Exploring Genetic Variability: Unraveling Correlations through Path and multivariate analysis in finger millet (*Eleusine coracana* L.)

ABSTRACT

The experiment was carried out using a Randomized Block Design (RBD) with three replicates. The trials were entirely composed of fifty-two genotypes for yield and their contributing characters for 13 different characters. For every attribute under study, an analysis of variance showed a highly significant difference. Among the genotypes studied, the evaluated characteristics showed varying degrees of heritability, genetic advancement, and variability. Both the genotypic and phenotypic coefficients of variation (PCV and GCV, respectively) ranged from low to high. particular for the percentage of fingers per ear (17.47% and 17.50%), ear weight per plant (g) (13.42% and 16.28%), and 1000 seed weight (g) (11.79% and 14.09%), the modest GCV and PCV values were observed respectively. Plant height (cm) (81.60%, 28.47) had the greatest wide sense heritability value, with the highest genetic advance, followed by ear weight per plant (g) (67.95%, 20.13). Thus, the findings of this study indicate that these genotypes have diversity in yield and other yield-related features, which should be exploited in subsequent breeding. The correlation and path coefficient analyses for yield and yield characteristics shows grain yield per plant showed a strong positive relationship both at the genotypic and phenotypic levels, with days to 50% flowering, days to maturity, ear weight per plant, and harvest index. Path analysis showed that for genotypic and phenotypic coefficients, harvest index (0.33, 0.46) and ear weight/plant (0.86, 0.39) showed the most positive direct effects. These characteristics might thus be applied as selection criteria to identify finger millet genotypes that show promising results in future breeding. Multivariate approaches such as principal component analysis and cluster analysis are crucial statistical tools for examining genetic diversity in plant breeding programs, as are their significant quantitative features. Based on principal component analysis, the entire variance was provided by six main components, of which PC-1 and PC-2 contributed 21.97% and 18.32%, respectively, to the total variability. Euclidean distance was used to divide the fifty-two genotypes into five groups. The largest number of genotypes (twenty-two) in Cluster I was followed by Cluster III, with 16 genotypes. As a result, genotypes from these clusters may be used as parents for hybridization.

Keywords: Finger millet, Genetic variability, Heritability, Genetic advance, Phenotypic coefficient of variation.

1. INTRODUCTION

The grass family Poaceae includes finger millet (*Eleusine coracana* (L.) 2n=36), a crop that is widely grown in arid and semi-arid regions of the world. Nonetheless, it is also known by other names such as Mandia and Ragi. Finger millet has high levels of calcium (0.38%),

protein (6–13%), fiber (18%), carbohydrates (65-75%), minerals (2.5–3.5%), fat (1.29%), and iron (3.90 mg/100g). It is also known to have antimicrobial, antitumorigenic, antidiabetic, and antiulcer properties. These attributes make it significant from a nutraceutical perspective [1],[2],[3]. Testa, which is often high in dietary fiber and micronutrients, is ground with finger millet to make flour, and the entire meal is used to make traditional dishes [4].

The millet is the most produced and exported from India worldwide. India produces 1601.46 tonnes of millets annually, with Karnataka accounting for 1125.73 tonnes of that total. It is extensively grown in Karnataka, Tamil Nadu, Orissa, Andhra Pradesh, Madhya Pradesh, and Jharkhand, according to the Indian Ministry of Agriculture and Farmers' Welfare (2011–2023). Given that the need for millets is increasing daily to meet the needs of an expanding population, one issue with finger millet is the absence of high-yielding cultivars, which results in poor productivity. The finger millet germplasm is widely available in India; it consists mostly of native and traditional varieties with a wide variety of alleles that may be exploited in crop improvement schemes [5]. As a result, for a certain per capita yield with quality, the rate at which new types are developed and their qualities also need to exceed what occurs as the population expands. Expanding the output requires an understanding of genetic variability, heritability, and sensitivity to selection. Finger millet has tremendous variability, indicating room for major improvements [6].

Through the integration of route analysis and correlation, a deeper comprehension of the causal linkages between various character pairs can be gained. Understanding character connections and the direct and indirect impacts of each character on yield will be helpful in the selection process. A complete knowledge of the link between yield and grain output is provided by correlation and route analyses, which determine the degree of dependency between yield and its constituent elements, as well as the relative importance of their direct and indirect impacts. Ultimately, this type of study might help breeders create selection plans to increase grain output.

Effective selection can be made by assessing the cause-and-effect relationship by splitting the path coefficient analysis into direct and indirect contributions (effects) of different traits to the dependent variable. This division was first proposed by Wright et. al., [7] and described by Dewey et. al., [8]. The current study was conducted to investigate the character connections in finger millet genotypes to boost output and per capita productivity in light of the aforementioned circumstances. Through the identification of the minimal number of components, PCA assists in explaining the highest variability of all variables contributing to the yield [9]. It reduces big datasets and identifies a limited number of critical independent variables without altering the main causes of genotype-to-genotype variability [10].

2. MATERIAL AND METHODS

2.1. Experimental materials

The 52 finger millet genotypes (Supplementary Table 1) used in this investigation were collected from various locations across India, including the M.S. Swaminathan Research Foundation in Jeypore, Odisha, and the Indian Institute of Millets Research in Hyderabad. The research was carried out during the Rabi season of 2021–2023, at the PG research farm, Department of Genetics and Plant Breeding, Centurion University of Technology and Management, Parlakhemundi, Odisha. Three replications and a randomized block design were used to set up the experiment.

2.2. Observations recorded

Observations were recorded from three randomly selected plants in each accession for 13 quantitative characters like, plant height (cm), number of tillers per plant, number of productive tillers per plant, number of fingers per ear, finger length (cm), finger width (cm), flag leaf area $(cm)^2$, ear weight per plant (g), 1000 seed weight (g), harvest index (%), and grain yield per plant while. Days to 50% flowering and days to maturity were recorded on plot basis, harvest index calculated as

"Harvest index "(%) = "Grain yield "/"Biological yield"×100.

2.3. Statistical analysis

2.3. 1. Analysis of variances

All gathered data were subjected to analysis of variance (ANOVA) using the appropriate computer software (SAS, version 9.3). The means and ranges for the relevant parameters were then separated using Tukey's range test (critical difference) at a probability of 0.05. A statistical study was conducted on the mean values of the five plants. Data for various characteristics were subjected to statistical analysis for significance using the analysis of variance approach [11].

2.3. 2. Phenotype and genotype variability

Range, mean, standard error, phenotypic and genotypic variance, and coefficient of variation were used to estimate the genotype variability. The resulting components of variance were then used to compute the phenotypic and genotypic variation and genetic progress as follows:

σ^2 g=(σ^2 t-σ^2 e)/r

Where, σ2 g = genotypic variance, σ2 t = mean square of treatment, σ2 e = error mean square, and r = number of replicates.

σ^2 p=σ^2 g+σ^2 e

Where, σ2 p = Phenotypic variance.

According to [12], the phenotypic and genotypic coefficients of variance, PCV and GCV, respectively, are expressed by the following formula:

GCV(%)=√(σ2 g)/x X100

PCV(%)=√(σ2 p)/x X100

According to [13], GCV and PCV levels were classified as low when less than 10%, moderate, 10–20%, and high, higher than 20%.

2.3. 3. Genetic Advance (GA), Heritability, and GA as a percentage of mean

The following formula was used to determine each trait's heritability in the broadest sense [14].

H^2 (%)=(σ^2 "g")/(σ^2 "p") "x" 100

The expected genetic advance (GA) under selection, assuming a selection intensity of 5%, was calculated as proposed [33]:

GA=X(√(σ2 P) (σ^2 "g")/(σ^2 "p") = k*h*√(σ2 P) = k*H*σ

σ = standard deviation), K = standardized selection differential.

GAM = (GA/X) x100

Where, GAM = Genetic expected mean, X = Grand mean.

2.3.4. Correlation coefficient: In a correlation study, this metric expresses the magnitude of the linear relationship between two variables. The proposed formula was used to estimate the correlation coefficients [15].

2.3.5. Path coefficient analysis: This is used to separate the direct and indirect effects through attributes by partitioning the correlations. Path coefficient analysis, using the formula suggested by Dewey et. al., [8].

2.3.6. Mahalanobis D2 analysis: D 2 statistics analysis is used for selection of genetically divergent parents in hybridization programme [16]

The data were subjected to statistical analysis using RStudio-4.2 [17].

3. RESULTS AND DISCUSSION

3.1. Descriptive statistics

The estimates of mean performance on grain yield per plant and its attributes showed that Bada mandia (21.99) had the highest grain yield per plant, followed by VR 1233 (21.08), and VR 1220 (20.58) (Table 3). The frequency distribution graph shows the plant height, days to 50% flowering, days to maturity, number of tillers per plant, number of productive tillers per plant, number of fingers per ear (cm), finger length (cm), finger width (cm), flag leaf area (cm2), ear weight per plant (g), 1000 seed weight (g), harvest index (g) (Supplementary figure 1).

