**Analysis of genetic diversity in Finger millet (*Eleusine coracana* L.)**

**Abstract**

The current study was conducted at Zonal Agricultural Research Station, Shenda Park, Kolhapur during kharif, 2023-24. The investigation consists of thirty seven (37) genotypes of finger millet. These genotypes were evaluated on the basis of twelve morphological characters for the diversity analysis. The diversity analysis distributed all genotypes into twelve consecutive clusters using tochers method. The D2 values were computed as inter and intra cluster distance which ranged from 46.37 to 1613.13. The highest value was seen between clusters X and XII, while the lowest value was found between clusters II and IX (46.37). Cluster X and XII (1613.13), Cluster IX and X (1498.81), Cluster III and XII (1359.00) had the largest inter-cluster distance, hence the genotypes present in this cluster viz., KFMG-2234, KFMG-2235, KFMG-2236, KFMG-2237, KFMG-2216, KFMG-2208 and KFMG-2208 could use in breeding programs to exploit the heterosis in terms of the hybrid progeny. The character productive tillers per plant, weight of 1000 grains, flag leaf blade width and peduncle length contribute mostly to the divergence. So the selection of parents can also rely on these characters in a breeding programme.

**Key words :** Diversity, Clusters, Genotypes, D2 value, Breeding

**Introduction**

Finger millet (*Eleusine coracana* (L.) Gaertn) commonly known as Ragi, is one of the important cereal crop largely grown in the arid and semi-arid areas of Africa and Asia. The cultivated finger millet is an allotetraploid with chromosome number 2n=4x=36, which have been evolved from *E. indica* (AA) and *E. floccifolia* or *E. tristachya* (BB). Finger mill*et al*so known as African millet, Ragi or Nachani. The common name Finger millet is derived from the finger-like branching of the panicle. The long history of cultivation of finger millet in India under diverse agro-climatic conditions and the associated human and natural selection has resulted in generation of large variability giving India the status of secondary centre of diversity.

It is an annual, erect growing herbaceous cereal crop. Finger millet is generally self-fertilized crop. The adventitious and fibrous roots of the plant are able to absorb moisture very efficiently and thoroughly from the soil. The tillers at the end of the culm bear finger like ear heads which are four to seven in number in which spikelets are crowded into two overlapping rows on the outer sides of the spike. The spikelet’s contain three to eight seeds which are very small in size and generally reddish-brown in colour. Finger millet is a short-day plant which requires optimum 12 hours of daylight for most varieties.

In world, among the different millets finger millet ranks fourth after sorghum, pearl millet and foxtail millet. It is cultivated almost in all states like Karanataka, Maharashtra, Uttarakhand, Tamil Nadu, Andhra Pradesh, Gujarat, Jharkhand, Bihar and Orisa. Nearly 80 per cent of the total production comes from these states. In Maharashtra it is mostly grown on either side of the western ghats mainly in the districts of Thane, Raigad, Ratnagiri, Sindhudurg, Dhule, Jalgaon, Nasik, Pune, Ahmednagar, Satara and Kolhapur. The largest acreage are found in the Konkan region comprising Thane, Raigad, Ratnagiri and Sindhudurg district. According to 1st Advance Estimates of Production of Food grains for 2021-22, ragi production estimate was 1.52 million tonnes as against 1.96 million tonnes in 2020-21. Out of these the area, production and productivity in Maharashtra *kharif* 2017-2018 was total area 0.801 lakh ha, production 0.848 lakh tones and productivity 1059 kg/ha (Directorate of Agriculuture, Government of Maharashtra, 2021).

