

Diversity Studies in Restorer Lines of Pearl Millet [*Pennisetum Glaucum* (L.) R. Br.] during Summer Season

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Abstract

The present investigation studied 77 restorer lines (R lines) of pearl millet [*Pennisetum glaucum* (L.) R. Br.], evaluated randomized block design (RBD) with two replications in summer season 2025 at Bajra Research Scheme, Govt. College of Agriculture, Dhule. (MS). All 77 genotypes were evaluated for nine different morphological and agronomical traits. The 30 genotypes were grouped into six clusters. The seventy-seven genotypes were grouped into six clusters. Cluster I contained the highest number of genotypes (62), followed by Cluster II with 6 genotypes, Cluster IV with 4 genotypes and Cluster V with 3 genotypes. The remaining clusters-III, VI, -each contained only a single genotype, making them solitary in terms of multivariate composition. Hybridization between genotypes from Cluster II and Cluster VI may result in greater heterosis due to maximum genetic divergence.

Key words : Genetic diversity; Pearl millet; Cluster; Genotypes; Phenotypes; D² value.

The term “millet” is randomly used for several types of small seeded annual grasses (FAO and ICRISAT, 1996). Pearl Millet [*Pennisetum glaucum* (L.) R.Br.] is one of the millets belongs to family Poaceae (Gramineae), subfamily Panicoideae and genus *Cenchrus*. Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is popularly known as bulrush millet, cattail millet or spiked millet, bajra, dukhn and as mhunga or mahango in different parts of southern Africa and Asia, is an important drought tolerant coarse grain cereal crop. It is a major crop in arid and semi-arid region of the world. It appears to have originated in Sahel zone of West Africa (Vavilov, 1950 and Murdock, 1959), which is known to be the crop's main centre of diversity, from where it spread to India and other countries. It is considered as cross-pollinated crop (allogamous) especially it shows protogyny condition. The chief pollinating agent is wind (anemophily). Pearl millet is diploid ($2n=2x=14$) and a C4 plant in nature. India is considered as the secondary centre of diversity (Brunken, 1977).

Pearl millet is not expensive like pearl but definitely has pearl-like quality which is beneficial to the body. 100 grams of pearl millet grain contains nutritional values as 360 calories energy, 12 g moisture, 12 g protein, 5 g fat, 2 g mineral, 1 g fiber, 67 g carbohydrate, 42 mg Calcium, 242mg phosphorus and 8mg iron (Malik, S., 2015). As a food crop, pearl millet grain own the peaked amount of calories per 100 g (Burton *et al.*, 1972). Among the mineral content, pearl millet grains contain Iron from 18 to 135ppm and Zinc from 22 to 92 ppm (Rai *et al.*, 2012).

India is currently the largest producer of millets in the world, contributing 38.4% of global production (DD News, 2025 and WPR, 2026). It is grown on 7.36 million ha with average production of 10.80 million tones and productivity of 1468 kg ha⁻¹ during 2024-25 (Directorate of Economics and Statistics 2025).

Genetic diversity is the principal requirement for any crop improvement programme. The genetic distance between pair of genotypes

provides the basis for grasping the structure of the diversity of any intra-species population. It assembles an all-to-all matrix to set out the distance between each sequence pair of genotypes, thereby directing plant breeder in their selection procedure (Adewale *et al.*, 2011). Phenotypic and genotypic characterization of R lines helps in clustering and grouping genotypes based on variability patterns, which aids in reducing efforts during parent selection for hybrid breeding. To assess genetic divergence among the collected genotypes, D^2 analysis was performed following the procedure outlined by Mahalanobis (1936). Subsequently, clustering of genotypes will be carried out according to the method proposed by Rao (1952), which groups genotypes based on their D^2 values to identify genetically diverse clusters.

Materials and methods

The experimental material used for the present research consisted of 77 restorer lines of pear millet [*Pennisetum glaucum* (L.) R. Br.], which were obtained from the Bajra Research Scheme, Govt. College of Agriculture, Dhule which were evaluated in Summer-2025. The list of genotypes used in the study is presented in Table 1.

