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GENETIC DIVERSITY ANALYSIS IN LITTLE MILLET (*PAnicum sumatrense* L.) GENOTYPES

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ABSTRACT

Genetic diversity is the foundation of crop improvement programs. The present investigation was undertaken to estimate the genetic divergence among thirty genotypes of little millet (*Panicum sumatrense* L.) using Mahalanobis D^2 statistics. The experiment was conducted in Kharif 2025-26 seasons in Randomized Block Design with three replications. Data on twelve yield contributing traits were recorded. Analysis of variance showed highly significant ($p<0.001$) differences among the genotypes for all the traits indicating the presence of significant genetic variability for divergence analysis. Tocher's method classified the genotypes into five distinct clusters based on D^2 values. Cluster II was the largest, comprising 13 genotypes, followed by Cluster I (11genotypes), Cluster III (3 genotypes), Cluster IV (2 genotypes) and cluster V containing one genotype, indicating their genetic uniqueness. The maximum inter-cluster distance was observed between Cluster I × Cluster III (84.36), suggesting that crosses between these clusters have the highest potential for generating transgressive segregants. Cluster mean analysis identified Cluster I and Cluster V as the most promising, Number of productive tillers per plant, 1000 Seed weight (g), Biological yield per plant (g), and Grain yield per plant (g). The traits contributing most to genetic divergence were1000 seed weight (33.56 %), biological yield per plant (18.16 %) and Harvest index (14.94 %). The results provide a clear basis for selecting genetically diverse parents for hybridization to enhance yield and adaptability in little millet.

Key words: Little millet, Genetic diversity, Clustering, Mahalanobis D^2, Tocher's method, Hybridization.

Introduction

Little millet (*Panicum sumatrense* L.) is one of the most important millet. It belongs to the family poaceae. Little Millet is nutritious small millet known for its very rich nutrient composition and health benefits. Per 100 g of raw grain, it provides about 329–341 kcal of energy, 67–68g carbohydrates, 7–8g protein, and 4–5 g fat rich in essential minerals such as iron (8–10mg), phosphorus (220–230mg), magnesium (90–100mg), calcium (15–20 mg), and potassium (200–220mg). Despite its agronomic and nutritional advantages, little millet remains under-researched and underutilized, resulting in low productivity levels. The lack of high-yielding, region - specific varieties and limited exploitation of available genetic diversity are major constraints to its improvement. Knowledge of genetic variability in respect of yield in any species is valuable in plant breeding program. It helps in choice of the best yield attributes either for selection or hybridization.

The success of breeding programs depends on the availability and use of genetic diversity. The use of heterosis and the genetic recombination in the following generations are determined by the selection of genetically diverse parents (Arunachalam, 1981). Univariate analyses allow for the examination of the variation of a single trait, while multivariate analyses, e.g. the Mahalanobis D^2 statistic, allow for a more robust estimate

of genetic divergence that considers simultaneously the variation in a set of traits (Rao, 1952). The method is efficient in measuring genetic distances and grouping genotypes into clusters, assisting breeders to select the most divergent parents for hybridization (Daniel *et al*., 2011). Several studies in little millet have employed D^2 analysis to understand genetic architecture Vetriventhan *et al.,* (2026), Amaravel *et al.,* (2023). However, continuous evaluation of new germplasm is essential to identify novel sources of variation.

Therefore, the estimation of variability, pattern of clustering and contribution of yield related traits is of immense importance to direct selection and hybridization strategies. Are fined understanding of genetic divergence will not only help in efficient parental selection but also ensure sustainable utilization of little millet genetic resources for yield improvement and adaptability under changing climatic conditions.

Materials and Methods

Experimental Site and Material

The experiment was conducted during the Kharif season of 2025-26 in the Research field of Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India. The experimental material consisted of 30 diverse little millet genotypes including improved varieties and advanced breeding lines collected from BAU, Sabour and Phule Ekadashi used as Check variety.

Experimental Design and Observations

This experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in plot size of 5.4 m^2 area with plant to plant spacing 10 × 10 cm. Recommended agronomic practices were followed to maintain healthy growth of the crop. Five competitive plants were selected at random from each replication for 12 quantitative characters (Days to 50 % Flowering, Days to maturity, Plant height (cm), Number of Productive tillers per plant, Flag leaf length (cm), Flag leaf width (cm), Panicle length (cm), Peduncle length (cm), 1000 seed weight (g), Grain yield per plant (g), Biological Yield (g), Harvest index (HI) were recorded.