3.2. Analysis of variance for different quantitative characters

The analysis of variance revealed significant differences among genotypes for all the characters under study due to their wide variability, which may be exploited for the selection of suitable traits for use in crop improvement programs (Supplementary 2). Analysis of variance revealed the mean sum of squares of genotypes for different characteristics like plant height (cm), days to 50% flowering, number of fingers, finger length (cm), flag leaf area (cm2), ear weight per plant (g), harvest index (%), 1000 seed weight (g), and grain yield per plant (g) showed significance at 0.01%. The number of tillers per plant, number of productive tillers per plant, and finger width (cm) were significantly different ($p < 0.05$). Analysis of variance revealed that all characters used in the study showed significant variation among the genotypes (Supplementary table 1).

3.3. Genetic variability, Heritability and Genetic advance

The genotypic coefficient of variation for all the characters under study was less than the phenotypic coefficient of variation, indicating an environmental effect on the characters (Supplementary 6). High PCV coupled with high GCV was observed for characters such as the number of fingers per ear (17.50, 17.47) ear weight per plant (g) (16.28,13.42) respectively. These characteristics should be selected for future studies. Similar results were also reported by Chunilal et al. [18], Deshmukh et al. [19], Devi et al. [20]. While, some of the characters showing like days to 50% flowering (4.60), days to maturity (4.34), and grain yield per plant (5.36) not selected because to higher influence of environment on traits.

All characters under study showed high to moderate heritability (Supplementary Table 4). Characteristics such as the number of fingers (99.64), finger length (91.19), number of tillers per plant (89.70), plant height (81.60), days to maturity (76.95), number of productive tillers per plant (75.20), 1000 seed weight (70.09), plant height (28.47), ear weight per plant (20.13) with high heritability, and high genetic advance should be selected for future finger millet crop improvement programs.

3.4. Correlation coefficient

In the present study, grain yield per plant was found to be significantly correlated each other at 1% and positively correlated with days to 50% flowering, ear weight per plant (g), and harvest index, indicating that these attributes were mainly influenced the grain yield in finger millet. The correlation between all possible combinations of the characters was estimated at the genotypic and phenotypic levels (Supplementary table 5 and 6). Selection for all positively correlated traits will improve both traits simultaneously, with a corresponding increase in yield. Similar results exhibiting highly significant and positive correlations between grain yield and other traits, as obtained in the present investigation, were also reported by Dewey et al. [21], Morrison et al. [22], Devi et al. [20].

3.5. Path coefficient analysis

In the present study, path coefficient analysis was performed at genotypic and phenotypic levels. Plant height, number of tillers per plant, number of fingers per ear, finger length (cm), ear weight per plant (g), and harvest index (%) had positive direct effects on grain yield per plant at both the genotypic and phenotypic levels (Supplementary 9 and 10). Characteristics such as days to maturity, number of productive tillers per plant, number of fingers per ear, finger width, flag leaf area and 1000 seed weight had a direct and negative effect on grain yield at the genotypic level. Characteristics such as days to 50% flowering, number of tillers per plant, number of productive tillers per plant, finger width, flag leaf area, and 1000 seed weight had shown direct and negative effects. The selection of these characters will increase the yield per plant, which will help in direct future improvement in finger millets, leading to an increase in yield. These characteristics have also been identified as major direct contributors to the grain yield in finger millet by former workers [22, 23, 24, 25, 26]. Selection of positive and indirect correlated traits i.e., days to 50% flowering, number of tillers per plant, finger length (cm), ear weight per plant (g), harvest index (%) (Supplementary table 7 and 8) leads to improvement in yield by selecting the trait of interest.

In addition, the residual effect was less for both genotypic and phenotypic traits in the path coefficient analysis, showing that the selected traits have significant contributions towards yield.

3.6. Principal component analysis (PCA)

PCA helps explain the maximum variability of total variables contributing to yield through the identified minimum number of components [27, 9].

The data presented Supplementary table 10 reveal that PCA can support the findings from the D^2 analysis and highlight the primary factors that contribute to genotype-to-genotype variability by condensing large data sets and identifying a small number of crucial independent variables without changing the original variability of the data [10]. In present study, the original data were recovered into six PCs with eigenvalues greater than one (Figure no. 1), which accounted for 76.58% of the overall variation among the fifty-two finger millet genotypes evaluated for 13 quantitative parameters (Supplementary table 9). The first few PCs have a considerable influence on overall variability, depending on a variety of plant properties [28].

The fig 2 biplot was made for the individuals and variables in PC1 and PC2, which were constitute a total variance of 21.97%. The characteristics associated with PC1 were grain yield, days to 50% flowering, days to maturity, harvest index these characters were positively associated with PC1. Genotypes VR 1214, FMCFMVZ, CFMV1, PR 202, and BR 9 are associated with grain yield.

The data shown in Supplementary table 9 indicate that the major contributors to PCs were determined from the loading factor values. The PC1 accounted for approximately 21.97% of the total variation. It can be seen from the harvest index (0.75), 1000 seed weight (0.51), ear weight/plant (0.50), and days to maturity (0.49), which had a maximum positive contribution towards divergence, and the number of productive tillers per plant (-0.69), number of tillers per plant (-0.62), and plant height (-0.40) had a negative contribution towards genetic divergence. PC1 was regarded as a major component of yield because it included several traits associated with grain yield per plant.

The PCII explained 18.32 % of total variation and highly positive scores for grain yield (0.82), plant height (0.49). Number of tillers per plant (- 0.67), 1000 seed weight (-0.55), and number of fingers per plant (-0.51) showed the maximum negative contribution towards divergence and the characters

The PCIII vector, which accounted for 13.59 percent total variance, the characters days to maturity (0.65), days to 50% flowering (0.64), number of fingers per ear (0.56), flag leaf area (0.50) had maximum positive contribution, while finger width (- 0.29), grain yield (-0.17) had maximum negative contribution towards genetic diversity respectively.

The PCIV vector had 8.85 percent of the total variance, and the characters followed by finger width (0.45), plant height (0.36), and days to maturity (0.17) had a maximum positive contribution, whereas the number of tillers per plant (-0.46), number of productive tillers per plant (-0.42), harvest index (-0.40), and ear weight per plant (-0.25) had the maximum negative contribution towards genetic diversity.

PCV had a variability of 7.37 percent of the total variance towards the genetic diversity and the characters finger width (0.61), ear weight per plant (0.44), number of tillers per plant (0.38), harvest index (0.25), plant height (0.25) had maximum positive contribution, whereas days to 50% flowering (-0.21), days to maturity (-0.12) had maximum negative contribution towards the genetic diversity.

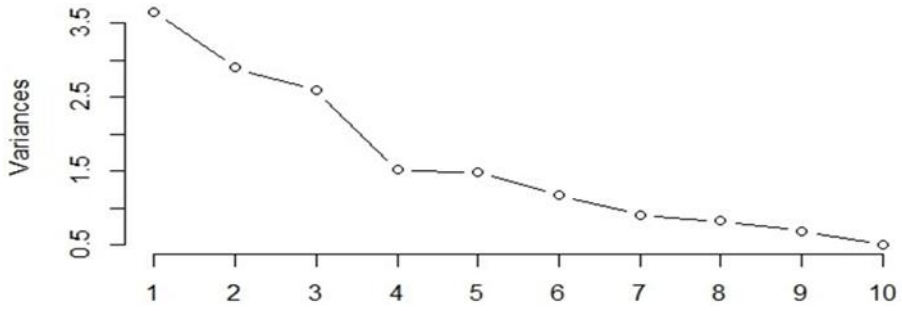

Fig 1: Scree Plot

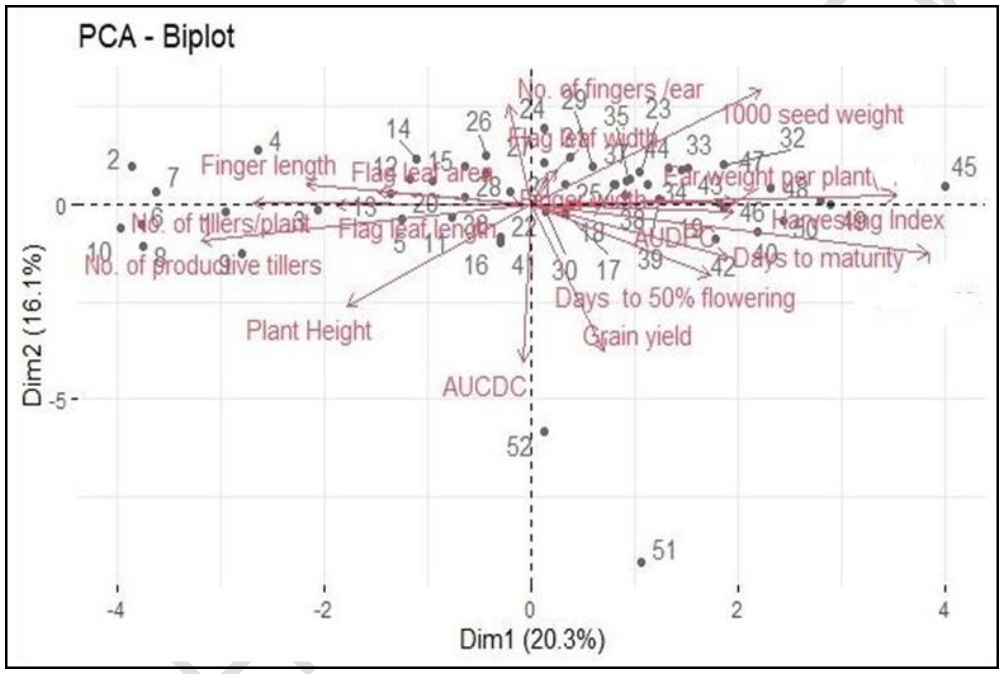

Fig 2: Biplot

3.7. Contribution of different characters towards divergence

The estimates of the percent contribution of each character to total genetic divergence are presented in Supplementary table 11. The results highlighted that the character flag leaf area(9.40%) was the major contributor to genetic divergence, followed by character ear weight per plant (9.04%), 1000 seed weight (8.31%), plant height (8.06%), finger width (8.05%), number of tillers per plant (6.71%), harvest index (6.14%), number of productive tillers per plant (5.57%), days to 50% flowering (4.88%), finger length (4.19), number of fingers per plant (2.83%), grain yield per plant (2.82%), and days to maturity (2.35%).

