Received: 26 Dec 2020 | Revised: 26 Feb 2021 | Accepted: 05 Mar 2021

Electronic Journal of Plant Breeding

Research Article

# Genetic diversity in foxtail millet genotypes

**Tirumala Jawahar Sri Gopi*, I. Shankergoud, L. N. Yoogesh, Ayyangowda Patil, B. V. Tembhurne, Basave Gowda and Mallikarjuna Kengnal**

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur-584104, India.
***E-Mail**: jaweesree@gmail.com

**Abstract**
A total of 80 foxtail millet genotypes were evaluated for ten quantitative characters at MARS (Main Agricultural Research Station), UAS (University of Agricultural Sciences), Raichur during *kharif* 2018 to assess the genetic diversity using Mahalanobis $D^2$ statistic. The eighty genotypes were grouped into twelve clusters. The highest inter-cluster distance (6623.62) was observed between cluster-VIII and cluster-XII. The highest intra-cluster distance was observed in cluster VII (529.01). A high mean grain yield was observed in cluster-XI (59.72g). Plant height (46.96%) and grain yield (46.39%) have the highest contribution to the total divergence. The crosses between genotypes of the divergent clusters VIII and XII would manifest wide variability.

**Key Words**
Foxtail millet, Mahalanobis D-Square, Clusters, Plant height, Grain yield and variability

## INTRODUCTION

Germplasm forms the raw material for any crop improvement programme. Around the world, more than 46,000 foxtail millet accessions were preserved and China holds the highest collection of foxtail millet germplasm. The successful utilization of these germplasm requires the characterization, evaluation, and identification of sources of useful traits and genes (Upadhyaya *et al.,* 2015). Characterization and evaluation of genotypes enable the effective utilization of genotypes for crop improvement. This relies on a thorough understanding of genetic diversity. The significance of the evaluation of genetic diversity was appreciated by breeders for a long time. Multivariate statistic methods like Mahalanobis $D^2$ were used to estimate the genetic diversity between genotypes. $D^2$statistic is a form of generalized distance which was first used by Mahalanobis, 1936. Rao (1952) proposed the use of this technique to assess genetic diversity in crop improvement programs. The genetic diversity has been analysed using various types of data like pedigrees, morphological, biochemical data attained from analysis of isoenzymes, seed proteins and molecular marker data.

## MATERIAL AND METHODS

The genetic material used for the current study consists, 75 foxtail millet genotypes and five check varieties viz. HMT 100-1, DHFT-109-3, HN-46, SiA 2644, SiA 3156. Among these 75 genotypes, 50 genotypes were obtained from AICRP on Small Millets, GKVK, Bengaluru and 25 genotypes from ARS, Hagari. An experiment was carried out during *kharif*-2018 at the Main Agricultural Research Station (MARS) of the University of Agricultural Sciences, Raichur. An experiment was laid in an augmented design without replication with five blocks and five check varieties. Five check varieties were randomized in each block. The plot size was a single row of 3 m length and the spacing maintained was 30 × 10 cm. The observations were recorded on traits *viz.,* Days to flowering, plant height (cm), the number of productive tillers per plant, panicle length (cm), panicle breadth (cm), panicle weight per plant (g), days to maturity, grain yield per plant (g) and test weight (g). The observations were recorded on ten randomly selected plants from the middle of the row avoiding the plants from the border and are tagged. Total variance among the genotypes and check entries were

separated into sources like 'genotypes + check entries', 'genotypes', 'check entries' and 'genotypes vs check entries' using Augmented design (Federer, 1956). The mean values of 10 plants in each genotype and check entries were used for genetic diversity estimation using Mahalanobis $D^2$ statistic. Mahalanobis (1936) D- Square distance was used to assess the genetic diversity between the genotypes.

