

RESEARCH PAPER

Genetic Diversity Studies of Little Millet (*Panicum sumatrense*)

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ABSTRACT

An experiment was conducted with 23 little millet genotypes laid out in randomized block design in three replications during *kharif*, 2018 at seven little millet growing locations in India. Data was recorded on six agronomic traits to study genetic divergence. The study revealed that genotypes were grouped into nine clusters and the highest inter cluster distance was found between clusters VI and VIII followed by clusters VI and VII. GLM 368 in cluster VII can be crossed with LMNDL-1 and GPUL 6 of clusters VI and VIII respectively to produce transgressive segregants which after proper evaluations may be released as varieties. Days to maturity contributed highest to total divergence indicating that there was more span in maturity among the genotypes considered in the study.

HIGHLIGHTS

- ① Significant difference was observed among 23 little millet genotypes by Analysis of variance.
- ② The genotypes were grouped into nine clusters among which seven were solitary.
- ③ GLM 368 recorded highest grain yield among all the genotypes studied in the experiment.
- ④ Highest inter cluster distance was found between clusters VI and VIII.

Keywords: Little millet, Genetic divergence, Mahanalobis D² statistics

Little millet (*Panicum sumatrense*) also known as samalu in Telugu, is grown in hilly areas by tribal farmers of high altitude and Tribal zone of Andhra Pradesh (Suryanarayana and Sekhar, 2018). It is a C4 grass crop species of *Poaceae* family which thrives well and produce more sugars in hot and dry conditions. It's high water use efficiency makes it a suitable crop to the changing climatic conditions in India. Besides its agronomic suitability, it also produces nutritionally balanced grain. It is rich in vitamin B, minerals like potassium, phosphorus, iron, zinc and magnesium. In addition, this crop requires very little amount of water to complete its life cycle (Selvi *et al.* 2015). However, there are only few released little millet varieties posing the need to develop new adaptable and climate resilient varieties in this crop.

Assessment of genetic diversity for yield and related traits in little millet crop breeding is essential requirement. Genetic diversity analysis is the study of genetic information within a species, population, or individual. It involves measuring and analyzing the genetic differences among individuals, populations, or species. In a quest, to develop such varieties, a breeder has to choose genetically divergent parents with desirable attributes for crossing and then further making selections in future generations for self-pollinated crops like little millet (Anuradha *et al.* 2017). Principal component

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analysis (PCA) and cluster analysis where grouping based on similarity, are two methods of multivariate analysis which are widely employed in identifying suitable genotypes for making hybridization. In this study, we aimed to identify diverse genotypes with desirable traits among 23 little millet lines by utilizing PCA and cluster analysis.

MATERIALS AND METHODS

The present investigation was carried out with 23 entries of little millet including checks (JK 8 and BL 6) during *kharif*, 2018 and the experiments were conducted in seven different locations in India *viz.*, Berhampur (Odisha), Perumallapalle (Andhra Pradesh), Ranchi (Jharkhand), Waghai (Gujarat), Karaikal (Puducherry), Athiyandal (Tamil Nadu) and Vizianagaram (Andhra Pradesh). The entry names were listed in Table 1. The design used for this experiment was Randomized complete block design with three replications. The data was recorded on six parameters *viz.*, plant height (PH; cm), number of productive tillers (NPT), days to 50% flowering (DFF), days to maturity (DM), grain yield (GY; q/ha), fodder yield (FY; q/ha). Data analysis was done using Indostat software for analysing analysis of variance, genetic parameters and genetic divergence using Mahalanobis generalized distance (D^2).

Table 1: List of 23 entries of little millet studied during *kharif*, 2018

Entry no.	Entry	Source State
1	WV 126	Gujarat
2	DHLT 28-4	Karnataka
3	OLM 217	Odisha
4	IIMR LM 7162	Telangana
5	TNPSu 186	Tamil Nadu
6	WV 125	Gujarat
7	WV 164	Gujarat
8	LMNDL-1	Andhra Pradesh
9	OLM 18	Odisha
10	BL 6	Chattisgarh
11	VS 13	Andhra Pradesh
12	GLM 368	Assam
13	GPUL 6	Karnataka
14	JK 8	Madhya Pradesh
15	GPUL 7	Karnataka
16	IIMRLM-8400-17	Telangana
17	IIMRLM-8437-17	Telangana
18	OLM 203	Odisha

