-0.55	0.65	0.92
Total green fodder yield		-0.91	0.22	-0.51	0.80	0.89

The hierarchical clustering analysis of forage pearl millet genotypes for pooled environments across different traits showed that Cluster IV had the highest positive mean for leaf length at 1.31, while negative values were observed in Cluster II and Cluster III. For total green fodder yield, Cluster IV had a mean of 0.80, while Cluster I displayed a negative mean of -0.91. (Table 5). Particularly Cluster IV exhibited the highest positive means for important attributes such as leaf length, leaf width, number of leaves, internodal length and stem thickness, green fodder and dry fodder yield in both cuts. This shows that the genotypes within Cluster IV possess superior growth characteristics, contributing positively to forage yield. Conversely, Clusters II and III displayed several negative mean values across traits, indicating a need for further investigation to enhance their performance. The cluster sizes also indicate the genetic diversity among the genotypes, Cluster III had the largest number of genotypes, which provides a broader genetic base for selection and improvement. These

findings show the importance of cluster analysis in identifying and characterizing genotypes with desirable traits, paving the way for targeted breeding strategies aimed at improving forage quality and yield in diverse environments.

The results of this study align well with the findings of Chaudhary *et al.*(2015), Ramya *et al.* (2017), Kumar *et al.* (2020), Jain and Diwan (2021), Tomar *et al.* (2021), Gupta *et al.*(2022) and Kalagare *et al.* (2022), which also identified important traits contributing to yield within the same clusters. This highlights the stability of cluster analysis in uncovering key traits associated with yield in pearl millet and suggests that these traits could serve as valuable targets in breeding programs aimed at enhancing yield potential and recovering high performing segregants through hybridization programs.

4. Conclusion

The present study identified leaf length, leaf width, number of leaves, plant height first cut, and number of tillers first cut as traits positively associated with total green fodder yield. These relationships were validated through principal component analysis, where four principal components explained 72% of total variation, with leaf characteristics and fodder yield components contributing significantly to the first two components (29% and 21% respectively). Hierarchical cluster analysis grouped genotypes into five clusters, with Cluster IV emerging as superior, showing high positive means for leaf length (1.31), leaf width (0.45), and total green fodder yield (0.80). The consistency of these trait associations across diverse analytical methods and clustering patterns provides robust selection criteria and identifies high-performing genotypes for forage traits. This comprehensive insight will guide future varietal and heterosis breeding programs in developing improved forage pearl millet varieties and hybrids, specifically adapted to thrive in arid and semi-arid regions.

5. References

- Andhale, G. R., Bhavsar, V. V., Goykar, M. B., Pawar, V. P., & Thorat, V. V. (2024). Study of Correlation Analysis and Path Analysis in Different Genotypes of Pearl Millet (*Pennisetum glaucum L.*). *International Journal of Environment and Climate Change*, 14(2), 30-44.
- Arya, R. K., Yadav, H. P., & Yadav, A. K. Deshraj 2009a: In: Forage symposium on "Emerging trends in Forage research and livestock production. Feb. 16-17, 2009 at CAZRI, RRS, Jaisalmer (Rajasthan) India.