The drought tolerance of finger millet may be attributed to an efficient antioxidant potential and increased signal perception. Being as hardy crop it is relatively easy to grow under stressful regimes, without affecting the net productivity. Finger millet is one of the minor cereals which is highly nutritious and non- glutinous. It is known for various health benefits and some of the health benefits are its dietary fibre contents and non acid forming food. Finger millet is commonly called as “Nutritious millet” as its grains are nutritionally superior over other cereals. It is considered one of the least allergenic and most digestible grains available. In the rainy or cold seasons finger millet is used to heat the body as it is the warming grain. It stands out as the richest source of calcium (380-450 mg/100g) among all the cereals. It has 10 times more calcium than brown rice, wheat or maize and 3-fold higher calcium than milk. Besides calcium, finger millet is also very rich source of iron (3.39 mg/100g), zinc (1.5 mg/100g), crude fibre (3.6 mg/100g), essential amino acids, valine (413 mg/100g of protein), leucine (594 mg/100g of protein) and slowly digestible starch and phytochemicals like polyphenols. The minerals, dietary fibre, vitamins and phenolics are present in the outer coat of the seed which form the part of the food and gives their nutritional and health benefits (Chandra *et al*., 2016). Finger millet contains high amounts of protein (3-6.5%), mineral nutrient as compared to other major cereals like sorghum, rice, wheat (Gupta *et al*. 2017). Finger millet is well known for its exceptionally high calcium (Ca) content having about 0.34% in whole seeds as compared with 0.01–0.06% in most other cereals (Kumar *et al*. 2016; Gupta *et al*. 2017). The seeds contain good amount of dietary fiber, iron, essential amino acids viz., isoleucine, leucine, methionine, phenylalanine, pytates and trypsin inhibitory factors, and are also gluten-free (Chandra *et al*. 2016; Sood *et al*. 2016).

Finger millet straw is excellent and nutritive as animal fodder contains a total of 60% digestible nutrients which can be fed hay or as green. It is rich source of dietary calcium and fiber for people suffering from calcium deficiencies. Finger millet is important but underutilized crops in tropical and semiarid regions of the world as it can be grown on low fertility soils and is not dependent on the use of chemical fertilizers. Finger millet got its popular name “famine crop” as it can resist storage pests for as long as 10 years and also ensures round the year food supply or even during a crop failure (Mgonja *et al*., 2007). It is also known to be one of the most efficient utilizer of nitrogen (Gupta *et al*. 2017).

The success of plant breeding programme mainly depend upon the efficiency of selection technique and the genetic variability available in breeding population. For choosing the diverse parents for purposeful hybridization the precise information on the degree and nature of genetic diversity helps the plant breeder. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like finger millet where hybridization is difficult, there being limited scope for making large number of crosses by random mating and hence, the information regarding the nature of genetic diversity of the parents to be used in the hybridization, is of paramount importance in finger millet breeding programme. The aim of manuscript is to depict diversity different genotypes of Finger millet to improved the breeding strategies.

**Materials and Methods :**

The present investigation, entitled was conducted at Zonal Agricultural Research Station, Shenda Park, Kolhapur during *kharif*, 2023-24. The experimental material for the genetic diversity consisted of 37 indigenous genotypes of finger millet collected from All India Co-ordinated Research Project on small millets ZARS, Kolhapur (Table 1). The experiment was conducted by following Randomized Block Design (RBD) with three replications. Sowing was carried by following dibbling method. Each entry was represented by four rows of 5.0 meter length. The spacing of 30 cm between the rows and 10 cm between plants i.e. 30 x 10 cm spacing . Two border rows along the length of each replication were grown to avoid the border effects. The required intercultural operations as well as nutrient management applied as per necessity.

The observations were recorded on five randomly selected plants from each treatment in each replication for all the eleven morphological characters except days to 50% flowering and days to maturity. However data on days to 50 per cent flowering and days to maturity was noted on plot basis. The observations on all eleven characters further used for statistical computation and for the genetic diversity study.