3.8. Genetic divergence analysis through D^2 statistics.

The estimated values of D^2 between genotypes were used to cluster the genotypes as the sum of squares of the differences between the mean values of all examined features. All fifty-two genotypes, including the checks, were classified into five major clusters using

torcher's approach [29]. All the fifty-two genotypes were divided into five primary clusters, with cluster I having the maximum number of genotypes, that is 22 (KMR656, FIN5164, FeZn84, DPLM2, VR 1225, PR-1639, TAYA, KOPN1056, Bhairabhi, PR202, VL 352, PR1506, BR9, VR1185, VR1222, FMCFMVZ, VR1218, VR1228, Muskuri, FeZn15,VR1226, Indaf-7). Cluster III includes (Chilli, DPLM3, FM1, FIN6164, Dangardi, Badtara, CFMV1, Telugu mandia, VR1214, Lalsuru mandia, Bada mandia, VR1220, VR1233, GPV67, Bada kumunda, VL400). Cluster II (TNEC1335, VR1217, VR1221, OEB610, KMR711, FIN5169), and cluster IV (WN572, Uduru, PR1630, FIN5167, FM4, DPLM3). Cluster V (VR1176).

3.9. Mean intra and inter cluster distance

The data shown in bold are intra cluster distances, while the other data represent inter cluster distances (Supplementary table 12), revealing that the estimates of intra cluster D values ranged from (0.00-148.90). Cluster III had the maximum D value (148.90), followed by cluster II (113.78), and cluster I (95.83). The highest inter cluster distance was recorded between cluster I and cluster V (229288.68), while the lowest distance was recorded between the inter cluster II and IV (32515.21).

3.10. Mean performance of clusters for quantitative traits in finger millet

The estimation of the mean performance of all characters for all clusters is presented in (Supplementary table 13). Clusters V (23.63) and IV (23.55) had the highest and lowest grain yield per plant, respectively. The genotypes in cluster IV had the highest mean plant height (87.38), whereas those in cluster II had the lowest mean plant height (83.34). Cluster I had the lowest days to 50% flowering (75.66), whereas cluster V had the longest days to 50% blooming (77.43). Cluster V (128.93) had the longest days to maturity, whereas Cluster I (126.35) had fewer days to maturity. The largest number of tillers per plant (7.61) was recorded for cluster III, whereas the lowest number (5.4) was recorded for cluster V. The genotypes in cluster III had more productive tillers per plant (6.47), whereas the genotypes in cluster V had the fewest tillers (4.33). Cluster III had the highest mean number of fingers (6.30), whereas cluster IV (6.11) had the lowest number of fingers. Cluster I reported a maximum mean finger length (6.38 cm) while cluster II recorded a minimum finger length of (5.71 cm). The genotypes found in cluster II had the highest mean finger width value (1.02 cm), whereas cluster IV had the lowest value (0.96 cm). Cluster V recorded the longest flag leaf area (41.59 cm), whereas cluster II recorded the shortest leaf area (34.44). The genotypes in cluster V had the highest average ear weight per plant (32.80 g), whereas cluster III had the lowest average ear weight per plant (25.31 g). Cluster IV recorded the highest mean harvest index value (49.07), whereas cluster III recorded the lowest value (40.51). The genotypes found in cluster I had a maximum mean value of 1000 seed weight (4.13 g), whereas cluster V had the lowest mean value (3.78 g). Cluster V had the highest grain yield (23.63 g), whereas cluster III had the lowest grain yield (20.77 g). Cluster I had the highest mean value (9.91), whereas Cluster II had the lowest mean value (8.22).

To achieve better heterosis and produce viable recombinants, it is vital to quantify genetic diversity within and between genotype groups. Several approaches have been suggested by Murthy et al. [30]. In contrast to indices based on morphological similarity and phylogenetic relationships, Mahalanobis generalized distance estimated by the D^2 statistic [29] is a special tool for population discrimination. Fifteen quantitative characters from fifty-two genotypes of finger millet were examined to measure diversity, and Mahalanobis generalized distance (D^2) was used to evaluate the fitness of the genotypes. Genetic divergence analysis aids in evaluating the nature of diversity to select genetically diverse genotypes for use in plant breeding programs.

3.11. Grouping of fifty-two finger millet genotypes based on D^2 analysis

The data shown in the (Supplementary table 14) revealed the working collection based on the D^2 value, fifty-two genotypes were grouped into five clusters. Among the five clusters, cluster I was the largest, comprising of (22 genotypes) followed by Cluster III (17 genotypes), Cluster II (6 genotypes), Cluster IV (6 genotypes), and Cluster V (one genotype). Additionally, depending on the intra- and inter cluster distances, genotypes within a cluster showed a limited range of genetic variation, whereas those between clusters showed a greater range of variability.

The clustering pattern showed that genotypes from various geographic regions formed distinct clusters, demonstrating that geographic diversity is not the primary determinant of genetic variation [31].

According to the aforementioned findings, in order to select genotypes with different genetic backgrounds, the material should be examined for important characteristics such grain yield per plot, flag leaf area, days to maturity, plant height, harvest index, and days to 50% flowering. These qualities facilitate the production of finger millet crops. Accordingly, there is no correlation between geographic variety and genetic diversity, and selection for these traits increases finger millet production. These findings are consistent with those of previous studies [32, 33, 34, 19, 21].

3.12. D^2 cluster analysis

The diversity of 52 finger millet genotypes was studied based on 13 quantitative characteristics using Mahalanobis D^2 statistics. Genetic divergence for yield and its attributing traits among the 52 finger millet genotypes are presented in (Supplementary 11). All 52 genotypes were grouped into five clusters. Among the five clusters, cluster I was the largest, comprising of (22 genotypes) followed by Cluster III (17 genotypes), Cluster II (6 genotypes), Cluster IV (6 genotypes), and Cluster V (one genotype). Additionally, depending on the intra- and inter cluster distances, genotypes within a cluster showed a limited range of genetic variation, whereas those between clusters showed a greater range of variability (Supplementary Table 14).

Supplementary table 12 shows that the estimates of intra-cluster D values ranged from (0.00-148.90). Cluster III had the highest D^2 value (148.90), followed by Cluster II (113.78), and Cluster I (95.83). The highest inter cluster distance was recorded between cluster I and cluster V (229288.68), while the lowest distance was recorded between the inter cluster II and IV (32515.21). The data shown in bold are intra cluster distance while, whereas the other data represent the inter cluster distance.

Clusters V (23.63) and IV (23.55) had the highest and lowest grain yield per plant, respectively. The genotypes in cluster IV had the highest mean plant height (cm) values (87.38), whereas those in cluster II had the lowest mean values (83.34). Cluster I had the lowest days to 50% flowering (75.66), whereas cluster V had the longest days to 50% blooming (77.43). Cluster V (128.93) had the longest days to maturity, whereas Cluster I (126.35) had fewer days to maturity. The largest number of tillers per plant (7.61) was recorded for cluster III, whereas the lowest number (5.4) was recorded for cluster V. The genotypes in cluster III had more productive tillers per plant (6.47), whereas the genotypes in cluster V had the fewest tillers (4.33). Cluster III had the highest mean number of fingers (6.30), whereas cluster IV(6.11) had the lowest number of fingers. Cluster I reported a maximum mean finger length (6.38 cm) while cluster II recorded a minimum finger length of (5.71 cm). The genotypes found in cluster II had the highest mean finger width value (1.02

cm), whereas cluster IV had the lowest value (0.96 cm). Cluster V recorded the longest flag leaf area (41.59 cm), whereas cluster II recorded the shortest leaf area (34.44). The genotypes in cluster V had the highest average ear weight per plant (32.80 g), whereas cluster III had the lowest average ear weight per plant (25.31 g). Cluster IV recorded the highest mean harvest index value (49.07), whereas cluster III recorded the lowest value (40.51). The genotypes found in cluster I had a maximum mean value of 1000 seed weight (4.13 g), whereas cluster V had the lowest mean value (3.78 g). Cluster V had the highest grain yield (23.63 g), whereas cluster III had the lowest grain yield (20.77 g) (Supplementary Table 13). These findings match those of earlier studies by [35, 36, 37, 19, 21].

