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Research Note

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

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Abstract
The genetic divergence among 105 finger millet genotypes was estimated using Mahalanobis' generalized distance using D^2 statistics. All the genotypes were grouped into fourteen clusters using Tocher's method. Cluster I was the largest comprising of maximum number of 30 genotypes followed by cluster II and VIII consisting of 22 genotypes each and cluster VI was aggregated with 21 genotypes. The remaining clusters III, IV, V, VII, IX, X, XI, XII, XIII and XIV were found to be solitary clusters. Among the characters studied grain protein content (32.6 %) contributed maximum to total variation followed by days to 50 % flowering (12.38 %) and grain iron content (9.18 %). Hybridization between genotypes of cluster XIII (VR 1122) with those of either cluster XI (IC0476229) or cluster XIV (FM 1918) with maximum inter cluster distance will be useful to obtain good hybrid vigour and desirable segregants.

Keywords: Finger millet, Genetic Divergence, D^2 statistics.

Finger millet (*Eleusine coracana* L. Gaertn) is an important food grain crop of semi arid tropics, particularly in India and East Africa and has the pride of place in having highest productivity among small millets, with a production of 1.79 Mt from the total cropped area of 1.17 M ha and also has the highest productivity (1591 kg/ha) followed by pearl millet (1130 kg/ha) and sorghum (883 kg/ha) (Meena *et al.,* 2021). Finger millet is commonly perceived as "super cereal" with exceptionally high nutritive values like carbohydrates, minerals, dietary fibre, calcium and micronutrients. In the era of growing nutritional crisis, these properties of finger millet must be harnessed to develop a crop with novel nutritional values to combat the malnutrition (Sood *et al.,* 2019). The COVID-19 pandemic slowly changed the food habits of the public from major cereals like rice to the millets in view of their nutritional properties (Reddy and Vengadessan, 2022). For example, finger millet (Ragi) has three times more calcium than milk and used to correct the nutrient deficiency in the consumers. In view of increase in public awareness on nutritional and health benefits of millets and their suitability for cultivation under adverse conditions, the United Nations (U.N.) has declared 2023 as the "International Year of Millets".

A logical way to start any breeding programme for crop improvement is to survey the variation present in the germplasm. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes (Shinde *et al*., 2013). Multivariate statistical methods and numerical taxonomy has been used widely in summarizing and describing variation

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and its pattern in a population of crop genotypes. The D^2 technique based on multivariate analysis developed by Mahalanobis (1936) is the most valuable method for quantifying the extent of genetic diversity among the genotypes. Crossing between more divergent parents is expected to generate a broad spectrum of variability giving ample scope for selection in the segregating populations. Keeping this in view, the present investigation was carried out to identify genetically diverse, nutrient rich and high yielding genotypes that can be used as parents to develop superior segregants in future breeding programmes.

One hundred and five finger millet genotypes, which were collected from ICAR-IIMR, Hyderabad, Agricultural Research Stations Vizianagaram, Perumallapalle and Peddapuram, were evaluated in Randomized Block Design during *kharif*, 2018 at Regional Agricultural Research Staton, Lam, Guntur with geographical positioning of 16.36° N and 80.43° E. The genotypes were raised in two replications with three rows of 3 m length with a spacing of 22.5 cm × 10 cm between and within the rows, respectively. Standard agronomic practices and recommended fertilizer doses were followed for raising the crop. Data were recorded on 14 characters including ten yield traits and four quality characters. Observations were recorded on five plants selected at random per genotype per replication and their means were used for analysis. However, observations on days to 50% flowering and days to maturity were recorded on plot basis.1000 grain weight and all the grain quality parameters *viz.*, protein, calcium, iron and zinc contents were recorded from the harvested produce as per the standard procedures. The nitrogen content (%) in each sample was estimated by Microkjeldahl method and protein content (%) of each sample was estimated as described by Sadasivam and Manickam (1996). For the estimation of grain iron and zinc contents, grains were ground into flour and estimated as per procedure given by Tandon (1999). Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936). The genotypes were grouped on the basis of minimum generalized distance using Tochers' method as described by Rao (1952).