**Table 1 : List of thirty seven Finger millet genotypes used under present study**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sr.****No.** | **Genotype** | **Sr.****No.** | **Genotype** | **Sr.****No.** | **Genotype** |
| **1** | KFMG-2201 | **15** | KFMG-2215 | **29** | KFMG-2229 |
| **2** | KFMG-2202 | **16** | KFMG-2216 | **30** | KFMG-2230 |
| **3** | KFMG-2203 | **17** | KFMG-2217 | **31** | KFMG-2240 |
| **4** | KFMG-2204 | **18** | KFMG-2218 | **32** | KFMG-2241 |
| **5** | KFMG-2205 | **19** | KFMG-2219 | **33** | KFMG-2242 |
| **6** | KFMG-2206 | **20** | KFMG-2220 | **34** | Phule Nachani |
| **7** | KFMG-2207 | **21** | KFMG-2221 | **35** | Phule Kasari |
| **8** | KFMG-2208 | **22** | KFMG-2222 | **36** | Dapoli-3 |
| **9** | KFMG-2209 | **23** | KFMG-2223 | **37** | VL-376 |
| **10** | KFMG-2210 | **24** | KFMG-2224 |  |  |
| **11** | KFMG-2211 | **25** | KFMG-2225 |  |  |
| **12** | KFMG-2212 | **26** | KFMG-2226 |  |  |
| **13** | KFMG-2213 | **27** | KFMG-2227 |  |  |
| **14** | KFMG-2214 | **28** | KFMG-2228 |  |  |

**Results and Discussion**

In current investigation the Mahalanobis distance statistic (D2) (1936) was used to calculate the genetic diversity between genotypes. Plant breeders uses it to categorise genetic stocks according to genetic divergence between populations.

The D2 values that were computed as inter and intra cluster distance which ranged from 46.37 to 1613.13 depicted in Table No. 2. The diagrammatic representation as a cluster diagram depicted in Fig 1. The highest value was seen between clusters X and XII, while the lowest value was found between clusters II and IX (46.37). Rao (1952) described Tocher's approach, which was used in the formation of the cluster. The all 37 genotypes were categorised into twelve clusters using D2 analysis. Cluster II and VI comprising six genotypes, were found to be the largest clusters based on cluster analysis. On the other hand, Cluster IV and V had five genotypes, while cluster I and III contained four genotypes and cluster VII comprising two genotypes. Single genotype was present in each of the clusters VIII, IX, X, XI and XII. Table 3 displays these clusters and the genotypes that fall under them.

Cluster VI had the highest intra-cluster distance (30.32), followed by cluster IV (29.14) while cluster III had the lowest intra-cluster distance (17.06), followed by cluster I (18.85). Because of solitary clusters there were no intra-cluster distances observed in the clusters VIII, IX, X, XI, and XII. When taking inter-cluster distance into consideration., between cluster X and XII (1613.13) had the largest inter-cluster distance, followed by cluster IX and X (1498.81) and cluster III and XII (1359.00) therefore genotypes from this clusters can utilized in hybrid development strategies. While on the other hand, cluster II and IX (46.37) had the lowest inter-cluster distance, followed by cluster I and VII (47.89) and cluster VI and VIII (48.57).

The average/mean performances for the twelve character cluster for the thirteen characters under study was depicted in Table 4. Regarding the twelve characters under study, there was a noticeable significant inter-cluster variation found among the different clusters. For days to 50% flowering, the cluster means ranged from 67.66 (cluster II) to 83.66 (cluster VIII and X).

For days to maturity, the cluster means ranged from lowest 99.53 (cluster VII) to highest 129.42 (cluster IX). For number of productive tillers per plant, the cluster means ranged from 1.09 (cluster IX) to 7.19 (cluster X). For plant height at maturity, the cluster means ranged from 77.21 cm (cluster VIII) to 104.07 cm (cluster X).