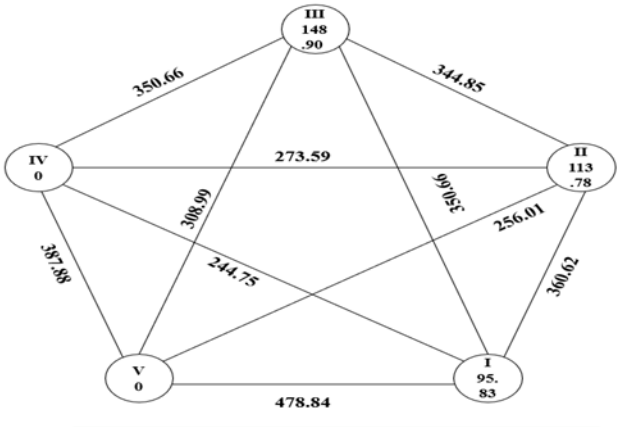

Fig 3: Mahalanobis Euclidean distance using Torcher's method

4. CONCLUSION

Analysis of variance revealed significant differences among the genotypes for all the characteristics under study. The estimates of mean performance on grain yield and its attributes highlighted that the genotype Bada mandia had the highest grain yield per plant, followed by VR 1233 and VR 1220, which may be exploited after critical evaluation. The estimates of phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation for all the characters under study, except days to 50% flowering, days to maturity, grain yield per plant, suggesting that environmental influences, in addition to genetic factors have a role in character expression. Genetic parameter analysis revealed that high GCV and PCV coupled with high heritability and high genetic advance as percentage of mean were observed for the number of fingers, ear weight per plant, finger width, finger length, and plant height. Characters had high GCV, low PCV, high heritability, high genetic advance, and high genetic advance as percent mean, suggesting a greater scope for the selection of superior genotypes for these traits. In general, correlation and path analysis concluded that the plant height, days to 50% flowering, days to maturity, ear weight per plant, harvest index, number of fingers per ear, number of tillers per plant, finger length influenced the grain yield more than any of the other characters. The maximum intra cluster D values were recorded between cluster III and cluster II, and the highest inter cluster distance was recorded between cluster I and cluster V. Hence, genotypes belonging to the diverse cluster can be focused for selection against contrasting traits of interest for further crop improvement. Genotypes such as FIN 5169 and FIN 5146 with characteristics like (late maturity), Lalsuru mandia, and DPLM 3 (early maturity) varieties when a cross can be made to produce a new hybrid variety. Genotypes such as PR 1506 and PR 1639, which have a

high grain yield per plant, are used to cross low-yielding varieties, such as Bada kumunda and chilli, to develop a new variety.

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Table 1: Analysis of variance (ANOVA) for thirteen quantitative traits of finger milletgenotypes

S.N.	Characters	Mean sum of squares		
		Replication df=2	Genotypes (df=51)	Error (df=102)
1	Plant height (cm)	85.61	100.22**	29.02
2	Days to 50% flowering	25.95	23.16**	9.08
3	Days to maturity	35.60	25.50*	11.96
4	Number of tillers per plant	1.33	2.07*	0.45
5	No. of productive tillers per plant	2.50	3.41*	0.88
6	Number of fingers per ear	0.17	0.26**	0.17
7	Finger length (cm)	1.44	3.14**	1.35
8	Finger width (cm)	0.00	0.03*	0.05
9	Flag leaf area (cm^2)	35.11	73.34**	11.56
10	Ears weight per plant (g)	42.97	149.60**	24.64
11	Harvest index (%)	28.87	128.46**	13.65
12	1000 seed weight (g)	1.49	1.11**	0.49
13	Grain yield per plant (g)	27.50	13.76**	3.41

*Significance level at 0.05; **Significance level at 0.01

Table 2: List of finger millet Genotypes along with respective collected institutions.

Sl. No	Variety	Collected from
1	Bada Mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
2	Lalsuru mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
3	Telugu Mandia	M.S. Swaminathan Research Foundation, Jeypore, Odisha
4	Badtara	M.S. Swaminathan Research Foundation, Jeypore, Odisha
5	Bhairabi	M.S. Swaminathan Research Foundation, Jeypore, Odisha
6	Taya	M.S. Swaminathan Research Foundation, Jeypore, Odisha
7	Bada kumunda	M.S. Swaminathan Research Foundation, Jeypore, Odisha
8	Madi Muskuri	M.S. Swaminathan Research Foundation, Jeypore, Odisha
9	Chilli	M.S. Swaminathan Research Foundation, Jeypore, Odisha
10	Dangardi	M.S. Swaminathan Research Foundation, Jeypore, Odisha
11	Muskuri	M.S. Swaminathan Research Foundation, Jeypore, Odisha
12	Arjun	M.S. Swaminathan Research Foundation, Jeypore, Odisha
13	VL mandua- 352	M.S. Swaminathan Research Foundation, Jeypore, Odisha
14	Chaitanya	M.S. Swaminathan Research Foundation, Jeypore, Odisha

15	OEB610	M.S. Swaminathan Research Foundation, Jeypore, Odisha
16	VL352	All India Coordinate Research Project (AICRP) Mandya, Karnataka
17	FMCFMVZ	All India Coordinate Research Project (AICRP) Mandya, Karnataka
18	PR202	Agricultural Research Station, Vizianagaram
19	VR1176	Agricultural Research Station, Vizianagaram
20	VR1185	Agricultural Research Station, Vizianagaram
21	VR 1220	Agricultural Research Station, Vizianagaram
22	KOPN1056	Agricultural Research Station, Vizianagaram
23	PR-1639	Agricultural Research Station, Vizianagaram
24	DPLM 3	Agricultural Research Station, Vizianagaram
25	KMR656	All India Coordinate Research Project (AICRP) Mandya, Karnataka
26	DPLM2	All India Coordinate Research Project (AICRP) Mandya, Karnataka
27	FeZN15	All India Coordinate Research Project (AICRP) Mandya, Karnataka
28	VR1218	Agricultural Research Station, Vizianagaram
29	VR1225	Agricultural Research Station, Vizianagaram
30	VR1214	Agricultural Research Station, Vizianagaram
31	VR1228	Agricultural Research Station, Vizianagaram
32	TNEC1335	All India Coordinate Research Project (AICRP) Mandya, Karnataka
33	VR1221	Agricultural Research Station, Vizianagaram
34	PR1639	Agricultural Research Station, Vizianagaram
35	VR1217	Agricultural Research Station, Vizianagaram
36	VR1226	Agricultural Research Station, Vizianagaram
37	VR1222	Agricultural Research Station, Vizianagaram
38	FeZN84	All India Coordinate Research Project (AICRP) Mandya, Karnataka
39	BR9	All India Coordinate Research Project (AICRP) Mandya, Karnataka
40	KMR711	All India Coordinate Research Project (AICRP) Mandya, Karnataka
41	VR1233	Agricultural Research Station, Vizianagaram

42	CFMV1	All India Coordinate Research Project (AICRP) Mandya, Karnataka
43	WN572	All India Coordinate Research Project (AICRP) Mandya, Karnataka
44	GPV67	All India Coordinate Research Project (AICRP) Mandya, Karnataka
45	PR1506	Agricultural Research Station, Vizianagaram
46	VL400	All India Coordinate Research Project (AICRP) Mandya, Karnataka
47	FIN6164	Indian Institute of Millets Research, Hyderabad
48	FIN5146	Indian Institute of Millets Research, Hyderabad
49	FIN5169	Indian Institute of Millets Research, Hyderabad
50	FIN5167	Indian Institute of Millets Research, Hyderabad
51	Uduru(Susceptible)	All India Coordinate Research Project (AICRP) Mandya, Karnataka
52	Indaf 7(Resistant)	All India Coordinate Research Project (AICRP) Mandya, Karnataka

Table 3: Mean performance of fifty-two genotypes for fifteen quantitative traits in finger millet

