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Genetic Diversity Studies in Local Germplasm of Peael Millet [*Pennisetum Glaucum* (L.) R. Br.] for Summer Season

G. D. Sirsat[1], K. K. Barhate[2], V. Y. Pawar[3*], J. M. Patil[4] , P. S. Munge[4] and S. D. Thorat[5]
Department of Agricultural Botany, College of Agriculture Dhule,
Mahatma Phule Krishi Vidyapeeth, Rahuri - 413 722 (India)
*Corresponding author E-mail : vypawar2gene@gmail.com

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Abstract

The objective of the current study was to determine the type and degree of genetic diversity between traits that contribute to seed yield. Present investigation studied 30 local genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.], evaluated randomized block design (RBD) with two replications in summer-2024 at Bajara Research Scheme, College of Agriculture, Dhule.(MS). All 30 genotypes were evaluated for different morphological and agronomical traitsthe 30 genotypes were grouped into nine clusters. Cluster I contained the highest number of genotypes (19), followed by Cluster VI with 3 genotypes, and Cluster VIII with 2 genotypes. The remaining clusters-II, III, IV, V, VII, and IX-each comprised a single genotype. In terms of multivariate composition, these clusters were therefore considered solitary. Hybridization between genotypes from Cluster VIII and Cluster IX may result in greater heterosis due to maximum genetic divergence.

Key words : Genetic diversity; Pearl millet; Cluster; Genotypes; Phenotypes; D^2 value.

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] belongs to the family Poaceae (Gramineae), subfamily Panicoideae, and the genus Cenchrus. It is considered a cross-pollinated (allogamous) crop, exhibiting protogyny (where the female reproductive parts mature before the male ones). The chief pollinating agent is wind (anemophily). Pearl millet is diploid (2n = 2x = 14) in nature. Genetic diversity is a crucial component in the improvement and sustainability of any crop species. In pearl millet, the wide genetic variation present within local landraces and wild relatives offers a rich reservoir of traits such as early maturity, disease resistance, abiotic stress tolerance, and yield stability. These genetic resources serve as the foundation for breeding programs aimed at developing improved cultivars with enhanced agronomic performance and resilience to climate change.

Genetic diversity is one of the key criteria for selecting parents in a hybridization programme. The quantification of genetic diversity through biometrical procedures, such as the Mahalanobis D^2 statistic, has made it possible to select genetically diverse parents. Divergence analysis plays a crucial role in the efficient selection of divergent parents for hybridization, aiming to exploit maximum heterosis for improving grain yield. Before initiating any breeding programme, it is essential to have a thorough understanding of the nature and magnitude of genetic variability, diversity, and the extent of association between yield and its components. Divergent genotypes will be obtained through collection from different agro-climatic regions to ensure genetic variability. To assess genetic divergence among the collected genotypes, D^2 analysiswill be 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 materials used for the

present research consisted of 30 local genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.], which were obtained from the Bajra Research Scheme, College of Agriculture, Dhule which were evaluated in Summer-2024. The list of genotypes used in the study is presented in Table 1.

Table 1. List of thirty local genotypes of pearl millet

Genotype	Genotype	Genotype
DHLGB-1	DHLGB-11	DHLGB-21
DHLGB-2	DHLGB-12	DHLGB-22
DHLGB-3	DHLGB-13	DHLGB-23
DHLGB-4	DHLGB-14	DHLGB-24
DHLGB-5	DHLGB-15	DHLGB-25
DHLGB-6	DHLGB-16	DHLGB-26
DHLGB-7	DHLGB-17	DHLGB-27
DHLGB-8	DHLGB-18	DHLGB-28
DHLGB-9	DHLGB-19	DHLGB-29
DHLGB-10	DHLGB-20	DHLGB-30

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 Mahalnobis (1936), as explained by Rao (1952), was used to analyze divergence, and Tocher's technique, as explained by Rao (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 squares for treatments 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 Subbulakshmi *et al.* (2018), Abdulhakeem *et al.* (2019), Mithlesh Kumar *et al.* (2020), also has reported variation among the various characters studied.