**Table No. 2 : Average intra and inter cluster D2 and D (in parenthesis) values in Finger millet**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster** | **I** | **II** | **III** | **IV** | **V** | **VI** | **VII** | **VIII** | **IX** | **X** | **XI** | **XII** |
| **I** | **18.85****(4.34)** | 199.62(14.12) | 399.54(19.98) | 68.16(8.25) | 60.487.77) | 189.59(13.75) | 47.89(6.92) | 253.50(15.92) | 285.57(16.89) | 536.01(23.15) | 56.32(7.50) | 336.34(18.33) |
| **II** |  | **28.13****(5.30)** | 1070.96(32.72) | 69.78(8.35) | 402.87(20.07) | 707.58(26.60) | 159.89(12.64) | 796.64(28.22) | 46.37(6.80) | 1311.75(36.21) | 307.73(17.54) | 68.71(8.28) |
| **III** |  |  | **17.06****(4.13)** | 701.81(26.49) | 195.10(13.96) | 80.58(8.97) | 484.97(22.02) | 98.78(9.93) | 1242.92(35.25) | 52.42(7.24) | 332.46(18.23) | 1359.00(36.86) |
| **IV** |  |  |  | **29.14****(5.39)** | 192.6313.87) | 410.64(20.26) | 68.22(8.25) | 487.97(22.02) | 113.16(10.63) | 886.60(29.77) | 145.56(12.06) | 149.30(12.21) |
| **V** |  |  |  |  | **21.64****(4.65)** | 69.17(8.31) | 100.99(10.04) | 127.005(11.26) | 502.75(22.42) | 295.89(17.20) | 65.85(8.11) | 581.05(24.10) |
| **VI** |  |  |  |  |  | **30.32****(5.50)** | 273.71(16.54) | 48.57(6.96) | 844.35(29.05) | 121.70(11.03) | 154.72(12.43) | 945.57(30.75) |
| **VII** |  |  |  |  |  |  | **20.21****(4.49)** | 368.43(19.19) | 216.88(14.72) | 684.0526.15) | 103.36(10.16) | 288.12(16.92) |
| **VIII** |  |  |  |  |  |  |  | **0** | 946.85(30.77) | 114.13(10.68) | 203.98(14.28) | 1099.20(33.15) |
| **IX** |  |  |  |  |  |  |  |  | **0** | 1498.81(38.714) | 414.26(20.35) | 65.50(8.09) |
| **X** |  |  |  |  |  |  |  |  |  | **0** | 457.92(21.39) | 1613.13(40.16) |
| **XI** |  |  |  |  |  |  |  |  |  |  | **0** | 481.13(21.93) |
| **XII** |  |  |  |  |  |  |  |  |  |  |  | **0** |

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# Fig 1 : Cluster Diagram of twelve clusters along with distance as D value

# Table No. 3 : Distribution of 37 genotypes of finger millet into different clusters

|  |  |  |
| --- | --- | --- |
| **Clusters** | **No. of genotypes included** | **Genotypes** |
| I | 4 | KFMG-2203, KFMG-2221, KFMG-2205, KFMG-2220 |
| II | 6 | KFMG-2226, KFMG-2229, KFMG-2217, KFMG-2225, KFMG-2207, KFMG-2214 |
| III | 4 | KFMG-2234, KFMG-2235, KFMG-2236, KFMG-2237 |
| IV | 5 | KFMG-2224, KFMG-2240, KFMG-2219, KFMG-2222, KFMG-2210 |
| V | 5 | KFMG-2201, KFMG-2206, KFMG-2232, KFMG-2204, KFMG-2212 |
| VI | 6 | KFMG-2215, KFMG-2211, KFMG-2209, KFMG-2202, KFMG-2230, KFMG-2228 |
| VII | 2 | KFMG-2227, KFMG-2218 |
| VIII | 1 | KFMG-2213 |
| IX | 1 | KFMG-2208 |
| X | 1 | KFMG-2208 |
| XI | 1 | KFMG-2242 |
| XII | 1 | KFMG-2216 |