S.N.	Genotype	PH		DF		DM		NT		NPT		NF		FL		FW	
		M	SD	M	SD	M	SD	M	SD	M	SD	M	SD	M	SD	M	SD
1	Bada Mandia	89.39	3.57	78.07	1.80	125.87	1.55	7.80	0.72	7.20	0.34	6.47	0.11	7.20	0.53	0.89	0.11
2	Lalsuru Mandia	88.18	10.00	71.00	1.96	118.80	3.14	8.20	0.72	7.07	0.61	6.70	0.26	6.78	0.89	0.98	0.20
3	Telugu Mandia	80.68	7.48	77.00	1.11	126.47	2.87	7.87	0.94	7.00	1.31	6.07	0.30	6.75	0.20	0.83	0.41
4	Badtara	77.29	2.73	70.40	1.60	124.40	4.66	8.40	0.40	6.33	0.50	6.67	0.50	6.81	0.78	1.13	0.90
5	Bhairabi	87.46	5.55	76.20	2.49	127.38	3.78	6.27	0.64	6.00	0.30	6.80	0.4	6.01	0.36	0.98	0.34
6	Taya	82.44	0.10	75.87	2.13	124.67	1.02	9.07	0.41	8.93	1.28	6.47	0.70	8.16	0.12	0.92	0.40
7	Bada Kumunda	90.53	13.40	72.67	5.87	129.20	3.46	8.27	0.80	7.67	0.11	6.80	0.2	7.37	0.34	1.12	0.19
8	Madi Muskuri	94.47	2.85	75.73	3.23	127.93	0.30	8.60	1.44	8.93	1.17	5.80	0.4	7.25	0.23	0.91	0.50
9	Chilli	97.70	8.53	78.47	3.36	130.07	2.15	7.40	0.34	6.60	1.09	6.53	0.41	6.52	0.20	0.91	0.75
10	Dangardi	97.39	8.32	77.27	3.58	124.80	2.90	9.27	0.61	8.53	0.41	6.53	0.11	6.53	0.40	1.00	0.11
11	Muskuri	79.43	8.19	74.07	2.20	125.93	1.94	6.00	0.40	6.67	1.33	6.53	0.41	5.46	0.46	0.97	0.23
12	Arjun	83.52	5.84	75.27	3.30	128.40	1.31	6.80	0.34	6.60	1	6.33	0.30	8.17	0.28	1.08	0.91
13	VL Mandua-352	85.38	7.62	74.33	1.80	121.93	2.60	7.40	0.40	6.00	0.2	6.43	0.20	7.30	0.75	0.81	0.46
14	Chaitanya	79.22	6.85	71.67	1.97	123.33	3.85	7.47	0.41	5.73	0.5	6.33	0.50	5.74	0.38	1.19	0.17
15	OEB610	82.46	4.95	71.93	3.52	123.60	4.32	7.13	0.41	5.60	0.4	6.60	0.4	5.95	0.22	0.99	0.98
16	VL352	88.46	4.58	75.47	5.06	128.93	2.78	6.60	1.20	6.93	0.50	6.13	0.61	5.71	0.23	0.92	0.60
17	FMCVZ	87.03	0.24	78.53	4.96	129.07	3.55	5.60	0.60	5.53	0.83	6.83	0.20	5.78	0.13	0.95	0.11
18	PR202	83.37	3.65	83.13	4.30	125.67	4.82	6.20	0.20	5.40	0.72	6.60	0.91	5.61	0.47	1.01	0.15
19	VR1176	81.65	4.05	77.40	4.68	128.93	3.78	5.40	1.20	4.33	0.50	6.13	0.41	5.48	0.29	1.03	0.46
20	VR1185	86.23	5.76	74.93	6.16	122.53	1.64	6.80	1.11	5.27	1.10	5.93	0.23	5.91	0.14	1.00	0.34
21	VR 1220	83.89	0.81	76.80	4.20	127.40	3.64	6.20	0.52	5.67	1.22	6.47	0.30	6.25	0.18	0.98	1.36
22	KOPN1056	86.49	4.10	75.80	1.90	125.20	0.52	6.47	0.50	5.13	0.75	6.33	0.30	6.26	0.32	0.95	0.30
23	PR-1639	72.67	8.99	78.47	4.80	125.53	5.51	7.93	0.11	7.13	0.50	6.20	0.34	5.79	0.20	0.98	0.10
24	DPLM 3	78.75	9.60	71.67	0.30	120.13	1.55	6.80	0.69	5.93	0.64	6.80	0.42	5.83	0.47	1.29	0.17
25	KMR656	84.61	2.87	73.73	0.70	124.08	3.00	6.93	1.10	5.47	1.36	6.20	0.44	7.19	0.25	0.86	0.16
26	DPLM2	82.77	3.35	72.67	1.70	121.47	2.61	7.00	0.60	6.27	0.50	6.40	0.32	7.30	0.62	0.92	0.11

27	FeZN15	89.03	5.20	74.20	2.62	124.27	3.44	7.80	0.52	5.93	0.80	6.33	0.30	6.21	0.29	1.08	0.60
28	VR1218	85.47	5.31	75.07	4.38	130.60	3.64	7.07	0.30	6.07	0.70	6.60	0.34	11.43	1.32	1.05	0.75
29	VR1225	86.43	2.65	73.73	2.00	126.20	2.08	7.13	0.64	5.83	0.94	6.27	0.30	5.35	0.11	1.03	0.61
30	VR1214	87.15	0.25	78.07	4.50	130.00	1.70	7.53	0.46	6.33	1.6	6.13	0.11	5.65	0.15	0.93	0.15
31	VR1228	82.32	4.48	74.33	5.40	127.33	1.67	8.40	1.05	7.27	1.10	6.60	0.40	5.85	0.56	0.97	0.30
32	TNEC1335	79.68	4.03	76.07	4.50	129.73	5.30	7.20	1.4	5.93	1.10	6.40	0.60	5.25	0.13	0.96	0.20
33	VR1221	84.48	3.45	74.47	1.70	125.80	1.77	6.87	0.50	5.40	0.8	6.00	0.34	5.73	0.16	1.09	0.11
34	PR1635	84.55	4.06	75.33	3.52	126.33	1.90	6.47	1.36	5.00	0.72	6.27	0.41	5.69	0.54	1.02	0.32
35	VR1217	83.88	3.14	73.47	1.13	123.93	3.32	7.20	0.34	5.47	0.98	6.07	0.30	6.22	0.42	1.25	0.90
36	VR1226	84.15	1.55	70.53	1.36	122.22	8.43	7.80	0.52	6.87	0.41	5.53	0.11	6.77	0.50	1.02	0.10
37	VR1222	81.80	6.69	73.78	2.00	124.60	4.33	6.87	0.98	4.57	0.90	6.00	0.6	5.51	0.23	1.00	0.72
38	FeZN84	87.64	2.67	78.53	2.06	129.42	1.93	7.07	0.30	5.00	0.40	6.27	0.90	6.39	0.16	1.13	0.41
39	BR9	85.37	2.69	75.97	0.56	127.92	0.61	6.27	0.23	4.80	0.52	6.13	0.61	6.66	0.34	1.10	0.11
40	KMR711	80.51	5.13	78.30	2.52	128.78	3.49	6.73	0.46	5.07	0.11	6.07	0.23	5.81	0.43	1.01	0.83
41	VR1233	81.30	0.41	77.40	2.77	125.53	4.10	6.47	0.41	8.07	3.94	6.13	0.11	5.90	0.14	0.89	0.70
42	CFMV1	86.45	3.89	80.67	2.41	129.93	2.08	7.53	0.61	6.13	0.41	6.20	0.42	5.63	0.18	1.08	0.52
43	WN572	82.87	7.68	73.13	1.41	126.00	6.68	7.33	0.30	6.00	0.6	6.40	0.34	6.70	0.36	0.96	0.20
44	GPV67	77.59	0.82	74.93	0.90	122.93	6.39	7.07	0.70	5.13	0.75	6.27	0.30	5.19	0.25	1.01	0.11
45	PR1506	75.09	7.55	79.73	3.84	129.47	3.52	5.27	0.41	4.13	0.64	6.40	0.34	5.72	0.27	0.86	0.20
46	VL400	80.93	4.63	76.67	3.71	126.60	1.8	6.87	0.30	5.00	0.52	5.77	0.25	5.16	0.24	1.01	0.75
47	FIN6164	73.35	5.18	79.73	0.80	129.33	4.14	7.53	0.23	6.80	0.91	6.27	0.11	5.83	0.36	0.81	0.61
48	FIN5146	84.69	6.47	79.00	0.20	130.87	2.08	7.13	0.98	5.20	0.72	6.60	0.4	5.74	0.14	1.03	0.41
49	FIN5169	84.52	3.36	79.33	0.41	131.07	1.80	7.47	0.41	6.07	0.41	6.53	1.10	5.53	0.41	0.93	0.30
50	FIN5167	95.55	3.89	78.93	2.56	129.93	2.54	7.07	0.61	6.27	1.20	6.17	0.35	6.21	0.80	1.07	0.23
51	Uduru(Susceptible)	97.77	2.55	77.47	4.44	126.87	1.55	7.07	0.11	6.47	0.11	5.67	0.30	5.66	0.32	1.01	0.23
52	Indaf (Resistant)	97.12	4.84	78.20	2.14	128.20	1.44	7.13	0.11	6.53	0.23	5.92	0.52	5.67	0.52	0.99	0.44
	Mean	**85.54**		**75.81**		**126.47**		**7.15**		**6.14**		**6.19**		**6.28**		**0.99**	
	SE(m)	0.77		0.37		0.38		0.11		0.14		0.03		0.14		0.01	
	CV%	6.5		3.5		2.2		12		17		3.8		16		10	
	CD%	4.2		2.3		2.7		0.5		0.7		0.3		0.9		0.6	
	SD	5.5		2.6		2.7		0.8		1.0		0.2		1.0		0.1	