- Aswini, M. S., Ganesan, K. N., & Ezhilarasi, T. (2023). The Correlation between Green Fodder Yield and Fodder Quality Traits in Hybrids of Pearl Millet [*Pennisetum glaucum* (L.) R. Br.]. *International Journal of Plant & Soil Science*, 35(19), 1975-1983.
- Bentley, A. R., Chen, C., & D'Agostino, N. (2022). Genome wide association studies and genomic selection for crop improvement in the era of Big Data. *Frontiers in Genetics*, 13, 873060.
- Bika, N. K., & Shekhawat, S. S. (2015). Character association studies in pearl millet [*Pennisetum glaucum* (L.) R. Br.] for green fodder yield and related traits. *Agricultural Science Digest-A Research Journal*, 35(3), 191-194.
- Bridges Jr, C. C. (1966). Hierarchical cluster analysis. *Psychological reports*, 18(3), 851-854.
- Chaudhary, Sunitha., Sagar, P., Hooda, B. K., & Arya, R. K. (2015). Multivariate analysis of pearl millet data to delineate genetic variation. *Forage Research*, 40(4), 201-208.
- Da Silva, K. J., Teodoro, P. E., Júlio, M. P. M., Borém, A., De Souza, V. F., Pimentel, L. D., De Menezes, C. B., & Da Silva, M. J. (2017). Contribution of morphoagronomic traits to grain yield and earliness in grain sorghum. *Genetics and Molecular Research*, 16(2). <https://doi.org/10.4238/gmr16029649>
- Daduwal, H. S., Bhardwaj, R., & Srivastava, R. K. (2024). Pearl millet a promising fodder crop for changing climate: A review. *Theoretical and Applied Genetics*, 137(7), 169.
- Dhedhi, K. K., Ansodariya, V. V., Chaudhari, N. N., Sanghani, J. M., Mehta, A. C., & Sorathiya, J. S. (2016). Fodder potential of pearl millet forage hybrids under rainfed conditions of Gujarat. *International Journal of Bio-resource and Stress Management*, 7(Jun, 3), 444-449.
- Gopalan, A., & Ramaswamy, K. R. (1981). Correlation and path-coefficient analyses in *Cenchrus ciliaris* L.
- Govintharaj, P., Duraisami, V. P., Atkari, D. G., Sumathi, P., Raveendran, M., Blummel, M., Gupta, S. K., Rathore, A., Maheswaran, M., & Kumar, V. A. (2018). Genotypic Variation in Forage Linked Morphological and Biochemical Traits in Hybrid Parents of Pearl Millet. *Animal Nutrition and Feed Technology*, 18(2), 163. <https://doi.org/10.5958/0974-181x.2018.00016.1>

- Gupta, D. E. E. P. A. K., & Khandelwal, V. I. K. A. S. (2022). Principal component analysis for yield and its attributing characters of pearl millet (*Pennisetum glaucum* [L.] R. Br.). *Annals of Plant and Soil Research*, 24(3), 408-14.
- Harinarayana, G., Melkania, N. P., Reddy, B. V. S., Gupta, S. K., Rai, K. N., & Kumar, P. S. (2005). Forage potential of sorghum and pearl millet. *Forage potential of sorghum and pearl millet*, 292-321.
- Huang, X., Wei, X., Sang, T., Zhao, Q., Feng, Q. I., Zhao, Y., ... & Han, B. (2010). Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature genetics*, 42(11), 961-967.
- Jain, S. K., & Diwan, D. (2021). Principal component and cluster analysis for quantitative traits to identify high yielding genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Forage research*, 46(4), 308-314.
- Javed, S., Rauf, S., Shahzad, M., Malinowski, D. P., Saleem, U., & Paderewski, J. (2016). Evaluation of Egyptian Clover (*Trifolium alexandrinum* L.) Germplasm through Redundancy Analysis for Forage Yield and Its Components. *Crop Science*, 56(3), 1179–1188. <https://doi.org/10.2135/cropsci2015.08.0518>
- Jeffers, J. N. R., & Richens, R. H. (1970). Multivariate analysis of the English elm population. *Silvae genetica*, 19(1), 31-38.
- Kaiser, H. F. (1959). Computer program for varimax rotation in factor analysis. *Educational and psychological measurement*, 19(3), 413-420.
- Kalagare, V. S., Ganesan, N. M., Iyanar, K., Chitdeshwari, T., & Chandrasekhar, C. N. (2022). Multivariate analysis in parental lines and land races of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Electronic Journal of Plant Breeding*, 13(1), 155-167.
- Kapoor, R. (2020). Variation and association studies for fodder yield and related traits in interspecific hybrids of bajra [*Pennisetum glaucum* (L.) R. Br.] × napier grass [*Pennisetum purpureum* (K.) Schum.]. *Range Management and Agroforestry*, 41(2), 363-367.
- Khandelwal, V., Narasimhulu, R., Choudhary, K. B., Renu Rani, S. J., Bhanwariya, S., & Tara Satyavathi, C. (2023). Multivariate analysis in pearl millet parental lines for

