RESEARCH ARTICLE

# Genetic Divergence Studies in Little Millet *(Panicum sumatrense)*

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10.18805/ag.D-4903


## Abstract

Genetic diversity was estimated in 50 little millet genotypes by Mahalanobis $D^2$ analysis for nine quantitative and eight physiological traits. In the present investigation based on $D^2$ analysis fifty genotypes were grouped into 7 clusters. Among the different clusters cluster I had maximum number 35 genotypes followed by cluster II contains 10 and clusters III, IV, V, VI, VII were solitary. Inter cluster distances were higher than intra cluster distances indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster IV and VII (131.19) followed by cluster II and IV (112.18) and cluster III and VII (104.28) indicated the existence of highly divergent genotypes. The genotypes from these clusters could be used as parents in hybridization programme to develop good recombinants. Days to 50% flowering, plant height, leaf area index at panicle initiation stage and 1000 seed weight contributed maximum towards genetic diversity. These traits could be given importance for selecting parents in crop improvement programme.


**Keywords:** Genetic divergence, Little millet, Physiological traits, Quantitative.

*Agricultural Science Digest* (2019)

## Introduction

Little millet (*Penicum sumatrence*) belongs to family *Poaceae* (*Gramineae*), having diploid chromosome number 2n =4x= 36 popularly known as Sama, samo, vari or kutki. It is an important reliable climate resistance small seeded crop grown in tribal areas and dry lands with poor resources. The advantage of millets lies in the fact that they can be grown in infertile soil, intense heat, and scanty rainfall (Gupta *et al.* 2014). Little millet Agricultural Research Station, Perumallapalle, Tirupati -517505, Andhra Pradesh, India is cultivated in Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Orissa, Bihar, Madhya Pradesh, Uttar Pradesh, Jharkhand, Chhattisgarh and Gujarat. Little millet is cultivated in an area of 2.34 lakh hectares with annual production of 1.27 lakh t and productivity of 544 kg $ha^{-1}$ in our country (Annual report, AICPMIP, 2017-2018). In Andhra Pradesh little millet is grown in an area of 7000 ha with production of 3000 t and productivity of 354 kg $ha^{-1}$ during the year 2017 -2018(AP statistics at a glance 2017-18).

In the last 50 years decline in little millet area and irregular cultivation resulted in lesser diversity. In little millet yields are very less; therefore it is essential to increase the yields by developing high yielding varieties. Genetic diversity is a powerful tool to identify the genetically appropriate divergent genotypes for hybridization to develop high yielding varieties (Bhatt, 1970). With the development of biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalonobis's $D^2$ statistics, it has become possible to estimate genetic diversity among the germplasm. For the development of promising genotypes with desirable traits, it is necessary to have divergent parents in the crossing programme. Joshi and Dhawan (1966) reported that genetic diversity was very much important factor for any hybridization programme aiming at genetic improvement of yield especially in self pollinated crops. They also inferred that Mahalonobis's $D^2$ statistics was a powerful tool choosing parents for hybridization aiming high yielding varieties. Very few studies are available on diversity analysis in little millet, therefore the present study was carried out to analyze the genetic divergence of 50 little millet genotypes for identification of divergent lines which could be used as parents in crop improvement programme.

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**How to cite this article:** 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

**Source of support:** Nil

**Conflict of interest:** None

**Submitted:** 07-03-2019 **Accepted:** 05-07-2019 **Published:** 03-10-2019

## Materials and Methods

The experiment was carried out with 50 little millet genotypes including improved lines developed from different research centres and released varieties at Agricultural Research Station, Perumallapalle, during *Kharif* 2018. The details of 50 little millet genotypes along with pedigree were presented in Table 1. The experiment was laid out in a randomized block design with three replications. Each genotype was sown in three rows of 3 m length with a spacing of 20 x 7.5 cm (plot size 1.8 sq.m). The crop was provided with fertilizer doses

