Electronic Journal of Plant Breeding

Research Note

Genetic divergence in finger millet (*Eleusine coracana* L.)

Bezawada Tarun reddy* and V. Vengadessan

Department of Plant Breeding and Genetics, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, U.T. of Pondicherry - 609 603
*E-Mail: tarun.bezawada.reddy@gmail.com

Abstract
Forty-two finger millet genotypes were raised in alpha lattice design during *kharif* , 2019 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal and the data were recorded on the 12 quantitative characters such as days to 50% flowering, plant height, number of tillers per plant, number of productive tillers, number of fingers per ear, main ear head length, finger length, days to maturity, test weight, ear head weight, threshing percentage and grain yield. The analysis of variance revealed that there is significant variation among 42 finger millet genotypes for 12 quantitative characters. The mean data recorded on quantitative characters were adjusted to eliminate the block variation. Genetic divergence was calculated using D^2 analysis and hierarchal cluster analysis in UPGMA method. Both methods of clustering analysis grouped genotypes into 10 clusters indicating existence of large genetic variation among 42 finger millet genotypes. Days to 50 % flowering showed the most diverse character based on ranking method in D^2 analysis. Both the clustering methods, genotype 32 (FMV-1162) and genotype 14 (FMV-1175) were identified as the most diverse genotypes in the population.

Keywords: Finger millet, quantitative characters, genetic divergence, D^2 analysis and hierarchal cluster.

Finger millet is an important millet crop grown in India and it is also known as African millet, *Ragi*, Bird's eye millet and *Nagali*. It is grown in wide range of environmental and climatic conditions prevailing in the country and it can be grown through-out the year if adequate moisture is available (Priyadharshini *et al.,* 2011). It is mostly cultivated as rainfed crop in India for its valued food grains, dry fodder and adaptability to wide range of geographical areas. In the recent years, demand for finger millet has been increased because of its nutritional properties and tolerance to various types of stress. This brings an urgent need for genetic improvement of the crop to meet the current demand. The logical way to start a breeding program was with finding the most diverse genotypes in the population and those diverse genotypes are used to develop a finger millet cultivar to increase the chance of getting a transgressive segregant in segregating population. In recent times, due to COVID-19 pandemic, the public slowly change the food habits from major

cereals like rice to the millets for nutritional properties. For example, finger millet (*Ragi*) has three times more calcium than milk and used to correct the nutrient deficiency in the consumers.

The clustering analysis helps in finding the amount of genetic divergence present in the population, useful in selecting most diverse parents for recombination breeding and to identify the most diverse character in population. If there is higher diversity between the parents, there will be better chance for getting transgressive segregants (Kumar *et al.,* 2010).

Forty – two finger millet genotypes comprising of initial and advanced breeding lines (**Table 1**), had been raised during *kharif,* 2019 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute in alpha lattice design with six blocks and three replications. The data were recorded on days to 50% flowering, plant height, number

of tillers per plant, number of productive tillers, number of fingers per ear, main ear head length, finger length, days to maturity, test weight, ear head weight, threshing percentage and grain yield. Analysis of variance was performed as suggested by Panse and Sukhatme (1978) and data for 12 quantitative characters were adjusted to eliminate the block variation from the genotypic values (Federer and Wolfinger, 2003) and these adjusted was used for further analysis. Among the clustering methods

the D^2 and Hierarchal clustering are important. The D^2 analysis suggested by Mahalanobis (1936) was used to estimate genetic divergence and grouped the genotypes into different clusters by following the Tocher's method (Rao, 1952). The hierarchal clustering with average linkage or UPGMA (Unweighted pair-group method using arithmetic averages) uses arithmetic means for construction of dissimilarity measures and groups the genotypes into various clusters.