S.N.	Genotype	FLA		EWP		HI		1000 SW		GY	
		M	SD	M	SD	M	SD	M	SD	M	SD
1	Bada Mandia	37.81	4.16	25.82	3.22	42.24	5.44	3.45	0.16	21.99	2.80
2	Lalsuru Mandia	35.99	2.02	23.06	1.14	33.33	3.43	3.54	0.38	17.67	2.73
3	Telugu Mandia	39.58	3.14	26.01	1.46	34.33	2.60	3.68	0.74	19.94	2.62
4	Badtara	41.35	2.46	24.89	3.33	39.96	8.05	3.31	0.47	19.42	1.31
5	Bhairabi	37.39	1.54	29.03	3.01	37.81	5.19	3.20	0.36	18.50	2.71
6	Taya	33.84	3.94	27.31	3.30	33.47	4.54	3.29	0.82	19.03	0.79
7	Bada Kumunda	41.66	6.00	20.11	1.75	34.45	3.63	3.10	0.36	14.47	1.14
8	Madi Muskuri	42.04	3.91	16.01	3.10	38.76	5.14	3.32	0.40	17.56	1.80
9	Chilli	43.10	6.32	17.23	2.52	38.81	4.28	3.61	0.77	17.51	2.69
10	Dangardi	43.32	4.43	27.60	0.57	32.18	1.10	2.95	0.26	18.76	0.62
11	Muskuri	36.65	1.33	20.67	1.28	37.98	1.81	3.04	0.13	19.30	0.93
12	Arjun	49.67	10.4	34.03	2.10	41.68	4.96	3.73	0.89	18.66	1.97
13	VL Mandua-352	38.42	3.04	24.67	1.94	36.65	6.87	3.42	0.67	18.14	1.18
14	Chaitanya	39.89	8.96	18.50	2.36	39.39	3.14	4.23	0.88	19.19	1.02
15	OEB610	41.74	3.23	25.67	3.14	34.02	6.53	3.30	0.37	19.33	0.51
16	VL352	37.25	0.60	27.52	2.29	38.94	3.55	4.19	1.35	19.44	2.35
17	CFMVZ	39.10	1.89	23.20	1.78	43.17	7.90	3.78	0.39	20.72	1.60
18	PR202	35.69	0.71	28.15	3.48	41.88	3.47	4.25	0.45	21.24	1.54
19	VR1176	41.59	5.20	32.80	2.32	44.26	6.04	3.78	0.75	18.64	3.08
20	VR1185	44.66	0.88	21.07	1.23	36.36	0.33	3.61	0.29	19.31	0.50
21	VR 1220	43.22	2.16	28.71	1.42	47.02	5.82	3.70	0.54	20.58	1.33
22	KOPN1056	38.48	0.16	33.65	2.44	38.87	1.30	3.90	0.86	19.91	3.77
23	PR-1639	29.05	0.98	35.48	2.10	47.58	4.50	3.52	1.02	24.53	2.39
24	DPLM 3	37.13	1.06	26.85	2.03	47.21	0.26	3.71	0.76	21.34	0.46
25	KMR656	35.47	0.41	26.80	1.43	50.41	5.02	4.04	0.70	23.03	2.06
26	FMDPLM2	34.66	0.99	22.49	0.18	40.21	0.95	4.42	0.40	20.05	0.75
27	FeZN15	35.85	0.92	27.51	0.45	43.42	3.30	4.24	1.01	23.40	2.81
28	VR1218	36.72	2.10	21.89	2.06	43.34	4.55	4.27	0.90	21.58	0.75
29	VR1225	40.94	1.23	22.03	0.57	44.48	2.56	4.02	0.94	18.75	3.95
30	VR1214	31.89	1.96	16.10	1.52	37.64	0.78	4.24	0.99	17.70	1.30
31	VR1228	31.06	0.79	33.66	2.63	39.65	1.45	5.09	0.12	17.49	1.22
32	TNEC1335	28.26	0.76	18.00	0.73	36.41	0.76	4.07	0.52	18.56	1.36
33	VR1221	32.30	0.28	22.44	1.86	39.88	3.04	5.03	0.16	20.28	0.63
34	PR1635	35.97	0.82	23.19	2.75	37.97	2.61	4.15	0.56	19.23	0.80
35	VR1217	23.84	0.29	18.44	0.76	40.86	1.53	3.72	1.11	18.07	0.79
36	VR1226	34.10	2.14	23.21	1.77	50.06	2.47	4.39	0.91	19.44	1.53
37	VR1222	34.38	3.08	19.83	0.46	42.82	3.60	4.44	0.31	18.55	1.12
38	FeZN84	37.76	3.97	21.89	1.64	35.62	3.82	4.43	0.66	18.06	1.80
39	BR9FM	34.42	2.07	23.43	0.88	38.46	1.17	3.96	0.85	19.98	0.98
40	KMR711	31.35	3.54	32.51	2.12	45.76	4.09	2.97	0.30	25.16	3.54
41	VR1233	28.49	3.73	21.63	2.32	41.55	1.50	3.25	0.55	21.08	2.53
42	CFMV1	28.19	4.78	35.69	1.15	45.08	2.12	3.95	1.13	22.23	1.23
43	WN572	36.38	2.25	27.07	1.53	57.53	1.50	3.66	0.64	23.53	0.28
44	GPV67	37.63	0.93	25.31	4.50	47.27	0.93	3.83	0.70	20.29	0.75

45	PR1506	32.99	1.89	25.71	2.35	56.85	1.18	3.23	0.78	25.63	1.36
46	VL400	43.52	6.11	30.05	3.88	50.31	3.97	4.03	0.24	21.30	1.02
47	FIN6164	41.06	5.08	33.73	3.91	59.12	0.60	4.84	0.41	20.83	2.38
48	FIN5146	39.98	5.24	40.19	4.37	55.12	0.37	4.56	0.74	22.90	3.22
49	FIN5169	41.80	2.56	47.66	7.52	54.37	1.19	4.03	1.19	19.46	3.08
50	FIN5167	40.93	1.54	50.55	5.67	49.36	4.66	4.70	1.53	22.38	1.67
51	Uduru(Susceptible)	34.23	2.03	23.95	1.73	43.23	1.15	2.30	0.21	19.94	1.98
52	Indaf (Resistant)	34.30	2.08	24.48	2.13	43.23	2.68	2.33	0.50	20.44	1.36
	Mean	**37.12**		**26.49**		**42.14**		**3.99**		**24.88**	
	SE(m)	0.70		0.97		1.07		0.08		3.02	
	CV%	14		27		18		15.9		92	
	CD%	2.6		3.8		2.8		0.5		1.4	
	SD	5.0		7.0		7.7		0.6		22.8	

Note: PH: Plant height(cm), DF: Days to 50 % flowering, DM: Days to maturity, NT: Number of tillers/ plant, NPT: Number of productive tillers/plant, NF: Number of finger/ear, FL: Finger length, FW: Finger width, FLA: Flag leaf area, EWP: Ear weight/plant, HI: Harvesting index, 1000 SW: 1000 seed weight, AUCDC: Chlorophyll content, AUDPC: Area under disease progress curve, GY: Grain Yield/plant. SE: Standard Error, CV %: Coefficient of Variation, CD%: Critical difference, SD: Standard Deviation, M: Mean

Table 4: Estimation of Genetic variability, heritability, and genetic advance of fifteen quantitative characters in fifty two finger millet genotypes.

Parameters	σ^2G	σ^2P	**GCV**	**PCV**	h^2	**GA**	**GA as % of mean**
Plant height (cm)	234.10	286.86	9.59	10.61	81.60	28.47	0.11
Days to 50% flowering	34.53	48.30	3.89	4.60	71.47	10.23	0.04
Days to maturity	55.02	71.50	3.80	4.341	76.95	13.40	0.03
No. of Tillers per plant	8.66	9.66	6.21	6.55	89.70	5.74	0.25
No. of productive tillers per plant	5.24	6.97	5.19	5.99	75.20	4.09	0.21
No. of fingers per ear	57.82	58.03	17.47	17.50	99.64	15.63	0.82
Finger length (cm)	20.16	22.11	10.63	11.13	91.19	8.83	0.49

Finger width (cm)	1.20	1.22	6.45	6.49	98.82	2.25	0.77
Flag leaf area (cm^2)	67.56	99.71	7.72	9.38	67.75	13.93	0.12
Ear weight per plant (g)	140.61	206.91	13.42	16.28	67.95	20.13	0.25
Harvest index(%)	110.38	162.30	9.34	11.32	68.00	17.84	0.14
1000 seed weight (g)	15.93	22.73	11.79	14.09	70.09	6.88	0.60
Grain yield/plant	10.46	17.33	4.16	5.36	60.39	8.10	0.13

Table 5: Genotypic Correlation coefficients of fifty-two finger millet genotypes for 15 different yield attributing traits

Traits	PH	DF	DM	NT	NPT	NF	FL	FW	FLA	EWP	HI	1000 SW	GY
PH	1	0.30*	0.45**	0.19	0.36**	-0.13	0.21	-0.07	0.29*	-0.05	-0.44**	-0.39*	0.30*
DF		1	1.18**	-0.36**	-0.02	0.17	-0.17	-0.39**	0.02	0.39*	-0.19	-0.07	0.47**
DM			1	-0.50**	-0.31*	0.21	-0.04	-0.29*	0.09	0.29*	0.35*	0.83	0.52**
NT				1	0.83**	0.05	0.30*	-0.03	0.04	-0.02	-0.34*	-0.13	-0.04
NPT					1	-0.01	0.33*	-0.35*	0.06	-0.08	-0.42**	-0.33*	0.02
NF						1	0.07	0.05	0.22	0.23	-0.07	0.27	-0.43*
FL							1	-0.01	0.16	-0.12	-0.19	-0.02	-0.11
FW								1	-0.03	-0.05	-0.05	0.07	-0.03
FLA									1	0.17	-0.06	-0.16	-0.08
EWP										1	0.53*	0.14	0.79**
HI											1	0.40*	0.66**
1000 SW												1	-0.38*
GY													1