Clustering Pattern of Genotypes : The thirty genotypes were grouped into nine clusters, as presented in Table 3. Cluster I contained the highest 19 genotypes, followed by Cluster VI with 3 genotypes and Cluster VIII with 2 genotypes. The remaining clusters-II, III, IV, V, VII and IX-each contained only a single genotype, making them solitary in terms of multivariate composition.

This is in conformity close with the result of Kumari *et al*., (2016) found that cluster I was the largest and consisted of fourteen genotypes, followed by cluster IV with four genotypes, whereas cluster II, III, V, VI, VII, IX, X, XI were unique, since, each had only one genotype, by Sumathi *et al*., (2016) grouped one thousand pearl millet genotypes can be grouped into eleven clusters, by Abubakar Abdulhakeem *et*

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

Characters	Mean sum of square		
	Replication	Genotype	Error
Days to 50% flowering	2.400	15.963**	0.400
Days to maturity	0.150	18.120**	0.667
Plant height at maturity (cm)	317.400	2979.503**	169.813
Productive tillers plant^{-1}	1.837	1.409**	0.068
Panicle length (cm)	0.010	56.363**	0.578
Panicle girth (cm)	1.500	3.448**	0.163
1000 seed weight (g)	3.178	5.600**	0.157
Grain yield plant^{-1} (g)	2.713	60.108**	1.924

*,** Exhibited significance at 5 % and1% level, respectively.

Table 3. Grouping of thirty Pearl millet genotypes into different clusters during summer season

Cluster number	No. of geno-types	Name of genotypes
I	19	DHLGB-25, DHLGB-26, DHLGB-24, DHLGB-4, DHLGB-6, DHLGB-28, DHLGB-22, DHLGB-18, DHLGB-27, DHLGB-21, DHLGB-23, DHLGB-29, DHLGB-20, DHLGB-12, DHLGB-2, DHLGB-30, DHLGB-3, DHLGB-9, DHLGB-13
II	1	DHLGB-10
III	1	DHLGB-1
IV	1	DHLGB-11
V	1	DHLGB-14
VI	3	DHLGB-15, DHLGB-19, DHLGB-16
VI	1	DHLGB-8
VIII	2	DHLGB-5, DHLGB-17
IX	1	DHLGB-9

al., (2019) recorded cluster analysis grouped the accession into four major clusters based on their morphological similarity, by Swamynatham *et al*.,(2020) investigated fifty germplasm using Mahalanobis D^2 statistics for fourteen different traits. D^2 clustering grouped the genotypes into sixteen clusters.

Intra and inter cluster divergence : The maximum inter-cluster distance was observed between clusters VIII to IX (D^2 = 24.97), followed by cluster VI to VIII (D^2 = 19.00), cluster I to IX (D^2 = 18.23), cluster V to VIII (D^2 = 17.40), cluster III to VIII (D^2 =17.17), cluster VII to VIII (D^2 = 16.79), cluster IV to VIII D^2 = 16.26), cluster II to VIII (D^2 = 16.18), cluster VII to IX (D^2 = 16.17) cluster II to VI (D^2 = 15.66), cluster VI to IX (D^2 = 15.22), cluster IV to IX (D^2 = 14.82), cluster V to VII (D^2 = 14.77), cluster VI to VII (D^2 = 14.63), cluster II to V (D^2 = 13.98), cluster V to IX (D^2 = 13.82), cluster I to VI (D^2 = 13.43), cluster IV to VI (D^2 = 13.26). While minimum inter-cluster distance was observed between cluster III to IV (D^2 = 6.64), cluster II to III (D^2 = 8.36), cluster V to VI (D^2 = 8.84), cluster III to VII (D^2 = 8.86), cluster II to IV (D^2 = 9.36), cluster IV to VII (D^2 = 10.09), cluster I to III (D^2 = 11.58) , cluster II to IX (D^2 = 11.62), cluster II to VII (D^2 =11.72), cluster I to V (D^2 =11.77), cluster I to IV (D^2 = 12.03), cluster I to II (D^2 = 12.18), cluster IV to V (D^2 = 12.25), cluster I to VIII (D^2 = 12.35), cluster III to V (D^2 = 12.38), cluster III to VI (D^2 = 12.96) , cluster I to VIII (D^2 =13.05), cluster III to IX (D^2 = 13.19).