All the finger millet genotypes under study were grouped into 14 distinct non-overlapping clusters using Tocher's method. (**Table 1 and Fig. 1**). Out of fourteen clusters formed, cluster I was the largest comprising of maximum number of 30 genotypes followed by cluster II and VIII consisting of 22 genotypes each. Cluster VI was aggregated with 21 genotypes. The remaining clusters III (IC0476563), IV (IC0476764), V (IC0477078), VII (IC0476282), IX (Vakula), X (IC0476585), XI (IC0476229), XII (VR 1131), XIII (VR 1122) and XIV (FM 1918) were monogenotypic clusters representing the existence of

Table 1. Clustering pattern of finger millet genotypes by Tocher's method

S. No.	Cluster number	Total number of genotypes	Genotypes
1	I	30	Saptagiri, Hima, IC077107, VR 1125, VR 1118, Sri Chaitanya, Bharathi, IC0476438, PPR 1027, VR 1081, GPU 67, PPR 1058, IC0476863, IC0476891, VR 988, PR 1044, PR 10-35, IC0476434, VR 1099, VR 1127, IC0476590, IC0476697, PPR 1021, IC0476834, IC0476594, VR 929, IC0476693, IC0476854, IC0477049 and IC0475759
2	II	22	IC0476554, IC0476269, IC0476516, IC0476690, IC0476544, IC0476591, IC0476362, IC04766656, IC0476668, IC0475578, IC0476608, IC0588011, IC0476664, IC0476273, VR 1136, IC0476665, VR 1011, IC0476896, IC0477200, VR 1144, VR 1128 and VR 1121
3	III	1	IC0476563
4	IV	1	IC0476764
5	V	1	IC0477078
6	VI	21	IC0475790, IC0476275, IC0475724, IC0476285, IC0476568, IC0476762, IC0476890, IC0476249, IC0475598, PPR 2885, IC0477419, IC0476819, Indira Ragi 1, VR 1112, PR-10-22, VR1116, IC0476993, IC0476607, VR 1117, VR 900 and VR 1125
7	VII	1	IC0476282
8	VIII	22	IC0476792, IC0475788, IC0476694, VR 1124, PPR 1080, IC0477106, IC0476227, VR 1126, VR 1066, IC0476419, PPR 2886, PPR 2773, VR 1076, Godavari, IC0476966, IC0476738, IC0476741, IC0476805, IC0475589, IC0476292, VR 1110 and IC0476699
9	IX	1	Vakula
10	X	1	IC0476585
11	XI	1	IC0476229
12	XII	1	VR 1131
13	XIII	1	VR 1122
14	XIV	1	FM 1918

