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Assessment of genetic diversity for yield and nutritional traits among finger millet (*Eleusine coracana* (L.) Geartn.) genotypes

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Abstract
A fundamental statistical method that makes it simple to evaluate significant polygenic characters which are very important in plant breeding programme is multivariate analysis. In a compact family block design, the current experiment was carried out in Kharif 2022 using 33 finger millet germplasm accessions at the Education and Research farm, Department of Agriculture Botany, Dapoli, Dist. Ratnagiri. The purpose of the current study was to determine which genotypes produce the highest yield by evaluating the degree of genetic diversity analysis. In addition to recording observations for seventeen characters, a multivariate technique was used, and cluster analysis was performed. Based on Euclidean distance, the thirty-three genotypes were sorted into six different clusters. There was a significant amount of diversity in Cluster II, which had the greatest number of genotypes (Thirteen), followed by Cluster I (Nine), Cluster IV (six), Cluster III (Three), and Cluster V & VI (One each). The greatest grain yield inter-cluster distances were found between Cluster III and VI, then Cluster I and VI, Cluster V and VI, Cluster II and VI, and Cluster III and V. This suggests that there is significant diversity among these clusters, and that genotypes from these clusters could be used as possible parents for hybridization. The study found that among the thirty-three finger millet genotypes under investigation, there was a significant variation in grain yield per plant, which the major factor was contributing to genetic divergence. For the majority of the desirable characteristics, including the number of ear heads per plant, grain yield per plant, straw yield per plant, biological output per plant, and iron content, Cluster I had the highest maximum cluster means.

Keywords: Finger millet, diversity, cluster analysis

Introduction
The popular name "Finger millet" is derived from the finger-like branching of the panicle on the plant *Eleusine coracana* (L.) Gaertn., commonly known as African millet or Ragi. It is a member of the Gramineae or Poaceae family. It is the third most significant millet in India, behind sorghum and pearl millet. It is a resilient crop that may be produced in a variety of climates, from virtually at sea level in south India to high lands in the Himalayas (altitudes of 1850 to 2300 meters), and from poor soils on hill slopes to rich soils in the Indogangetic plains region. An allotetraploid crop called ragi has the chromosomal number 2n=4x=36 (AABB). It is frequently referred to as the "poor man's crop." Although it is a self-pollinated crop, cross-fertilization has only been shown to contribute to less than 1% of the pollination. In many regions of India, finger millet serves as a staple food for a sizable portion of the agriculture-dependent and economically marginalized communities. There is a huge range of morphological variation in finger millet. For instance, a variety of seed colours that are associated with calcium and protein content can be developed (Vadivoo *et al*., 1998) [18].

It is a sustainable crop that can thrive at high elevations, on marginal terrain, and with ease in saline and drought environments. Compared to other crops, it requires substantially less irrigation and other inputs. In India, finger millet is cultivated on an area of 1.26 million hectares with a production of 1.79 million tonnes. (Anonymous, 2017- 18) [1]. In Maharashtra, Finger millet occupies an area of about 80,130 hectares with a production of 84,850 tonnes (Anonymous, 2018-19) [2]. The 30,200 hectares area is found in the Konkan region of Maharashtra comprising Raigad, Thane, Palghar, Sindhudurg and Ratnagiri districts with a production of 33, 200 tones with a productivity of 1100 kg /ha. In Konkan region the varieties Dapoli 1, Dapoli 2, Dapoli 3, and Dapoli Safed developed and released by the D.B.S.K.K.V. Dapoli are helpful to increase millet production and withstand vagaries of climate change.

In comparison to other important grains like wheat, rice, and sorghum, it has significant levels of protein and minerals (Gupta *et al*., 2017; Sharma *et al*., 2017) [8, 15]. The whole seeds of finger millet contain about 0.34% calcium (Ca), which is significantly more than the other cereals. In addition to being gluten-free, the seeds are a rich source of dietary fibre, iron, and the important amino acids isoleucine, leucine, methionine, phenylalanine, and phytates (Chandra *et al*., 2016; Sood *et al*., 2016) [5, 16]. The grain is a nutritious nourishment for newborns as well as a source of flour used to make cakes, bread, and other pastries (Mgonja *et al*., 2007; Ceasar and Ignacimuthu, 2011) [10, 4].