- diversity estimation and association study of yield contributing traits for genetic improvement of hybrids. *Annals of Arid Zone*, 62(1), 65-75.
- Kumar, M., Rani, K., Ajay, B. C., Patel, M. S., Mungra, K. D., & Patel, M. P. (2020). Multivariate diversity analysis for grain micronutrients concentration, yield and agromorphological traits in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *International Journal of Current Microbiology and Applied Sciences*, 9(3), 2209-2226.
- Kumari, J., Bag, M. K., Pandey, S., Jha, S. K., Chauhan, S. S., Jha, G. K., ... & Dutta, M. (2016). Assessment of phenotypic diversity in pearl millet [*Pennisetum glaucum* (L.) R. Br.] germplasm of Indian origin and identification of trait-specific germplasm. *Crop and Pasture Science*, 67(12), 1223-1234.
- Olivoto, T., & Lúcio, A. D. C. (2020). metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, 11(6), 783-789.
- Parmar, A. B., Patel, V. R., Choubey, M., Desai, D. N., Patel, N. M., & Baishya, A. (2022). Evaluation of tropical top feed species for their nutritional properties, in vitro rumen digestibility, gas production potential and polyphenolic profile. *Range Management and Agroforestry*, 43(1), 146-153.
- Patil, S. H. (2020). Genetic analysis studies in pearl millet [*Pennisetum glaucum* L.] (Doctoral dissertation, *Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani*).
- Ramya, A. R., Ahamed, M. L., & Srivastava, R. K. (2017). Genetic diversity analysis among inbred lines of pearl millet [*Pennisetum glaucum* (L.) R. Br.] Based on grain yield and yield component characters. *International Journal of Current Microbiology and Applied Sciences*, 6(6), 2240-2250.
- Sathya, M., Sumathi, P., Senthil, N., Vellaikumar, S., & Joel, A. J. (2014). Genetic studies for yield and its component traits in RIL population of pearl millet (*Pennisetum glaucum* [L.] R. Br.). *Electronic Journal of Plant Breeding*, 5(2), 322-326.
- Shalini, P., Surana, P. P., & Shinde, G. C. (2020). Development and evaluation of new Bajra × Napier grass hybrids for green fodder yield and quality traits.
- Singh, S., Sharma, R., Pushpavathi, B., Gupta, S. K., Durgarani, C. V., & Raj, C. (2018). Inheritance and allelic relationship among gene (s) for blast resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Plant Breeding*, 137(4), 573-584.

Sneath, P. H. A., & Sokal, R. R. (1973). *Numerical taxonomy: The Principles and Practice of Numerical Classification*. W H Freeman & Company.

Thomas, S. L., & Thomas, U. C. (2019). Innovative techniques in fodder production-a review. *Forage Res*, 44(4), 217-223.

Tomar, M., Bhardwaj, R., Kumar, M., Singh, S. P., Krishnan, V., Kansal, R., & Sachdev, A. (2021). Nutritional composition patterns and application of multivariate analysis to evaluate indigenous Pearl millet ((*Pennisetum glaucum* (L.) R. Br.) germplasm. *Journal of Food Composition and Analysis*, 103, 104086.

Yadav, O. P., Gupta, S. K., Govindaraj, M., Sharma, R., Varshney, R. K., Srivastava, R. K., & Mahala, R. S. (2021). Genetic gains in pearl millet in India: insights into historic breeding strategies and future perspective. *Frontiers in Plant Science*, 12, 645038.

Zerbini, E., & Thomas, D. (2003). Opportunities for improvement of nutritive value in sorghum and pearl millet residues in South Asia through genetic enhancement. *Field Crops Research*, 84(1-2), 3-15.

Kumar, S., Babu, C., Revathi, S. and Sumathi P. (2017a). Genetic variation deliniation among fodder pearl millet [*Pennisetum glaucum* (L.)] accessions and Napier grass germplasm using SSR markers. *Indian Journal of Ecology*. 44(4): 186-189

Kumar, S., Babu, C., Revathi, S. and Sumathi P. (2017b). Estimation of genetic variability, heritability and association of green fodder yield with contributing traits in fodder pearl millet [*Pennisetum glaucum* (L.)]. *International Journal of Advanced Biological Res*. 7(1): 131-136

Rani S, Khandelwal V. Stability Analyses of pearl Millet Genotypes (*Pennisetum glaucum*) and its Related Traits Using the Freeman and Perkins Model. *International Journal of Plant & Soil Science*. 2023 Aug 3;35(18):1504-10.

Meena RC, Ram M, Ambawat S, Satyavathi CT, Khandelwal V, Meena RB, Kumar M, Bishnoi JP, Mungra KD. Screening of pearl millet genotypes for high temperature and drought tolerance based on morpho-physiological characters. *Int J Environ Climate Change*. 2021;11(9):74-80.