## RESULTS AND DISCUSSION

The data was collected on ten traits and was subjected to analysis of variance using the augmented RCBD package in R software. The mean sums of squares of all the ten traits were presented in **Table. 1**. Analysis of variance indicated high significant differences between genotypes for most of the traits *viz.,* days to fifty per cent flowering, plant height, panicle length, panicle weight, days to maturity, the number of productive tillers and grain yield per plant except panicle breadth, test weight and harvest index which recorded non-significant difference between entries. The information on genetic diversity between the genotypes helps in the selection of parents for the hybridization program. The distance between the genotypes was estimated by Mahalabonis $D^2$ statistic (Mahalanobis, 1936). The genotypes were then clustered into groups using Tocher's optimization method.

**Table 1. Analysis of variance for morphological traits in foxtail millet genotypes during *Kharif*-2018**

| Source of variation | df | Days to fifty per cent flowering | Plant height | Panicle length | Panicle breadth | Panicle weight | Days to maturity | Number of productive tillers/ plants | Grain yield per plant | Test weight | Harvest index |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Blocks | 4 | 1.24 | 0.75 | 0.97 | 0.16 | 0.24 | 1.24 | 1.26 | 30.45 | 0.40 | 45.76 |
| Entries(Genotypes + Checks) | 79 | 7.97** | 241.77** | 8.37** | 0.34 | 2.09** | 13.1** | 2.69** | 146.26** | 1.11 | 27.14 |
| Genotypes | 74 | 7.04** | 245.51** | 8.56** | 0.19 | 1.92** | 12.46** | 2.49** | 121.31** | 0.54 | 25.07 |
| Checks | 4 | 25.74** | 232.45** | 5.83* | 0.34 | 1.70** | 25.74** | 5.96** | 246.04** | 1.16 | 67.19 |
| Genotypes vs Checks | 1 | 5.60** | 2.67 | 4.18 | 0.78 | 16.81** | 9.72** | 4.08** | 1593.68** | 0.04 | 19.76 |
| Residual | 16 | 0.64 | 1.19 | 1.46 | 0.44 | 0.67 | 0.64 | 0.53 | 14.54 | 0.71 | 23.14 |

* - Significance at 5 per cent level of probability ** - Significance at 1 per cent level of probability

The eighty genotypes were clustered into twelve clusters (**Table 2**). The cluster analysis indicated that cluster I have the highest number (56) of genotypes, followed by cluster VIII (6 genotypes) and cluster VII (5 genotypes) and cluster III (5 genotypes). The clusters II, IV, V, VI, IX, X, XI, and XII were solitary with only a single genotype. The results revealed that genetic diversity has no relationship with the geographical distribution and the selection of parents for hybridization must be done based on genetic diversity and not on geographic diversity (Arunachalam and Jawahar Ram, 1967).

**Table 2. Clustering of foxtail millet genotypes based on Mahalanobis $D^2$ values**

| Cluster | Number of genotypes in cluster | Genotypes |
|---|---|---|
| **I** | 56 | GS21, GS289, GS45, GS111, GS200, HN46, SiA3156, SiA2644, GS310, DHFT 35-3, GS266, TNSi345, SiA3205, GS121, GS8, SiA3219, GS301, GS53, GS140, GS105, GS5, GS158, GS26, GS56, SiA2622, GS293, SiA3163, GS282, GS6, GS47, DHFT 5-6, RFM-68, GS246, GS78, GS271, GS33, GS71, GS42, GS212, PPSS-7, HG-9, DHFT-100-1, GS285, GS335, GS243, GS280, TNSi337, GS103, Cori Navanai, GS103, GS276, GS64 |
| **II** | 1 | GS17 |
| **III** | 5 | SiA326, DHFT 2-5-3, HMT-100-1, GS337, PKS22 |
| **IV** | 1 | GS96 |
| **V** | 1 | GS62 |
| **VI** | 1 | GS60 |
| **VII** | 5 | IIMRFTM-1, SiA2644, Cori Navanai, SiA3212, HN-1 |
| **VIII** | 6 | SiA3164, SiA3159, DHFTMV 2-5, GS336, GS316, GS12 |
| **IX** | 1 | GS91 |
| **X** | 1 | GS106 |
| **XI** | 1 | GS35 |
| **XII** | 1 | GS250 |