Material and Methods

This study was conducted in Kharif 2022 at the Department of Agriculture Botany, Education and Research Farm in Dapoli, District Ratnagiri, using a compact family block design with a spacing of 20 cm between rows and 15 cm between plants, respectively. Thirty-three finger millet genotypes, along with three varietal checks, comprised the material for the present research. The following checks were obtained from Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth in Dapoli: Dapoli-1, Dapoli-2, and Dapoli-3. Thirty germplasms were obtained from different Dapoli localities. A random selection of five plants in each treatment were used to record the observations based on seventeen characters: plant height (cm), days to 50% flowering, days to maturity, number of tillers per plant, number of earheads per plant, number of fingers per earhead, finger length (cm), 1000 grain weight (g), grain density, grain yield per plant (g), straw yield per plant (g), biological yield per plant (g), harvest index (%), protein content (%), calcium content (mg/100 gm), iron content (mg/100 gm), and fibre content (%). The statistical analysis was carried out using the average data from these five plants. The Standardized Euclidean Square Distance method was used to perform the cluster analysis for the quantitative data, and Tocher's method was used to classify thirty-three finger millet genotypes into clusters based on 17 quantitative characteristics. Based on the performances of different genotypes in each cluster, inter- and intra-cluster distances as well as cluster means were determined for specific characters. The Mahalanobis D^2 statistic was used in multivariate analysis to evaluate the genetic divergence among genotypes.

Result and Discussion

Using Mahalanobis D2 statistics, the genotype diversity of thirty-three finger millet genotypes was examined based on seventeen quantitative characteristics. It performed a quantitative analysis of the thirty-three finger millet genotypes shown in Tables 1 to 4 to determine genetic divergence for yield and its contributing features. Based on the closeness of the genotypes with respect to their D^2 values in Table 1, the genotypes were divided into six distinct clusters. Table 2 displays the average intra- and inter-cluster distances that were calculated whereas inter-cluster distance indicated relational difference between the clusters, intra-cluster distance revealed genetic divergence within a cluster. Additionally, the analysis shows that each of these features contribute to overall divergence, clustering pattern, and intra- and inter-cluster distances. The Mahalanobis euclidean distance method and Tocher's method were used to produce the cluster diagram and dendrogram, respectively. The following is a list of the various clusters with full descriptions:

Table 1: Thirty-three finger millet genotypes were grouped into six clusters based on D^2 analysis.

Cluster	Number of genotypes	Name of the Genotypes
I	9	N-54, N-56, N-55, N-49, N-7, N-35, N-34, N-33 & N-48
II	13	N-3, N-9, N-18, N-29, N-50, N-36, N-10, N-28, N-16, N-47, N-14, N-13 & N-12
III	3	N-1, N-11 & N-26
IV	6	N-53, N-22, N-27, N-17, N-21 & N-19
V	1	N-15
VI	1	N-51

Table 2: Finger millet genotypes grouped into six clusters based on the intra- and inter-cluster distance (D^2)

Cluster	I	II	III	IV	V	VI
I	289.25	621.73	657.24	580.91	818.97	1520.59
II		368.24	832.49	852.07	546.73	1347.55
III			383.43	1000.22	1320.53	2199.45
IV				527.89	831.85	994.39
V					0.00	1375.58
VI						0.00

Table 3: Cluster mean for seventeen characters of thirty-three genotypes in finger millet among six clusters