Statistical Analysis

The mean data were subjected to Analysis of Variance (ANOVA) using Indostat 9.2 software to test the significance of genotypic differences. Genetic divergence was assessed using Mahalanobis D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into clusters following Tocher's method as outlined by Rao (1952). Intra and inter-cluster distances were calculated, and the relative contribution of each character to the total divergence was determined by ranking the characters based on their Mahalanobis distance.

Table 1: Analysis of variance (ANOVA) for yield and yield attributing traits.

Source of Variations	Mean sum of Square		
	Replication	Treatments	Error
Degree of freedom	2	29	58
Days to50% flowering	33.011	4.077*	2.092
Days to maturity	40.078	119.947**	7.974
Flag leaf length (cm)	46.974	29.157**	8.090
Flag leaf width (cm)	0.075	0.021**	0.010
Peduncle length (cm)	6.348	4.098**	0.918
Panicle length (cm)	54.107	24.152**	8.125
No. of effective tillers per plant	2.003	3.670**	0.893
Plant height (cm)	812.204	463.443**	146.222
1000SeedWt. (gm)	0.015	1.401**	0.049
Biological yield per plant(g)	41.908	264.406**	14.717
Harvest index (%)	82.65	79.111**	13.909
Grain yield per plant(g)	7.693	16.833**	0.769

Results and Discussion

Analysis of variance

Analysis of variance (ANOVA) showed significant differences ($p<0.01$) among the 30 genotypes for all the twelve traits studied (Table 1). This indicates the existence of a significant genetic variability in the experimental material, which is a good basis for further analysis of divergence. Similar findings of significant genetic variability in little millet have been reported by Vetriventhan *et al.,* (2026), Amaravel *et al.,* (2023), Suryanarayana *et al.,* (2018), Patel *et al., (*2018), Selvi *et al*., (2015), Manimozhi *et al*., (2015).

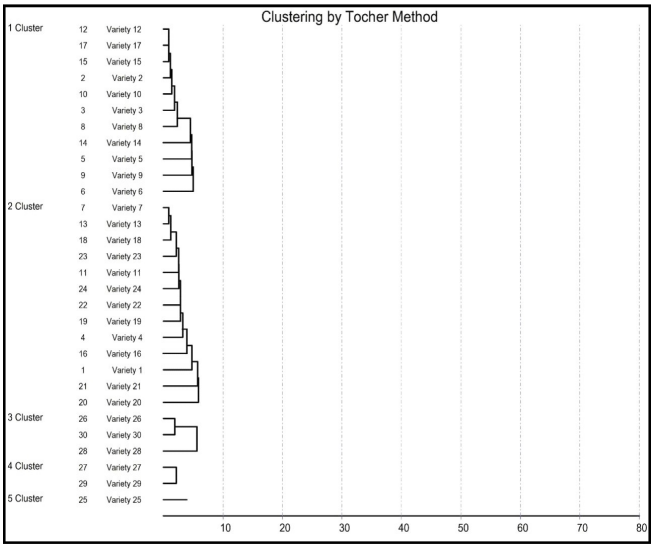


Fig. 1: Clustering pattern of 30 little millet genotypes into five distinct groups using Tocher's method.

Table 2: Composition of little millet genotypes in five clusters (Tocher's method).

Cluster	Number of Genotypes	Genotypes
I	11	IPmr1006, IPmr1035, IPmr1020, IPmr722, IPmr1002,IPmr857, IPmr990, IPmr1015, IPmr868, IPmr991, IPmr 880
II	13	IPmr885, IPmr1014, IPmr1038, IPmr1057, IPmr1003, IPmr1058, IPmr1053, IPmr1042, IPmr865, IPmr1032, IPmr700, IPmr1050, IPmr1047
III	3	BL6, Phule Ekadashi, GPUL6
IV	2	GNV3,GV2
V	1	IPmr1059