The $D^2$ values ranged from 48.68 to 6623.62 which indicated the presence of a large amount of genetic diversity between the genotypes in the present material. The results of the inter cluster and intra cluster distances were presented in **Table 3**. The distance between genotypes within the clusters (intra cluster distance) was much lower than the distance between genotypes of a different cluster (inter cluster distance), which suggested, the heterogeneous and homogeneous nature between and within clusters, respectively. The maximum intra-cluster distance was observed in cluster-VII (529.01) followed by VII (422.54), I (255.89) and III (187.71). Since there is one genotype in each of clusters II, IV, V, VI, IX, X, XI and XII the intra cluster divergence was found to be zero. The maximum inter-cluster distance was observed between the clusters VIII and XII (6623.62) followed by VIII and XI (5399.50). The lowest inter-cluster distance was observed between clusters IV and VI (48.68) followed by II and IV (61.59). The crosses between the genotypes of diverse clusters were expected to produce wide variability in segregating generations. The crosses between genotypes of the diverse clusters VIII and XII would manifest wide variability.

**Table 3. Inter and intra cluster distances among twelve clusters in foxtail millet**

| | Cluster Distances | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Cluster 1** | **Cluster 2** | **Cluster 3** | **Cluster 4** | **Cluster 5** | **Cluster 6** | **Cluster 7** | **Cluster 8** | **Cluster 9** | **Cluster 10** | **Cluster 11** | **Cluster 12** |
| **Cluster 1** | 255.89 | 451.01 | 730.82 | 509.68 | 451.47 | 655.12 | 616.89 | 2665.68 | 948.19 | 912.65 | 1566.31 | 1203.11 |
| **Cluster 2** | | 0.00 | 1671.56 | 61.59 | 145.19 | 130.09 | 882.22 | 3962.44 | 236.96 | 122.15 | 467.56 | 468.52 |
| **Cluster 3** | | | 187.71 | 1846.29 | 1309.64 | 2075.46 | 1311.95 | 2585.03 | 2705.33 | 2571.90 | 3725.22 | 2380.27 |
| **Cluster 4** | | | | 0.00 | 365.62 | 48.68 | 718.54 | 3559.43 | 119.66 | 130.62 | 373.13 | 786.77 |
| **Cluster 5** | | | | | 0.00 | 455.32 | 1245.30 | 4521.54 | 731.28 | 417.43 | 996.24 | 229.32 |
| **Cluster 6** | | | | | | 0.00 | 905.56 | 3808.61 | 172.99 | 120.86 | 378.23 | 818.10 |
| **Cluster 7** | | | | | | | 422.54 | 1743.43 | 939.09 | 1280.31 | 1662.14 | 2341.81 |
| **Cluster 8** | | | | | | | | 529.01 | 3975.17 | 4718.54 | 5399.50 | 6623.62 |
| **Cluster 9** | | | | | | | | | 0.00 | 131.00 | 141.93 | 1113.10 |
| **Cluster 10** | | | | | | | | | | 0.00 | 181.22 | 559.56 |
| **Cluster 11** | | | | | | | | | | | 0.00 | 1072.87 |
| **Cluster 12** | | | | | | | | | | | | 0.00 |