Table 1. Details of finger millet genotypes used in experiment

G. No	Source	Lines
G1	AVT-Finger millet	FMV-1137
G2	AVT-Finger millet	GPU 45
G3	AVT-Finger millet	FMV-1116
G4	AVT-Finger millet	FMV 1117
G5	AVT-Finger millet	PR 202
G6	AVT-Finger millet	FMV-1114
G7	AVT-Finger millet	VL-376
G8	AVT-Finger millet	FMV 1144
G9	AVT-Finger millet	FMV 1147
G10	AVT-Finger millet	FMV 1151
G11	AVT-Finger millet	FMV 1148
G12	IVT-Finger millet	FMV-1171
G13	IVT-Finger millet	FMV-1178
G14	IVT-Finger millet	FMV-1175
G15	IVT-Finger millet	FMV-1181
G16	IVT-Finger millet	GPU 67
G17	IVT-Finger millet	FMV-1173
G18	IVT-Finger millet	FMV-1168
G19	IVT-Finger millet	FMV-1163
G20	IVT-Finger millet	VL-376
G21	IVT-Finger millet	FMV-1180
G22	IVT-Finger millet	FMV-1165
G23	IVT-Finger millet	GPU 45
G24	IVT-Finger millet	FMV-1183
G25	IVT-Finger millet	FMV-1159
G26	IVT-Finger millet	FMV-1169
G27	IVT-Finger millet	FMV-1157
G28	IVT-Finger millet	PR 202
G29	IVT-Finger millet	FMV-1182
G30	IVT-Finger millet	FMV-1177
G31	IVT-Finger millet	FMV-1166
G32	IVT-Finger millet	FMV-1162
G33	IVT-Finger millet	FMV-1160
G34	IVT-Finger millet	FMV-1164
G35	IVT-Finger millet	FMV-1167
G36	IVT-Finger millet	FMV-1170
G37	IVT-Finger millet	FMV-1172
G38	IVT-Finger millet	FMV-1176
G39	IVT-Finger millet	FMV-1161
G40	IVT-Finger millet	FMV-1158
G41	IVT-Finger millet	FMV-1174
G42	IVT-Finger millet	FMV-1179

Analysis of variance revealed that there is significant variation among 42 finger millet genotypes for 12 quantitative characters indicating the existence of large genetic variation among 42 finger millet genotypes for 12 quantitative characters and analysis of variance was presented in **Table 2**. Block including of replication was found to be significant for the characters for plant height, number of tillers per plant, number of productive tillers, number of fingers per ear, main ear head length, ear head weight and grain yield which showed that these characters are more influenced by environment or block or field variation.

Genetic divergence in this study was evaluated using the clustering analyses such as D²analysis and hierarchal clustering. The distribution of genotypes into different clusters in both the analyses was presented in **Table 3**.

The D² analysis grouped the 42 genotypes into ten clusters, performed by subjecting the data recorded on 12 quantitative characters. The intra and inter cluster distances for ten clusters are presented in **Table 4**. The cluster I was the largest with 25 genotypes followed by cluster III with five genotypes, and the clusters II, VII, VIII, IX and X are mono-genotypic. Among the ten clusters the intra cluster distance was maximum of 5.71 for the cluster IV because heterogenous composition of genotypes which was also reported by Das *et al.* (2013) and Wolie and Belete (2013) and minimum of 0.00 for the clusters II, VII, VIII, IX, X. The maximum inter cluster distance of 14.75 was observed between the clusters V containing genotype 36 (FMV-1170) and genotype 38 (FMV-1176) and X containing genotype 14 (FMV-1175) indicating these are the most diverse genotypes. The least inter cluster distance of 5.83 was recorded between cluster I and II.

Table 2. Analysis of variance for 12 quantitative characters in finger millet

S. No.	Characters	Treatment adjusted	Replication	Block including replication	Error
		41	**2**	**15**	**67**
		Mean sum of squares			
1	Days to 50% flowering	165.93**	17.21	10.64	9.17
2	Plant height	142.07**	20.52	95.34**	21.80
3	Number of tillers per plant	0.50**	0.14	0.37*	0.20
4	Number of productive tillers	0.53**	0.27	0.43*	0.20
5	Number of fingers per ear	2.89**	0.23	1.50**	0.54
6	Finger length	4.37**	1.98	1.85	1.30
7	Main ear head length	3.27**	0.19	1.50**	0.41
8	Days to maturity	189.71**	2.39	12.01	10.50
9	Test weight	0.18**	0.01	0.04	0.04
10	Ear head weight	43.22**	9.65	21.72**	6.16
11	Threshing percentage	267.43**	1.04	63.22	36.20
12	Grain yield	9.28**	5.18	6.04**	2.11

** & * Significant at 1% & 5 % level

Table 3. Distribution of genotypes in both cluster analyses

Cluster Number	Genotypes as per D² analysis	Genotypes as per Hierarchal clustering
I	G10, G19, G8, G2, G9, G42, G20, G31, G5, G3, G13, G35, G24, G33, G26, G11, G22, G4, G34, G18, G1, G16, G25, G28, G29	G1, G5, G15, G22 and G24
II	G15	G2, G3, G8, G9, G10, G11, G13, G18, G19, G20, G21, G25, 26, 28, 31, 33, G34, G35 and G42
III	G7, G37, G40, G32, G23	G4 and G16
IV	G17, G6	G6, G7, G17, G23, G37 and G40
V	G36, G38	G12
VI	G27, G41, G39	G14
VII	G21	G27, G39 and G41
VIII	G12	G30
IX	G30	G32
X	G14	G36, G38