	Plant height (cm)	Days to 50% flowering	Days to Maturity	Number of tillers per plant	Number of earheads per plant	Number of fingers per plant
Cluster 1	88.68	101.87	129.82	3.86	3.70	8.04
Cluster 2	85.77	106.46	134.96	3.70	3.42	8.28
Cluster 3	88.60	107.83	134.50	3.63	3.50	7.50
Cluster 4	87.55	103.58	132.08	3.76	3.23	7.76
Cluster 5	90.80	104.00	133.00	4.00	3.50	9.10
Cluster 6	81.75	106.00	138.00	3.25	3.15	6.20

	Finger length (cm)	Grain density	1000 Grain weight (g)	Grain yield per plant (g)	Straw yield per plant (g)	Biological yield per plant
Cluster 1	8.59	80.28	2.83	15.24	26.60	41.84
Cluster 2	8.72	81.69	2.68	12.38	23.32	35.70
Cluster 3	9.41	89.00	2.73	9.77	19.40	28.87
Cluster 4	8.85	83.83	2.59	9.22	20.10	29.32
Cluster 5	6.82	96.50	2.33	13.84	19.45	33.29
Cluster 6	7.66	63.50	3.24	8.51	22.65	31.16

	Harvest Index (%)	Protein (%)	Calcium (mg/100 g)	Iron (mg/100 g)	Fibre (%)
Cluster 1	36.16	7.00	228.35	3.50	2.61
Cluster 2	34.44	6.98	111.69	2.63	1.77
Cluster 3	32.41	7.24	240.33	1.67	1.51
Cluster 4	31.07	4.75	192.92	3.08	2.74
Cluster 5	40.70	5.56	94.00	2.03	2.15
Cluster 6	27.31	3.06	128.50	1.96	1.19

Table 4: Each character contribution to the finger millet's genetic divergence

Sr. No.	Source	Contribution %
1	Plant height (cm)	3.98
2	Days to 50% flowering	2.80
3	Days to Maturity	1.70
4	Number of tillers per plant	4.55
5	Number of earheads per plant	3.54
6	Number of fingers per earhead	8.90
7	Finger length (cm)	2.84
8	Grain density (grains/cm)	0.76
9	1000 Grain weight (g)	10.32
10	Grain yield per plant (g)	16.78
11	Straw yield per plant (g)	12.22
12	Biological yield per plant (g)	5.49
13	Harvest Index (%)	3.54
14	Protein (%)	4.31
15	Calcium (mg/100g)	5.67
16	Iron (mg/100g)	7.10
17	Fibre (%)	5.50

Group constellation

The largest number of genotypes (Thirteen) was found in Cluster II, with nine genotypes in Cluster I, six genotypes in Cluster IV, three genotypes in Cluster III, and one genotype each in Cluster V & VI. These clusters showed significant diversity within and between the set as a whole. Desai (2012) [6] and Nagargoje (2015) [11] used these methods in their studies as well. Kumar *et al*., (2010) [9] grouped 140 genotypes in 10 clusters.

Intra and inter-cluster distances

Based on the average D2 values, the intra- and inter-cluster relationships were determined. Table 2 displays the average D2 values for intra- and inter-cluster distances. The D2 values of the intra cluster average varied between 0.00 and 527.89. Cluster IV (527.89) had the greatest intra-cluster distance among the clusters, followed by cluster III (383.43), cluster II (368.24), and cluster I (289.25). Cluster V (0.00) and cluster VI (0.00) had the lowest intra-cluster distances. The varied composition of Cluster IV contributed to its high intra-cluster genetic distance. Collaborative results have also been given by Wolie and Belete (2013) [19] Bedis *et al*., 2007 [13] and Negi *et al.* (2017) [12].

The lowest inter-cluster D2 value was found between cluster II and cluster V (546.73), while the highest inter-cluster D2 value was observed between cluster III and VI (2199.45). Cluster III and VI (2199.45) had the greatest inter-cluster genetic distance, followed by cluster I and VI (1520.59), cluster V and VI (1375.58), cluster II and VI (1347.55), cluster III and V (1320.53), cluster III and IV (1000.22), cluster IV and VI (994.39), cluster II and IV (852.07), cluster II and III (832.49), cluster IV and V (831.85), cluster I and cluster V (818.97), cluster I and cluster III (657.24), cluster I and cluster II (621.73), cluster I cluster IV (580.91), and cluster II and cluster V (546.73). High genetic diversity was present in the genotypes included in clusters with larger inter-cluster distances. Because heterotic hybrids can arise from the convergence of various genes dispersed in parents to progeny, hybridization between genotypes in these clusters may arise.