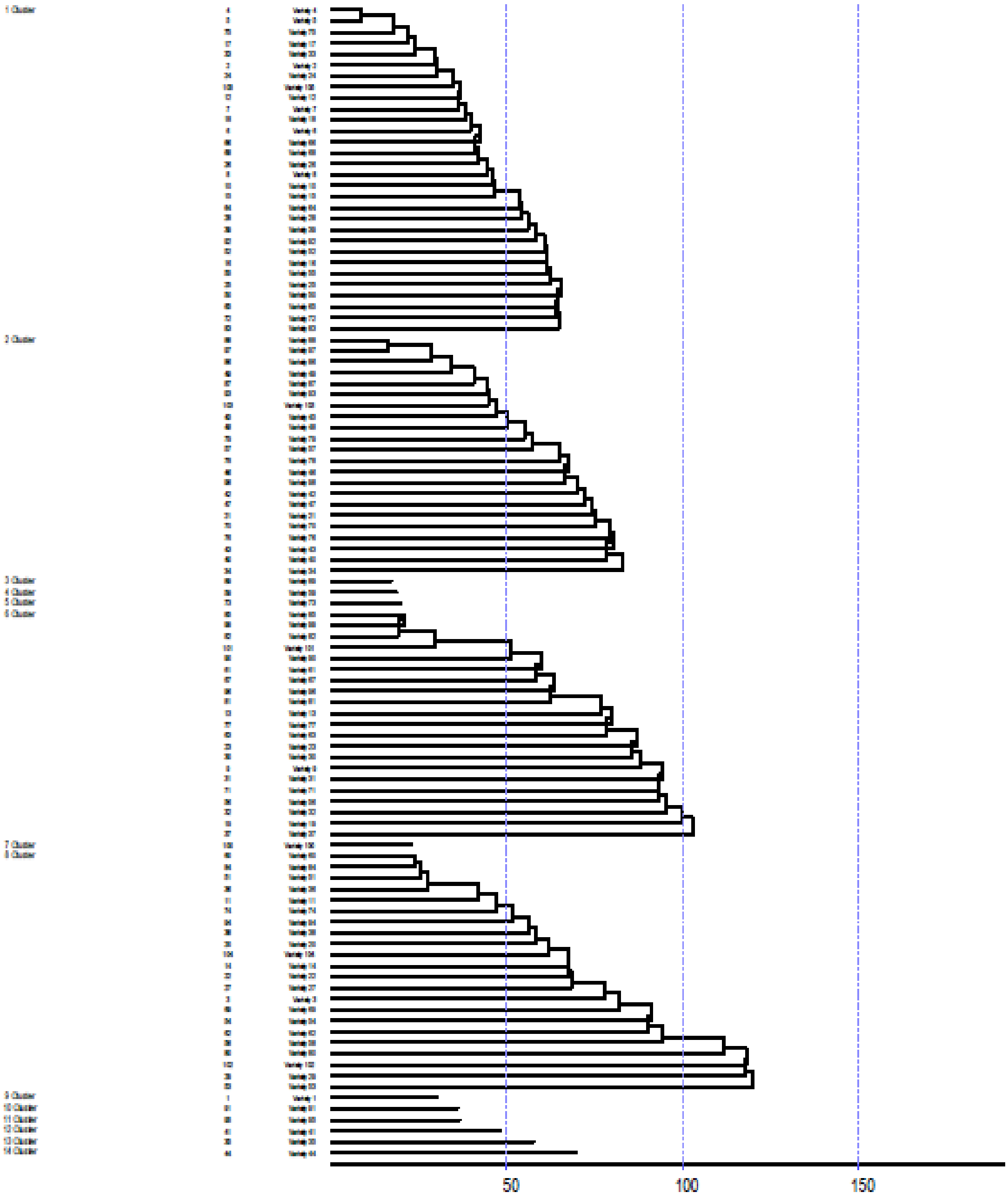

Fig. 1. Dendrogram showing clustering pattern among 105 genotypes of finger millet based on Mahalanobis' D^2 values using Tocher's method.

wide diversity among the genotypes, which may be useful in crop improvement.

The genotypes and germplasm obtained from Vizianagram, Perumallapalle, Peddapuram and other geographical regions were scattered in all the clusters randomly indicating that clustering of genotypes did not follow their geographic location distribution and thus revealing the non-correspondence of geographic origin with genetic diversity. These results were in agreement with findings of Meera (2021) in finger millet.

Relative contribution of different characters in the present study was represented in the **Table 2**. Among the characters studied grain protein content (32.6 %) contributed maximum to total variation followed by days to 50 % flowering (12.38 %), grain iron content (9.18 %), earhead weight (9.07 %), productive tillers per plant

Table 2. Contribution of different characters towards genetic divergence among finger millet genotypes

S. No.	Character	Times ranked 1st	Contribution %
1	Grain protein content (%)	1780	32.60 %
2	Days to 50 % flowering	676	12.38 %
3	Grain iron content (mg/100g)	501	9.18 %
4	Earhead weight (g)	495	9.07 %
5	Productive tillers per plant	397	7.27 %
6	Finger length (cm)	342	6.26 %
7	Grain calcium content (mg/100g)	304	5.57 %
8	Grain zinc content (mg/100g)	272	4.98 %
9	Earhead length (cm)	234	4.29 %
10	Plant height (cm)	223	4.08 %
11	1000-grain weight (g)	122	2.23 %
12	Fingers per earhead	101	1.85 %
13	Days to maturity	9	0.16 %
14	Grain yield per plant (g)	4	0.07 %

(7.27 %), finger length (6.26 %), grain calcium content (5.57 %), grain zinc content (4.98 %), earhead length (4.29 %), plant height (4.08 %), 1000 grain weight (2.23 %), fingers per earhead (1.85 %), days to maturity (0.16 %) and grain yield per plant (0.07 %).

The average intra and inter-cluster distances (D^2 values) were estimated and are presented in **Table 3 and Fig. 2**. Intra-cluster D^2 values ranged from 0.00 (III, IV, V, VII, IX, X, XI, XII, XIII and XIV) to 93.90 (VIII). The maximum intra cluster D^2 value was observed for cluster VIII (93.90) followed by cluster VI (91.71), cluster II (73.68) and cluster I (56.45). The intra cluster distance indicates the divergence among the genotypes with in a cluster. Comparison between inter and intra cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values (**Table 4**). The inter cluster distance ranged from 37.40 (between cluster III and V) to 359.00 (between cluster XI and XIII). Maximum inter-cluster distance was observed between the clusters XI and XIII (359.00), followed by clusters XIII and XIV (354.54), clusters VII and XIV (335.39), clusters X and XI (322.62), clusters V and XI (307.37). This suggested that there was wide genetic diversity between these clusters. Based on these studies, crosses were proposed between the genotypes VR 1122 of cluster XIII and ICO476229 of cluster XI and the genotypes FM 1918 of cluster XIV and ICO476282 of cluster VII, which were expected to give desirable segregants. Inter crossing between the genotypes which are divergent in nature lead to