Genetic Divergence and Clustering Pattern

The genetic divergence analysis using Mahalanobis D^2 statistic grouped the 30 genotypes into five distinct clusters (Table 3). Cluster II was the largest, consisting of 13 genotypes (IPmr885, IPmr1014, IPmr1038, IPmr1057, IPmr1003, IPmr1058, IPmr1053, IPmr1042, GPUL 6, IPmr1032, IPmr700, IPmr1050, and IPmr1047), indicating a close genetic relationship among them. Cluster I contained 11 genotypes, and Cluster III contained 3, Cluster IV contained 2, Notably, Cluster V (IPmr 1059) were solitary, housing only one genotype. This monotypic nature emphasizes their significant genetic divergence from other genotypes and makes them unique parents for hybridization. The pattern of clustering is illustrated in Fig. 1.

Intra-and Inter-Cluster Distances

The average intra- and inter-cluster distances (D^2 values) are presented in Table 3. The intra-cluster distances, which measure diversity within a cluster, were highest for cluster III (16.71) followed by cluster II (11.97), Cluster I (10) and Cluster IV (5.70). The high intra-cluster distance in Cluster III The highest contribution of genetic diversity was exhibited by 1000 seed weight (33.56 %) followed by biological yield per plant (18.16 %) and Harvest index (14.94 %). These 5 traits together with biological yield per plant (18.16 %), harvest index (14.94 %), days to maturity (11.95), Peduncle length (5.98%) and1000 seed weight (33.56 %) contributed more than 84 % of total genetic divergence. Hence, these traits should form the basis for the selection of parents for hybridization to attain maximum genetic gains. Similar findings were reported by Pavithra *et al.,* (2025), Narasimhulu *et al*., (2023), where yield-related traits were major contributors to divergence. Suggests

Table 3: Intra and inter-cluster distances (D^2 values) among the five clusters.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster1	10.89	23.21	84.36	47.34	37.01
Cluster2		11.97	55.13	22.81	20.50
Cluster3			16.71	60.83	70.86
Cluster4				5.70	34.14
Cluster5					0.00

considerable variability among its constituent genotypes, offering scope for selection within the cluster. In contrast, V had zero intra-cluster distances, as expected for solitary clusters. Inter-cluster distances, representing genetic distance between clusters, were variable. The highest inter-cluster distance was recorded between cluster I and III (84.36) suggesting that genotypes from these two clusters are highly divergent. This was followed by cluster III and V (70.86) and cluster III and IV (60.83).

Mahalanobis (1936) suggested that crosses between genotypes belonging to the most divergent clusters are likely to produce a wide range of variability and high heterotic effects, which may lead to superior transgressive segregants. Hence, hybridization between genotypes from cluster I and III is expected to be most rewarding. Similar conclusions on exploiting maximum inter-cluster distances have been made in little millet by Selvi *et al.,* (2015), Suryanarayana *et al.,* (2018).

Cluster Mean Analysis

The mean performance of the five clusters for the twelve traits is summarized in Table 4. Cluster I and V had highest number of traits i.e. Number of productive tillers per plant (7.60), 1000 Seed weigh t(g) (3.40), Biological yield per plant (g) (43.19), Grain yield per plant

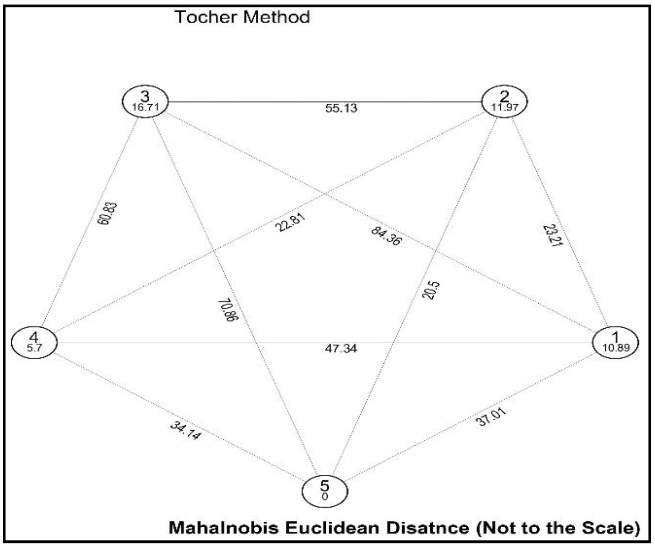


Fig. 2: Mahalanobis Euclidean distance using Tocher's method among 30 little millet genotypes.