Table 4. Average intra (diagonal) and inter cluster D² values among ten clusters in finger millet

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**4.68**	5.83	6.68	7.60	6.82	8.67	7.06	9.16	10.69	12.01
II		**0.00**	8.14	8.64	8.61	7.58	6.87	10.34	8.10	10.07
III			**4.67**	5.99	6.32	11.19	10.09	6.71	11.91	13.91
IV				**5.71**	6.46	10.41	10.02	6.67	11.48	13.38
V					**4.59**	11.24	9.20	8.09	12.53	14.75
VI						**5.12**	6.94	11.79	7.72	6.13
VII							**0.00**	11.85	7.18	9.98
VIII								**0.00**	12.13	14.05
IX									**0.00**	6.99
X										**0.00**

The mean performance of 12 quantitative characters were presented in the **Table 5**. Based on the mean performance the cluster II recorded the lowest mean performance for the characters number of tillers per plant (2.90), number of productive tillers (2.90) and number of fingers per ear (5.03). The cluster III recorded the highest mean performance for threshing percentage (74.20 %) and least mean performance for days to maturity (92.13 days). The cluster IV recorded the highest mean performance for number of tillers per plant (4.22) and least mean performance for the characters main ear head length (7.27 cm) and finger length (5.37 cm). The cluster V recorded highest mean performance for test weight (3.04 g) and least mean performance for the characters ear head weight (9.41 g) and grain yield (5.67g). The cluster VI recorded highest mean performance for plant height (98.33 cm). The cluster VII recorded highest mean performance for days to 50 % flowering (88.33 days). The cluster VIII recorded least mean performance for the characters days to 50 % flowering (58 days) and plant height (76.33 cm) and highest mean performance for number of fingers per ear (9.07). The cluster IX recorded least mean performance for test weight (2.23 g). The cluster X recorded the highest mean performance for number of productive tillers (4.13), main ear head length (12.61 cm), finger length (11.13 cm), days to maturity (118.67 days), ear head weight (29.64 g) and grain yield (14.27 g) and least mean performance for threshing percentage (48.17 per cent).

The contribution of different characters to the total diversity was presented in **Table 6**. The days to 50 % flowering contributed maximum to the total genetic divergence (22.53 per cent) by appearing 194 times in first rank followed grain yield (16.38 %) by appearing 141 times in first rank and number of fingers per ear (14.40 %) by appearing 124 times in first rank. The contribution of other characters to total divergence are plant height (9.76 %), number of tillers per plant (2.67 %), number of productive tillers (2.44 %), main ear head length (9.99 %), finger length (1.16 %), days to maturity (5.11 %), test weight (6.97 %), ear head weight (5.34 %) and threshing percentage (3.25 %).

Table 5. Mean values of ten clusters estimated by D² statistics in finger millet

Cluster Number	DF	PH	NT	PT	NF	EL	FL	DM	TW	EW	TH	GY
I	71.96	95.11	4.06	3.93	5.71	8.26	6.37	106.16	2.94	15.48	72.75	11.11
II	75.33	87.53	2.90	2.90	5.03	9.29	7.12	111.33	2.42	13.98	68.89	9.66
III	60.60	85.40	3.93	3.83	6.92	7.57	6.34	92.13	2.71	14.83	74.20	10.95
IV	62.00	82.58	4.22	4.07	7.50	7.27	5.37	95.17	2.69	16.31	58.55	9.42
V	64.67	92.53	3.85	3.73	6.53	7.29	6.35	94.00	3.04	9.41	60.30	5.67
VI	81.78	98.33	4.20	4.09	5.98	9.69	8.50	116.67	2.82	24.51	50.19	12.09
VII	88.33	96.47	4.00	4.00	5.20	8.57	6.27	114.00	2.85	17.44	59.25	10.35
VIII	58.00	76.33	4.17	3.47	9.07	7.46	9.30	91.33	2.84	15.75	67.74	10.66
IX	85.33	84.87	3.47	3.47	7.13	11.08	9.70	111.33	2.23	20.84	53.46	11.12
X	83.33	97.73	4.13	4.13	6.87	12.61	11.13	118.67	2.82	29.64	48.17	14.27

DF: Days to 50% flowering, PH: Plant height (cm), NT: Number of tillers per plant, PT: Number of productive tillers, NF: Number of fingers per ear, EL: Main ear head length (cm), FL: Finger length (cm), DM: Days to maturity, TW: Test weight (g), EW: Ear head weight (g), TH: Threshing percentage, GY: Grain yield (g)