19	TNPSu 203	Tamil Nadu
20	TNPSu 177	Tamil Nadu
21	TNPSu 202	Tamil Nadu
22	TNPSu 176	Tamil Nadu
23	Local check	Respective local

RESULTS AND DISCUSSION

Analysis of variance presented in Table 2 shows there is significant differences among the 23 genotypes studied in this experiment, which implies that there is a good scope for selection of the studied characters. The mean values of all seven locations for all the six traits were presented in Table 3. The overall mean of plant height was 128 cm and it ranged from 114 cm in GPUL 6 to 146 cm in GLM 368. Number of productive tillers ranged from 4.16 (TNPSU 202) to 6.33 (DHLT 28-4) with a mean value of 5.19. Days to 50% flowering recorded a mean value of 69.50. The genotype TNPSu 203 (59 days) has flowered early whereas GLM 368 (85 days) was late to flower. The duration ranged between 87 days (TNPSU 203) to 118 days (GLM 368) with a mean of 100 days. GLM 368 has recorded highest grain and fodder yield of 13.94 q/ha and 73.52 q/ha respectively and GPUL 6 has recorded lowest grain and fodder yield of 7.90 q/ha and 35.18 q/ha respectively.

Grouping of genotypes into clusters

In our study, twenty-three little millet genotypes were grouped into nine clusters (Table 4). Out of nine clusters, cluster I was noticed to be accommodating highest number of genotypes followed by cluster II. WV 126, DHLT 28-4, OLM 217, IIMR LM 7162, WV 125, WV 164, OLM 18, IIMRLM-8400-17, IIMRLM-8437-17, TNPSU 203, TNPSU 177, OLA 203 were the 12 genotypes clustered into cluster I. TNPSU 186, GPUL 7, BL 6, JK 8 were four genotypes grouped into cluster II. TNPSU 176, Local check, TNPSU 202, LMNDL-1, GLM 368, GPUL 6, GPUL 6 and VS 13 were genotypes which were solitarily grouped into cluster III, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII and cluster IX respectively. Fig. 1 provides the categorization of 23 little millet genotypes into nine different clusters. Similar findings were reported by Shankar and Kumari, A (2022), Venkataratnam *et al.* (2019) and Amaravel *et al.* (2023).

**Table 2:** Analysis of variance (ANOVA) for six traits studied in 23 little millet genotypes

Source of variation	Df	PH	NPT	DFF	DM	GY	FY
Genotypes	22	1895.82*	6.74*	1128.29***	1366.58***	51.07***	1544.72***
Replications	2	244.34	9.29	34.62	10.42	3.56	65.47
Environment	6	39555.34***	502.24***	11463.76***	20409.77***	674.39***	35505.38***
Interactions	12	230.83	3.36	6.01	3.52	2.94	80.09
Error	440	1121.16	4.02	340.33	414.82	22.06	493.62
Total	20	12029.53***	153.62***	3446.19***	6126.08***	204.48***	10706.21***