The Panse and Sukhatmate (1995) approach was used to perform the analysis of variance. Analysis of variance for the individual characters studied was worked out as per RBD to test the significance among the genotypes. The D^2 Statistic of Mahalanobis (1936), as explained by Rao (1952), was used to analyze divergence, and Tocher's technique, as explained by Rao

Table 1. List of seventy-seven restorer lines (R lines) of pearl millet

Genotype	Source	Genotype	Source	Genotype	Source
IC-DHLBIR-2024-1	ICRISAT	IC-DHLBIR-2024-27	ICRISAT	IC-DHLBIR-2024-53	ICRISAT
IC-DHLBIR-2024-2	ICRISAT	IC-DHLBIR-2024-28	ICRISAT	IC-DHLBIR-2024-54	ICRISAT
IC-DHLBIR-2024-3	ICRISAT	IC-DHLBIR-2024-29	ICRISAT	IC-DHLBIR-2024-55	ICRISAT
IC-DHLBIR-2024-4	ICRISAT	IC-DHLBIR-2024-30	ICRISAT	IC-DHLBIR-2024-56	ICRISAT
IC-DHLBIR-2024-5	ICRISAT	IC-DHLBIR-2024-31	ICRISAT	IC-DHLBIR-2024-57	ICRISAT
IC-DHLBIR-2024-6	ICRISAT	IC-DHLBIR-2024-32	ICRISAT	IC-DHLBIR-2024-58	ICRISAT
IC-DHLBIR-2024-7	ICRISAT	IC-DHLBIR-2024-33	ICRISAT	IC-DHLBIR-2024-59	ICRISAT
IC-DHLBIR-2024-8	ICRISAT	IC-DHLBIR-2024-34	ICRISAT	IC-DHLBIR-2024-60	ICRISAT
IC-DHLBIR-2024-9	ICRISAT	IC-DHLBIR-2024-35	ICRISAT	IC-DHLBIR-2024-61	ICRISAT
IC-DHLBIR-2024-10	ICRISAT	IC-DHLBIR-2024-36	ICRISAT	IC-DHLBIR-2024-62	ICRISAT
IC-DHLBIR-2024-11	ICRISAT	IC-DHLBIR-2024-37	ICRISAT	IC-DHLBIR-2024-63	ICRISAT
IC-DHLBIR-2024-12	ICRISAT	IC-DHLBIR-2024-38	ICRISAT	IC-DHLBIR-2024-64	ICRISAT
IC-DHLBIR-2024-13	ICRISAT	IC-DHLBIR-2024-39	ICRISAT	IC-DHLBIR-2024-65	ICRISAT
IC-DHLBIR-2024-14	ICRISAT	IC-DHLBIR-2024-40	ICRISAT	IC-DHLBIR-2024-66	ICRISAT
IC-DHLBIR-2024-15	ICRISAT	IC-DHLBIR-2024-41	ICRISAT	IC-DHLBIR-2024-67	ICRISAT
IC-DHLBIR-2024-16	ICRISAT	IC-DHLBIR-2024-42	ICRISAT	IC-DHLBIR-2024-68	ICRISAT
IC-DHLBIR-2024-17	ICRISAT	IC-DHLBIR-2024-43	ICRISAT	IC-DHLBIR-2024-69	ICRISAT
IC-DHLBIR-2024-18	ICRISAT	IC-DHLBIR-2024-44	ICRISAT	IC-DHLBIR-2024-70	ICRISAT
IC-DHLBIR-2024-19	ICRISAT	IC-DHLBIR-2024-45	ICRISAT	IC-DHLBIR-2024-71	ICRISAT
IC-DHLBIR-2024-20	ICRISAT	IC-DHLBIR-2024-46	ICRISAT	IC-DHLBIR-2024-72	ICRISAT
IC-DHLBIR-2024-21	ICRISAT	IC-DHLBIR-2024-47	ICRISAT	IC-DHLBIR-2024-73	ICRISAT
IC-DHLBIR-2024-22	ICRISAT	IC-DHLBIR-2024-48	ICRISAT	IC-DHLBIR-2024-74	ICRISAT
IC-DHLBIR-2024-23	ICRISAT	IC-DHLBIR-2024-49	ICRISAT	IC-DHLBIR-2024-75	ICRISAT
IC-DHLBIR-2024-24	ICRISAT	IC-DHLBIR-2024-50	ICRISAT	IC-DHLBIR-2024-76	ICRISAT
IC-DHLBIR-2024-25	ICRISAT	IC-DHLBIR-2024-51	ICRISAT	IC-DHLBIR-2024-77	ICRISAT
IC-DHLBIR-2024-26	ICRISAT	IC-DHLBIR-2024-52	ICRISAT		