Table 3. Average intra and inter-cluster distances (D^2 values) among 14 clusters of finger millet genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**56.45**	114.24	79.41	84.52	100.89	92.58	134.17	107.55	147.66	80.2	182.34	131.61	148.80	163.97
II		**73.68**	160.29	128.58	174.47	144.64	89.92	131.37	164.54	210.95	96.56	151.16	223.30	197.26
III			**0**	110.65	37.40	106.81	248.78	202.47	232.12	70.21	247.60	171.89	249.37	164.79
IV				**0**	78.37	67.58	177.30	133.91	118.80	113.99	248.15	97.20	203.14	119.02
V					**0**	84.06	278.28	214.10	190.76	107.48	307.37	151.03	249.20	107.40
VI						**91.71**	179.98	155.15	136.64	127.72	244.11	127.40	201.51	155.49
VII							**0**	100.53	143.01	238.29	94.98	168.49	160.05	335.39
VIII								**93.90**	142.37	156.06	180.64	145.92	137.47	253.36
IX									**0**	238.78	251.82	64.64	187.40	269.50
X										**0**	322.62	168.15	123.20	247.39
XI											**0**	263.23	359.00	283.26
XII												**0**	161.91	273.34
XIII													**0**	354.54
XIV														**0**

Diagonal bold values are intra cluster distances

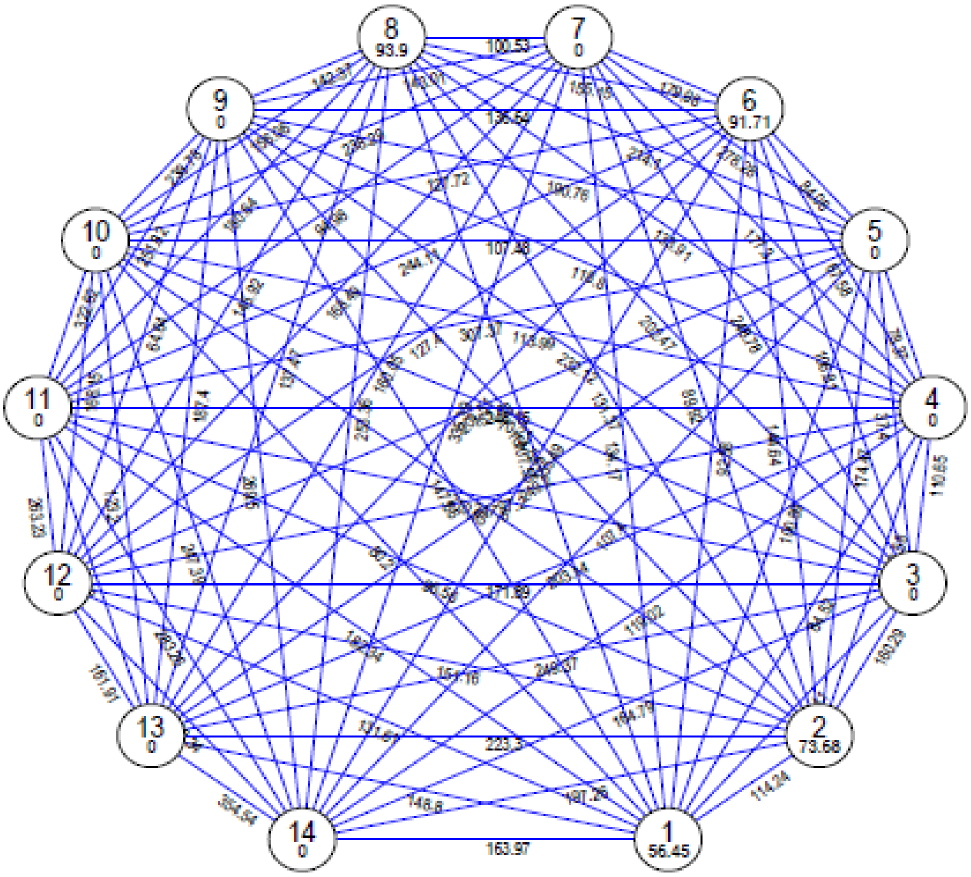

Fig. 2. Intra and inter-cluster distance of 105 finger millet genotypes in fourteen clusters based on Tocher's method