Table 3: Mean values and summary statistics of 23 little millet genotypes

Sl. No.	Genotype	PH (cm)	NPT	DFF (days)	DM (days)	GY (q/ha)	FY (q/ha)
1	WV 126	137.72	5.35	72.29	105.24	12.28	67.52
2	DHLT 28-4	139.35	6.33	70.38	104.24	10.38	60.52
3	OLM 217	130.35	5.58	62.95	96.38	10.93	54.64
4	IIMR LM 7162	135.76	5.94	60.57	94.19	11.07	64.09
5	TNPSU 186	134.12	5.85	74.48	108.86	13.02	61.79
6	WV 125	130.31	5.31	61.76	95.38	10.25	62.42
7	WV 164	135.98	5.15	74.86	103.95	10.34	61.15
8	LMNDL-1	135.60	5.42	77.05	100.29	10.28	65.88
9	OLM 18	137.14	4.99	73.71	104.24	11.98	64.49
10	BL 6 (C)	135.68	5.95	83.24	116.76	12.84	63.63
11	VS 13	115.89	5.55	78.26	106.29	10.15	45.36
12	GLM 368	146.70	4.51	85.24	118.57	13.94	73.52
13	GPUL 6	114.19	4.72	74.90	108.00	7.90	35.18
14	JK 8 (C)	124.56	4.60	68.52	99.52	12.95	59.90
15	GPUL 7	116.34	5.26	69.43	103.05	10.01	46.71
16	IIMRLM-8400-17	124.90	5.06	61.48	93.43	9.12	55.92
17	IIMRLM-8437-17	131.94	5.57	63.81	97.71	10.76	53.69
18	OLM 203 (C)	133.57	5.00	64.48	95.24	10.30	53.84
19	TNPSU 203	118.62	5.09	59.52	87.76	9.70	59.89
20	TNPSU 177	115.08	4.51	63.05	91.24	9.07	52.07
21	TNPSU 202	116.67	4.16	62.29	88.24	11.99	51.22
22	TNPSU 176	118.91	4.23	67.57	95.95	9.44	46.79
23	Local check	122.05	5.46	68.76	95.62	8.49	56.05
Mean		128.32	5.19	69.50	100.44	10.75	57.23
Minimum		114.19	4.16	59.53	87.77	7.90	35.18
Maximum		146.70	6.33	85.24	118.57	13.94	73.52
Co-efficient of variance (%)		26.09	38.55	26.54	20.28	43.70	38.83
Standard error		7.31	0.44	4.03	4.44	1.03	4.85

Inter and intra cluster distances of nine clusters

Table 5 provides inter and intra cluster distances between and within the nine clusters and Fig. 2 illustrates cluster diagram of the present study. The highest inter-cluster distance (0.32) was found to be between cluster VIII and cluster VI, followed by cluster VII and cluster VI (0.23), cluster II and cluster

VI (0.23) and cluster VIII and cluster V (0.21). These results indicate LMNDL-1 (in cluster VI) and GPUL 6 (in cluster VIII) and LMNDL-1 (in cluster VI) and GLM 368 (in cluster VII) were genetically divergent from one another and performing crossings between them can yield transgressive segregants. The intra cluster distance was recorded 0.04 for cluster I and cluster II, while the remaining clusters were solitary