Table 2. Analysis of variance for nine characters in Pearl millet during summer 2025 season

Characters	Mean sum of square		
	Repli- cation	Geno- type	Error
Days to 50% flowering	4.733	62.711**	1.194
Days to maturity	3.435	18.061**	1.948
Plant height at maturity (cm)	0.026	511.072**	10.881
Productive Tillers plant ⁻¹	0.002	1.289**	0.079
Panicle length (cm)	0.104	61.918**	2.288
Panicle girth (cm)	0.514	3.287**	0.162
1000seedweight(g)	0.800	7.563**	0.485
Grain yield plant ⁻¹ (g)	2.974	764.415**	32.393
Dry fodder yield plant ⁻¹ (g)	0.416	941.198**	128.468

*, ** Exhibited significance at 5 % and 1% level, respectively.

(1952), was used to generate clusters. In accordance with Arunachalam and Bandopadhyaya (1984), the potential boundaries of parental divergence where heterosis was likely to occur were computed. Transformation was done by using the pivotal condensation method. The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

Result and Discussion

Analysis of variance shows significant differences among genotypes, as indicated by the mean sum of square for treatment being significant for all traits Table 2. This confirms the presence of substantial genetic variation among the genotypes. However, the differences due to replications were not statistically significant, indicating that the experimental field was uniform and homogeneous.

Previous study of Andhale *et al.*, (2024), Sharma *et al.*, (2024), Sabitha *et al.*, (2025), Sirsat *et al.*, (2026), also has reported variation among the various character studied.

Clustering Pattern of Genotypes : The seventy-seven genotypes were grouped into six clusters, as presented in Table 3 and Figure 1. Cluster I contained the highest number of genotypes (62), followed by Cluster II with 6 genotypes, Cluster IV with 4 genotypes and Cluster V with 3 genotypes. The remaining clusters III, VI, each contained only a single genotype, making them solitary in terms of multivariate composition.

This is in conformity close with the result of Devaliya *et al.*, (2017) studied sixty-eight genotypes, based on genetic distances the sixty-eight genotypes under study were grouped into eight clusters cluster I contains highest sixty genotypes, followed by VII (2 genotypes) and cluster III contains (2 genotypes) while the remaining six clusters were solitary, Karunya *et al.*, (2021) From the D² analysis, five major groups were formed as clusters I, II, III, IV and V consisting of 18, 1, 4, 1 and 1 genotypes, respectively; Amudha *et al.*, (2024) Studied Genetic diversity was determined in 50 pearl millet germplasm accessions based on yield and yield components using multivariate diversity analysis, cluster analysis categorized the 50 genotypes into nine clusters with largest number of genotypes (31) present in cluster I.

Intra and inter cluster divergence : The intra-cluster distance (D²) ranged from 4.87 to 12.21. Among the clusters, Cluster V (D² = 12.21) recorded the highest intra-cluster distance, followed by Cluster II (D² = 8.49), Cluster I (D² = 8.43) and Cluster IV (D² = 4.87). Clusters, III and VI were monogenotypic and, therefore, had no intra-cluster distance (D² = 0).

The maximum inter-cluster distance was observed between clusters II to VI (D² = 23.27), followed by cluster IV to VI (D² = 23.21), cluster IV to V (D² = 22.40), cluster II to V (D² = 19.02), cluster III to VI (D² = 18.46), cluster III to IV (D² = 18.29), III to V cluster (D² = 17.49), cluster

Table 3. Grouping of seventy-seven Pearl millet genotypes into different clusters