The following clusters had the lowest estimated inter-cluster distances: cluster II and cluster V (546.73), cluster I and IV (580.91), cluster I and III (657.24), and cluster I and II (621.73). Indicating that the genotypes in these cluster pairs were genetically near to one another, are the clusters with the lowest inter-cluster distances. Promising recombinants were expected to be produced in the segregating generations by crossings between genotypes from clusters separated by a low inter-cluster distance. Similar results have also been obtained by Sahu and Pradhan (2012) [13] and Kumar *et al*., (2010) [9].

Cluster means analysis for different characters

Table 3 lists the cluster group means for the seventeen characters combined with the six clusters. The majority of the traits under study showed significant variations between clusters.

The highest cluster mean for the number of earheads per plant, grain yield per plant, straw yield per plant, biological yield per plant, and iron content was found in Cluster I, which contained nine genotypes. The lowest cluster mean was found for the days to 50% blooming and days to maturity. The finger length, calcium content, and protein content cluster means were highest in Cluster III, which had three genotypes. The greatest cluster mean for fibre content was found in Cluster IV, which included six genotypes. The highest cluster mean was found for plant height, number of tillers per plant, number of fingers per earhead, grain density, and biological yield per plant in Cluster V, which comprised a single genotype. The greatest cluster mean for 1000 grain weight was shown by Cluster VI, which consisted of a single genotype Cluster I exhibited the greatest maximum cluster means for a majority of the desired characteristics, including the number of earheads per plant, grain yield per plant, straw yield per plant, biological yield per plant, and iron content, as

can be seen from the above results. As a result, genotypes belonging to this cluster can be utilized to simultaneously increase a multitude of iron content, seed yield, and yield-contributing traits. Earlier workers Bedis *et al*., 2007 [13], Desai (2012) [6] and Sahu *et al*., 2012 [13] also reported wide variability among clusters for yield and most of the yield contributing characters.

Contribution of various traits in relation to divergence

Proportion of contribution of each character to total divergence presented in Table 4 and Figure1. Each character was ranked on the basis of percent contribution of that character.

The result showed that grain yield per plant contributed maximum (16.78%) to the total divergence among the thirty-three finger millet genotypes studied, followed by straw yield per plant (12.22%), 1000 grain weight (10.32%), number of fingers per earhead (8.90%), iron content (7.10%), calcium content (5.67%), fibre content (5.50%), biological yield per plant (5.49%), number of tillers per plant (4.55%), protein content (4.31%), plant height (3.98%), harvest index (3.54%), number of earheads per plant (3.54%), fingers length (2.84%), days to 50% flowering (2.80%), days to maturity (1.70%) However, the contribution of grain density (0.76%) recorded lowest contribution towards divergence. Characters such as number of fingers per earhead, grain yield per plant, straw yield per plant, and 1000 grain weight are important determinants in the genetic divergence, according to the current study. Similar results were reported by Suryanarayana *et al*. (2014) [17], Sapkal *et al*. (2019) [14] and Devaliya *et al*. (2017) [7].