Table 4. Cluster means of nine clusters estimated by Tocher's method in finger millet genotypes

Character	**Cluster number**													
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**
Days to 50 % flowering	81.60	73.55	86.50	76.50	82.50	79.01	73.00	74.05	63.50	85.50	79.50	62.00	69.50	84.00
Days to maturity	110.85	103.61	116.00	108.00	112.50	109.31	103.00	103.56	97.50	112.50	102.50	87.00	101.50	115.00
Plant height (cm)	106.44	101.23	115.40	97.85	105.30	104.70	119.70	100.95	115.01	115.70	104.50	110.40	115.95	64.35
Productive tillers per plant	3.89	3.16	4.57	4.31	4.55	4.48	3.35	3.11	3.60	4.65	2.43	4.55	3.80	3.50
Fingers per panicle	7.92	6.50	8.50	8.00	8.35	8.42	5.40	6.96	8.75	9.90	7.75	8.40	6.65	7.00
Earhead length (cm)	8.56	8.04	9.55	10.75	10.60	9.49	6.40	8.03	9.75	9.55	6.40	9.50	9.65	12.05
Finger length (cm)	6.96	6.59	7.40	9.10	9.20	8.25	5.45	6.39	7.70	6.50	5.55	8.15	4.85	9.70
Earhead weight (g)	8.41	7.50	8.55	10.75	10.35	9.95	7.10	7.42	8.60	9.55	4.40	8.65	9.75	9.10
1000 grain weight (g)	2.67	2.33	2.82	2.84	2.31	2.53	2.12	2.32	3.04	2.39	2.07	2.64	1.92	2.52
Grain protein content (%)	5.89	8.46	7.59	6.55	7.45	6.60	6.55	4.56	5.70	3.84	9.51	5.62	2.75	8.46
Grain calcium content (mg/100g)	368.10	319.80	450.00	225.00	545.00	390.93	260.00	327.48	496.00	335.00	257.50	400.00	420.00	420.00
Grain iron content (mg/100g)	4.25	3.89	6.60	4.94	6.23	4.31	2.49	3.98	2.45	6.46	3.00	4.90	3.29	2.95
Grain zinc content (mg/100g)	2.73	2.52	3.19	2.40	3.23	2.37	1.40	2.17	1.35	3.52	1.65	2.65	3.25	3.33
Grain yield per plant (g)	22.98	17.74	26.75	21.40	25.45	24.01	14.50	17.88	19.40	24.00	14.30	34.30	26.50	28.60

wide genetic base in the source population and greater opportunity for crossing over to occur, which releases the hidden variability by breaking undesirable linkages.

The cluster means signifies mean performance of all the genotypes present in a cluster. Mean performance of top clusters with their promising characters by Tocher's method was presented in **Table 4**. Cluster III showed highest cluster mean for days to fifty % flowering (86.50), days to maturity (116.00) and grain iron content (6.60). Cluster XII showed lowest cluster mean for days to 50 % flowering (62.00) and days to maturity (87.00). Hence, the genotype of this cluster can be used in future breeding programmes for developing early maturing varieties. Lowest cluster mean for plant height (64.35) was showed by cluster XIV; hence genotypes from this cluster may be recommended in future breeding programmes for developing dwarf varieties which are lodging resistant.

The monogenotypic clusters like cluster IV consisting of germplam accession ICO476764 with highest cluster mean for earhead weight (10.75 g), cluster V with germplam accession ICO477078 with highest mean grain calcium content (545.00 mg/100g), cluster XI consisting of ICO476229 with highest mean grain protein content (9.51 %), cluster IX with accession Vakula with highest mean 1000-grain weight (3.04 g) and cluster X with germplasm accession ICO476585 having highest cluster means for productive tillers per plant (4.65), fingers per earhead (9.90) and grain zinc content (3.52 mg/100g) can be used for improvement of both grain yield and nutritional quality. Cluster XIV with FM 1918 showed highest mean earhead length (12.05) and finger length (9.70) which are major yield attributing characters that can be incorporated through breeding program for the improvement of grain yield. The genotypes in clusters III, V, X and XI showed highest cluster means for grain iron, calcium, zinc and iron contents, respectively. This highlighted that nutritional superiority of these genotypes from diverse clusters can be utilized for biofortification of finger millet cultivars in future crop improvement programmes.

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