**Table 1:** List of pedigree details of 50 little millet genotypes

| *S. No* | *Genotype* | *Pedigree* | *Center* |
|---|---|---|---|
| 1 | BL-2 | CO-2 × OLM-56 | Jagdalpur |
| 2 | BL-4 | CO-2 × TNAU-97 | Jagdalpur |
| 3 | BL-8 | CO-2 × OLM-56 | Jagdalpur |
| 4 | BL-41-3 | Paiyur-2 × TNAU-97 | Jagdalpur |
| 5 | BL-150 | Paiyur-2 × DLM-369 | Jagdalpur |
| 6 | CO-2 | Pure line selction | Coimbatore |
| 7 | DhLtMV-10-2 | CO-4 × Paiyur-2 | Hanumanamatti |
| 8 | DhLtMV-14-1 | CO-2 × TNAU-110 | Hanumanamatti |
| 9 | DhLtMV-21-1 | CO-2 × TNAU-26 | Hanumanamatti |
| 10 | DhLtMV-28-4 | CO-2 × TNAU-26 | Hanumanamatti |
| 11 | DhLtMV-36-3 | CO-4 × Paiyur-2 | Hanumanamatti |
| 12 | DhLtMV-39-1 | CO-4 × Paiyur-2 | Hanumanamatti |
| 13 | DLM-8 | Pure line selection from local germplasm | Dindori |
| 14 | DLM-14 | Pure line selection from local germplasm | Dindori |
| 15 | DLM-89 | Pure line selection from local germplasm | Dindori |
| 16 | DLM-95 | Selection from local germplasm | Rewa |
| 17 | DLM-103 | Pure line selection from local germplasm | Dindori |
| 18 | RLM-186 | Selection from local germplasm of Rewa | Rewa |
| 19 | DhLt-28-4 | CO-2 × TNAU-26 | Hanumanamatti |
| 20 | GPUL-1 | JK-8 × Peddasame | Banglore |
| 21 | GPUL-2 | Pure line selection from peddasame | Banglore |
| 22 | GPUL-3 | JK-8 × Peddasame | Banglore |
| 23 | GPUL-4 | JK-8 × Peddasame | Banglore |
| 24 | GPUL-5 | JK-8 × Peddasame | Banglore |
| 25 | GV-2-1 | Mutant of Gujarat Vari-1 | Waghai |
| 26 | IIMRLM-7012 | Selection from IPMR-699 | IIMR, Hydrabad |
| 27 | IIMRLM-7162 | Selection from GPMR-1153 | IIMR, Hydrabad |
| 28 | KADIRI-1 | Selection from Kadiri local | Bangalore |
| 29 | KOPLM-53 | IPS from local germplasm | Kolhapur |
| 30 | NALLASAMA | Selection from local | ARS, Perumallapalle |
| 31 | OLM-217 | Selection from Udayagiri local | Berhampur |
| 32 | OLM-233 | Selection from L55 | Berhampur |
| 33 | RLM-37 | Selection from local germplasm No 37 | Rewa |
| 34 | RLM-238 | Selection from local germplasm of Rewa | Rewa |
| 35 | RLM-367 | Selection from local germplasm No. 367 | Rewa |
| 36 | TNAU-152 | Paiyur-1 × PM-29 | Coimbatore |
| 37 | TNAU-159 | TNAU-81 × TNAU-25 | Coimbatore |
| 38 | TNAU -160 | TNAU-91 × MS-4729 | Coimbatore |
| 39 | TNPsu-167 | CO-2 × TNAU-26 | Coimbatore |
| 40 | TNPsu-170 | CO-4 × IPM-113 | Coimbatore |
| 41 | TNPsu-171 | CO-2 × TNAU-28 | Coimbatore |
| 42 | TNPsu-174 | CO-2 × IPM-113 | Coimbatore |
| 43 | TNPsu-183 | CO-2 × MS-4729 | Athiyandal |
| 44 | TNPsu-186 | MS-507 × MS-1211 | Athiyandal` |
| 45 | WV-125 | Local collection from Waghai | Waghai |
| 46 | WV-126 | Local collection from Dangas | Waghai |
| 47 | WV-167 | Local selection from Subir | Waghai |
| 48 | BL-6 | Paiyur-1 × OLM-29 | Jagdalpur |
| 49 | JK-8 | Selection from local germplasm | Rewa |
| 50 | OLM-203 | Pure line selection from Lakshmipur local | Berhampur |

20:20:20 N: P: K Kg ha$^{-1}$. Recommended package of practices were followed during the crop period. Observations were recorded from five randomly selected plants from each entry in three replications for 9 quantitative traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), main panicle weight (g), 1000 seed weight (g), grain yield plot$^{-1}$ (kg), fodder yield plot$^{-1}$ (kg) and 8 physiological traits *viz.,* leaf area index at both panicle initiation and 15 days after panicle initiation, society for cardiovascular magnetic resonance (SCMR) at panicle initiation and 15 days after panicle initiation, specific leaf weight at panicle initiation and 15 days after panicle initiation, harvest index (%) and relative injury (%) at 15 days after panicle initiation. Genetic divergence studies were done by following Mahalanobis $D^2$ statistics and genotypes were grouped into different clusters according to Tocher's method as given by Rao, (1952).