# Table 4 : Mean performance of 12 clusters for 12 characters in finger millet

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster No.** | **Days to 50% flowering (No.)** | **Days to maturity (No.)** | **Productive tiller per plant (No.)** | **Plant height at maturity****(cm)** | **Flag leaf blade length****(cm)** | **Flag leaf blade width****(cm)** | **Peduncle length (cm)** | **Finger length (cm)** | **Finger width (cm)** | **Fingers per plant (No.)** | **1000****grain weight (g)** | **Grain yield per plant (g)** |
| I | 77.50 | 113.10 | 3.67 | 91.15 | 27.62 | 0.85 | 19.82 | 6.99 | 0.75 | 7.50 | 2.35 | 8.38 |
| II | 78.27 | 108.25 | 1.79 | 78.58 | 25.18 | 0.88 | 21.71 | 5.01 | 0.87 | 8.27 | 2.21 | 6.08 |
| III | 67.66 | 102.59 | 6.59 | 101.88 | 25.02 | 0.87 | 22.97 | 9.47 | 0.87 | 9.08 | 3.10 | 13.01 |
| IV | 78.26 | 119.43 | 2.66 | 87.19 | 27.70 | 0.88 | 21.30 | 6.10 | 0.86 | 8.26 | 2.49 | 7.25 |
| V | 78.86 | 113.60 | 4.69 | 94.43 | 27.43 | 0.90 | 23.52 | 7.71 | 0.79 | 8.20 | 2.57 | 9.61 |
| VI | 82.05 | 116.89 | 5.65 | 94.97 | 27.44 | 0.88 | 21.58 | 8.59 | 0.83 | 7.88 | 2.86 | 10.81 |
| VII | 73.33 | 99.53 | 3.42 | 86.14 | 27.16 | 0.81 | 27.80 | 6.48 | 0.86 | 8.16 | 2.28 | 7.77 |
| VIII | 83.66 | 123.60 | 5.74 | 77.21 | 24.46 | 0.86 | 18.66 | 8.81 | 0.93 | 7.66 | 2.96 | 10.84 |
| IX | 78.33 | 129.42 | 1.09 | 78.11 | 28.10 | 0.96 | 28.70 | 5.40 | 0.90 | 8.00 | 2.05 | 5.34 |
| X | 83.66 | 120.53 | 7.19 | 104.07 | 24.60 | 0.90 | 19.26 | 9.83 | 0.66 | 8.33 | 3.21 | 13.71 |
| XI | 75.00 | 102.56 | 4.21 | 89.97 | 29.23 | 1.23 | 19.36 | 7.31 | 0.93 | 7.33 | 3.53 | 8.91 |
| XII | 81.33 | 121.45 | 1.37 | 100.49 | 27.26 | 0.96 | 21.60 | 4.48 | 0.86 | 9.66 | 2.11 | 5.47 |

For flag leaf blade length, the cluster means ranged from 24.46 cm (cluster VIII) to 29.23 cm (cluster XI) and for flag leaf blade width, the cluster means ranged from 0.81 cm (cluster VII) to 1.23 cm (cluster XI). For peduncle length, the cluster means ranged from 18.66 cm (cluster VII) to 28.70 cm (cluster IX). For finger length, the cluster means ranged from 4.48 cm (cluster XII) to 9.83 cm (cluster X). For finger width, the cluster means ranged from 0.66 cm (cluster X) to 0.93 cm (cluster VIII and XI). For number of fingers per plant, the cluster means ranged from 7.33 (cluster XI) to 9.66 (cluster XII). For 1000 grain weight, the cluster means ranged from 2.05 g (cluster IX) to 3.53 g (cluster XI). For grain yield per plant, the cluster means ranged from 5.34 g (cluster IX) to 13.71 g (cluster X).

The aforementioned results indicated that the selection of better parents for a hybridization programme is based on cluster divergence and cluster formation. Twelve clusters were formed in the current study as a result of the Tocher's approach. The majority of the genotypes were found in cluster I and cluster VI. Cluster IV and V had five genotypes, while cluster I and III contained four genotypes and cluster VII comprising two genotypes. Single genotype was present in each of the clusters VIII, IX, X, XI and XII. Twelve clusters based on genotype grouping showed a comparatively high level of genetic variation in the sample under study. As the clusters VIII, IX, X, XI and XII were mono-genotypic, there was significant variation between them and the remaining population. This means that these genotypes differ greatly from each other in terms of their genetic composition.