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

Table 4. Average intra and inter cluster distance (D^2 values) for eight characters in Pearl millet during summer season

Cluster	I	II	III	IV	V	VI.	VII	VIII	IX
I	10.31	12.18	11.58	12.03	11.77	13.43	13.05	12.35	18.23
II		0.00	8.36	9.36	13.98	15.66	11.72	16.18	11.62
III			0.00	6.64	12.38	12.96	8.86	17.17	13.19
IV				0.00	12.25	13.26	10.09	16.26	14.82
V					0.00	8.84	14.77	17.40	13.82
VI						9.53	14.63	19.00	15.22
VII							0.00	16.79	16.17
VIII								8.26	24.97
IX									0.00

Table 5. Cluster means for eight characters in nine clusters of thirty Pearl millet genotypes during summer season

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 weight (g)	Grain yield plant^{-1} (g)
I	55.11	86.92	186.76	2.31	29.81	12.01	10.79	59.53
II	58.00	90.00	224.50	1.15	31.80	11.70	8.23	52.56
III	60.50	91.50	186.00	2.65	34.50	10.50	9.88	64.75
IV	60.50	91.50	278.00	2.50	32.00	10.50	12.18	60.67
V	55.50	87.50	213.00	3.50	36.65	12.00	11.15	56.22
VI	54.00	86.00	188.50	1.93	38.67	10.47	13.05	64.64
VII	60.50	96.00	132.50	1.65	31.65	9.30	10.68	60.15
VIII	51.75	83.75	222.75	2.33	20.33	11.40	11.26	57.04
IX	58.50	91.00	202.50	1.30	42.70	10.35	7.95	50.58
Average	57.15	89.35	203.83	2.14	33.12	10.91	10.57	58.46

clusters for eight characters (Table 5), it was observed that Cluster VII exhibited late days to 50% flowering and days to maturity. Cluster IV recorded the highest plant height, while Cluster V showed the highest number of productive tillers per plant as well as the maximum panicle girth. Cluster IX exhibited the maximum panicle length, Cluster VI recorded the highest 1000-seed weight (test weight), and Cluster III showed the highest grain yield per plant.

Cluster VIII was characterized by early 50% flowering, early maturity, and shorter panicle length. Cluster VII recorded the least plant height and panicle girth, as well as the lowest test weight and grain yield. Cluster II exhibited the minimum number of productive tillers per plant.

The contribution of different characters to total genetic divergence is presented in Table 6. The application of D^2 analysis for assessing the proportional contribution of individual traits enhances the precision and significance of genetic divergence studies.

Panicle length contributed the most to genetic diversity, accounting for 38.16% by securing the first rank 166 times out of 435

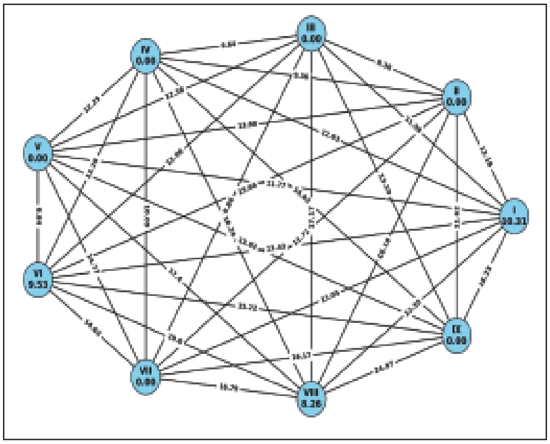

Fig. 1. cluster diagram of thirty genotypes in pearl millet during summer season

Table 6. Relative percent contribution of different characters towards total genetic divergence in pearl millet during summer season

Characters	No. of times ranked 1st	Per cent contribution
Days to 50% flowering	69	15.86
Days to maturity	4	0.92
Plant height at maturity(cm)	23	5.29
Productive tillers plant^{-1}	27	6.21
Panicle length(cm)	166	38.16
Panicle girth(cm)	30	6.90
1000 seed weight(g)	98	22.53
Grain yield plant^{-1} (g)	18	4.14

Table 7. Characters improvement on the basis of source clusters during summer season