Table 6. Contribution of various characters towards total divergence in finger millet

S. No	Characters	Rank	Per cent contribution
1	Days to 50% flowering	194	22.53
2	Plant height	84	9.76
3	Number of tillers per plant	23	2.67
4	Number of productive tillers	21	2.44
5	Number of fingers per ear	124	14.40
6	Main ear head length	86	9.99
7	Finger length	10	1.16
8	Days to maturity	44	5.11
9	Test weight	60	6.97
10	Ear head weight	46	5.34
11	Threshing percentage	28	3.25
12	Grain yield	141	16.38

The hierarchal clustering of genotypes by agglomerative cluster analysis using adjusted mean values of 12 quantitative characters grouped the 42 genotypes into 10 clusters. Among all clusters, the cluster II was maximum with 20 genotypes followed by cluster IV with 6 genotypes. The cluster I was with 5 genotypes, cluster III with two genotypes, cluster VII with 3 genotypes, cluster X with two genotypes and the clusters V, VI, IX and X were with single genotype.

The circular diagram showing the clustering of genotypes in cluster was presented in **Fig. 1** and mean values for 12 quantitative characters were presented in the **Table 7**. The cluster I recorded least mean performance for the characters number of tillers per plant (3.35) and number of productive tillers (3.09), the cluster III recorded highest mean performance for plant height (98.7 cm), number of tillers per plant (4.82), number of productive tillers (4.62), test weight (3.26 g), threshing percentage (76.23 %) and least mean performance for number of fingers per ear. The cluster IV recorded least mean performance for finger length (5.99 cm). The cluster V recorded highest mean performance for the number of fingers per ear (9.35) and least mean performance for the characters days to 50 % flowering (57.93 days), plant height (79.9 cm) and days to maturity (91.29 days). The cluster VI recorded highest mean performance for the characters main ear head length (12.54 cm), finger
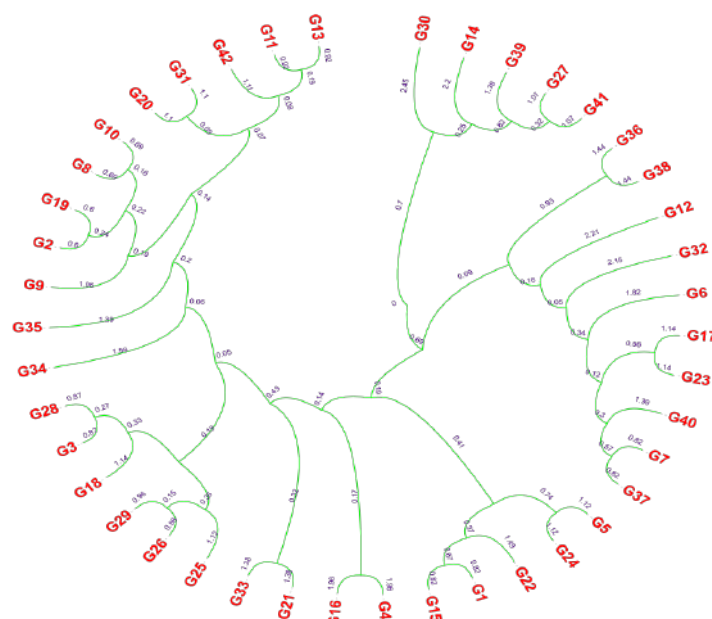

Fig. 1. Circular display of hierarchal clusters in finger millet generated using iTOL software.

Table 7. Mean values of ten clusters estimated by hierarchal cluster analysis in finger millet

Cluster number	DF	PH	NT	PT	NF	EL	FL	DM	TW	EW	TH	GY
I	72.67	91.28	3.35	3.09	5.53	8.41	6.73	106.95	2.59	14.57	70.01	10.2
II	72.14	95.51	4.1	4.02	5.77	8.32	6.32	105.96	2.96	15.43	72.25	10.98
III	78.41	98.7	4.82	4.62	5.05	7.93	6.47	112.66	3.26	17.61	76.23	13.21
IV	60.67	82.84	4.04	3.96	7.07	7.65	5.99	93.17	2.68	14.86	68.68	9.93
V	57.93	79.9	4.17	3.54	9.35	7.68	9.41	91.29	2.84	16.44	66.75	10.89
VI	83.26	96	4.13	4.08	6.95	12.54	11.07	118.68	2.82	29.04	48.47	13.94
VII	81.88	96.51	4.2	4.07	5.71	9.39	8.39	116.68	2.82	24.36	50.63	12.15
VIII	85.25	83.96	3.47	3.39	7.16	10.93	9.65	111.35	2.23	20.15	54.08	10.84
IX	62.64	96.95	3.87	3.81	7.38	7.62	6.61	92.03	2.88	20.49	74.25	15.02
X	64.62	92.69	3.85	3.71	6.55	7.2	6.36	93.95	3.04	9.43	60.2	5.71