## Results and discussion

Analysis of variance in the study revealed the significant difference for all the traits studied indicated the presence of sufficient variability among 50 genotypes. Based on the $D^2$ values 50 genotypes were grouped into 7 clusters by Tocher's method (Table 2). Among the different clusters cluster I had maximum number 35 genotypes followed by cluster II contains 10 and clusters III, IV, V, VI, VII were solitary. Solitary clusters revealed that presence of wide genetic divergence for various characters among these genotypes. Clustering pattern of genotypes revealed that little millet accessions from different origin were accommodated in same cluster indicating their close affinity. On the other hand the accessions collected from the same origin were distributed in different clusters indicating that geographical diversity may not be necessarily related with genetic diversity. Therefore, the selection of genotypes for hybridization to generate new gene combination should be based on genetic diversity rather than geographical diversity.

Cluster means for nine quantitative traits and eight physiological traits were presented in Table 3 and Table 4. Considerable differences were observed among the cluster means for most of the traits studied. Early flowering genotype was observed in cluster IV (49 days), while delayed flowering genotype was in cluster II (75 days). Among seven clusters, cluster IV showed higher mean values for days to 50% flowering, day to maturity, panicle length, thousand seed weight and grain yield plot$^{-1}$. Cluster VI also recorded higher mean values for number of productive tillers plant$^{-1}$, fodder yield and grain yield (Table 3). Among seven clusters, cluster IV was recorded higher mean value for physiological traits *viz.,* SCMR at both panicle initiation and 15 days after panicle initiation, SLW at panicle initiation and also recorded the low relative injury. Therefore hybridization between the promising genotypes having desirable traits in divergent clusters could be attempted to develop high yielding varieties.

Intra and inter cluster distance ($D^2$) among seven clusters of little millet is presented in Fig 1. Among the clusters, maximum intra cluster distance was observed in the cluster

**Table 2:** Cluster composition of 50 little millet genotypes (Tochers method)

| *Cluster no* | *No of genotypes* | *genotypes* |
|---|---|---|
| I | 35 | DhLtMV-36-3, DhLt-28-4, DLM-8, TNAU-160, TNAU-152, DhLtMV-39-1, BL-2, GPUL-4, BL-6, JK-8, RLM-238, RLM-37, DLM-14, DLM-89, BL-41-3, OLM-233, RLM-367, NALLASAMA, RLM-186, TNPsu-171, GPUL-5, DLM-103, TNPsu-174, DhLtMV-10-2, TNPsu-170, KADIRI-I, BL-150, TNPsu-167, DhLtMV-28-4, DhLtMV-14-1, IIMRLM-7162, CO-2, WV-167, DLM-95 and BL-4. |
| II | 10 | GPUL-2, OLM-203, GV-2-1, KOPLM-53, GPUL-1, GPUL-3, WV-126, OLM-217, DhLtMV-21-1and WV- 125 |
| III | 1 | TNAU-159 |
| IV | 1 | BL-8 |
| V | 1 | TNPsu-186 |
| VI | 1 | TNPsu-183 |
| VII | 1 | IIMRLM- 7012 |

**Table 3:** Cluster means for yield and yield attributing traits in little millet

| *Cluster* | *DFF* | *DM* | *PH* | *NPT* | *PL* | *MPW* | *TSW* | *FYPP* | *GYPP* |
|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 53.61 | 83.74 | 120.30 | 7.70 | 27.10 | 1.80 | 2.30 | 1.09 | 0.20 |
| Cluster II | 75.43 | 105.10 | 111.67 | 5.58 | 25.03 | 1.92 | 1.95 | 1.37 | 0.17 |
| Cluster III | 53.67 | 83.67 | 138.33 | 6.60 | 32.23 | 1.51 | 2.14 | 0.86 | 0.18 |
| Cluster IV | 49.33 | 79.33 | 124.00 | 8.00 | 32.28 | 1.68 | 2.58 | 0.83 | 0.22 |
| Cluster V | 52.33 | 82.33 | 127.00 | 6.07 | 25.50 | 2.07 | 2.50 | 1.07 | 0.19 |
| Cluster VI | 63.33 | 93.33 | 123.33 | 9.40 | 32.47 | 1.71 | 2.56 | 1.43 | 0.31 |
| Cluster VII | 61.00 | 94.67 | 114.33 | 5.67 | 21.47 | 4.57 | 1.94 | 1.32 | 0.22 |

DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPT: Number of productive tillers plant$^{-1}$; PL: Panicle length (cm); MPW: Main panicle weight (g); TSW: Thousand seed weight (g); FYPP: Fodder yield plot$^{-1}$ (kg); GYPP: Grain yield plot$^{-1}$ (kg).

**Table 4:** Cluster means for physiological characters in little millet

| Cluster | LAI (PI) | LAI (15 DA PI) | SCMR (PI) | SCMR (15 DA PI) | SLW (PI) | SLW (15DA PI) | RI | H.I |
|---|---|---|---|---|---|---|---|---|
| Cluster I | 1.17 | 1.57 | 37.04 | 29.55 | 0.03 | 0.03 | 32.49 | 19.65 |
| Cluster II | 1.61 | 2.10 | 38.42 | 28.50 | 0.04 | 0.03 | 30.07 | 12.96 |
| Cluster III | 1.74 | 2.45 | 34.89 | 33.26 | 0.03 | 0.04 | 28.68 | 20.52 |
| Cluster IV | 0.50 | 0.86 | 45.47 | 36.96 | 0.04 | 0.04 | 26.18 | 26.14 |
| Cluster V | 2.34 | 2.67 | 34.79 | 28.95 | 0.04 | 0.06 | 39.58 | 17.63 |
| Cluster VI | 2.07 | 2.26 | 33.54 | 29.22 | 0.02 | 0.03 | 44.54 | 26.48 |
| Cluster VII | 1.93 | 2.15 | 41.70 | 29.86 | 0.04 | 0.03 | 40.22 | 20.80 |

LAI (PI): Leaf area index at panicle initiation stage; LAI (15 DAPI): Leaf area index at 15 days after panicle initiation stage;
SCMR (PI): SPAD chlorophyll meter reading at panicle initiation stage;
SCMR (15 DA PI): SPAD chlorophyll meter reading at 15 days after panicle initiation stage;
SLW (g $cm^{-2}$) (PI): Specific leaf weight panicle initiation stage;
SLW (g $cm^{-2}$) (15 DAPI): Specific leaf weight at 15 days after panicle initiation stage;
RI: Relative injury (%) at 15 days after panicle initiation stage; HI: Harvest index (%)