**Table 4. Cluster means for ten morphological traits in foxtail millet**

| | **Days to fifty *per cent* flowering** | **Plant height (cm)** | **Panicle length (cm)** | **Panicle breadth (cm)** | **Panicle weight (g)** | **Days to maturity** | **Number of productive tillers** | **Grain yield *per* plant (g)** | **Test weight (g)** | **Harvest index (%)** |
|---|---|---|---|---|---|---|---|---|---|---|
| **Cluster 1** | 42.41 | 145.47 | 17.78 | 2.40 | 4.14 | 87.41 | 5.89 | 25.07 | 3.17 | 35.40 |
| **Cluster 2** | 42.00 | 156.00 | 19.20 | 2.96 | 2.98 | 87.00 | 6.00 | 38.99 | 3.10 | 31.30 |
| **Cluster 3** | 43.67 | 140.33 | 19.23 | 2.37 | 4.97 | 88.67 | 6.00 | 5.38 | 2.48 | 45.71 |
| **Cluster 4** | 43.00 | 150.40 | 21.00 | 2.67 | 4.22 | 88.00 | 4.00 | 42.47 | 4.58 | 29.05 |
| **Cluster 5** | 42.00 | 162.80 | 18.40 | 2.42 | 4.08 | 87.00 | 7.00 | 29.92 | 3.37 | 34.97 |
| **Cluster 6** | 42.00 | 151.40 | 25.20 | 2.58 | 2.67 | 87.00 | 5.00 | 43.34 | 4.99 | 27.22 |
| **Cluster 7** | 42.67 | 130.63 | 14.97 | 2.28 | 4.91 | 87.67 | 6.00 | 34.36 | 3.10 | 35.58 |
| **Cluster 8** | 36.67 | 99.07 | 13.67 | 2.79 | 4.35 | 79.50 | 4.67 | 19.47 | 2.39 | 30.93 |
| **Cluster 9** | 42.00 | 149.60 | 18.60 | 1.63 | 4.34 | 87.00 | 7.00 | 52.21 | 2.80 | 27.28 |
| **Cluster 10** | 40.00 | 158.60 | 23.20 | 1.97 | 3.72 | 85.00 | 7.00 | 47.86 | 3.61 | 28.15 |
| **Cluster 11** | 41.00 | 157.80 | 18.40 | 2.82 | 4.55 | 86.00 | 4.00 | 59.72 | 5.13 | 26.68 |
| **Cluster 12** | 42.00 | 176.60 | 22.00 | 2.57 | 5.14 | 87.00 | 5.00 | 34.44 | 3.15 | 34.43 |

The cluster means of eight quantitative traits were presented in **Table 4**. Mean values of traits varied in different clusters. Low mean days to 50 % flowering (36.37 days) and days to maturity was recorded in cluster-VIII (79.50 days). The high mean for plant height (176.60 cm) and panicle weight (5.14 g) were recorded in cluster-XII.

The highest mean values for panicle length (25.20 cm) and test weight (4.99 g) were observed in cluster-VI. The highest mean values for the number of productive tillers (7) were recorded in Cluster V, IX, X. Highest mean values for grain yield were observed in cluster XI (59.72g). A high mean value for harvest index (45.71%) was observed in cluster-III. The desirable traits were highly dispersed among clusters. It is always desirable to identify genotypes with more than one favourable trait as in the case of cluster XII which was superior for plant height, panicle weight and VI which was superior for panicle length and test weight. The crosses involving genotypes of clusters VI and XII could release transgressive segregants for grain yield. The crosses involving cluster VII and cluster IX could produce recombinants that are high yielding as well as early maturing.

**Table 5. Contribution of traits towards divergence in foxtail millet**

| Traits | Contribution ( %) | Times ranked first |
|---|---|---|
| **Days to fifty per cent flowering** | 1.36 | 43 |
| **Plant height** | 46.96 | 1484 |
| **Panicle length** | 1.93 | 61 |
| **Panicle breadth** | 0.00 | 0 |
| **Panicle weight** | 0.09 | 3 |
| **Days to maturity** | 0.19 | 6 |
| **Number of productive tillers/ plants** | 1.14 | 36 |
| **Grain yield per plant** | 46.39 | 1466 |
| **Test weight** | 0.19 | 6 |
| **Harvest index** | 1.74 | 55 |

The contribution of individual traits towards diversity was presented in **Table 5**. Of the ten morphological and agronomic traits studied plant height (46.96%) and grain yield (46.39%) contributed maximum towards total divergence. Similar results of the maximum contribution of grain yield and plant height to genetic divergence were reported by Gangurde *et al*. (2016); Geethanjali and Jegadeeswaran (2016). These traits have to be given high weightage while selecting diverse parents for hybridization.

## ACKNOWLEDGEMENT

The authors are highly thankful to AICRP on Small Millets, GKVK, Bengaluru and ARS, Hagari for providing the experimental materials for conducting the experiment.

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