DF: Days to 50% flowering, PH: Plant height (cm), NT: Number of tillers per plant, PT: Number of productive tillers, NF: Number of fingers per ear, EL: Main ear head length (cm), FL: Finger length (cm), DM: Days to maturity, TW: Test weight (g), EW: Ear head weight (g), TH: Threshing percentage, GY: Grain yield (g)

length (11.07 cm), days to maturity (118.68 days), ear head weight (29.04 g) and the least mean performance for threshing percentage (48.47 per cent). The cluster VIII recorded the highest mean performance for the characters days to 50 % flowering (85.25 days) and least mean performance for test weight (2.23 g). The cluster IX recorded highest mean performance for grain yield.

Selection for diverse genotypes will broaden the genetic variability of quantitative characters in segregating populations, which should be done using the cluster distances and genotypes with highest mean performance in each cluster. Genetic improvement of the yield and its component characters can be achieved by crossing diverse genotypes because it results high heterosis in F_1 and better transgressive segregates in further generations which was line with findings of Kadam 2008 and Kumar *et al.* 2010.

In both the methods a total number of ten clusters are formed. There is a considerable similarity was observed between the two clusters analysis, five out of ten clusters exactly contain same genotypes in both cluster analysis. However, the distribution of few genotypes in D^2 analysis varies from the hierarchal cluster analysis. The reason could be usage replicated data for D^2 analysis and adjusted phenotypic mean data for hierarchal cluster analysis.

In both the clusters there is no relationship between the place of origin of variety and the genetic diversity. The genotypes from same geographical regions are grouped in to different clusters and genotypes of different geographical regions are grouped into same cluster. This may be due the selection and procedure followed in development of a variety. This finding was also reported by Sao *et al.* (2018)**.**

The diversity through clustering analyses showed that the characters days to 50 % flowering, plant height, days to maturity, days to maturity, ear head weight, and threshing percentage are the diverse characters. The genotype 32 (FMV-1162) and genotype 14 (FMV-1175) are most diverse genotypes and including these genotypes in the breeding program will bring high chance in getting transgressive segregants in segregating population. The alpha lattice design helps to give precise results when the number of entries is more than 20 by dividing the field into homogenous blocks and eliminating the block effect from the genotypic mean values.In respect to the future view the growing demand for finger millet in public brings tremendous scope for finger millet breeding or improvement programs in the region and this study forms a base for future programs.

REFERENCES

Das, R., Sujatha, M., Pandravada, S.R. and Sivasankar, A. 2013. Genetic divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn) germplasm. *Indian J.*, **6(4):** 373-376.

Federer, W. T. and Wolfinger, R. D. 2003. Analysis for an experiment designed as an augmented lattice square design. Handbook of formulas and software for plant geneticists and breeders: Pp. 283-289.

Kadam, D. D. 2008. Genetic divergence in finger millet (Nachani/ Ragi/Nagali /Eluesine coracana). *Journal of Soils and Crops,* **18(1):** 138-142.

Kumar, D., Tyagi, V., Ramesh, B. and Pal, S. 2010. Genetic diversity in finger millet (*Eleusine coracana* L.). *Crop improvement,* **37(1):** 25-28.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. In: *Proc. Natl. Inst. Sci. India*, **12:** 49-55.

Panse, V.G. and Sukhatme, P.V. 1978. Statistical methods for agricultural workers. III Rev. Ed., ICAR, New Delhi. Pp.103-108.

Priyadharshini, C., Nirmalakumari, A., Joel, A. J. and Raveendran, M. 2011. Genetic variability and trait relationships in finger millet (*Eleusine coracana* (L.) Gaertn.) hybrids. *Madras Agricultural Journal,* **98(1-3):** 18-21.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons. Inc., New York. 390p.

Sao, A., Singh, P., Kumar, P. and Panigrahi, P. 2018. Genetic analysis for estimation of yield determinants in finger millet (*Eleusine coracana* (L.) Gaertn.). *Int. J. Agric. Sci.,* **10 (14):** 6665-6668.

Wolie, A. and Belete, K. 2013. Genetic divergence and variability studies in some Ethiopian finger millet germplasm collections. *Scholary J. of Agri. Sci.,* **3(4):** 110-116.