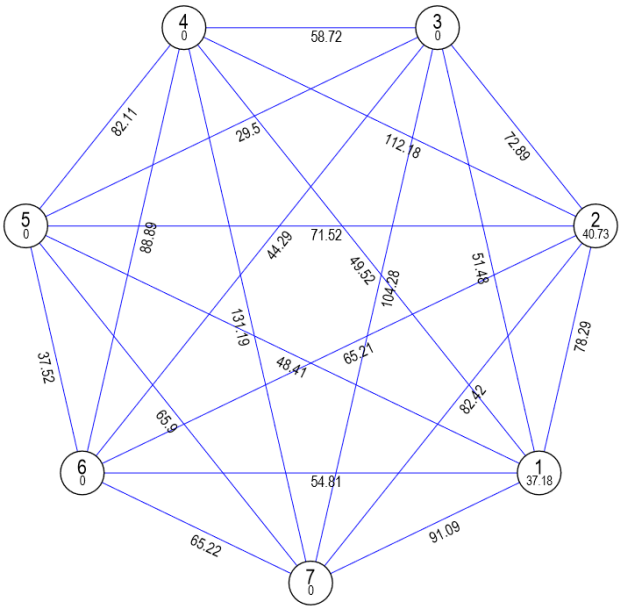



**Fig. 1:** Intra cluster (D) and inter cluster distance ($D^2$) among seven clusters of little millet

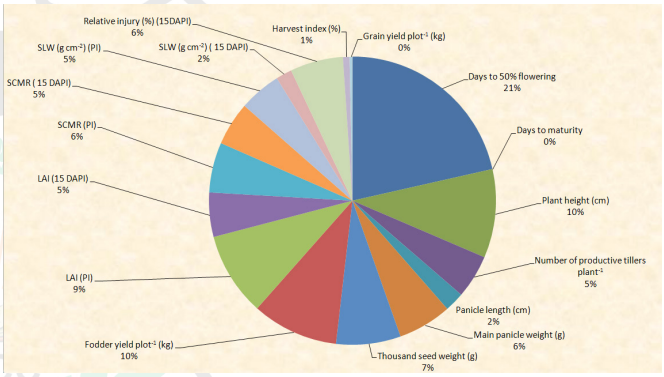



**Fig. 2:** Percentage contribution of yield and yield attributes to the genetic diversity in little millet

II (40.73) and cluster I (30.47) indicating that genotypes within the cluster were similar. Remaining clusters III, IV, V, VI, VII recorded was zero intra cluster distance because these clusters possessed only one genotype which revealed that the presence of wide genetic diversity for various traits between the genotypes. Arunachalam *et al.* (2005) and selvi *et al.* (2015) were observed solitary clusters in their studies in little millet. Maximum inter cluster $D^2$ value was observed between cluster IV and VII (131.19) followed by between cluster II and IV (112.18) and cluster III and VII (104.29) suggested that genotypes present in these clusters are genetically divergent and could be used as a parents in hybridization progrme for high heterotic response in little millet. Similar results were reported earlier by Arunachalam *et al.* (2005), Selvi *et al.* (2015), Nagar *(*2015) and Patel *et al.* (2018) in little millet.

Contribution of different traits towards genetic divergence is presented in Fig.2. Among the 17 traits studied days to fifty percent flowering contributed maximum to the divergence (21.47%) followed by plant height (9.96%), fodder yield $plot^{-1}$ (9.71) and leaf area index panicle (LAI) initiation (9.39) which implying that these traits could be helpful in crop improvement programme in little millet. Similar results of maximum contribution of divergence for days to 50% flowering was reported earlier by Arunachalam *et al.* (2005) in little millet, Selvi *et al.* (2015) in little millet for plant height and thousand seed weight; Nagar *(*2015) in little millet for days to 50% flowering; Thippeswamy *et al.* (2018) in foxtail millet for days to 50% flowering, thousand seed weight, fodder yield and Bheemesh *et al.* (2018) in foxtail millet for fodder yield. However, grain yield per plot contributed very less to the genetic divergence indicating narrow range of diversity among the genotypes under study.

Based on mean performance of genotypes, genetic divergence and cluster means clusters III, IV, V, VI and VII were identified as best clusters and genotypes in these clusters viz., TNPsu-183, BL–8, IIMRLM- 7012 and TNPsu -186 were

**Table 5:** List of selected desirable clusters and promising genotypes based on divergence and *per se* performance for agronomic traits

| *Clusters* | *Characters* | *Genotypes* |
|---|---|---|
| Cluster III | Plant height | TNAU-159 |
| Cluster IV | Days to 50% flowering, days to maturity, thousand seed weight, SCMR at both panicle and 15 day after panicle initiation, SLW at panicle initiation stage and RI at 15 days after panicle initiation | BL-8 |
| Cluster V | LAI at both panicle and 15 days after panicle initiation stage and SLW at 15 days after panicle initiation | TNPsu-186 |
| Cluster VI | Number of productive tillers plant$^{-1}$, panicle length, fodder yield and grain yield and harvest index, panicle length and harvest index | TNPsu-183 |
| Cluster VII | Main panicle weight and SLW at panicle initiation | IIMRLM-7012 |

identified as promising genotypes for yield and physiological traits (Table 5).

## Conclusion

From the study it was concluded that hybridization among the promising genotypes are expected to give more desirable recombinants in segregating generations. The crosses *viz.*, BL-8 (cluster-IV) × IIMRLM-7012 (cluster-VII) for short duration, grain yield and drought tolerance, BL-8 (cluster IV) × TNPsu-183 (cluster-VI) for short duration, high yielding and drought tolerance, TNAU-159 (cluster-III) × IIMRLM-7012 (cluster-VII) for more plant height and main panicle weight and TNPsu-186 (cluster-V) × TNPsu-183 (cluster-VI) for high yielding and drought tolerance were proposed for in future breeding programme for little millet crop improvement.

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