Cluster X and XII were determined to have the greatest inter-cluster distance. The cluster VI had the greatest intra-cluster distance, indicating that the genotypes inside these clusters may have distinct genetic compositions. The five monogenic clusters, VIII, IX, X, XI and XII, demonstrated zero intra-cluster distance, which is consistent with the findings of Reddy *et al*. (1993). It is shown that there was a large range of variability among the clusters for every character based on the mean performances of the 12 clusters.

The per cent contribution of each character in estimating divergence among the 37 finger millet genotypes was in Table No. 5. The character productive tillers per plant (50.60%) out of the 12 characters under study had the most contribution to divergence. The weight of 1000 grains (20.00%), flag leaf blade width (12.19%) and peduncle length (9.08%) were the next three characters. The least amount of input to divergence was shown by the character finger width (0.03%), which was followed by the flag leaf blade length (0.15%), days to 50 % flowering (0.30%), days to maturity (0.30%), grain yield per plant (0.75%), fingers per plant (1.80%), plant height at maturity (2.25%) and finger length (2.55).

The similar findings were reported by Desai (2012) for plant height at maturity, days to 50 per cent flowering and days to maturity. The comparable results also reported by Charitha *et al*. (2023) and Hema *et al*. (2025). Also Bedis *et al*. (2007) exhibited similar outcomes for plant height at maturity and number of productive tillers per plant. Jaylal and Haider (1994) for number of productive tillers per plant.

# Table 5: Per cent contribution of 12 characters for divergence in finger millet

|  |  |  |  |
| --- | --- | --- | --- |
| **Sr.****No.** | **Source** | **Times ranked first** | **Contribution percentage** |
| **1** | Days to 50% flowering (No.) | 2 | 0.30% |
| **2** | Days to maturity (No.) | 2 | 0.30% |
| **3** | Productive tiller per plant(No.) | 337 | 50.60% |
| **4** | Plant height at maturity (cm) | 15 | 2.25% |
| **5** | Flag leaf blade length (cm) | 1 | 0.15% |
| **6** | Flag leaf blade width (cm) | 108 | 12.19% |
| **7** | Peduncle length (cm) | 167 | 9.08% |
| **8** | Finger length (cm) | 17 | 2.55% |
| **9** | Finger width (cm) | 0 | 0.03% |
| **10** | Fingers per plant (No.) | 12 | 1.80% |
| **11** | 1000 grain weight (g) | 5 | 20.00% |
| **12** | Grain yield per plant (g) | 2 | 0.75% |
|  |  | Total | 100 |

**Conclusion :**

According to the current study electing parents based on the highest genetic divergence for the majority of yield-contributing characters would be preferable. The 37 genotypes were categorized into twelve clusters using D2 analysis. The highest value was found between clusters X and XII, while the lowest value was found between clusters II and IX. Also, Cluster X and XII, Cluster IX and  Cluster III and X  show the largest inter-cluster distance, hence the genotypes present in this cluster viz., KFMG-2234, KFMG-2235, KFMG-2236, KFMG-2237, KFMG-2216, KFMG-2208 and KFMG-2208 can be employed in upcoming breeding programs for development of hybrids.

The character productive tillers per plant, weight of 1000 grains, flag leaf blade width and peduncle length contributed most to the genetic divergence hence it indicate relative significance of this characteristics in the selection of parents for a hybridization programme

Effective breeding programs hinge on selecting parent plants that prominently display desirable, economically valuable traits. Consequently, genetic diversity is a cornerstone of successful crop improvement. While various parent selection methods exist, leveraging diversity offers unique advantages. This study aimed to quantify the genetic variability among different genotypes, providing valuable insights for identifying optimal parent combinations for future crosses. These findings can guide breeders in creating new varieties with enhanced performance and resilience.

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