Clusters	No. of genotypes	Name of genotype
I	62	IC-DHLBIR-2024-53, IC-DHLBIR-2024-63, IC-DHLBIR-2024-62, IC-DHLBIR-2024-54, IC-DHLBIR-2024-65, IC-DHLBIR-2024-33, IC-DHLBIR-2024-43, IC-DHLBIR-2024-9, IC-DHLBIR-2024-49, IC-DHLBIR-2024-46, IC-DHLBIR-2024-18, IC-DHLBIR-2024-37, IC-DHLBIR-2024-48, IC-DHLBIR-2024-51, IC-DHLBIR-2024-29, IC-DHLBIR-2024-15, IC-DHLBIR-2024-30, IC-DHLBIR-2024-26, IC-DHLBIR-2024-27, IC-DHLBIR-2024-19, IC-DHLBIR-2024-17, IC-DHLBIR-2024-39, IC-DHLBIR-2024-8, IC-DHLBIR-2024-21, IC-DHLBIR-2024-28, IC-DHLBIR-2024-22, IC-DHLBIR-2024-55, IC-DHLBIR-2024-41, IC-DHLBIR-2024-57, IC-DHLBIR-2024-7, IC-DHLBIR-2024-34, IC-DHLBIR-2024-6, IC-DHLBIR-2024-61, IC-DHLBIR-2024-38, IC-DHLBIR-2024-31, IC-DHLBIR-2024-20, IC-DHLBIR-2024-56, IC-DHLBIR-2024-16, IC-DHLBIR-2024-47, IC-DHLBIR-2024-12, IC-DHLBIR-2024-14, IC-DHLBIR-2024-11, IC-DHLBIR-2024-10, IC-DHLBIR-2024-68, IC-DHLBIR-2024-2, IC-DHLBIR-2024-24, IC-DHLBIR-2024-5, IC-DHLBIR-2024-13, IC-DHLBIR-2024-58, IC-DHLBIR-2024-67, IC-DHLBIR-2024-70, IC-DHLBIR-2024-32, IC-DHLBIR-2024-40, IC-DHLBIR-2024-52, IC-DHLBIR-2024-50, IC-DHLBIR-2024-64, IC-DHLBIR-2024-23, IC-DHLBIR-2024-36, IC-DHLBIR-2024-4, IC-DHLBIR-2024-42, IC-DHLBIR-2024-66, IC-DHLBIR-2024-60.
II	6	IC-DHLBIR-2024-74, IC-DHLBIR-2024-76, IC-DHLBIR-2024-73, IC-DHLBIR-2024-71, IC-DHLBIR-2024-35, IC-DHLBIR-2024-59.
III	1	IC-DHLBIR-2024-44.
IV	4	IC-DHLBIR-2024-75, IC-DHLBIR-2024-77, IC-DHLBIR-2024-69, IC-DHLBIR-2024-72.
V	3	IC-DHLBIR-2024-1, IC-DHLBIR-2024-3, IC-DHLBIR-2024-45.
VI	1	IC-DHLBIR-2024-25.

I to VI ($D^2=17.48$), cluster V to VI ($D^2=16.60$).

While minimum inter-cluster distance was observed between cluster I to III ($D^2=11.17$), cluster I to II ($D^2=11.87$), cluster II to I V ($D^2=13.64$), cluster I to V ($D^2=13.85$), cluster I to IV ($D^2=13.91$), cluster II to III ($D^2=14.19$).

The inter-cluster distances were greater than the intra-cluster distances, indicating the existence of substantial genetic diversity among the genotypes. The genotypes in these clusters can be utilized as potential parents, and crosses between them are likely to result in high heterotic expression for yield and its components.

Based on the average performance of

clusters for nine characters (Table 5), it was observed that Cluster IV exhibited late days to 50% flowering and days to maturity, grain yield per plant as well as dry fodder yield per plant. Cluster VI recorded the highest plant

Table 4. Average intra and inter cluster distance (D^2 values) for nine characters in pearl millet

Cluster	I	II	III	IV	V	VI
I	8.43	11.87	11.17	13.91	13.85	17.48
II		8.49	14.19	13.64	19.02	23.27
III			0.00	18.29	17.49	18.46
IV				4.87	22.40	23.21
V					12.21	16.60
VI						0.00

(Bold figure indicate intra-cluster D^2 values)