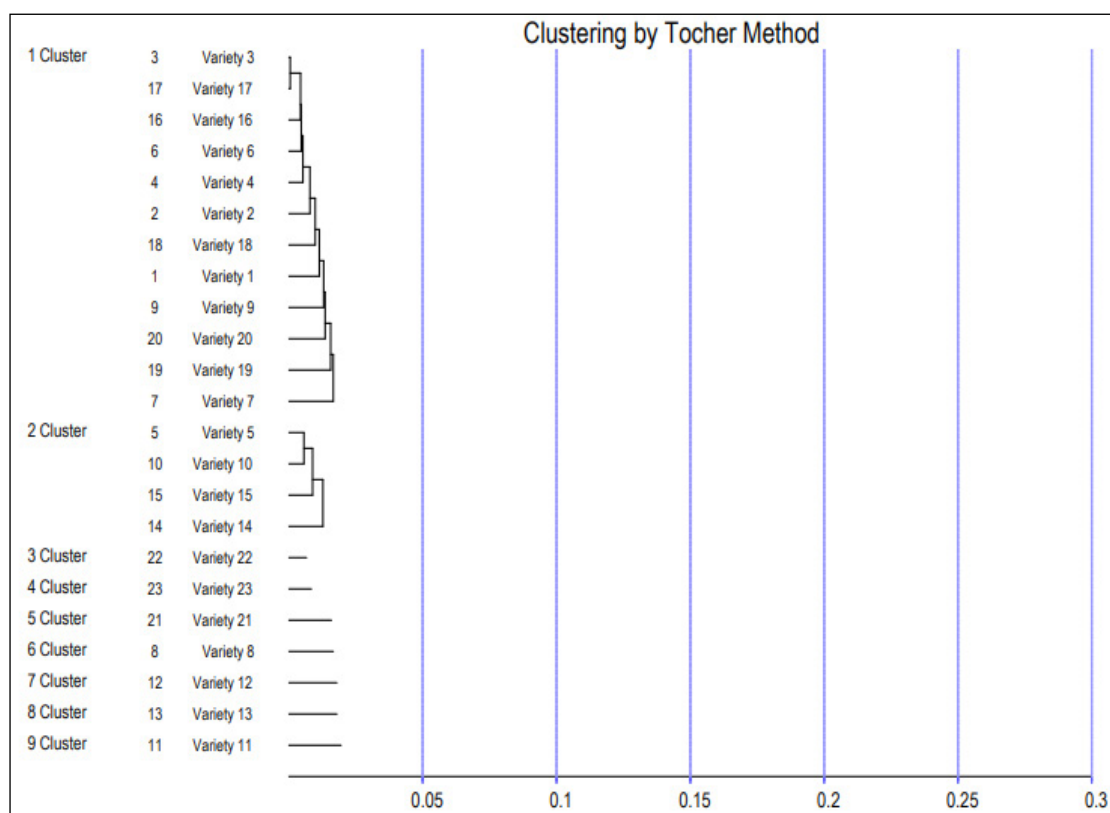


Fig. 1: Clustering of genotypes by Tocher's method

Table 4: Clustering pattern of 23 little millet genotypes based on six traits by Tochers' method

Clusters	No. of genotypes	Genotypes
Cluster I	12	WV 126, DHLT 28-4, OLM 217, IIMR LM 7162, WV 125, WV 164, OLM 18, IIMRLM-8400-17, IIMRLM-8437-17, TNPSU 203, TNPSU 177, OLA 203
Cluster II	4	TNPSU 186, GPUL 7, BL 6, JK 8
Cluster III	1	TNPSU 176
Cluster IV	1	Local check
Cluster V	1	TNPSU 202
Cluster VI	1	LMNDL-1
Cluster VII	1	GLM 368
Cluster VIII	1	GPUL 6
Cluster IX	1	VS 13

Table 5: Inter and intra cluster distances between nine clusters studied on six traits for 23 little millet genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	0.04	0.07	0.05	0.06	0.09	0.15	0.12	0.14	0.10
II		0.04	0.08	0.12	0.10	0.23	0.08	0.11	0.07
III			0.00	0.05	0.05	0.13	0.11	0.08	0.05
IV				0.00	0.10	0.04	0.18	0.17	0.07
V					0.00	0.15	0.16	0.21	0.10
VI						0.00	0.23	0.32	0.14
VII							0.00	0.18	0.15
VIII								0.00	0.08
IX									0.00



with single genotype and recorded 0 distance. The smallest inter cluster distance was observed between cluster VI and cluster IV. Smaller the distance between clusters, greater the similarity of genotypes of those clusters. Larger distance between the clusters implies the presence of great genetic divergence between the genotypes, hence high chances of developing high performing hybrids by crossing those genotypes.