Values with * are different from 0 with a significance level alpha=0.05 Values with ** are different from 0 with a significance level alpha=0.01 PH: Plant height (cm), DF: Days to 50 % flowering, DM: Days to maturity, NT: Number of tillers/ plant, NPT: Number of productive tillers/plant, NF: Number of finger/ear, FL: Finger length (cm), FW: Finger width (cm), FLA: Flag leaf area (cm2), EWP: Ear weight/plant, HI: Harvest index, 1000 SW: 1000 seed weight, GY: Grain yield/plant

Table 6: Phenotypic Correlation coefficient of fifty-two finger millet genotypes for 15 different yield attributing traits

Traits	PH	DF	DM	NT	NPT	NF	FL	FW	FLA	EWP	HI	1000 SW	GY
PH	1	0.11	0.08	0.16*	0.26**	-0.04	0.18*	0.17*	0.26**	-0.04	-0.26**	-0.20*	-0.12
DF		1	0.74**	-0.13	-0.03	0.14	-0.11	-0.13	0.02	0.22**	0.16*	-0.09	0.22**
DM			1	-0.15	-0.02	0.10	-0.05	-0.08	0.07	0.11	0.15	0.07	0.18*
NT				1	0.62**	-0.08	0.21**	0.03	0.04	-0.04	-0.24**	-0.10	-0.17*
NPT					1	-0.11	0.25**	-0.09	0.12	-0.08	-0.32**	-0.14	-0.19*
NF						1	-0.01	0.08	0.07	0.12	0.01	0.06	0.15
FL							1	-0.06	0.40**	-0.02	-0.12	-0.08	0.07
FW								1	0.16*	-0.04	0.10	-0.01	-0.01
FLA									1	0.12	-0.06	-0.10	0.06
EWP										1	0.47**	0.11	0.58**
HI											1	0.31**	0.61**
1000 SW												1	0.16*
GY													1

Values in * are different from 0 with a significance level alpha=0.05 Values in ** are different from 0 with a significance level alpha=0.01
PH: Plant height(cm), DF: Days to 50 % flowering, DM: Days to maturity, NT: Number of tillers/ plant, NPT: Number of productive tillers/plant, NF: Number of finger/ears, FL: Finger length (cm), FW: Finger width (cm), FLA: Flag leaf area (cm2), EWP: Ear weight/plant, HI: Harvest index, 1000 SW: 1000 seed weight, GY: Grain yield/plant

Table 7: Estimates of Genotypic Path Coefficients for yield and its contributing traits in finger millet genotypes

Variables	PH	DF	DM	NT	NPT	NF	FL	FW	FLA	EWP	HI	1000 SW	GY
PH	0.20	0.65	-0.51	0.37	-0.74	-0.77	0.44	-0.32	-1.10	0.34	0.09	-0.04	0.37
DF	0.27	1.22	-0.93	0.53	-0.88	-1.38	0.55	-0.50	-0.14	1.20	0.40	-0.14	0.47
DM	0.60	2.56	-1.98	1.23	-1.80	-3.13	1.41	-1.23	-0.32	2.09	0.88	-0.34	0.52
NT	0.12	0.41	-0.34	0.41	-0.84	-0.64	0.39	-0.23	-0.07	0.30	0.05	-0.04	-0.04
NPT	0.08	0.22	-0.16	0.27	-0.76	-0.31	0.28	-0.04	-0.03	0.08	-0.05	0.07	0.02
NF	0.24	1.02	-0.84	0.62	-0.93	-1.15	0.68	-0.53	-0.17	0.89	0.32	-0.16	-0.43
FL	0.09	0.26	-0.24	0.24	-0.52	-0.43	0.48	-0.17	-0.06	0.07	0.02	-0.03	-0.11
FW	0.10	0.37	-0.33	0.24	-0.14	-0.54	0.28	-0.42	-0.04	0.17	0.13	-0.06	-0.03
FLA	0.07	0.22	-0.18	0.14	-0.23	-0.37	0.20	-0.08	-0.12	0.32	0.06	-0.01	-0.08
EWP	0.02	0.22	-0.14	0.07	-0.06	-0.22	0.03	-0.04	-0.03	0.86	0.19	-0.02	0.79
HI	0.02	0.22	-0.17	0.03	0.09	-0.24	0.02	-0.10	-0.02	0.55	0.33	-0.05	0.66
1000 SW	0.04	0.31	-0.26	0.12	0.06	-0.48	0.17	0.17	-0.02	0.32	0.23	-0.11	-0.38

Residual effect: 0.1825

PH: Plant height(cm), DF: Days to 50 % flowering, DM: Days to maturity, NT: Number of tillers/ plants, NPT: Number of productive tillers/plants,NF: Number of finger/ears, FL: Finger length, FW: Finger width, FLA: Flag leaf area, EWP: Ear weight/plant, HI: Harvest index, 1000 SW: 1000 seed weight, GY: Grain Yield/ plant

Table 8: Estimates of Phenotypic Path Coefficients for yield and its contributing traits in finger millet genotypes

Variables	PH	DF	DM	NT	NPT	NF	FL	FW	FLA	EWP	HI	1000 SW	GY
PH	**0.06**	-0.00	0.00	-0.00	-0.00	-0.00	0.00	-0.02	-0.01	-0.01	-0.12	0.00	-0.12
DF	0.00	**-0.02**	0.04	0.00	0.00	0.01	-0.00	0.01	-0.00	0.08	0.07	0.00	0.22
DM	0.00	-0.01	**0.06**	0.00	0.00	0.01	-0.00	0.01	-0.00	0.04	0.07	-0.00	0.18
NT	0.01	0.00	-0.00	**-0.01**	-0.01	-0.00	0.00	-0.00	-0.00	-0.01	-0.11	0.00	-0.17
NPT	0.01	0.00	-0.00	-0.00	**-0.02**	-0.01	0.00	0.01	-0.00	-0.03	-0.15	0.00	-0.19
NF	-0.00	-0.00	0.00	-0.00	0.00	**0.09**	-0.00	-0.00	-0.00	0.04	0.00	-0.00	0.15
FL	0.01	0.00	-0.00	-0.00	-0.00	-0.00	**0.01**	0.00	-0.00	-0.03	-0.05	-0.00	0.07
FW	0.01	0.00	-0.00	-0.00	0.00	0.00	-0.00	**-0.11**	-0.00	-0.00	-0.01	-0.00	-0.00
FLA	0.01	-0.00	0.00	-0.00	-0.00	0.00	0.00	-0.00	**-0.04**	0.04	-0.02	0.00	0.00
EWP	-0.00	-0.00	0.00	0.00	0.00	0.01	-0.00	0.00	-0.00	**0.39**	0.22	-0.00	0.58
HI	-0.01	-0.00	0.00	0.00	0.00	0.00	-0.00	0.00	0.00	0.18	**0.46**	-0.00	0.61
1000 SW	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	-0.00	0.00	0.04	0.14	**-0.02**	0.16
GY	-0.00	0.00	-0.00	-0.00	-0.00	0.00	0.00	0.02	-0.00	-0.09	-0.07	0.00	**0.05**

Residual effect: 0.2489

PH: Plant height(cm), DF: Days to 50 % flowering, DM: Days to maturity, NT: Number of tillers/ plant, NPT: Number of productive tillers/plant, NF: Number of finger/ear, FL: Finger length, FW: Finger width, FLA: Flag leaf area, EWP: Ear weight/plant, HI: Harvest index, 1000 SW: 1000 seed weight, AUCDC: Chlorophyll content, AUDPC: Area under disease progress curve, GY: Grain Yield/ plant

Table 9: Principal component analysis in finger millet genotypes

Principal components (PCs)	Eigenvalues	Variability%	Cumulative%
PC1	3.51	21.97	21.97
PC2	2.93	18.32	40.29
PC3	2.17	13.59	53.89
PC4	1.41	8.85	62.75
PC5	1.18	7.37	70.12
PC6	1.03	6.45	76.58

Table 10: Contribution of each principal component towards different characters.