Table 5. Cluster means for nine characters in six clusters of seventy-seven pearl millet genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Panicle girth (cm)	1000 Seed wt. (g)	Dry fodder yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)
I	56.02	86.04	153.48	3.87	25.04	10.33	9.78	43.82	99.43
II	52.08	83.50	128.50	3.45	19.75	11.87	11.22	28.06	70.75
III	52.50	85.00	160.00	5.80	27.50	12.65	12.50	101.85	145.00
IV	68.88	92.50	122.63	3.13	19.75	11.24	11.49	21.19	57.75
V	50.00	84.17	178.33	3.03	31.83	7.78	6.55	21.58	102.67
VI	62.50	89.50	180.50	3.70	55.00	10.75	13.35	28.60	125.00
Average	57.00	86.79	153.91	3.83	29.81	10.77	10.82	40.85	100.10

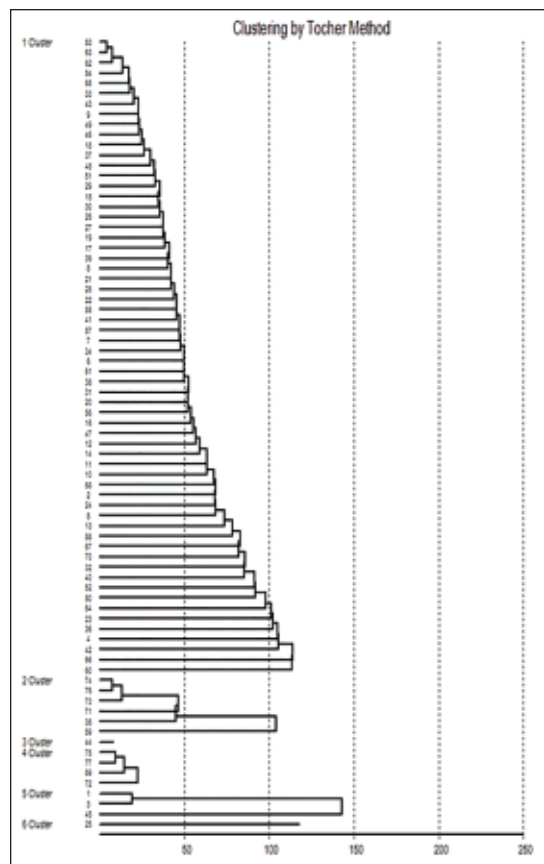
height, while Cluster V showed the lowest number of productive tillers per plant. Cluster II, IV exhibited the minimum panicle length, Cluster V recorded the lowest and 1000-seed weight (test weight).

Cluster V was characterized by early 50% flowering, cluster II recorded for early maturity, and cluster IV shorter plant height. Cluster III recorded the maximum number of productive tillers per plant and panicle girth. Cluster VI had maximum panicle length, as well as the 1000-seed weight (test weight). Cluster III showed the highest grain yield per plant and dry fodder yield per plant.

The Relative Contribution of Different Characters to Diversity : The contribution of different characters to total genetic divergence is presented in Table 6. The application of D² analysis for assessing the proportional contribution of individual traits enhances the precision and significance of genetic divergence studies.

Days to 50% flowering contributed the most to genetic diversity, accounting for 30.79% by securing the first rank 901 times out of 2926 combinations in this study. It was followed by plant height, contributing 23.10% with 676 first ranks; panicle girth, contributing 11.11% with

325 first ranks; 1000 seed weight, contributing 10.05 with 294 first ranks; panicle length, contributing 10.01% with 293 first ranks; grain

**Fig. 1.** Cluster diagram as per Tocher Method for seventy seven pearl millet genotypes

yield plant⁻¹, contributing 8.54% with 2503 first ranks; productivetillersperplant, contributing 5.91% with 173 first ranks; days to maturity, contributing the least at 0.48% with 14 times first ranks and dry fodder yield plant⁻¹.