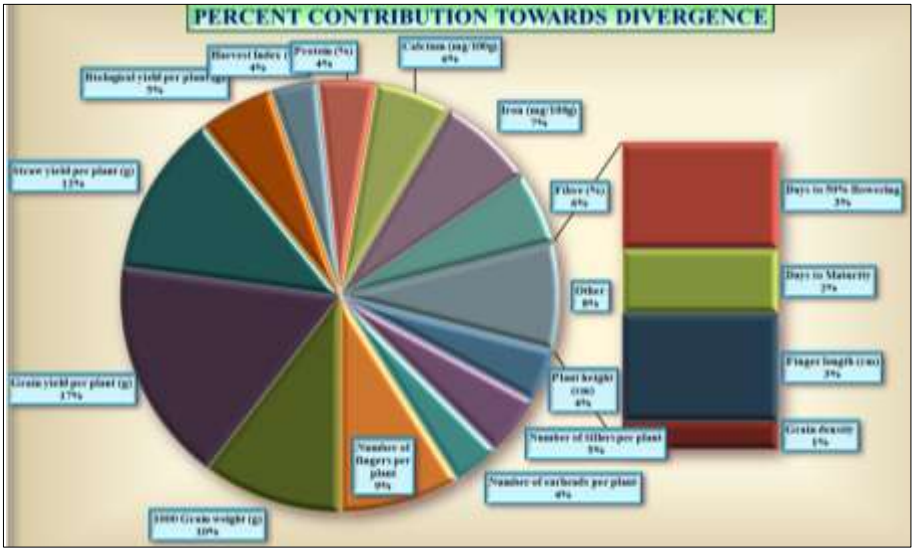

Fig 1: Pie chart showing each character's contribution to the genetic divergence of finger millet

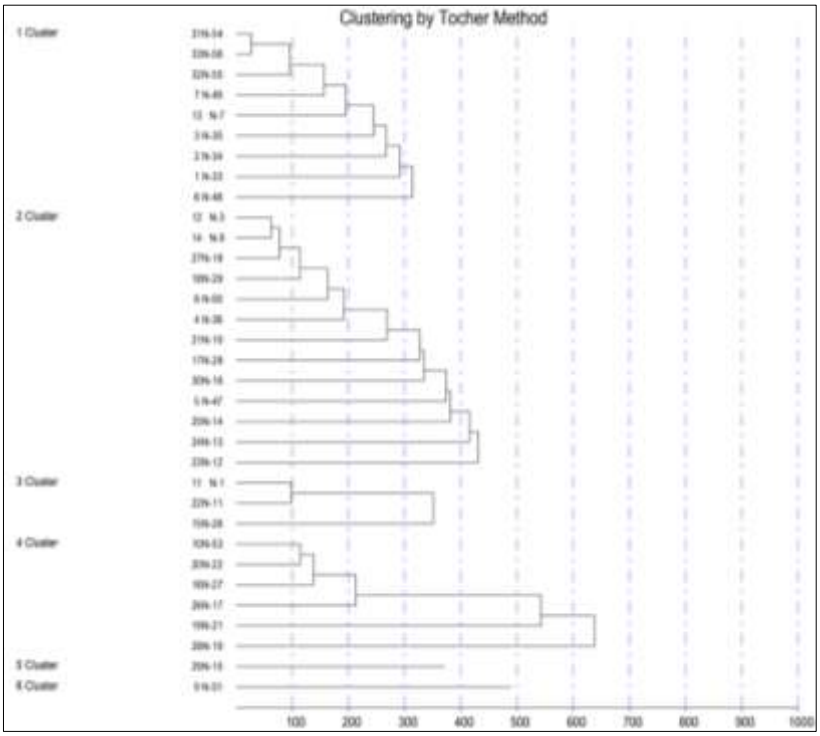

Fig 2: Using 17 quantitative characteristics, the Tocher method produced a dendrogram (Cluster diagram) that illustrates the relationships between 33 finger millet genotypes.

Conclusion

Genotypes that belong to the same cluster are likely do not vary much from one another as assessed by character aggregates. There is significant variation between these clusters, as shown by the highest inter-cluster distances for grain yield that were found between Cluster III & VI and Cluster I and V, respectively. To produce desired recombinants, genotypes from these clusters can therefore be selected for a hybridization procedure. The largest percentage of genetic divergence in thirty-three finger millet genotypes was attributed to grain yield per plant, indicating a high degree of diversity in these characteristics among the genotypes under study.

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