Characters	Source clusters
Days after 50 per cent flowering Early)	VIII, VI, III
Days to maturity (Early)	VIII, VI, III
Plant height at maturity (cm) (Mid Tall)	IX, V
Productive tillers plant^{-1} (Maximum)	V, III
Panicle length (cm) (Maximum)	IX, VI
Panicle girth(cm) (Maximum)	I, V
1000 seed weight(g) (Maximum)	VI, IV
Grain yield plant^{-1} (g) (Maximum)	I, III,

combinations in this study. It was followed by 1000 seed weight, contributing 22.53% with 98 first ranks; days to 50 percent flowering, contributing 15.86% with 69 first ranks; panicle girth, contributing 6.90% with 30 first ranks; number of productive tillers per plant, contributing 6.21% with 27 first ranks; plant height, contributing 5.29% with 23 first ranks; grain yield, contributing 4.14% with 18 first ranks; and days to maturity, contributing the least at 0.92% with 4 times first ranks.

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 Abubakar Abdulhakeem *et al*., (2019)into four major clusters based on their morphological similarity; Sharma *et al*., (2024) crude protein content, plant height, number of tillers per plant. Considering all the above aspects, the following

Table 8. Tentative suggested future crossing programme during summer season

Characters to be improved	Cluster combination with inter-cluster distance	Genotypes Possible	Crosses
Earliness (50 flowering) and Days to maturity Earliness	VIII xVI = 19.00	DHLGB-5, DHLGB-17, DHLGB-15, DHLGB-19, DHLGB-16.	DHLGB-5 X DHLGB-15 DHLGB-5 X DHLGB-19 DHLGB-5 X DHLGB-16 DHLGB-17 X DHLGB-15 DHLGB-17 X DHLGB-19 DHLGB-17 X DHLGB-16
	VIII xIII=17.17	DHLGB-5, DHLGB-17, DHLGB-1.	DHLGB-5 X DHLGB-1 DHLGB-17 X DHLGB-1
Plant height (Mid Tall)	IX x V=13.82	DHLGB-7, DHLGB-14.	DHLGB-7 X DHLGB-14
Productive tillers per plant	V x III=12.38	DHLGB-14, DHLGB-1.	DHLGB-14 X DHLGB-1
Panicle length (cm)	IX x VI=15.22	DHLGB-7, DHLGB-15, DHLGB-19, DHLGB-16.	DHLGB-7 X DHLGB-15 DHLGB-7 X DHLGB-19 DHLGB-7 X DHLGB-16
Panicle girth (cm)	I x V=11.77	DHLGB-25, DHLGB26, DHLGB-14.	DHLGB-25 X DHLGB-14 DHLGB-26 X DHLGB-14
1000 seed weight(g)	VI x IV=13.26	DHLGB-15, DHLGB19, DHLGB-16, DHLGB-11.	DHLGB-15 X DHLGB-11 DHLGB-19 X DHLGB-11 DHLGB-16 X DHLGB-11
Grain yield (g) maximum	I x III = 11.58	DHLGB-22, DHLGB-28, DHLGB-21, DHLGB-1.	DHLGB-22 X DHLGB-1 DHLGB-28 X DHLGB-1 DHLGB-21 X DHLGB-1

genotypes identified in the present study DHLGB-1, DHLGB-5, DHLGB-15, DHLGB-19,DHLGB-21, DHLGB-22, DHLGB-25, and DHLGB-28 may be regarded as potential parents for future breeding programmes aimed at improving seed yield and yield-related traits in pearl millet.

Conclusion

The cluster analysis revealed that thirty genotypes were grouped into nine clusters. Cluster I contained the highest number of genotypes (19), followed by Cluster VI with 3 genotypes, and Cluster VIII with 2 genotypes. The remaining clusters-II, III, IV, V, VII, and IX-each comprised a single genotype. In terms of multivariate composition, these clusters were therefore considered solitary. The maximum inter-cluster distance was observed between clusters VIII to IX (D^2 = 24.97). Considering inter-cluster distance, cluster means, genotype per se performance, and divergence class, the genotypes DHLGB-1, DHLGB-5, DHLGB-15, DHLGB-19,DHLGB-21, DHLGB-22, DHLGB-25, and DHLGB-28 can be utilized in future breeding programmes to generate a broad spectrum of variability for various yield-contributing traits, facilitating the development of superior genotypes.

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