In light of the current findings and previous research, it can be concluded that the yield indicators responsible for divergence differ substantially. Higher contribution towards genetic divergence was also observed by Athoni *et al.*, (2016) for seed yield and panicle girth; Basavaraj *et al.*, (2017) for panicle girth and Ramya *et al.*, (2017) for plant height, dry matter yield plant⁻¹, test weight and productive tillers

Table 6. Relative per cent contribution of different characters towards total Genetic Divergence in Pearl millet

Characters	No. of times ranked 1 st	Per cent contribution
Days to 50% flowering	901	30.79
Days to Maturity	14	0.48
Plant Height at maturity (cm)	676	23.10
Productive Tillers plant ⁻¹	173	5.91
Panicle Length (cm)	293	10.01
Panicle Girth (cm)	325	11.11
1000 Seed Weight (g)	294	8.54
Grain yield plant ⁻¹ (g)	250	10.05
Dry fodder yield plant ⁻¹ (g)	0	0

Table 7. Characters improvement on the basis of source clusters

Characters	Source clusters
Days to 50 per cent flowering (Early)	V, II, III, I
Days to maturity (Early)	II, V, III, I
Plant height at maturity(cm) (Mid Tall)	I, III
Productive tillers plant ⁻¹ (Maximum)	III, I, VI
Panicle length (cm) (Maximum)	VI, V
Panicle girth (cm) (Maximum)	III, II, IV
1000 seed weight (g) (Maximum)	VI, III, IV, II
Grain yield plant ⁻¹ (g) (Maximum)	III, I
Dry fodder yield plant ⁻¹ (g) (Maximum)	III, IV, V

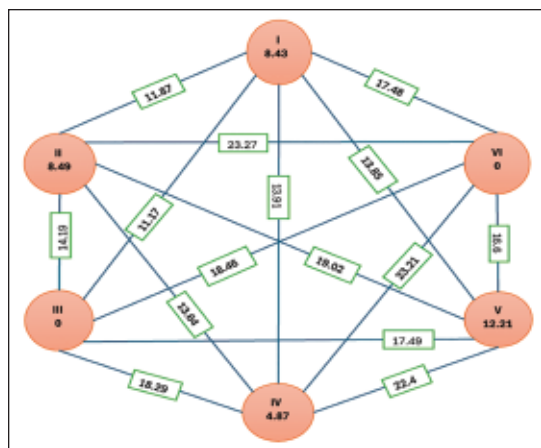


Fig. 2. Cluster diagram of seventy-seven genotypes in pearl.

plant⁻¹; Shashibhushan (2022) for days to and panicle length; Sharma *et al.*, (2024) crude protein content, plant height, number of tillers plant⁻¹.

Considering all the above aspects, the following genotypes identified in the present study may be regarded as potential parents for future breeding programmes aimed at improving seed yield and yield-related traits in pearl millet.

1. IC-DHLBIR-2024-23
2. IC-DHLBIR-2024-31
3. IC-DHLBIR-2024-34
4. IC-DHLBIR-2024-36
5. IC-DHLBIR-2024-41
6. IC-DHLBIR-2024-42
7. IC-DHLBIR-2024-44
8. IC-DHLBIR-2024-57
9. IC-DHLBIR-2024-58

Conclusion

The genotypes investigated have a lot of genetic variability. Six clusters were formed from the seventy-seven genotypes. Cluster I contained the highest number of genotypes (62), followed by Cluster II with 6 genotypes, Cluster IV with 4 genotypes and Cluster V with 3 genotypes. The remaining clusters-III, VI, -each contained only a single genotype, making them solitary in terms of multivariate composition. There was no

correlation between genetic diversity and geographic dispersion. The maximum inter-cluster distance was observed between clusters II to VI ($D^2=23.27$). On considering inter-cluster distances, cluster mean and per se performance, and divergence class observed in the present study, the genotypes viz., IC-DHLBIR-2024-23, IC-DHLBIR-2024-31, IC-DHLBIR-2024-34, IC-DHLBIR-2024-36, IC-DHLBIR-2024-41, IC-DHLBIR-2024-, IC-DHLBIR-2024-44, IC-DHLBIR-2024-57, IC-DHLBIR-2024-58 and IC-DHLBIR-2024-59 were distinct and diverse and can be classified as promising genotypes. These genotypes can be used for inter-crossing to obtain wider variability in pearl millet. Hybridization between the genotypes of cluster II and cluster VI may result in exploiting more heterosis with maximum genetic divergence and are likely to produce desirable transgressive segregants in segregating generations for further crop improvements.

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