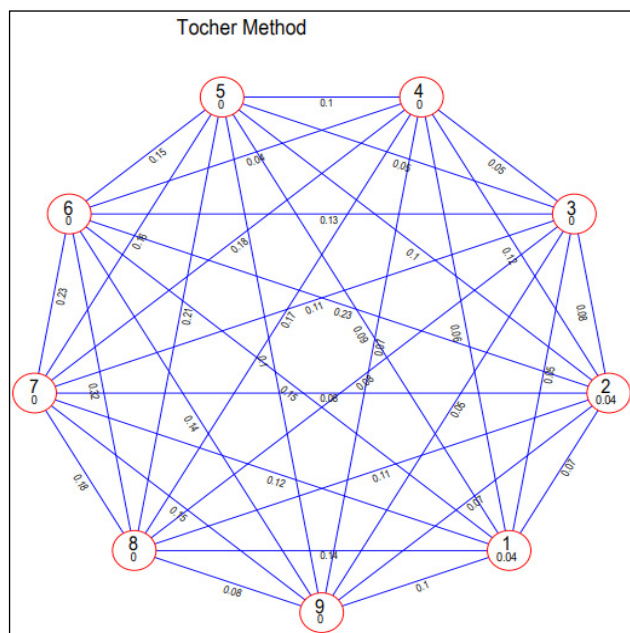


Fig. 2: Cluster diagram of 23 genotypes in nine clusters by Tocher's method

Cluster means

The highest mean for plant height was recorded by cluster VII (146.70cm) and lowest was recorded by cluster VIII (114.19cm). Nine cluster means of six traits were shown in Table 6. For number of productive tillers, the highest mean was observed in cluster IX (5.55), whereas lowest was observed in cluster V (4.16). Cluster V has recorded lowest mean value of 62.29 days to 50% flowering, whereas cluster VII has recorded late flowering with 85.24 days. Same is the case with days to maturity, where cluster VII has lowest mean value of 88.24 days and cluster VII scored highest mean value of 118.57 days. Grain yield and fodder yield were recorded highest in cluster VII with mean values of 13.94 q/ha and 79.52 q/ha respectively. Cluster VIII has recorded lowest mean values of 7.90 q/ha for grain yield and 35.18 q/ha for fodder yield. Hence cluster VII and cluster VIII have recorded highest and lowest

mean values for three traits *viz.*, plant height, grain yield and fodder yield. GLM 368 in cluster VII has recorded highest values of plant height, days to 50% flowering, days to maturity, grain yield and fodder yield.

Table 6: Cluster means of six traits studied on 23 little millet genotypes

Clusters	PH (cm)	NPT	DFE (days)	DM (days)	GY (q/ha)	FY (q/ha)
I	130.89	5.32	65.74	97.42	10.52	59.19
II	127.68	5.41	73.92	107.05	12.21	58.01
III	118.91	4.23	67.57	95.95	9.44	46.79
IV	122.05	5.46	68.76	95.62	8.49	56.05
V	116.67	4.16	62.29	88.24	11.99	51.22
VI	135.60	5.42	77.05	100.29	10.28	65.88
VII	146.70	4.51	85.24	118.57	13.94	73.52
VIII	114.19	4.72	74.90	108.00	7.90	35.18
IX	115.89	5.55	78.26	106.29	10.15	45.36

Percent contribution

In our present study, days to maturity (32.02%) held highest percentage contribution towards total divergence, followed by days to 50% flowering (25.30%), grain yield (15.81%), fodder yield (13.04%), number of productive tillers (7.11%) and plant height (6.72%). Table 7 shows the percent contributions of various characters towards total divergence and times they were ranked first.

Table 7: Per cent contribution of six traits in 23 little millet genotypes

Sl. No.	Character	Contribution %	Times ranked 1 st
1	Plant height	6.72	17
2	Number of productive tillers	7.11	18
3	Days to 50% flowering	25.30	64
4	Days to maturity	32.02	81
5	Grain yield	15.81	40
6	Fodder yield	13.04	33

CONCLUSION

It can be concluded that 23 little millet genotypes had significant differences between them for the studied characters based on the results of ANOVA and indicating presence of large amount of variability among genotypes. Maximum number of genotypes were grouped into cluster I which included 12

genotypes. In the present study the highest inter cluster distance was found between clusters VI and VIII and clusters VI and VII. Genotypes belonging to these clusters may be used as parents to produce transgressive segregants

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REFERENCES

- Anuradha, N., Patro, T.S.S.K., Divya, M., Rani, Y.S and Triveni. U. 2017. Application of principal component analysis in judging little millet genetic diversity. *Frontiers in Crop Improvement*, 5(1): 50-53.
- Shankar, C. and Kumari, A. 2022. Morpho-Molecular Genetic Diversity Analysis of Little Millet (*Panicum sumatrense*) using Yield Attributing Traits and ISSR Markers to Evaluate its Performance as a Summer Crop. *Environment and Ecology*, 41(3B): 1788- 1798.
- Selvi, M.V., Nirmalakumari, A. and Senthil, N. 2015. Genetic diversity for zinc, calcium and iron content of selected little Millet Genotypes. *Journal of Nutrition and Food Sciences*, 5(6): 1.
- Suryanarayana, L. and Sekhar, D. 2018. Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) genotypes. *The Pharma Innovation Journal*, 7(7): 908-910.
- Venkataratnam, T., Latha, L.M., Sekhar, M.R. and Nirmal, A.R.K. 2019. Genetic divergence studies in Little Millet (*Panicum sumatrense*). *Agricultural Science Digest.*, 39(3): 210-214.
- Amaravel, M., Nirmalakumari, A., Geetha, S., Sathya, K. and Renuka, R. 2023. Understanding the Genetic Basis of Yield-related Traits in Little Millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) Germplasm through Association and Diversity Analysis. *Agricultural Science Digest.*, 43(6): 733-740.