Particulars	PC1	PC2	PC3	PC4	PC5
Plant height (cm)	-0.40	0.49	0.34	0.36	0.25
Days to 50% flowering	0.45	0.45	0.64	0.03	-0.20

Days to maturity	0.49	0.32	0.65	0.17	-0.12
No. of tillers per plant	-0.62	-0.67	0.15	-0.46	0.38
No. of productive tillers per plant	-0.69	0.12	0.32	-0.42	0.10
No. of fingers per ear	0.11	-0.51	0.56	-0.02	-0.02
Finger length (cm)	-0.44	-0.17	0.26	-0.05	0.25
Finger width (cm)	0.01	-0.18	-0.29	0.45	0.61
Flag leaf area (cm^2)	-018	-0.06	0.50	0.25	0.19
Ear weight per plant (g)	0.50	0.06	0.42	-0.25	0.44
Harvest index (%)	0.75	0.09	-0.07	-0.40	0.25
1000 seed weight (g)	0.51	-0.55	-0.05	-0.24	0.08
Grain yield	0.00	0.82	-0.17	0.00	0.15

Table 11: Percentage contribution of morphological characters towards diversity inthe finger millet genotypes

S.N.	Characters	Percentage (%)
1	Plant height (cm)	8.06
2	Days to 50% flowering	4.88
3	Days to maturity	2.35
4	Number of tillers/plant	6.71
5	Number of productive tillers/plant	5.57
6	Number of fingers/plant	2.83
7	Finger length (cm)	4.19
8	Finger width (cm)	8.05
9	Flag leaf area	9.40
10	Ear weight/Plant	9.04
11	Harvesting index	6.14
12	1000 seed weight/plant	8.31
15	Grain yield/plant	2.82

Table 12: Mean intra and inter cluster distance in finger millet

Cluster	I	II	III	IV	V
I	**9183.57** (95.83)	130051.12 (**360.62**)	74855.96 (**273.59**)	59904.32 (**244.75**)	229288.68 (**478.84**)
II		**12947.61** (113.78)	118925.65 (**344.85**)	32515.21 (**180.31**)	65545.81 (**256.01**)
III			**22172.45** (148.90)	122965.99 (**350.66**)	95475.27 (**308.99**)
IV				**0.00**	150456.87 (**387.88**)
V					**0.00**

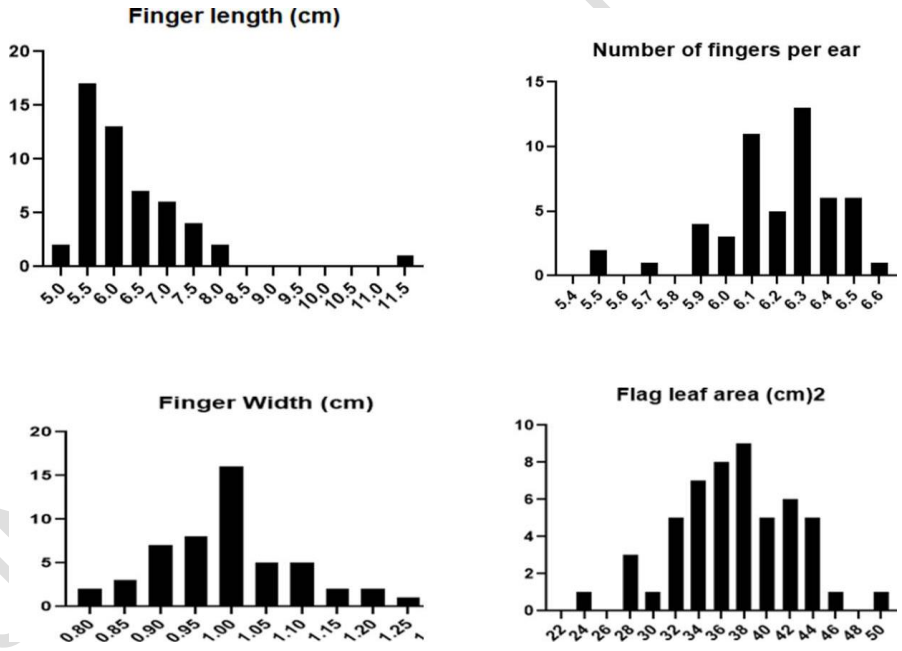
***The values in brackets core D values**

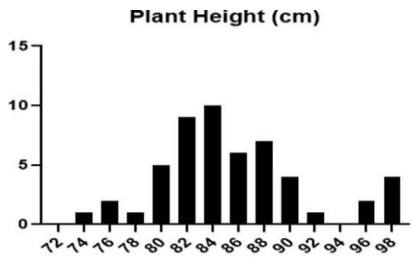
Table 13: Cluster mean performance for different characters in finger millet genotypes

Parameters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Plant height (cm)	85.18	83.34	85.01	87.38	84.98
Days to 50% flowering	75.66	76.12	75.76	75.94	77.4
Days to maturity	126.35	127.71	125.95	126.65	128.93
No. of tiller/ plant	6.93	7.12	7.61	7.37	5.4
No. of productive tillers/ plant	5.95	5.65	6.47	6.38	4.33
Number of fingers per ear	6.15	6.25	6.30	6.11	6.13
Finger length (cm)	6.38	5.71	6.21	6.33	5.48
Finger width (cm)	0.98	1.02	1.01	0.96	1.03
Flag leaf area (cm^2)	36.12	34.44	39.15	35.81	41.59
Ear weight/ plant (g)	26.30	30.38	25.31	32.45	32.8
Harvest index (%)	42.47	44.38	40.51	49.07	43.26
1000 seed weight (g)	4.13	4.15	3.84	3.88	3.78
Grain yield/ plant (g)	22.55	22.93	20.77	23.55	23.63

Table 14: Grouping of fifty-two finger millet genotypes based on D^2 analysis

Cluster	Number of genotypes	Genotypes
I	22	KMR656, FIN5146, FeZn84, DPLM2, VR 1225,PR-1639, Taya, KOPN1056, Bhairabhi, PR202, VL352, PR1506, BR9, VR1185, VR1222, CFMVZ, VR1218, VR1228, Muskuri, FeZn15, VR1226, INDAF,
II	6	TNEC1335, VR1217, VR1221, OEB610, KMR711, FIN5169
III	17	Chilli, DPLM3, FM1, FIN6164, Dangardi, Badtara, CFMV1, Telugu mandia, VR1214, Lalsuru mandia, Bada mandia, VR1220, VR1233, GPV67, Bada kumunda, VL400
IV	6	WN572, UDURU, PR1630, DPLM3 FIN5167, FM4
V	1	VR1176




Plant Height (cm)
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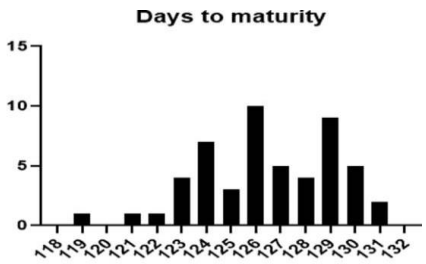
10
5
0
72 74 76 78 80 82 84 86 88 90 92 94 96 98


Days to maturity
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10
5
0
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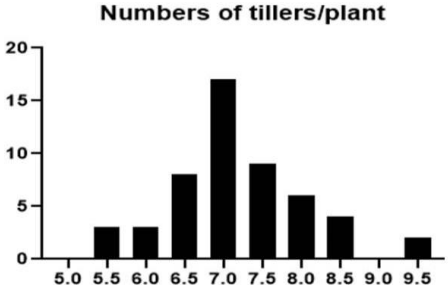
Numbers of tillers/plant
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15
10
5
0
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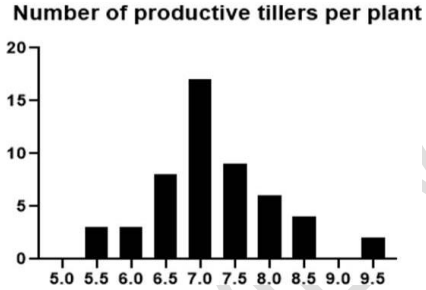
Number of productive tillers per plant
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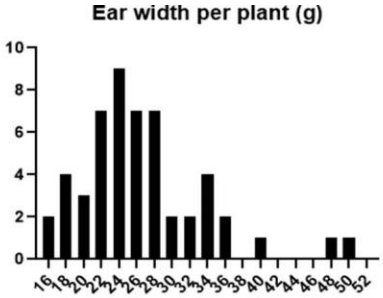
15
10
5
0
5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5


Ear width per plant (g)
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8
6
4
2
0
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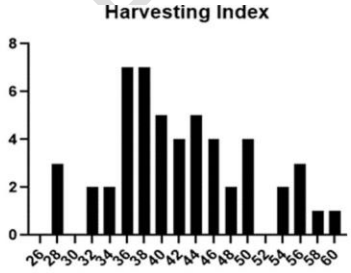
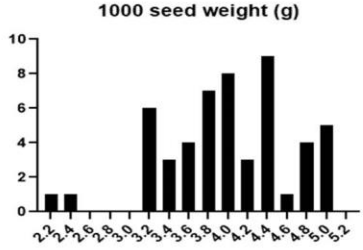
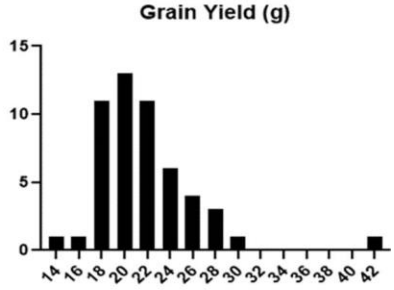

Harvesting Index
8
6
4
2
0
26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60


1000 seed weight (g)
10
8
6
4
2
0
2.2 2.4 2.6 2.8 3.0 3.2 3.4 3.6 3.8 4.0 4.2 4.4 4.6 4.8 5.0 5.2


Grain Yield (g)
15
10
5
0
14 16 18 20 22 24 26 28 30 32 34 36 38 40 42

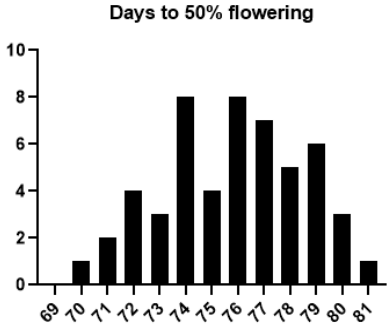

Days to 50% flowering
10
8
6
4
2
0
69 70 71 72 73 74 75 76 77 78 79 80 81

Fig. 4: Frequency Distribution Graphs of different yield attributing traits of finger millet