Table 4: Cluster mean of 12 characters for 30 little millet genotypes.

CA	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
DF	96.88	96.77	96.67	97.17	95.33
DM	125.42	125.90	106.11	127.50	126.00
FLL	23.21	20.61	22.87	20.29	28.38
FLW	0.88	0.89	0.85	0.84	1.01
PDL	7.39	7.67	9.68	5.58	7.24
PL	25.52	22.13	23.35	19.25	26.44
NPT	7.60	6.16	6.53	6.55	6.44
PH	119.72	114.58	118.85	84.88	129.76
SW	3.40	2.67	1.94	2.52	1.72
BYP	43.19	36.11	22.55	21.85	42.67
HI	27.88	25.12	19.94	36.71	24.79
GYP	11.68	8.84	4.39	7.99	10.58

CA: Characters; DF: Days to 50% flowering; DM: Days to maturity; FLL: Flag leaf length (cm); FLW: Flag leaf width(cm); PDL: Peduncle length(cm); PL: Panicle length(cm); NPT: Number of productive tillers/plant; PH: Plant height(cm); SW: 1000 Seed Wt.(gm); BYP: Biological yield per plant (g); HI: Harvest index (%); GYP: Grain yield per plant (g)

(g) (11.68) and Days to 50% flowering (95.33), Flag leaf length (cm) (28.38), Flag leaf width(cm) (1.01), Panicle length (cm) (26.44), Cluster IV also showed promising traits, plant height (cm) (84.88), Harvest index (36.71 %). Cluster III performed well for days to maturity (106.11) and peduncle length (9.68). The diverse mean values across clusters reflect the genetic diversity revealed by the D^2 analysis and assist in the identification of clusters with specific desirable traits for targeted breeding.

Contribution of Traits to Genetic Divergence

The percentage contribution of each character to the total genetic divergence is presented in Table 5. The highest contribution of genetic diversity was exhibited by 1000 seed weight (33.56 %) followed by biological yield per plant (18.16 %) and Harvest index (14.94 %). Together with 1000 seed weight (33.56 %), biological yield per plant (18.16 %), harvest index (14.94 %), days to maturity (11.95), and Peduncle length (5.98 %) these 5 traits contributed to more than 84% of the total divergence. Thus, in selecting parents for hybridization, these characteristics should be prioritized to get maximum genetic gain. Similar findings were reported by Pavithra *et al.,* (2025), Narasimhulu *et al*., (2023), where yield-related traits were major contributors to divergence.

Table 5: Percentage contribution of characters to total genetic divergence.

Source	TRF	CB
Daysto50% flowering	9	2.07
Days to maturity	52	11.95
Flag leaf length (cm)	6	1.38
Flag leaf width(cm)	2	0.46
Peduncle length(cm)	26	5.98
Panicle length(cm)	4	0.92
Number of effective tillers per plant	16	3.68
Plant height(cm)	8	1.84
1000 Seed Wt.(gm)	146	33.56
Biological yield per plant (g)	79	18.16
Harvest index (%)	65	14.94
Grain yield per plant(g)	22	5.06

TRF: Times ranked first; CB: Contribution%

Conclusion

The study revealed significant genetic diversity among the 30 little millet genotypes, successfully grouping the minimum to five distinct clusters. The high inter-cluster distances particularly between cluster I and III (84.36) indicates a strong possibility of heterosis and generation of desirable variability through their hybridization. The unique genotype in solitary cluster i.e., Cluster V (IPmr 1059) are valuable genetic resources. The cluster means provide a clear guide for selecting parents for specific traits, with Cluster I and Cluster III being ideal for combining high yield and early maturity. The analysis underscores that 1000 seed weight, biological weight per plant, and harvest index are the most critical traits for distinguishing genotypes. The results provide a scientifically sound strategy to little millet breeders to select diverse parents and design efficient crossing programmes for developing high yielding and adaptable cultivars.

Author Contributions

I have done my research work under the supervision of Dr. Ranju Kumari and DR. Anand Kumar, and other advisory team.

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